

# *Chil1* Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-8-23**

# Project Overview

**Project Name**

*Chill*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Chil1* gene has 8 transcripts. According to the structure of *Chil1* gene, exon3-exon5 of *Chil1-201* (ENSMUST00000082060.9) transcript is recommended as the knockout region. The region contains 413bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Chil1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice show impaired OVA-induced Th2 responses with reduced splenocyte proliferation, cytokine production and IgE levels, impaired dendritic cell recruitment, higher CD4 T cell, macrophage and eosinophil apoptosis, and reduced CD4 T cell and alternatively activated macrophage numbers.
- The *Chill* 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Chil1 chitinase-like 1 [Mus musculus (house mouse)]

Gene ID: 12654, updated on 31-Jan-2019

### Summary



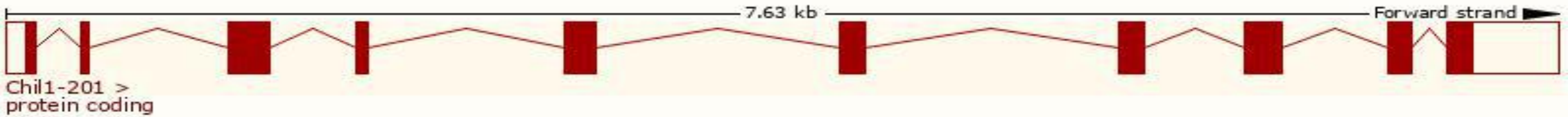
<b>Official Symbol</b>	Chil1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	chitinase-like 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1340899</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000064246</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</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>	AW208766, Brp39, Chi3l1, Gp39
