

Itgae Cas9-CKO Strategy

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Design Date:

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Project Overview

Project Name

Itgae

Project type

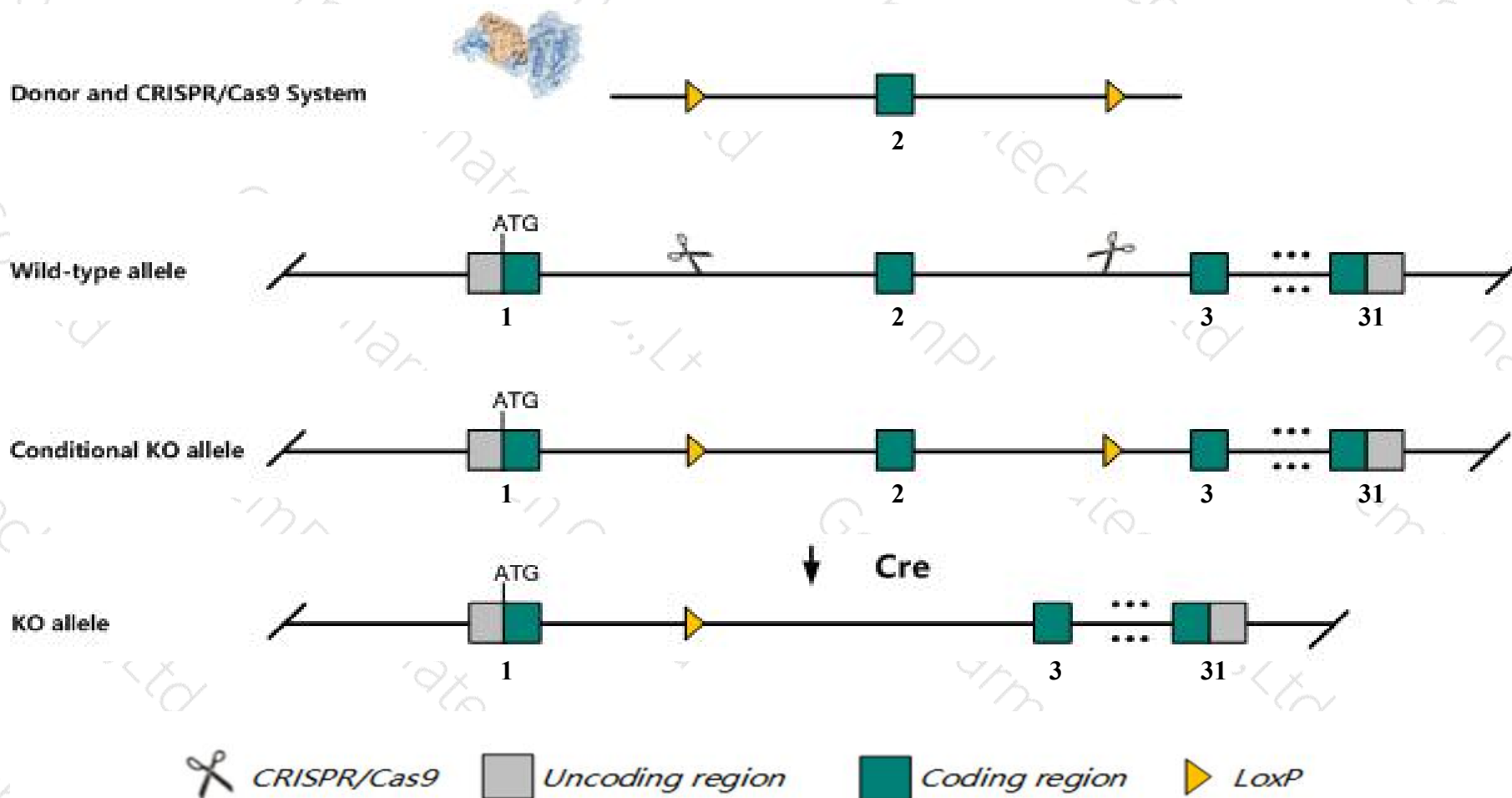
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Itgae* gene has 2 transcripts. According to the structure of *Itgae* gene, exon2 of *Itgae-201* (ENSMUST00000006101.3) transcript is recommended as the knockout region. The region contains 124bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Itgae* 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, Homozygotes for a targeted null mutation exhibit reductions in the numbers of intestinal and vaginal intraepithelial lymphocytes and of T lymphocytes of the lamina propria.
- The *Itgae* gene is located on the Chr11. 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)

