

Dock10 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Dock10

Project type

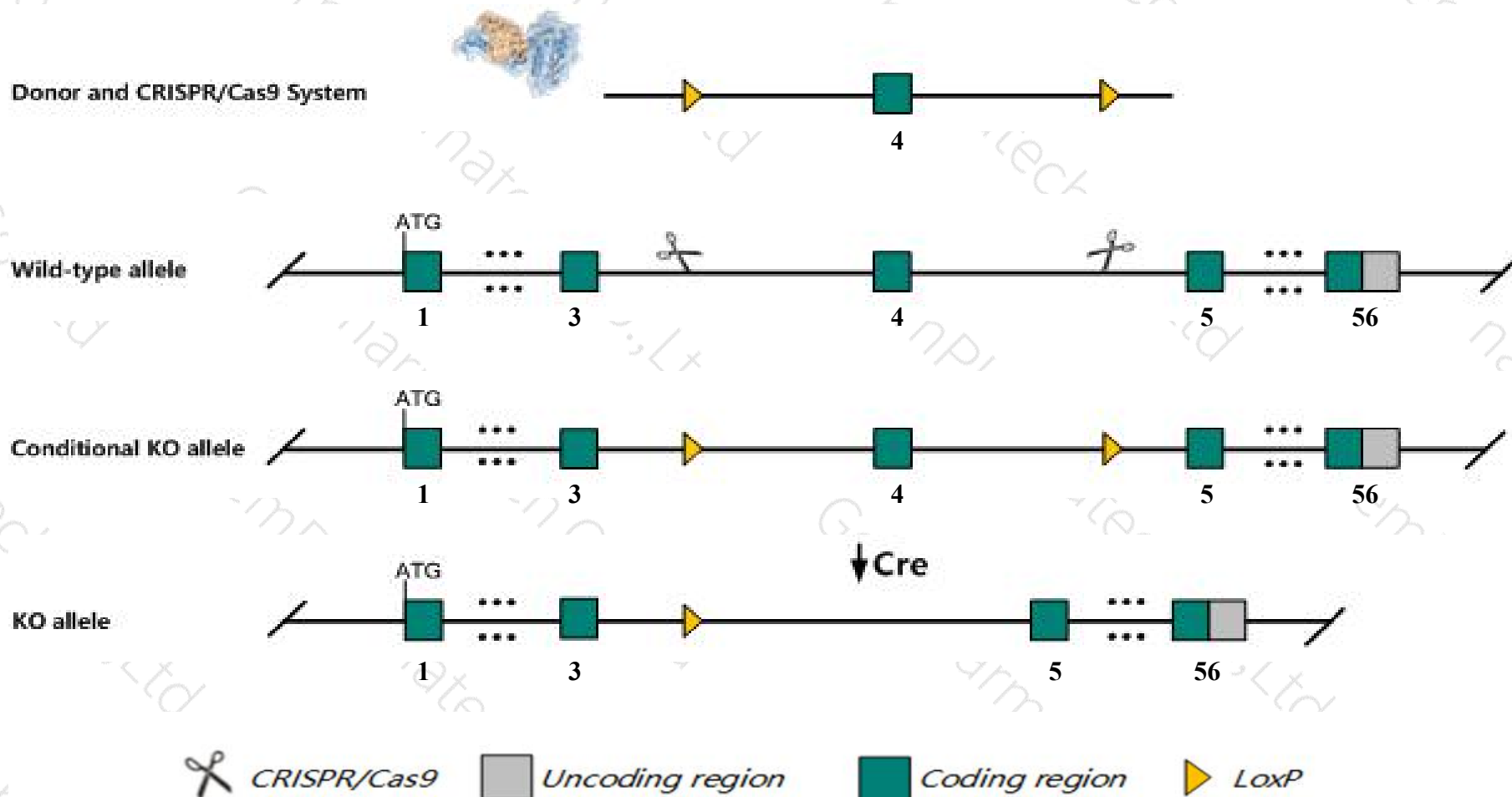
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dock10* gene. The schematic diagram is as follows:



Technical routes

- The *Dock10* gene has 11 transcripts. According to the structure of *Dock10* gene, exon4 of *Dock10-201* (ENSMUST00000077946.11) transcript is recommended as the knockout region. The region contains 83bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dock10* 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, Mice homozygous for a knock-out allele exhibit a reduction of B cell numbers in secondary lymphoid organs. Follicular B cells show membrane CD23 overexpression.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Dock10* 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)

