

# *Ahi1* Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-8-8**

# Project Overview

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<b>Project Name</b>	<b><i>Ahi1</i></b>
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<b>Project type</b>	<b>Cas9-KO</b>
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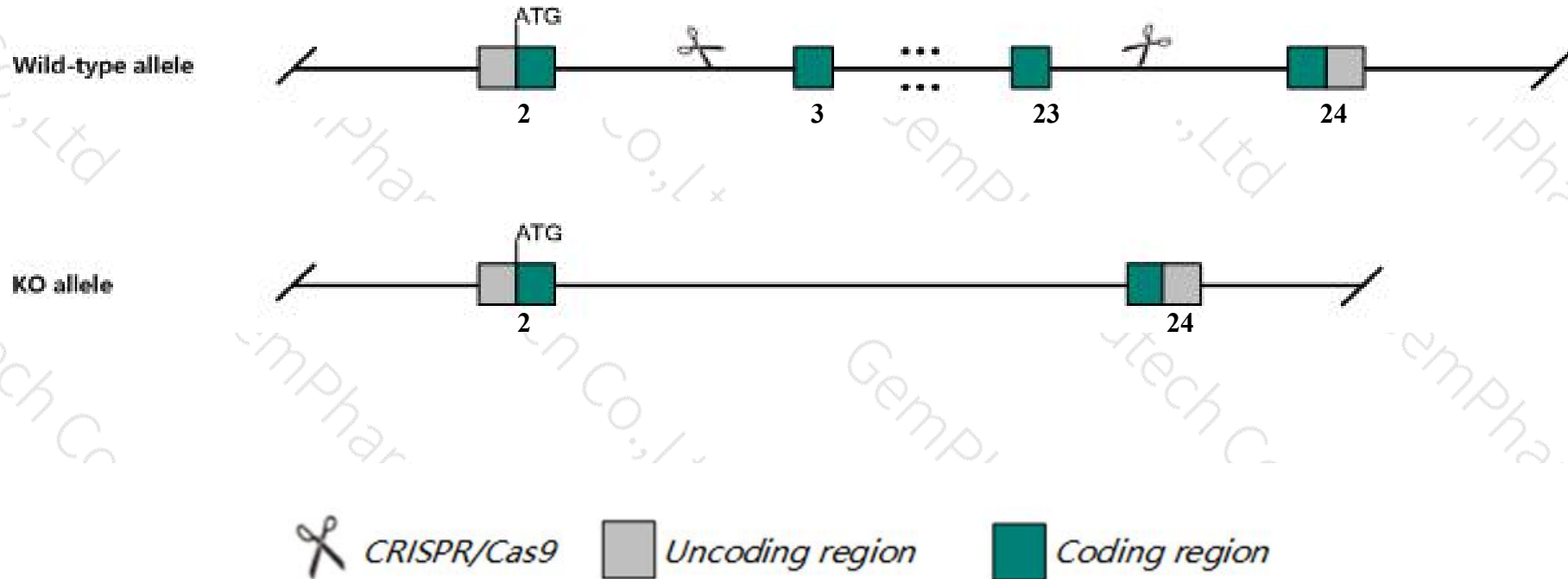
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<b>Strain background</b>	<b>C57BL/6JGpt</b>
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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ahi1* gene. The schematic diagram is as follows:



- The *Ahi1* gene has 7 transcripts. According to the structure of *Ahi1* gene, exon3-exon23 of *Ahi1-201* (ENSMUST00000105525.11) transcript is recommended as the knockout region. The region contains 2830bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ahi1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mouse embryonic fibroblasts homozygous for one knock-out allele exhibit reduced and abnormal cilia. Mice homozygous for another knock-out allele exhibit premature death and abnormal kidney morphology and physiology.
- The *Ahi1* 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)

## Ahi1 Abelson helper integration site 1 [Mus musculus (house mouse)]

Gene ID: 52906, updated on 10-Feb-2019

### Summary



<b>Official Symbol</b>	Ahi1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Abelson helper integration site 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:87971</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000019986</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1700015F03Rik, Ahi-1, D10Bwg0629e
<b>Expression</b>	Biased expression in CNS E18 (RPKM 44.9), frontal lobe adult (RPKM 34.7) and 6 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