<b>Expression</b>	Restricted expression toward lung adult (RPKM 398.3) <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

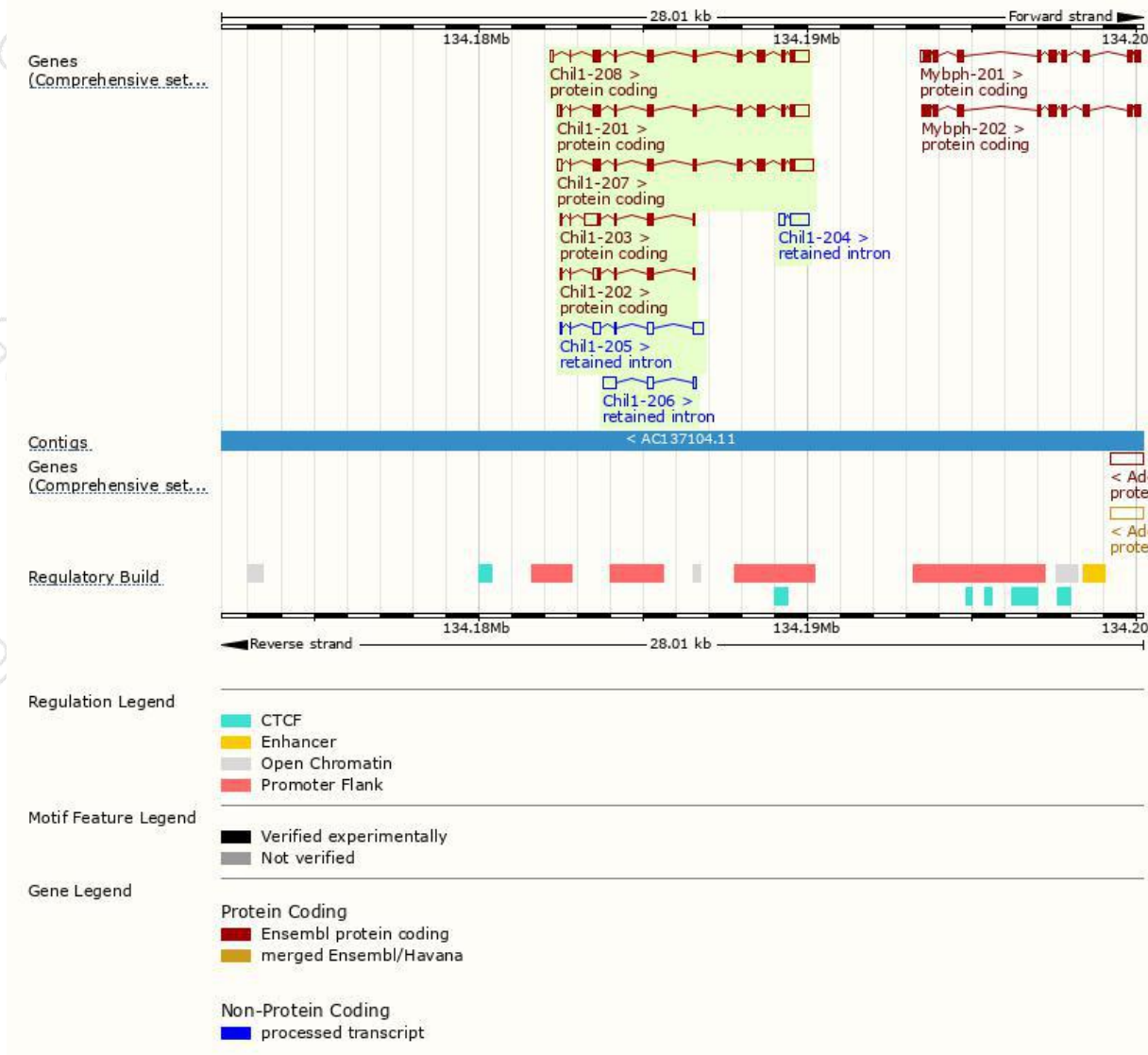
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chil1-201	<a href="#">ENSMUST00000082060.9</a>	1687	<a href="#">389aa</a>	Protein coding	<a href="#">CCDS48368</a>	<a href="#">Q61362</a>	TSL:1 GENCODE basic APPRIS P2
Chil1-207	<a href="#">ENSMUST00000153856.7</a>	1839	<a href="#">381aa</a>	Protein coding	-	<a href="#">Q61362</a>	TSL:1 GENCODE basic APPRIS ALT2
Chil1-208	<a href="#">ENSMUST00000156873.7</a>	1645	<a href="#">379aa</a>	Protein coding	-	<a href="#">Q61362</a>	TSL:5 GENCODE basic APPRIS ALT2
Chil1-203	<a href="#">ENSMUST00000133701.7</a>	828	<a href="#">106aa</a>	Protein coding	-	<a href="#">D3Z2Z5</a>	CDS 3' incomplete TSL:5
Chil1-202	<a href="#">ENSMUST00000132873.7</a>	585	<a href="#">110aa</a>	Protein coding	-	<a href="#">D3YXU4</a>	CDS 3' incomplete TSL:5
Chil1-205	<a href="#">ENSMUST00000139254.7</a>	848	No protein	Retained intron	-	-	TSL:2
Chil1-204	<a href="#">ENSMUST00000134812.1</a>	735	No protein	Retained intron	-	-	TSL:2
Chil1-206	<a href="#">ENSMUST00000144819.1</a>	647	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Chil1-201* transcript,The transcription is shown below

