

Coro1a Cas9-CKO Strategy

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Reviewer: Shilei Zhu

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Project Overview

Project Name

Coro1a

Project type

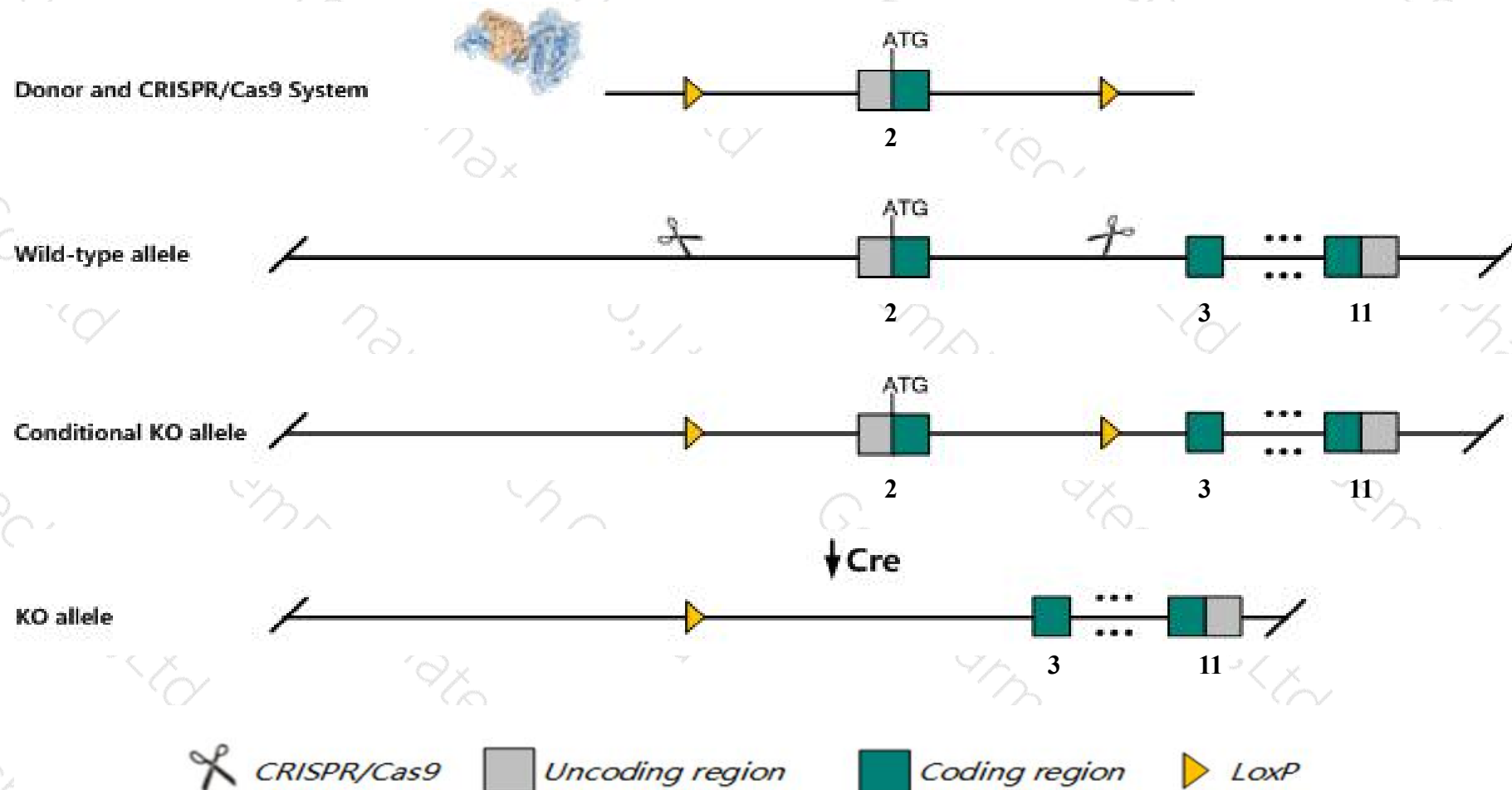
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Coro1a* gene has 12 transcripts. According to the structure of *Coro1a* gene, exon2 of *Coro1a-202*(ENSMUST00000106364.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Coro1a* 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 null or hypomorph alleles of this gene display lower peripheral T cell counts resulting from defects in T cell migration and increased rates of apoptosis.
- The *Coro1a* gene is located on the Chr7. 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)