Itgae integrin alpha E, epithelial-associated [Mus musculus (house mouse)]

Gene ID: 16407, updated on 17-Feb-2019

Summary



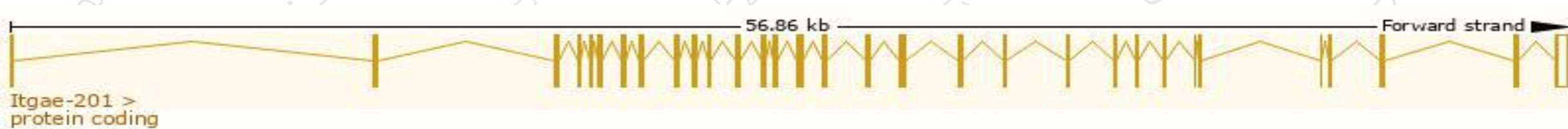
Official Symbol	Itgae provided by MGI
Official Full Name	integrin alpha E, epithelial-associated provided by MGI
Primary source	MGI:MGI:1298377
See related	Ensembl:ENSMUSG00000005947
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A530055J10, CD103, aM290, alpha-E1, alpha-M290
Expression	Biased expression in thymus adult (RPKM 6.0), testis adult (RPKM 5.9) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

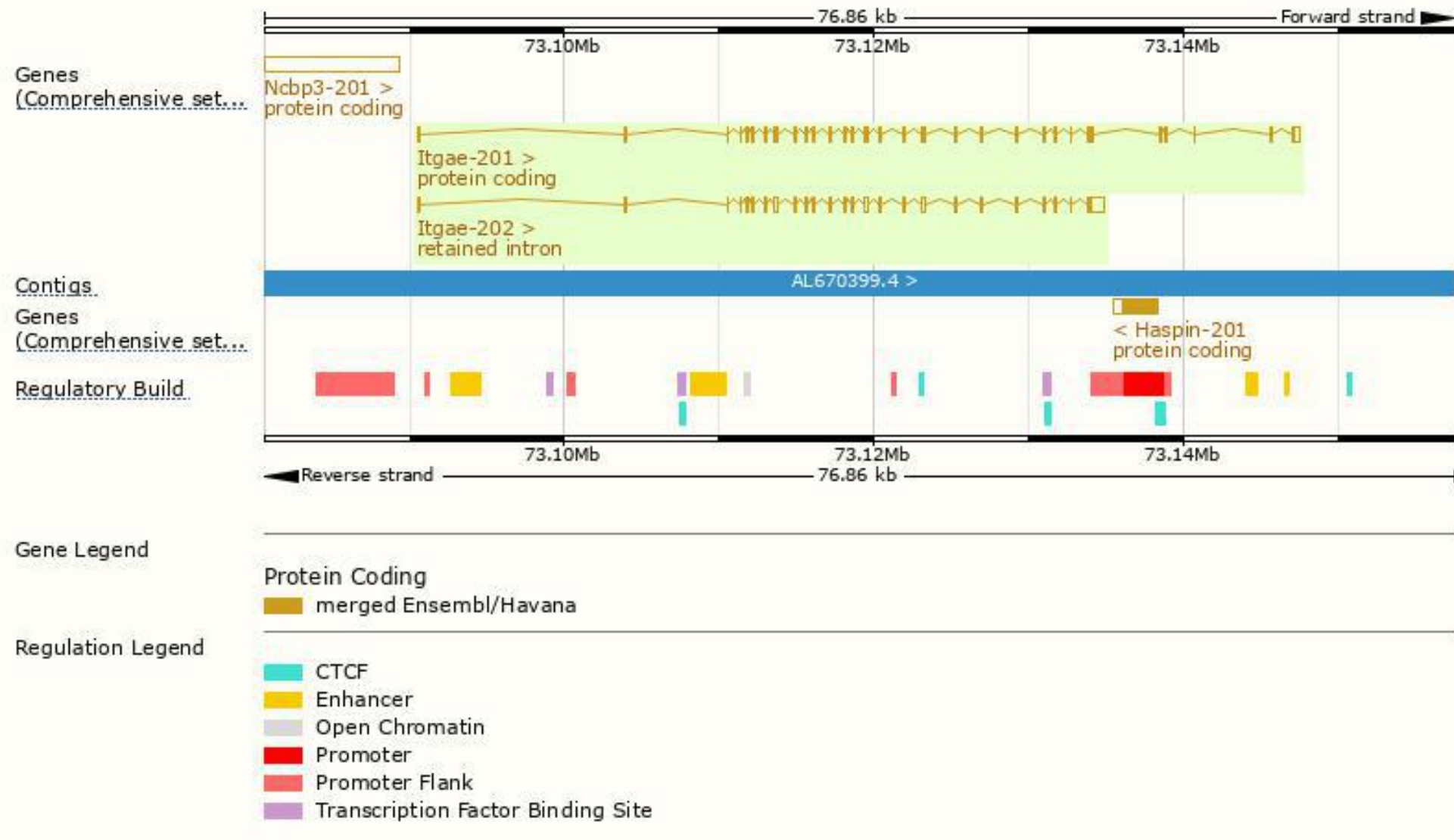
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Itgae-201	ENSMUST00000006101.3	3845	1167aa	Protein coding	CCDS24995	Q60677	TSL:1 GENCODE basic APPRIS P1
Itgae-202	ENSMUST00000102537.9	3825	No protein	Retained intron	-	-	TSL:1

