

# ***Ahctf1 Cas9-KO Strategy***

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**Reviewer :**

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# Project Overview

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**Project Name**

*Ahctf1*

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**Project type**

**Cas9-KO**

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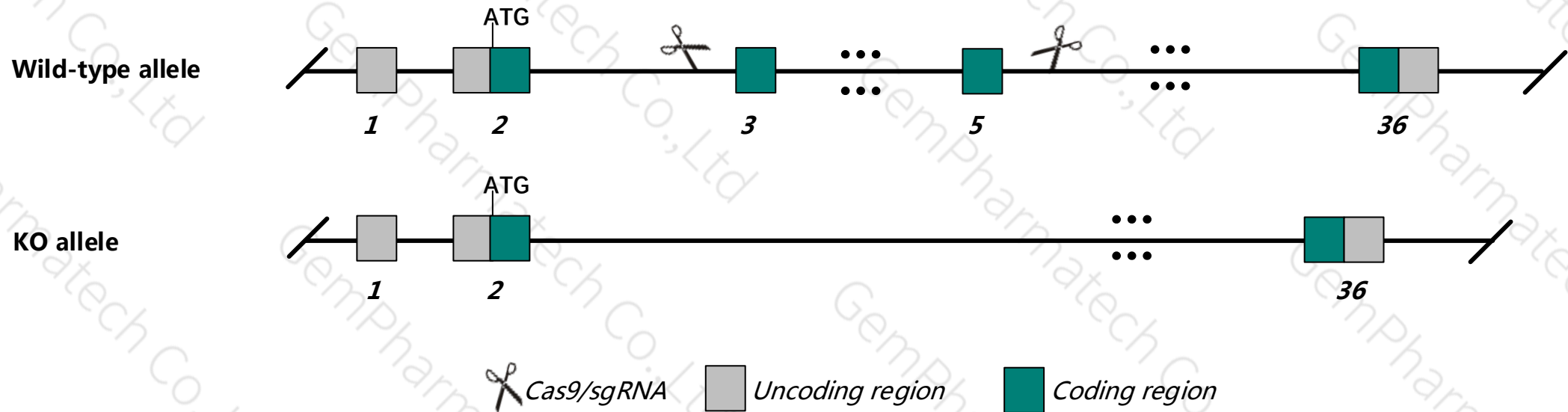
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ahctf1* gene. The schematic diagram is as follows:



# Technical routes

- The *Ahctf1* gene has 9 transcripts. According to the structure of *Ahctf1* gene, exon3-exon5 of *Ahctf1*-201 (ENSMUST00000027768.13) transcript is recommended as the knockout region. The region contains 715bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ahctf1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9, sgRNA 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.

- According to the existing MGI data , Homozygous null mice die between E3.5 and E5.5. The inner cell mass cells exhibit impaired proliferation and apoptosis when grown in culture.
- Transcript *Ahctf1-204 and Ahctf1-205* may not be affected.
- The *Ahctf1* gene is located on the Chr1. 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 knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information ( NCBI )

## Ahctf1 AT hook containing transcription factor 1 [ *Mus musculus* (house mouse) ]

Gene ID: 226747, updated on 12-Aug-2019

### Summary

Official Symbol	Ahctf1 provided by <a href="#">MGI</a>
Official Full Name	AT hook containing transcription factor 1 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1915033</a>
See related	<a href="#">Ensembl:ENSMUSG00000026491</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Elys; AV011447; 6230412P20Rik
Expression	Ubiquitous expression in testis adult (RPKM 11.3), placenta adult (RPKM 10.3) and 25 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