Coro1a coronin, actin binding protein 1A [Mus musculus (house mouse)]

Gene ID: 12721, updated on 13-Mar-2020

Summary

Official Symbol Coro1a provided by [MGI](#)

Official Full Name coronin, actin binding protein 1A provided by [MGI](#)

Primary source [MGI:MGI:1345961](#)

See related [Ensembl:ENSMUSG00000030707](#)

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

Also known as Clabp, Lmb3, TACO, p57

Summary This gene encodes a member of the WD repeat coronin family. The encoded protein may bind actin and interact with microtubules. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2014]

Expression Biased expression in thymus adult (RPKM 522.1), spleen adult (RPKM 445.6) and 7 other tissues [See more](#)

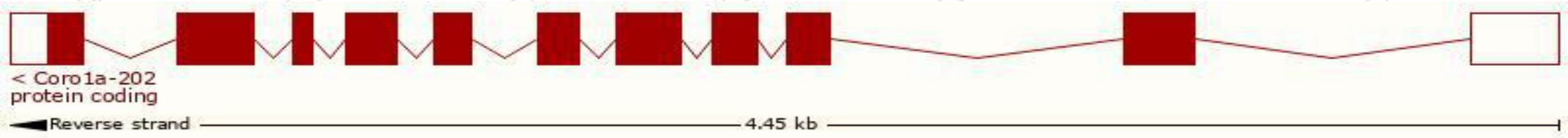
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

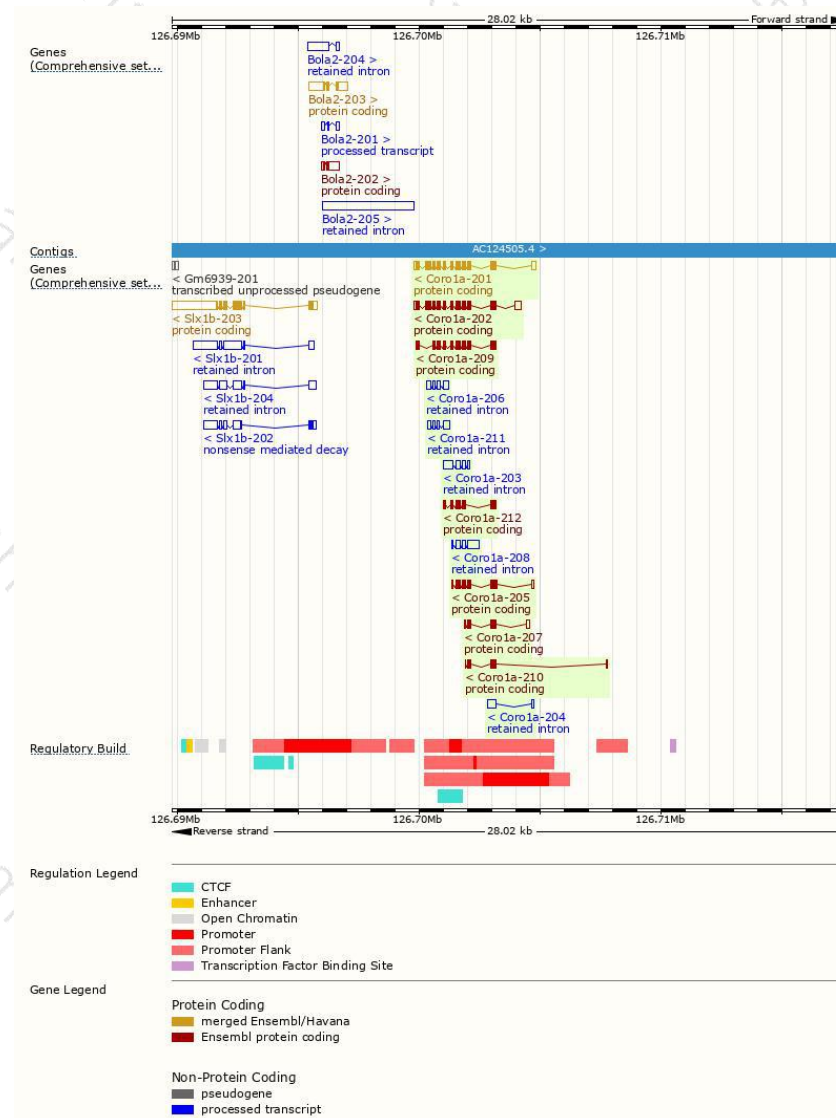
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Coro1a-202	ENSMUST00000106364.7	1747	461aa	Protein coding	CCDS21840	O89053 Q3U1N0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Coro1a-201	ENSMUST00000032949.13	1660	461aa	Protein coding	CCDS21840	O89053 Q3U1N0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Coro1a-209	ENSMUST00000173108.7	1170	389aa	Protein coding	-	G3UYK8	TSL:5 GENCODE basic
Coro1a-205	ENSMUST00000131415.7	824	233aa	Protein coding	-	D3YW57	CDS 3' incomplete TSL:3
Coro1a-212	ENSMUST00000205515.1	739	246aa	Protein coding	-	A0A0U1RPY8	CDS 3' incomplete TSL:5
Coro1a-207	ENSMUST00000135087.7	471	116aa	Protein coding	-	D3YXM2	CDS 3' incomplete TSL:2
Coro1a-210	ENSMUST00000173116.1	388	113aa	Protein coding	-	G3UX53	CDS 3' incomplete TSL:3
Coro1a-208	ENSMUST00000140896.1	862	No protein	Retained intron	-	-	TSL:2
Coro1a-203	ENSMUST00000123511.7	824	No protein	Retained intron	-	-	TSL:2
Coro1a-206	ENSMUST00000133718.7	602	No protein	Retained intron	-	-	TSL:2
Coro1a-211	ENSMUST00000174579.1	520	No protein	Retained intron	-	-	TSL:5
Coro1a-204	ENSMUST00000126193.1	445	No protein	Retained intron	-	-	TSL:2