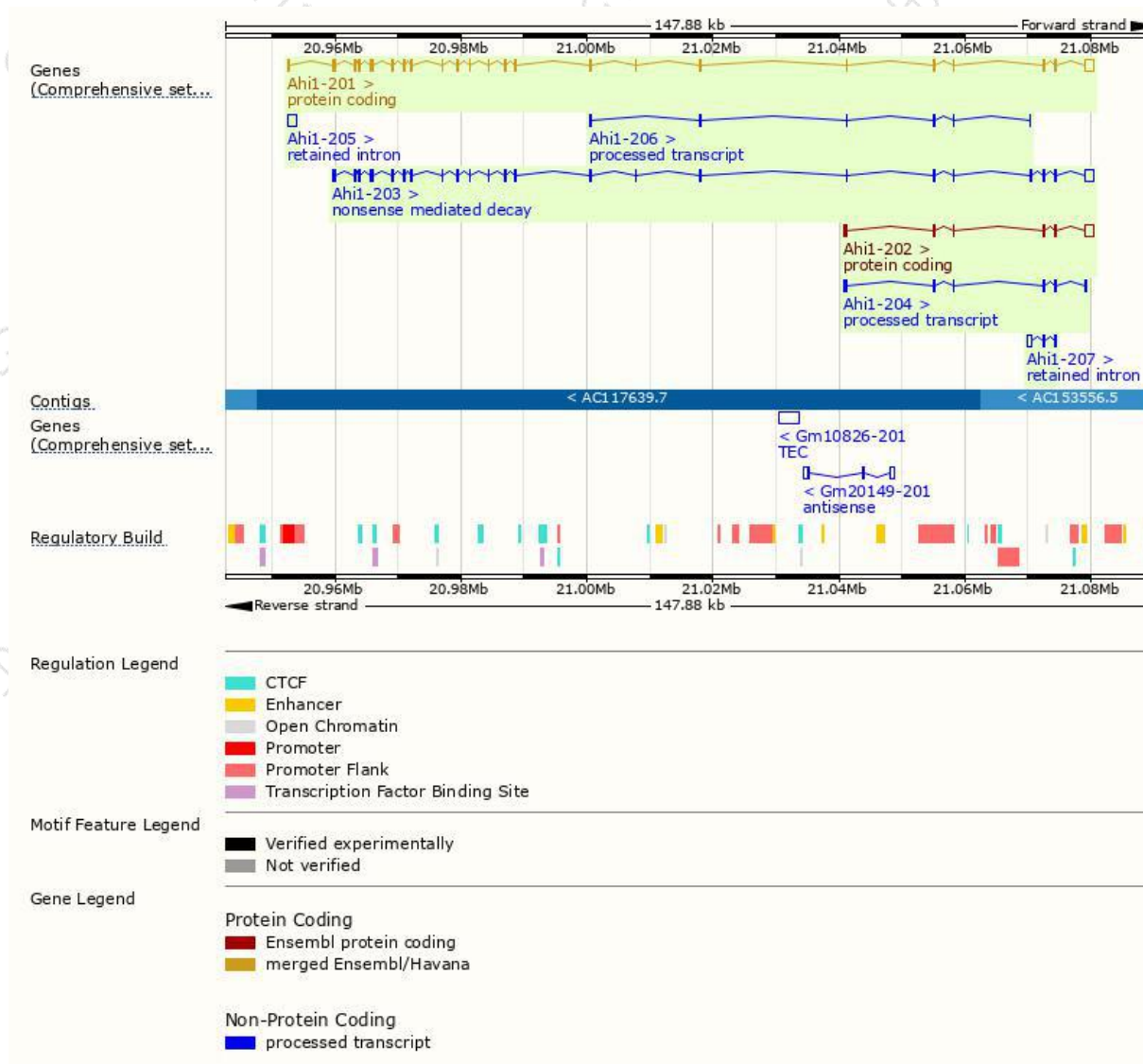
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ahi1-201	<a href="#">ENSMUST00000105525.11</a>	4851	<a href="#">1047aa</a>	Protein coding	<a href="#">CCDS35860</a>	<a href="#">E9QP54</a>	TSL:1 GENCODE basic APPRIS P1
Ahi1-202	<a href="#">ENSMUST00000163505.2</a>	2067	<a href="#">142aa</a>	Protein coding	<a href="#">CCDS48512</a>	<a href="#">E9Q552</a>	TSL:1 GENCODE basic
Ahi1-203	<a href="#">ENSMUST00000213104.1</a>	4829	<a href="#">1005aa</a>	Nonsense mediated decay	-	<a href="#">A0A1L1SQE2</a>	TSL:2
Ahi1-204	<a href="#">ENSMUST00000213852.1</a>	1038	No protein	Processed transcript	-	-	TSL:1
Ahi1-206	<a href="#">ENSMUST00000214893.1</a>	788	No protein	Processed transcript	-	-	TSL:5
Ahi1-205	<a href="#">ENSMUST00000214745.1</a>	1375	No protein	Retained intron	-	-	TSL:NA
Ahi1-207	<a href="#">ENSMUST00000215543.1</a>	790	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Ahi1-201* transcript,The transcription is shown below