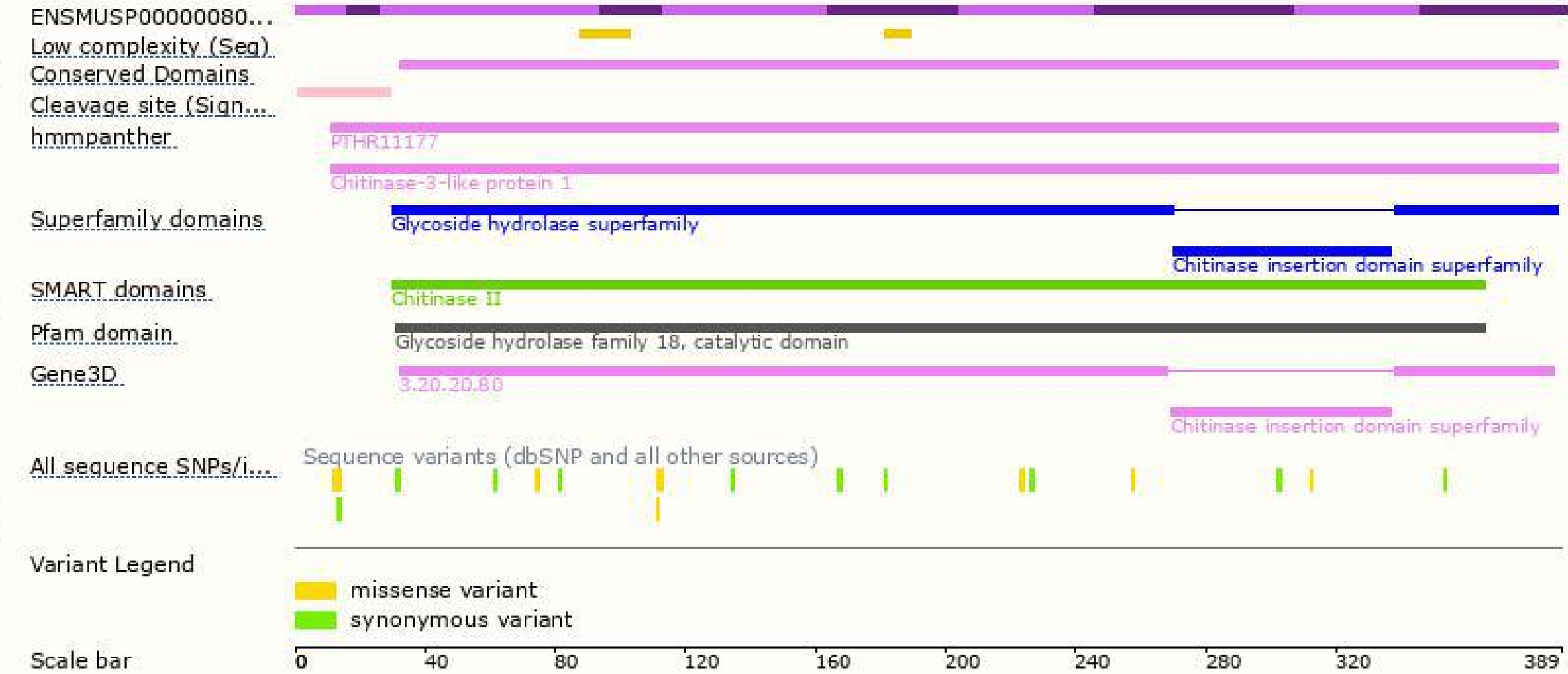


# Genomic location distribution

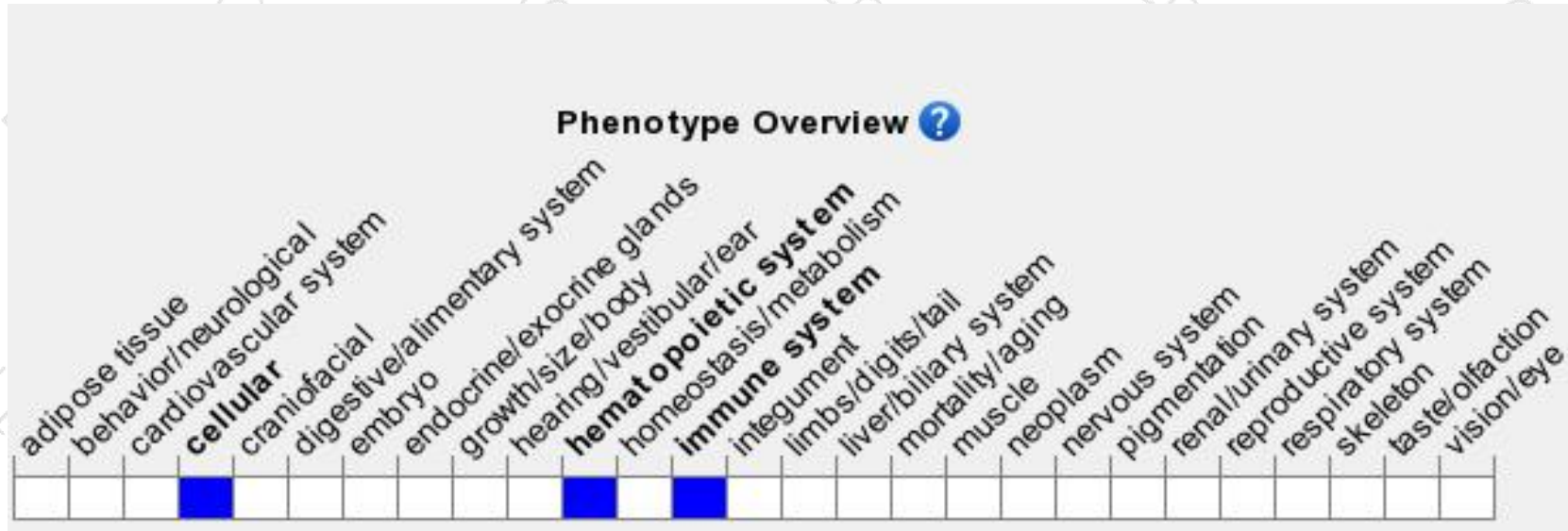




# Protein domain



# 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 show impaired OVA-induced Th2 responses with reduced splenocyte proliferation, cytokine production and IgE levels, impaired dendritic cell recruitment, higher CD4 T cell, macrophage and eosinophil apoptosis, and reduced CD4 T cell and alternatively activated macrophage numbers.

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

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