

***Stat4* Cas9-CKO Strategy**

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Project Overview

Project Name

Stat4

Project type

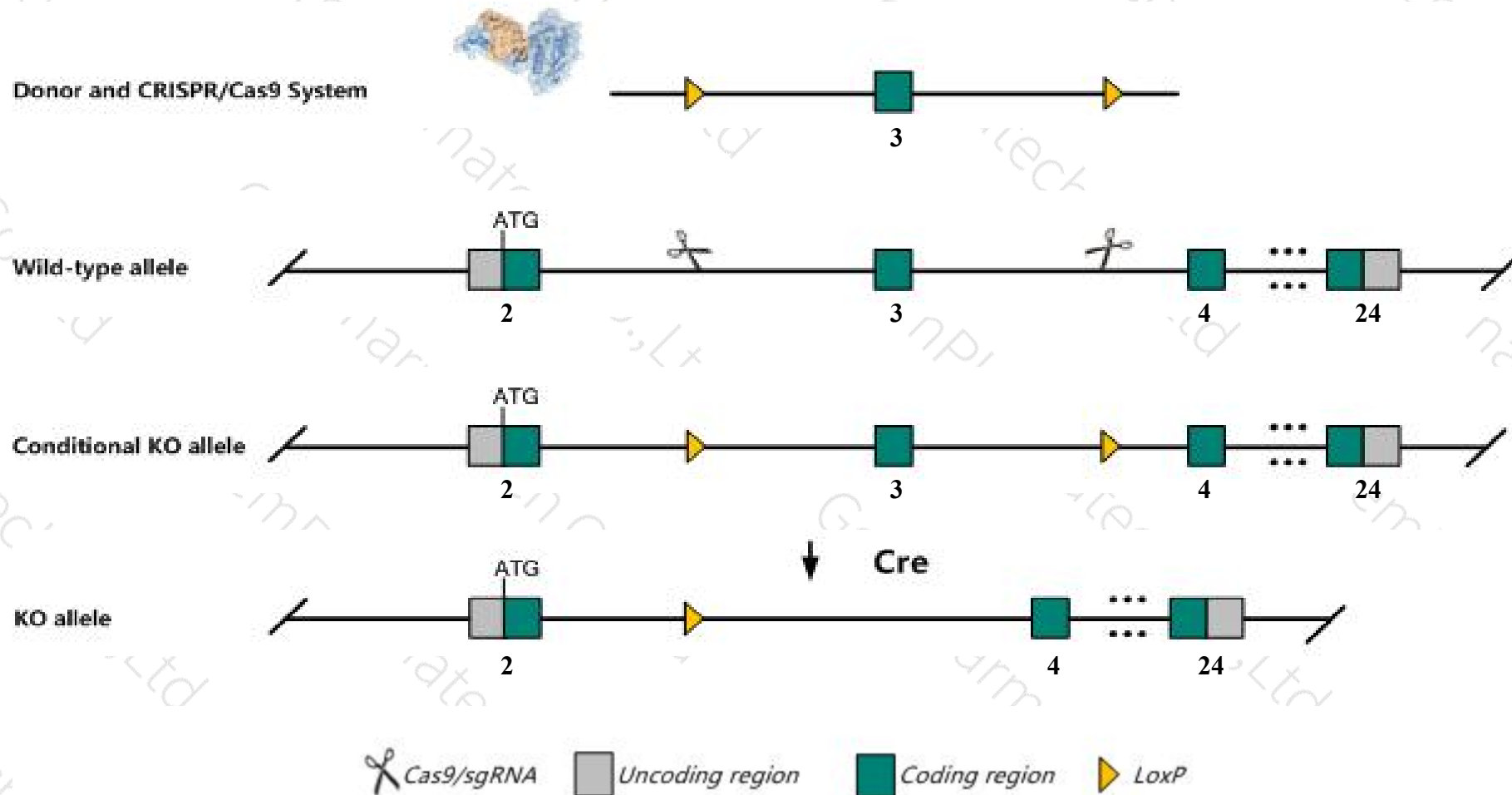
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stat4* gene. The schematic diagram is as follows:



- The *Stat4* gene has 4 transcripts. According to the structure of *Stat4* gene, exon3 of *Stat4-201* (ENSMUST00000027277.6) transcript is recommended as the knockout region. The region contains 145bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stat4* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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 inactivation of this gene leads to altered cytokine production of T-cells, impaired IL-12 responses, enhanced Th2 cell development, decreased susceptibility to autoimmune diabetes, altered NK cell responses during viral infection, and increased susceptibility to Salmonella infection.
- Transcript *Stat4*-204 may not be affected.
- The *Stat4* 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)