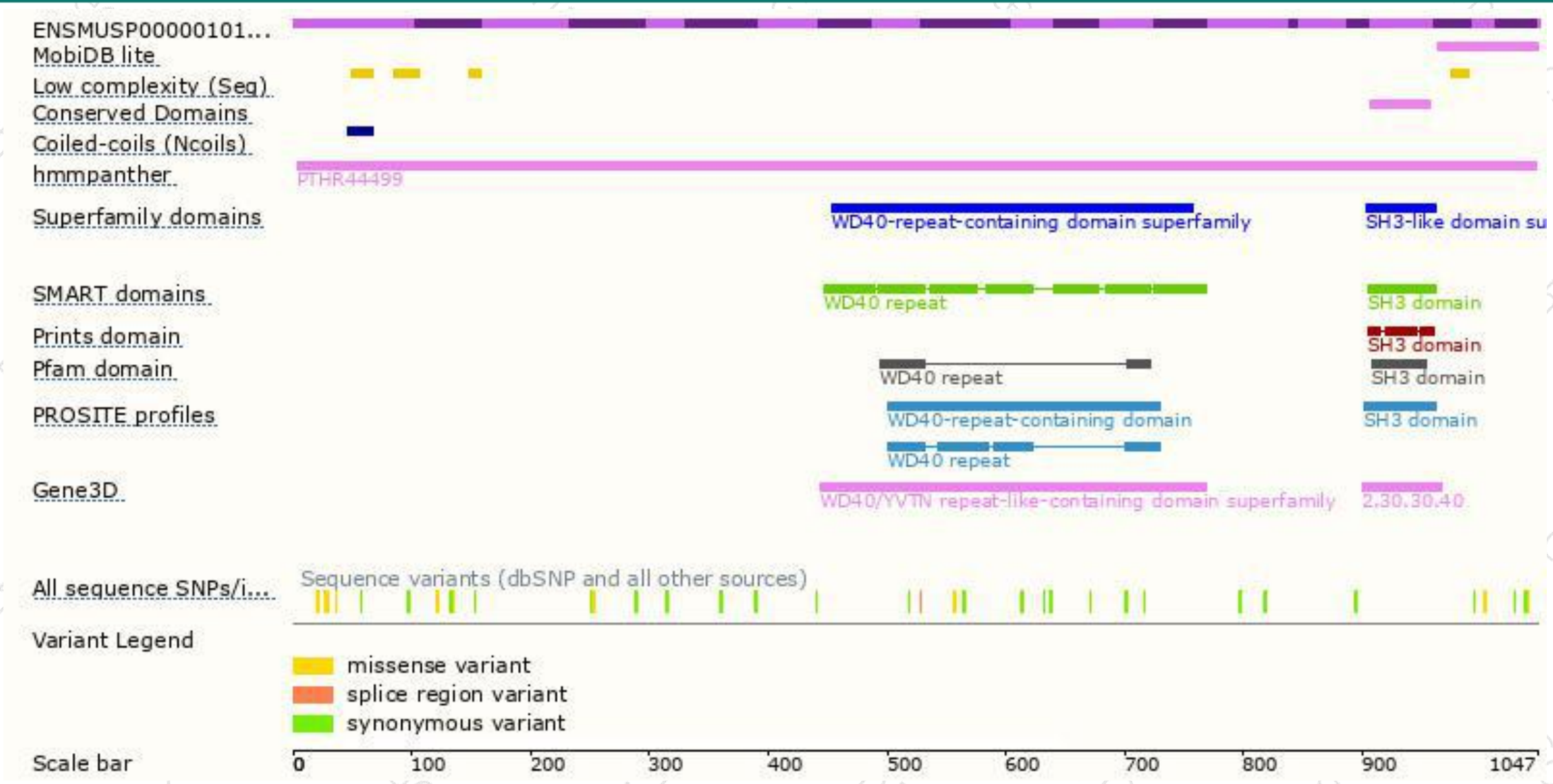


# Genomic location distribution

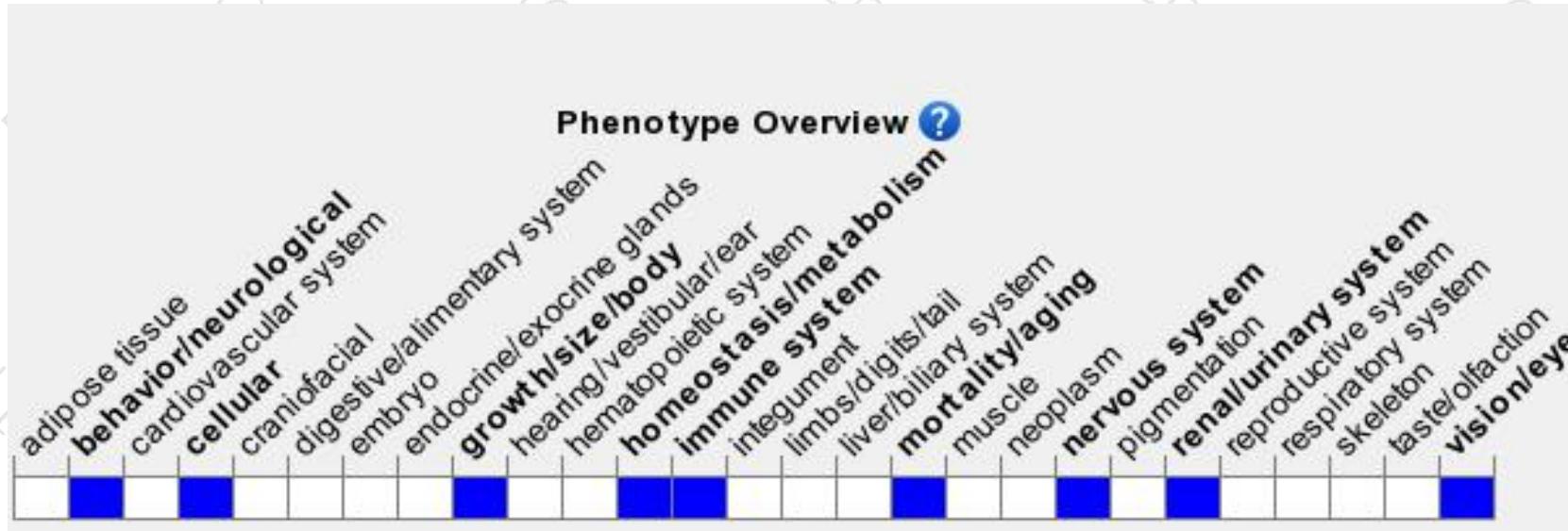




# Protein domain



# 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 fibroblasts homozygous for one knock-out allele exhibit reduced and abnormal cilia. Mice homozygous for another knock-out allele exhibit premature death and abnormal kidney morphology physiology.

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

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