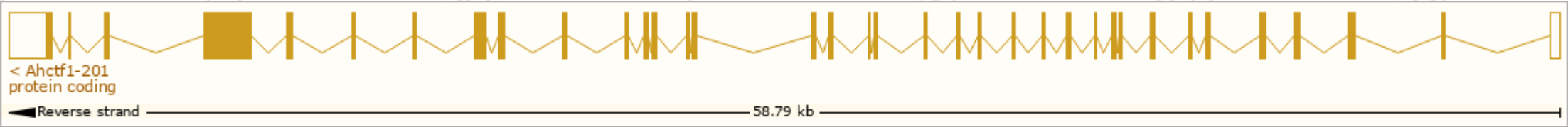


# Transcript information ( Ensembl )

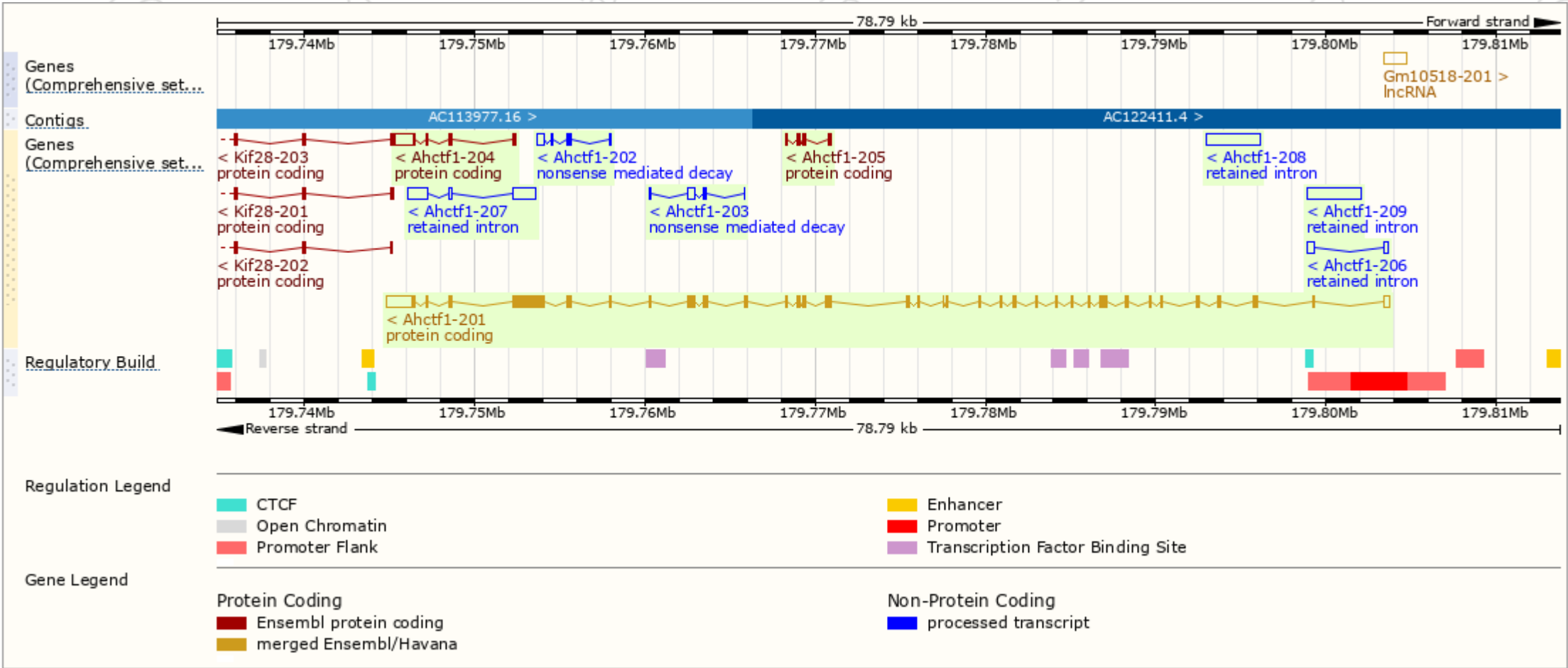
The gene has 9 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ahctf1-201	<a href="#">ENSMUST00000027768.13</a>	8506	<a href="#">2243aa</a>	Protein coding	<a href="#">CCDS15564</a>	<a href="#">Q8CJF7</a>	TSL:1 GENCODE basic APPRIS P1
Ahctf1-204	<a href="#">ENSMUST00000140489.1</a>	1494	<a href="#">116aa</a>	Protein coding	-	<a href="#">F6S6E4</a>	CDS 5' incomplete TSL:1
Ahctf1-205	<a href="#">ENSMUST00000145968.2</a>	530	<a href="#">176aa</a>	Protein coding	-	<a href="#">F6SJR1</a>	CDS 5' and 3' incomplete TSL:5
Ahctf1-202	<a href="#">ENSMUST00000125816.1</a>	769	<a href="#">104aa</a>	Nonsense mediated decay	-	<a href="#">F6QTR3</a>	CDS 5' incomplete TSL:3
Ahctf1-203	<a href="#">ENSMUST00000127250.1</a>	680	<a href="#">35aa</a>	Nonsense mediated decay	-	<a href="#">F6XUM6</a>	CDS 5' incomplete TSL:2
Ahctf1-209	<a href="#">ENSMUST00000194536.1</a>	3232	No protein	Retained intron	-	-	TSL:NA
Ahctf1-208	<a href="#">ENSMUST00000192645.1</a>	3156	No protein	Retained intron	-	-	TSL:NA
Ahctf1-207	<a href="#">ENSMUST00000151734.1</a>	2570	No protein	Retained intron	-	-	TSL:1
Ahctf1-206	<a href="#">ENSMUST00000147137.1</a>	746	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Ahctf1*-201 transcript, The transcription is shown below