Stat4 signal transducer and activator of transcription 4 [Mus musculus (house mouse)]

Gene ID: 20849, updated on 2-Apr-2019

Summary



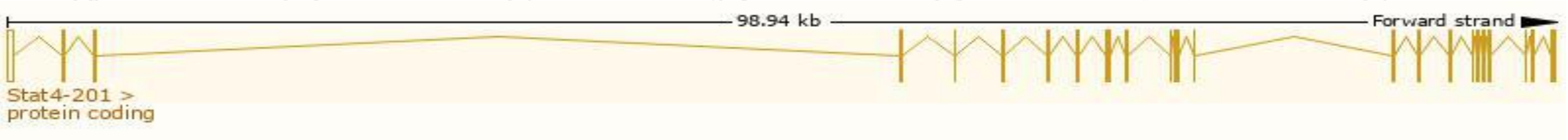
Official Symbol	Stat4 provided by MGI
Official Full Name	signal transducer and activator of transcription 4 provided by MGI
Primary source	MGI:MGI:103062
See related	Ensembl:ENSMUSG00000062939
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	The protein encoded by this gene is a member of the STAT family of transcription factors. In response to cytokines and growth factors, STAT family members are phosphorylated by the receptor associated kinases, and then form homo- or heterodimers that translocate to the cell nucleus where they act as transcription activators. Homozygous knockout mice for this gene exhibit reduced inflammation and cytokine production in response to immune challenge. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2015]
Expression	Biased expression in testis adult (RPKM 66.2) and spleen adult (RPKM 2.1) See more
Orthologs	human all

Transcript information (Ensembl)

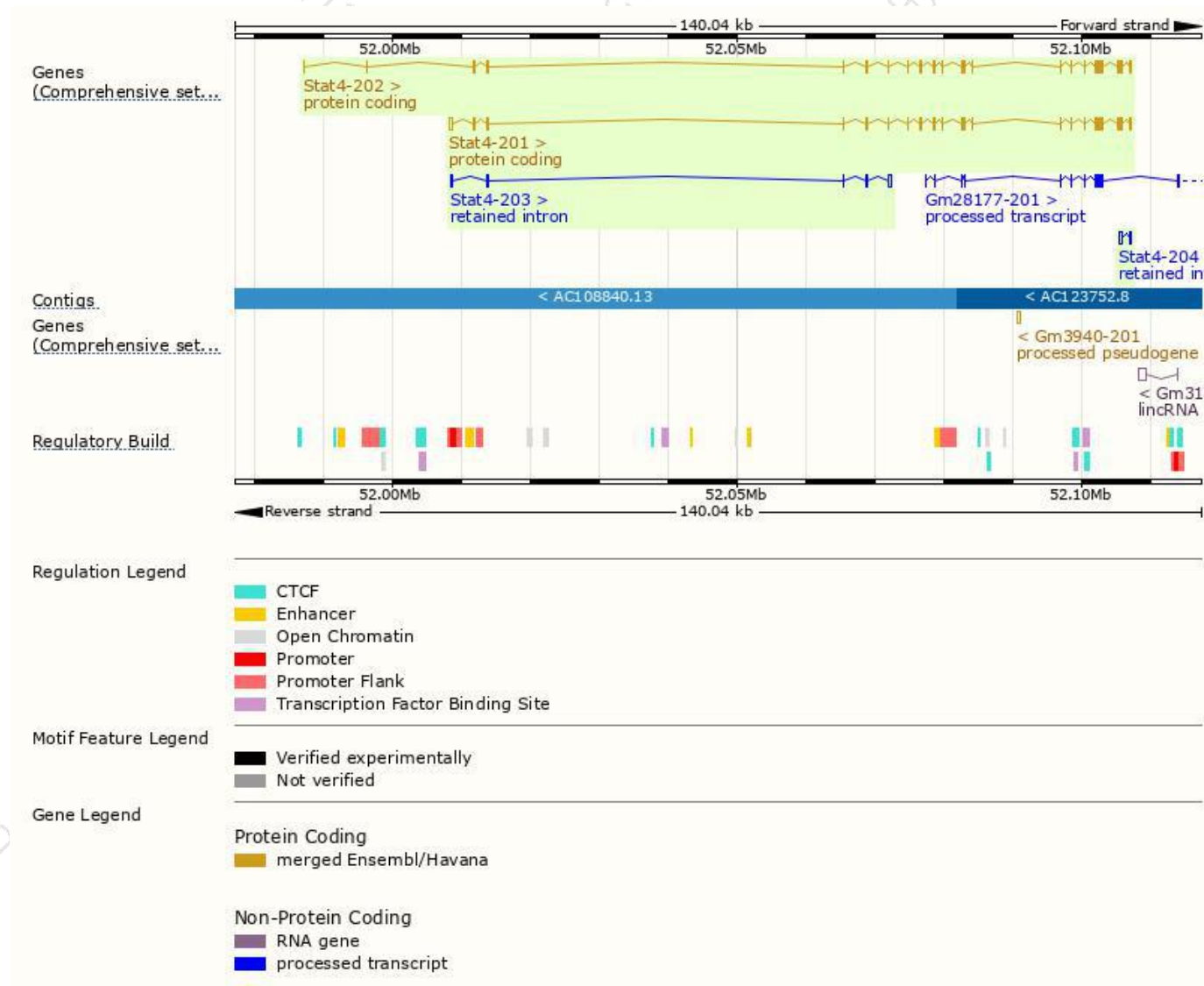
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stat4-201	ENSMUST00000027277.6	2982	748aa	Protein coding	CCDS14943	Q3V157	TSL:1 GENCODE basic APPRIS P1
Stat4-202	ENSMUST00000168302.7	2662	748aa	Protein coding	CCDS14943	Q3V157	TSL:1 GENCODE basic APPRIS P1
Stat4-203	ENSMUST00000187053.1	1024	No protein	Retained intron	-	-	TSL:2
Stat4-204	ENSMUST00000187554.1	607	No protein	Retained intron	-	-	TSL:2

