

Chil1 Cas9-CKO Strategy

Designer:

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Design Date:

2019-8-23

Project Overview

Project Name

Chill

Project type

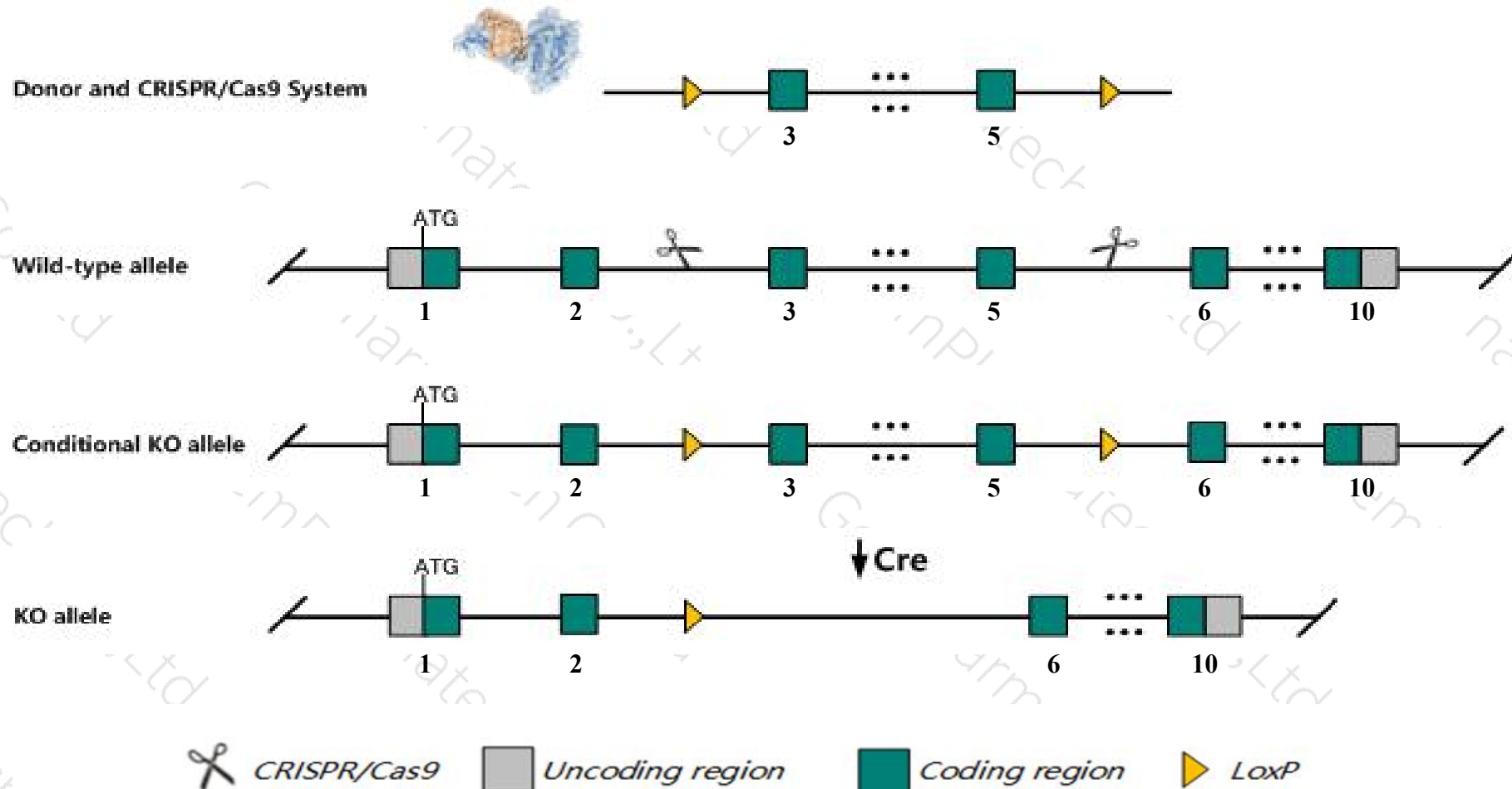
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Chill* gene has 8 transcripts. According to the structure of *Chill* gene, exon3-exon5 of *Chill*-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 *Chill* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