Dock10 dedicator of cytokinesis 10 [Mus musculus (house mouse)]

Gene ID: 210293, updated on 19-Mar-2019

Summary



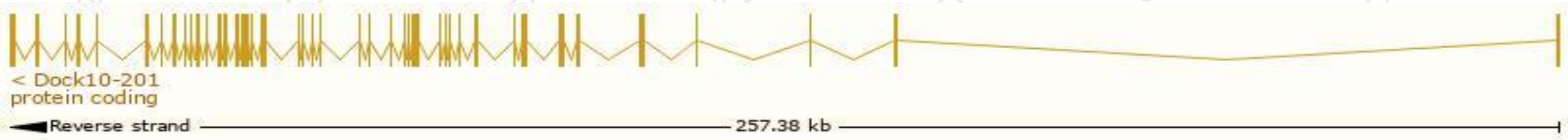
Official Symbol	Dock10 provided by MGI
Official Full Name	dedicator of cytokinesis 10 provided by MGI
Primary source	MGI:MGI:2146320
See related	Ensembl:ENSMUSG00000038608
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9330153B10Rik, A630054M16Rik, Jr4, Jr5, R75174, ZIZ3, Zizimin3, mKIAA0694
Expression	Broad expression in spleen adult (RPKM 3.8), frontal lobe adult (RPKM 3.8) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

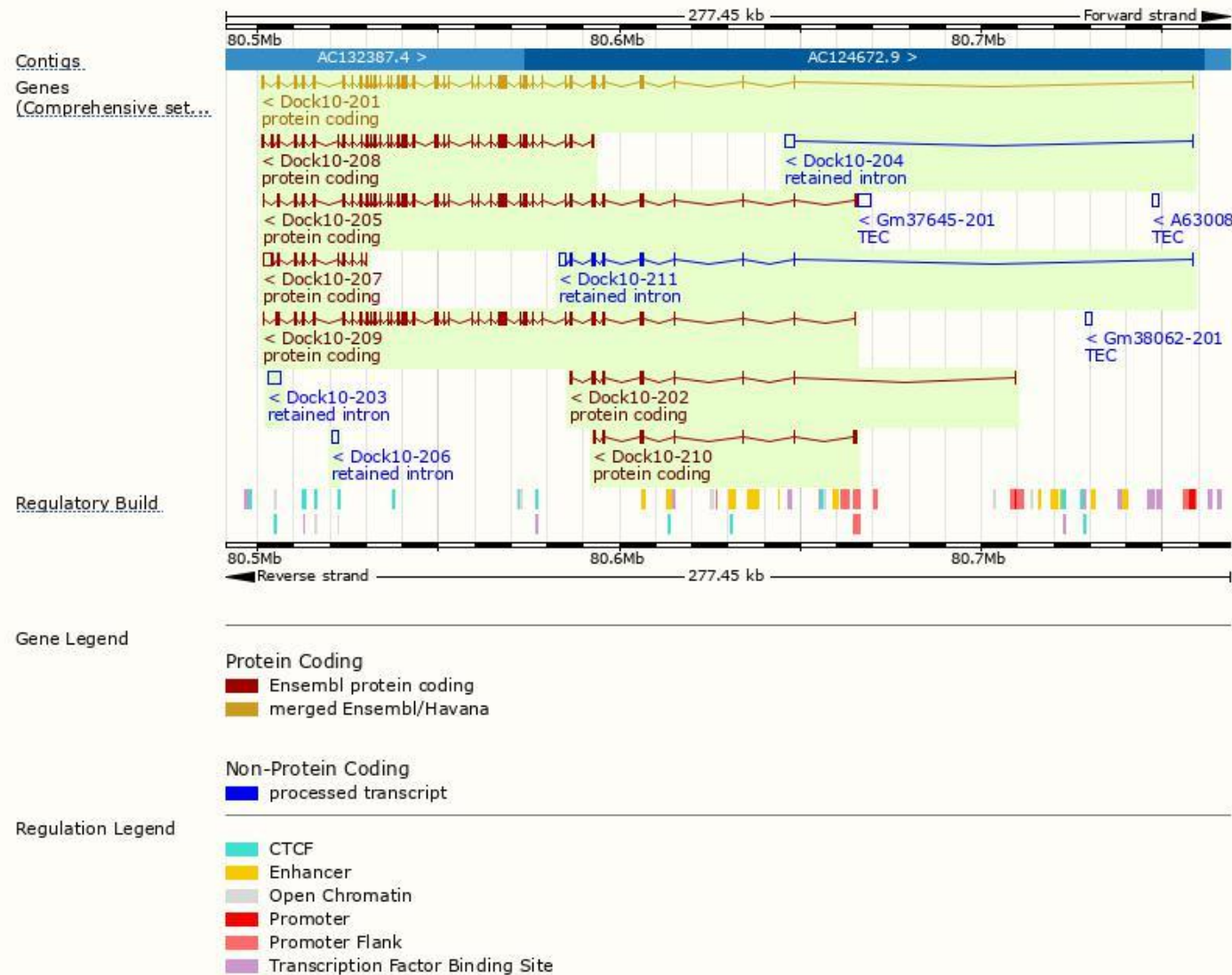
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dock10-201	ENSMUST00000077946.11	7198	2187aa	Protein coding	CCDS48297	E9QM99	TSL:5 GENCODE basic APPRIS P3
Dock10-205	ENSMUST00000187774.6	6796	2175aa	Protein coding	CCDS78626	A0A087WQ86	TSL:1 GENCODE basic APPRIS ALT 2
Dock10-209	ENSMUST00000190983.6	6672	2151aa	Protein coding	-	A0A087WRP5	TSL:1 GENCODE basic APPRIS ALT 2
Dock10-208	ENSMUST00000190595.6	6025	1816aa	Protein coding	-	A0A0R4J2B7	CDS 5' incomplete TSL:5
Dock10-207	ENSMUST00000189486.6	3639	564aa	Protein coding	-	A0A087WS26	CDS 5' incomplete TSL:5
Dock10-202	ENSMUST00000186087.6	1688	546aa	Protein coding	-	A0A087WQA1	CDS 3' incomplete TSL:5
Dock10-210	ENSMUST00000191449.1	1384	373aa	Protein coding	-	Q8BLX9	CDS 3' incomplete TSL:1
Dock10-211	ENSMUST00000191505.1	3472	No protein	Retained intron	-	-	TSL:1
Dock10-203	ENSMUST00000186835.1	3420	No protein	Retained intron	-	-	TSL:NA
Dock10-204	ENSMUST00000187698.1	2789	No protein	Retained intron	-	-	TSL:1
Dock10-206	ENSMUST00000187885.1	1899	No protein	Retained intron	-	-	TSL:NA