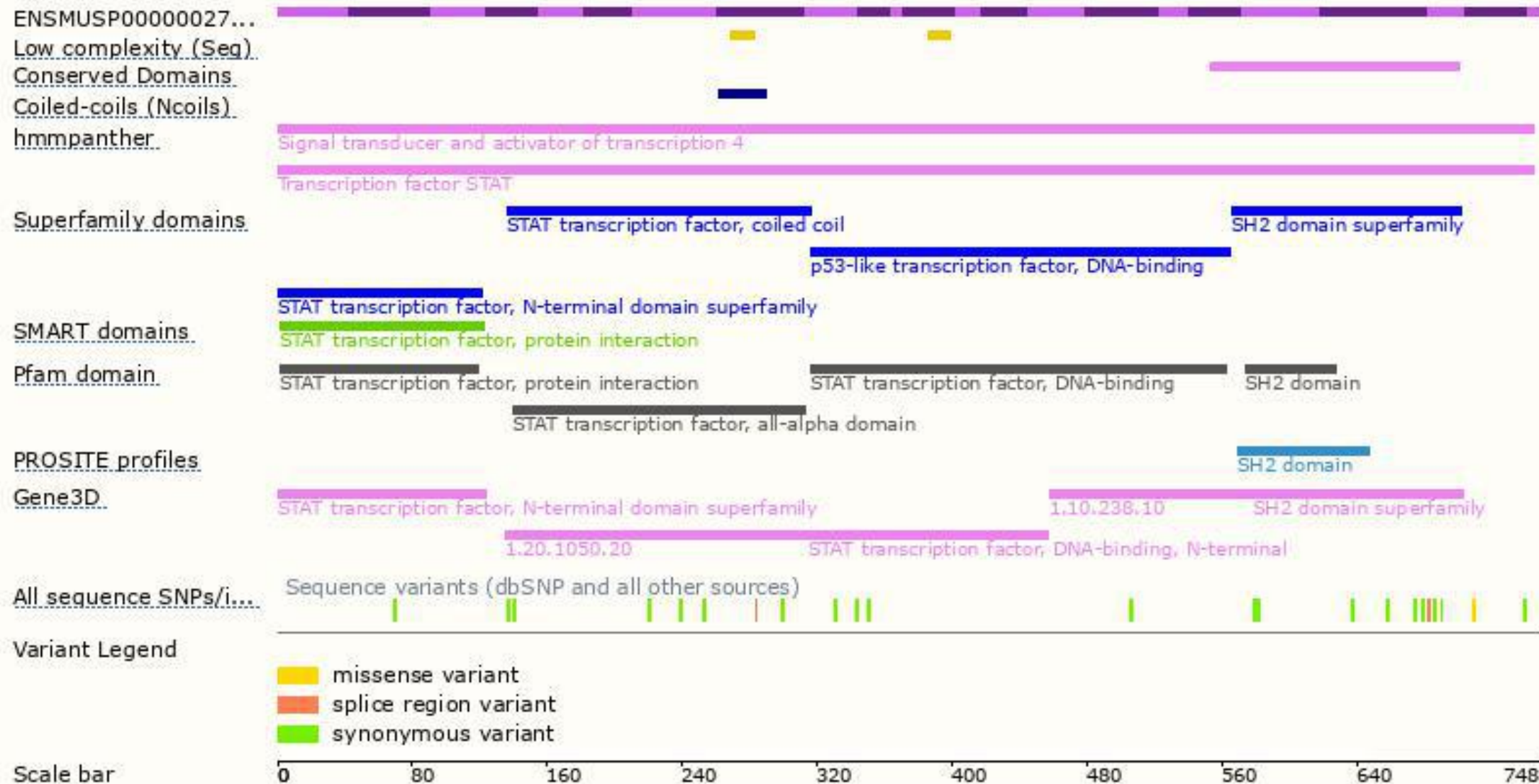
The strategy is based on the design of *Stat4-201* transcript,The transcription is shown below