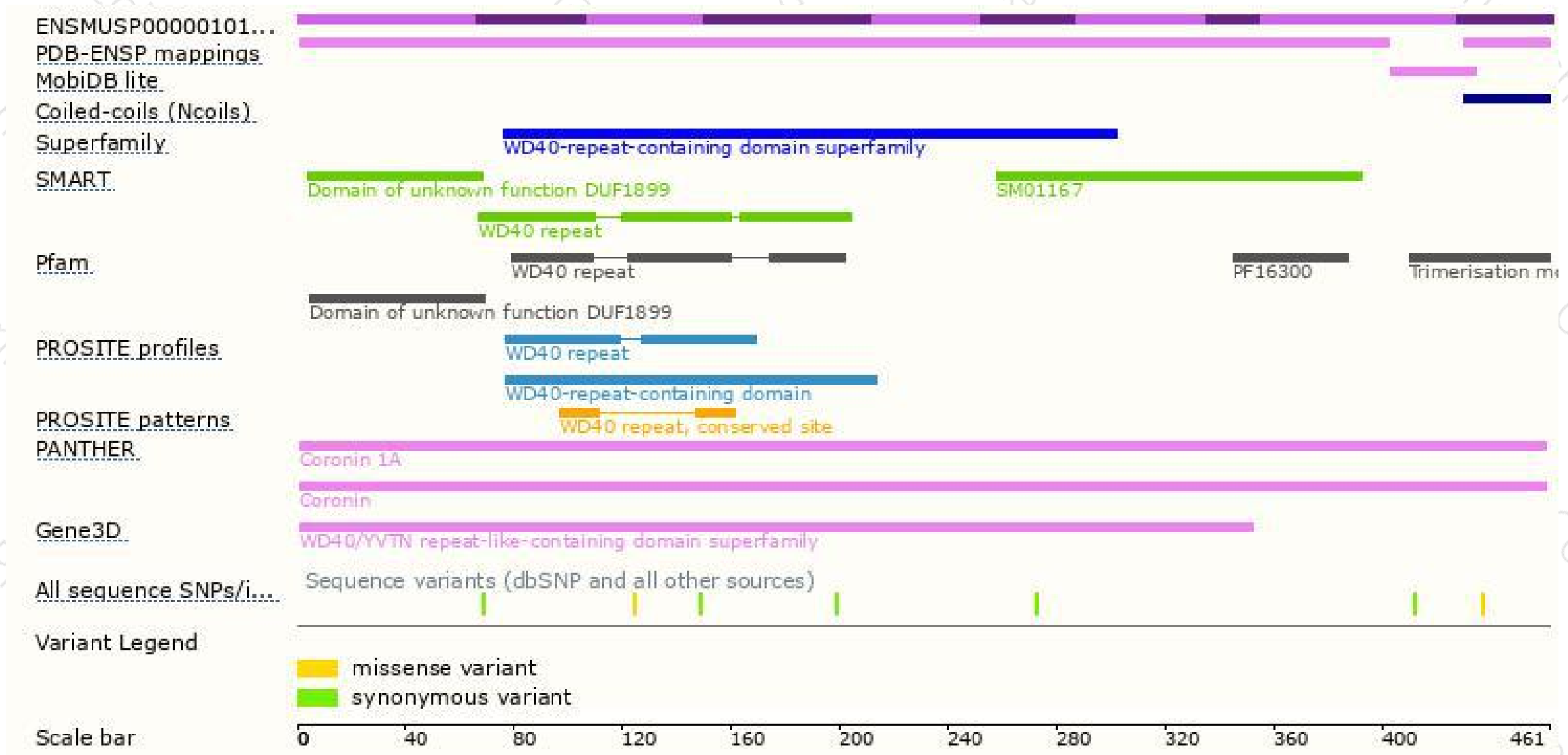
The strategy is based on the design of *Coro1a-202* transcript,the transcription is shown below:



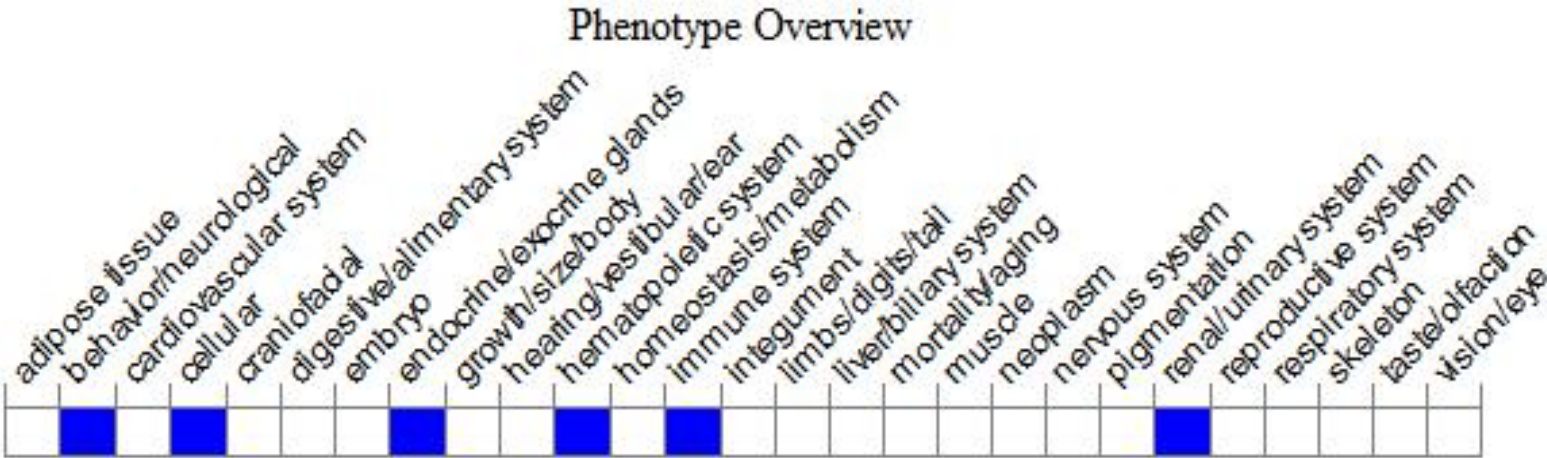
Genomic location distribution



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 null or hypomorph alleles of this gene display lower peripheral T cell counts resulting from defects in T cell migration and increased rates of apoptosis.

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

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