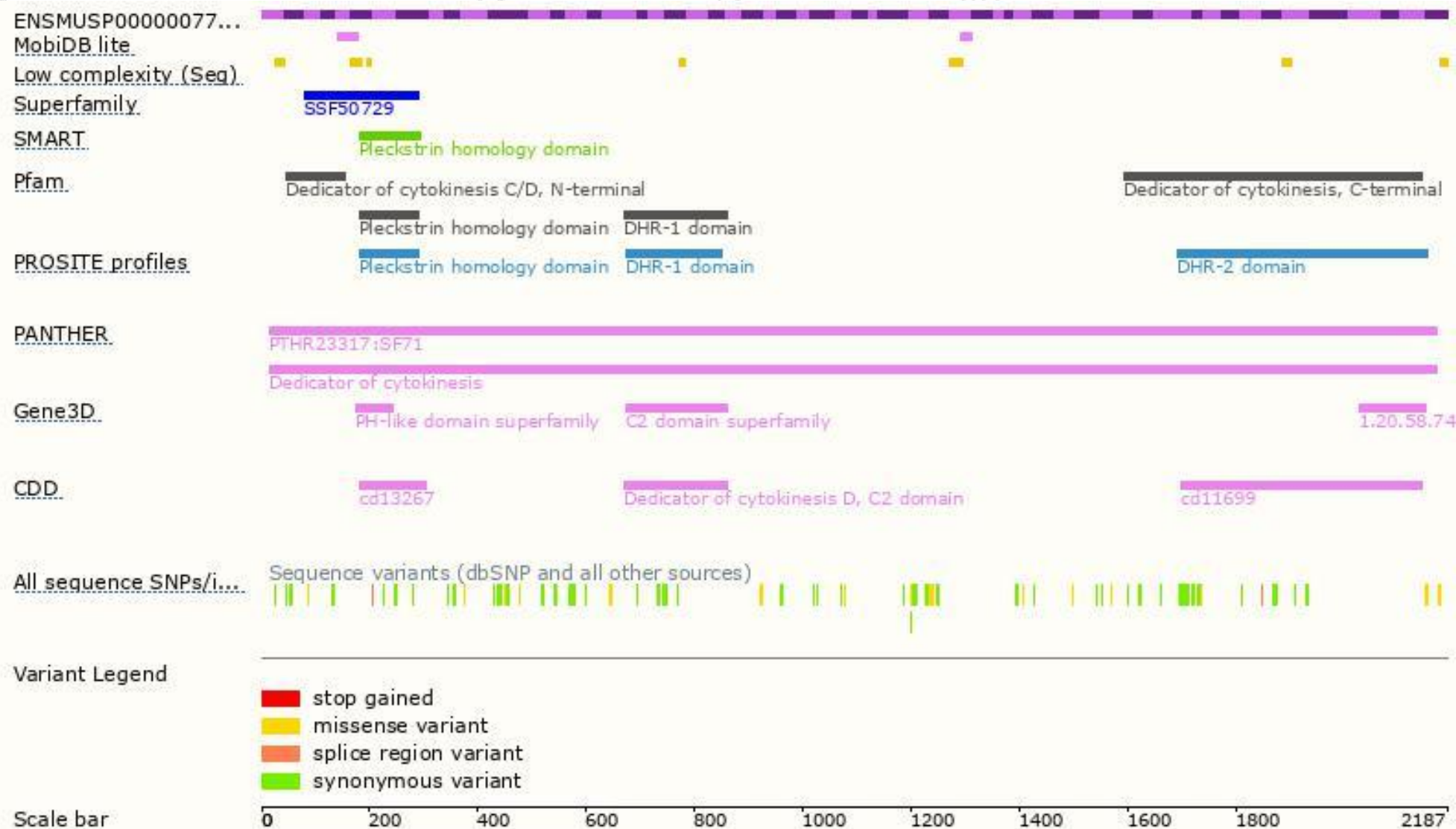
The strategy is based on the design of *Dock10-201* transcript,The transcription is shown below