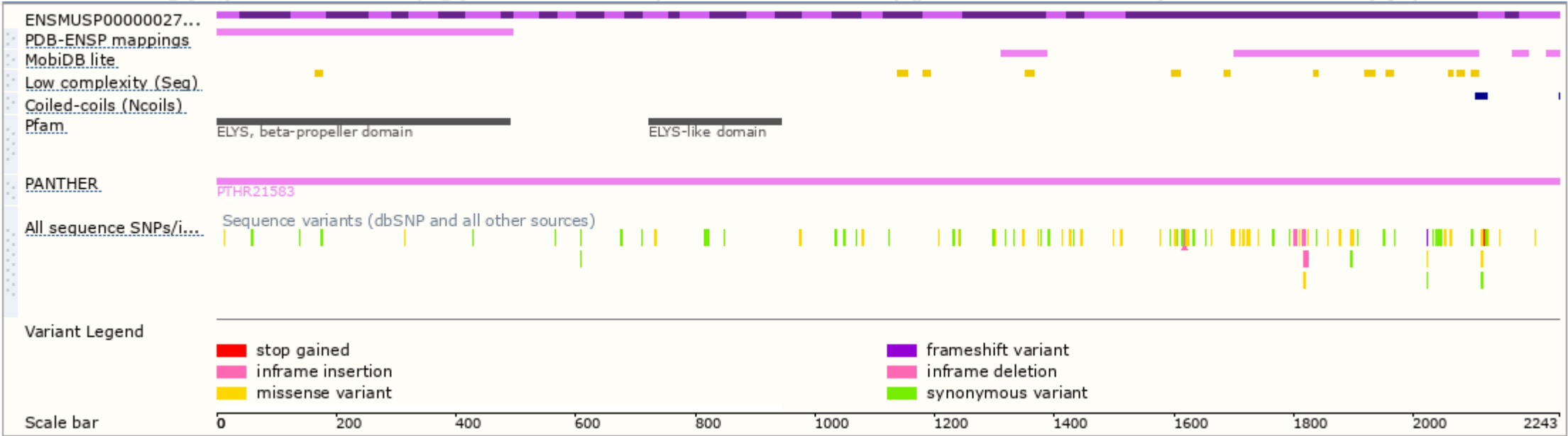


# Genomic location distribution

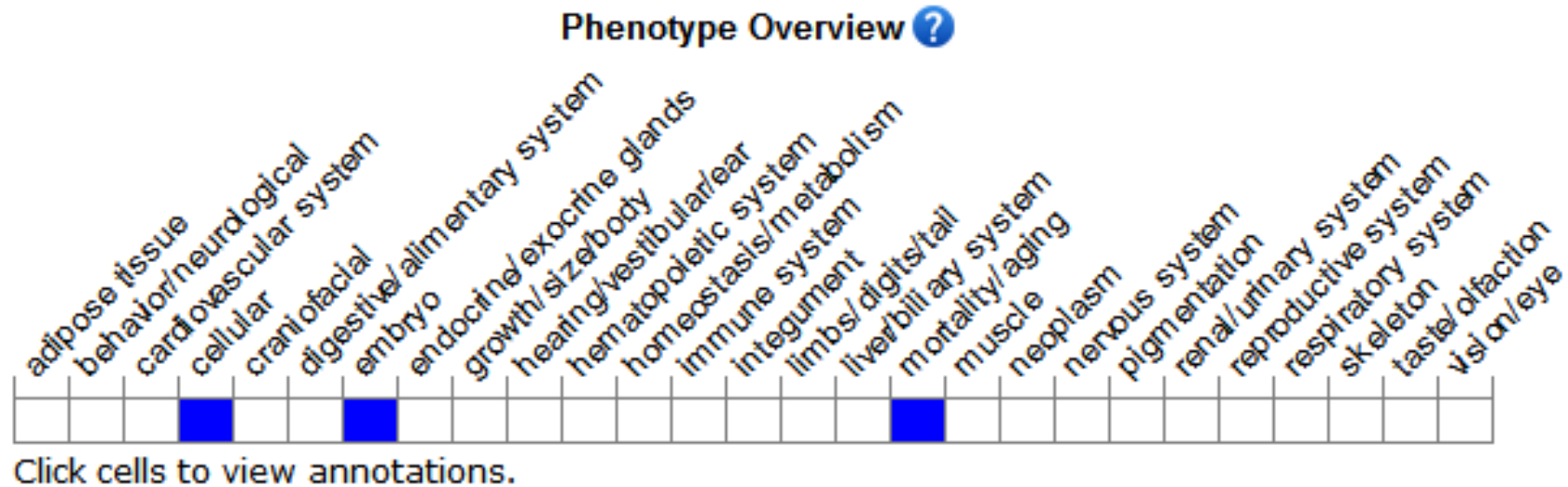




# Protein domain



# 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 null mice die between E3.5 and E5.5. The inner cell mass cells exhibit impaired proliferation and apoptosis when grown in culture.

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