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

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

Summary



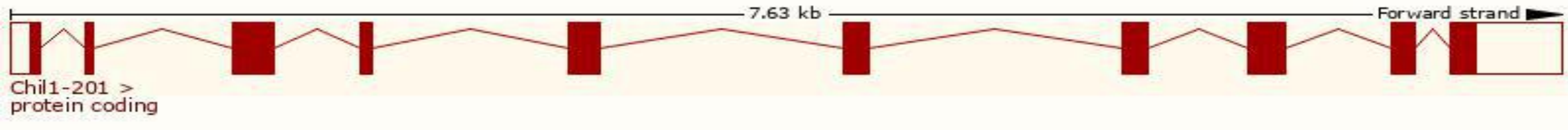
Official Symbol	Chil1 provided by MGI
Official Full Name	chitinase-like 1 provided by MGI
Primary source	MGI:MGI:1340899
See related	Ensembl:ENSMUSG00000064246
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW208766, Brp39, Chi3l1, Gp39
Expression	Restricted expression toward lung adult (RPKM 398.3) See more
Orthologs	human all

Transcript information (Ensembl)

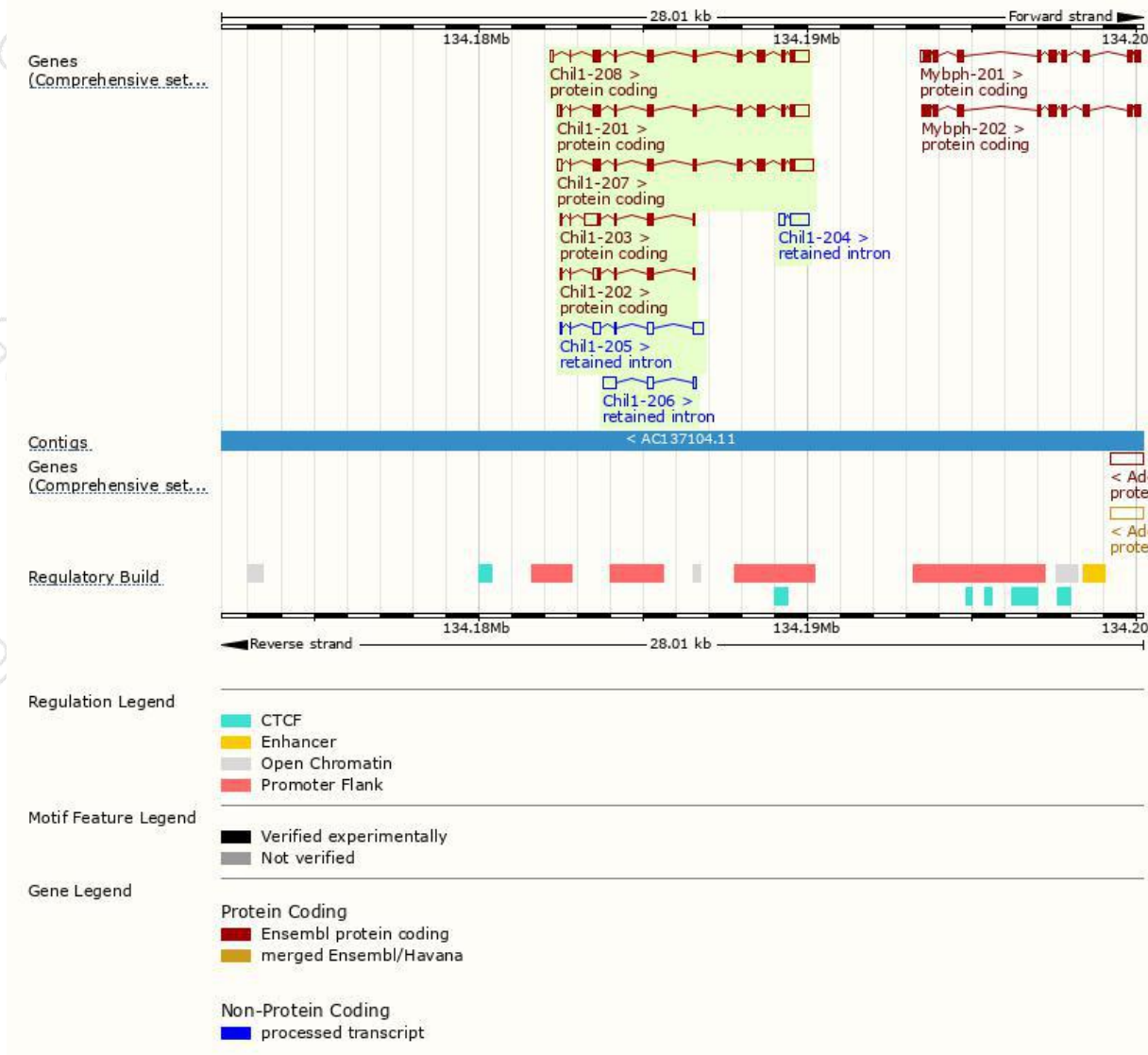
The gene has 8 transcripts,all transcripts are shown below:

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

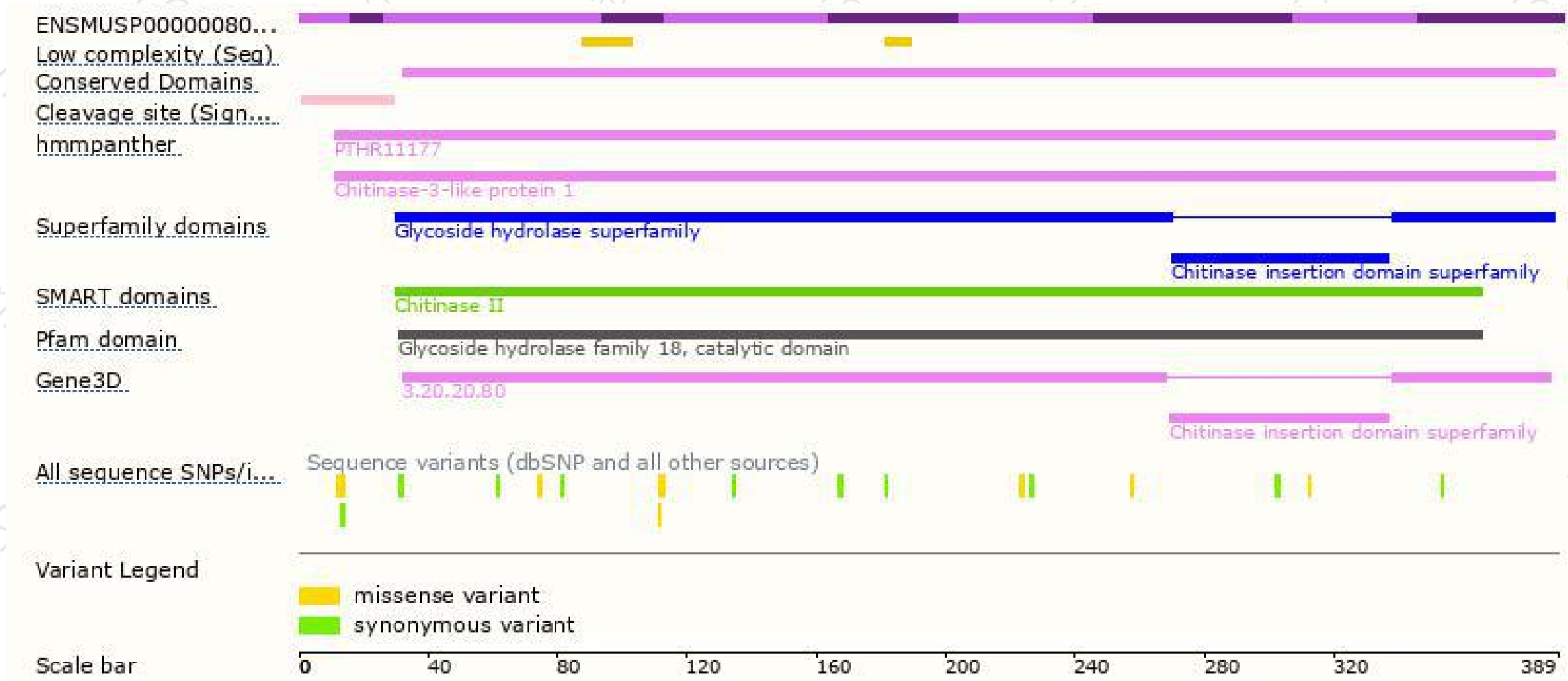
The strategy is based on the design of *Chil1-201* transcript,The transcription is shown below