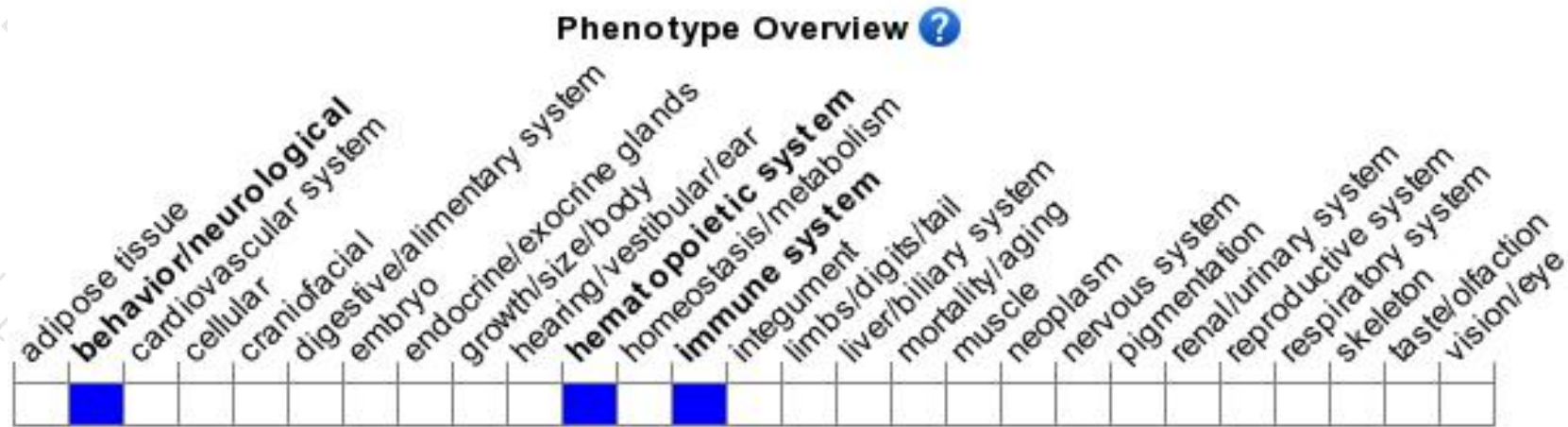
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit a reduction of B cell numbers in secondary lymphoid organs. Follicular B cells show membrane CD23 overexpression.

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

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