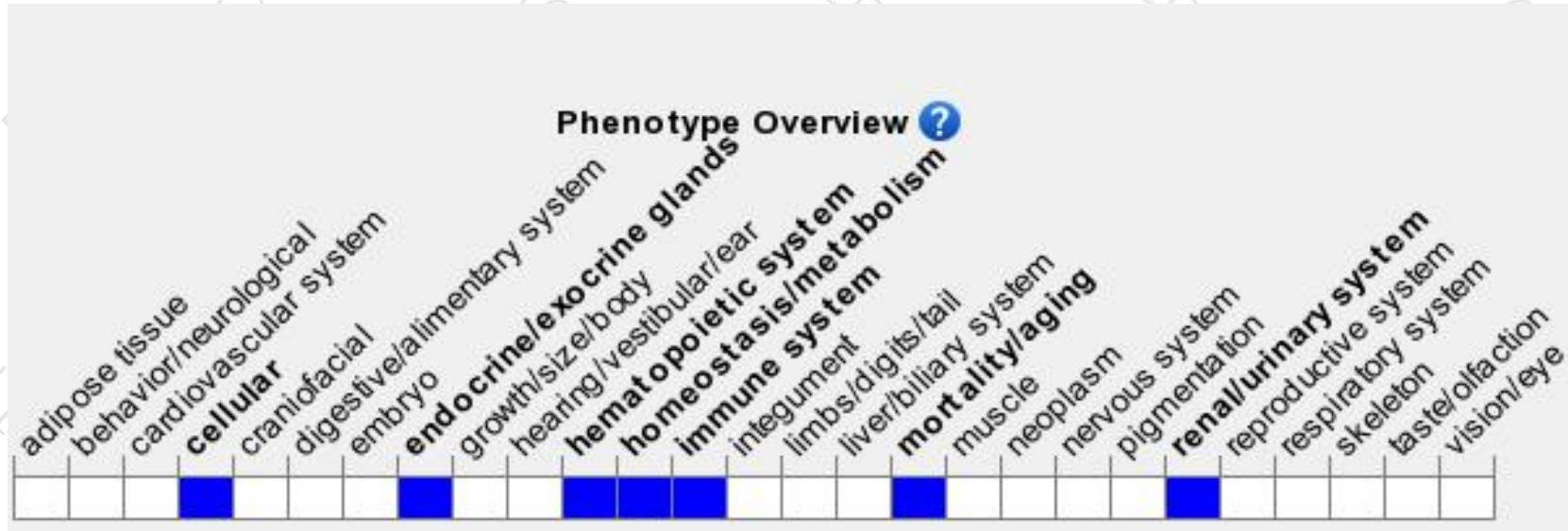
Genomic location distribution



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 inactivation of this gene leads to altered cytokine production of T-cells, impaired IL-12 responses, enhanced Th2 cell development, decreased susceptibility to autoimmune diabetes, altered NK cell responses during viral infection, and increased susceptibility to Salmonella infection.

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

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