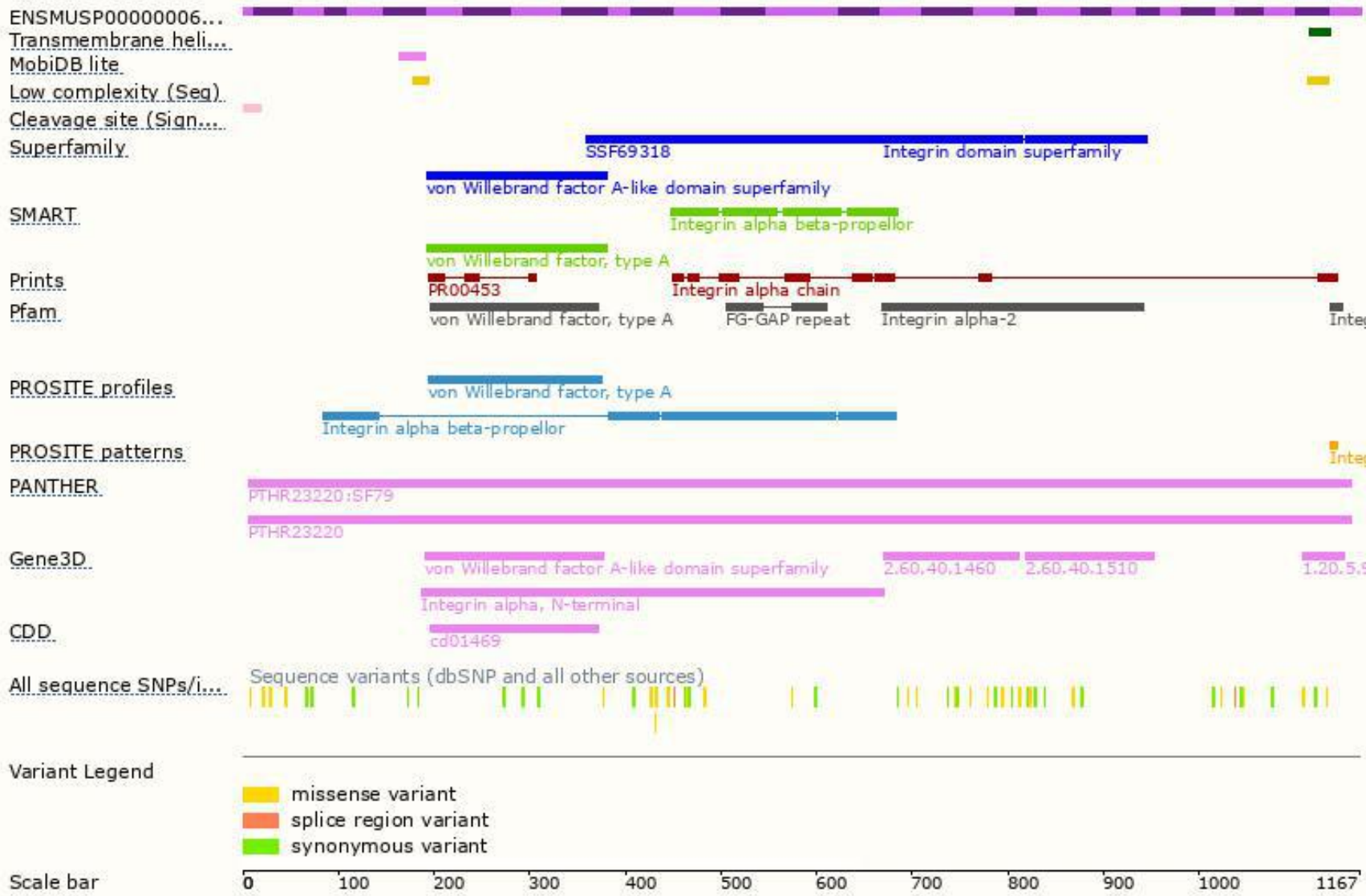
The strategy is based on the design of *Itgae-201* transcript, The transcription is shown below