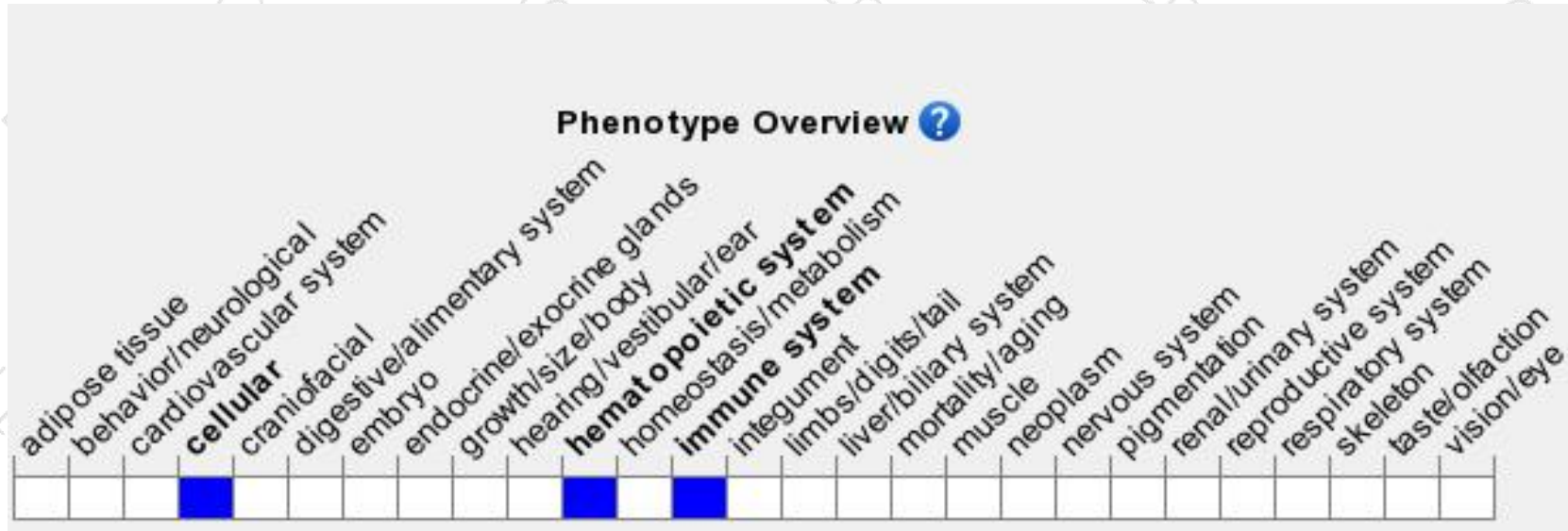
Genomic location distribution



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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