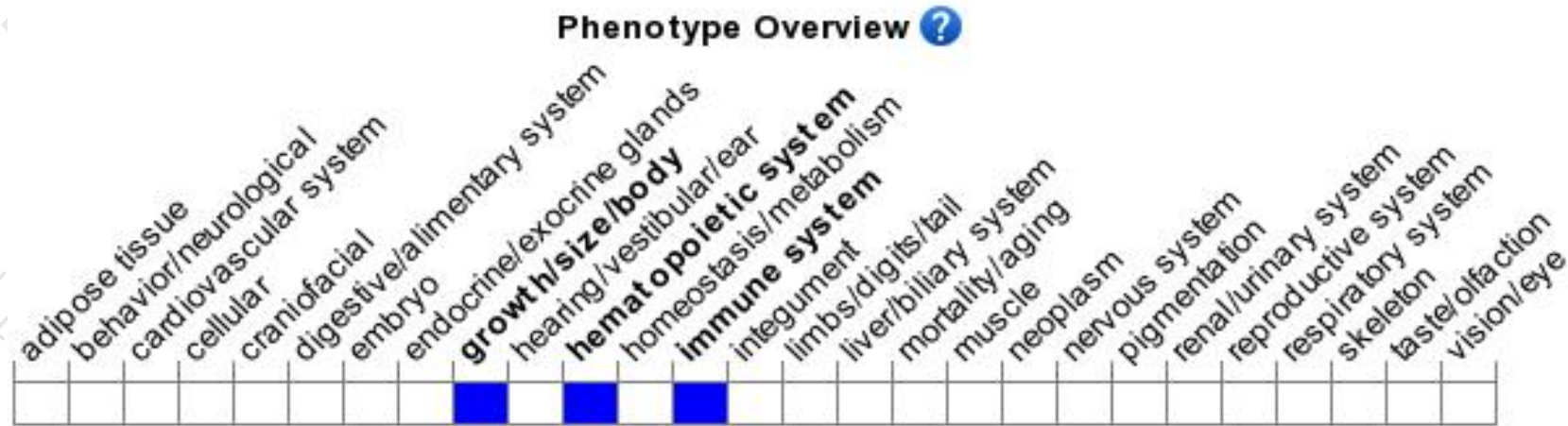
Genomic location distribution



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, Homozygotes for a targeted null mutation exhibit reductions in the numbers of intestinal and vaginal intraepithelial lymphocytes and of T lymphocytes of the lamina propria.