

Foxp3 Cas9-KO Strategy

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Design Date: 2019-9-12
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Project Overview

Project Name

Foxp3

Project type

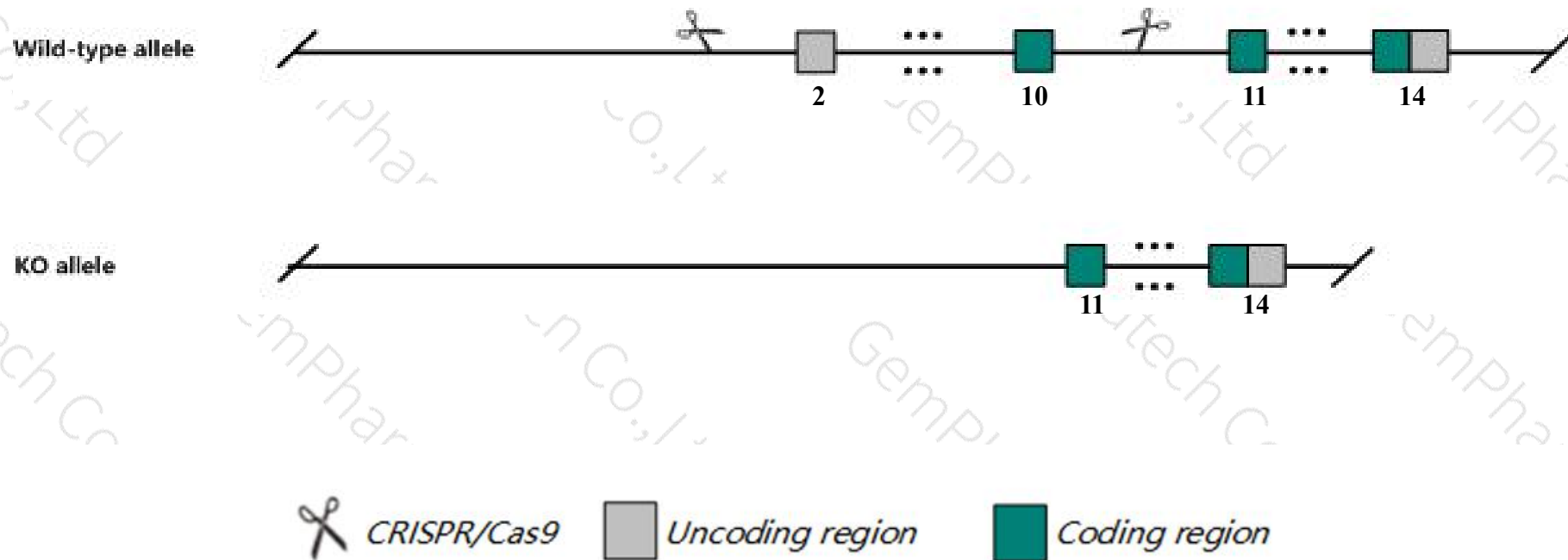
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxp3* gene. The schematic diagram is as follows:



- The *Foxp3* gene has 10 transcripts. According to the structure of *Foxp3* gene, exon2-exon10 of *Foxp3*-204 (ENSMUST00000115740.8) transcript is recommended as the knockout region. The region contains 813bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Foxp3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Hemizygous mutant males exhibit scaly skin, reddening and swelling of genital papilla, small undescended testes, depressed platelet and red cell counts, and lymphohistiocytic proliferation in various organs. Mutants die around weaning age.
- The *Foxp3* gene is located on the ChrX. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Foxp3 forkhead box P3 [Mus musculus (house mouse)]

Gene ID: 20371, updated on 9-Apr-2019

Summary



Official Symbol Foxp3 provided by [MGI](#)

Official Full Name forkhead box P3 provided by [MGI](#)

Primary source [MGI:MGI:1891436](#)

See related [Ensembl:ENSMUSG00000039521](#)

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 JM2, scurfin, sf

Summary The protein encoded by this gene is a member of the forkhead/winged-helix family of transcriptional regulators. Defects in this gene result in the scurfy phenotype (sf). Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2015]

Expression Ubiquitous expression in spleen adult (RPKM 3.0), thymus adult (RPKM 2.4) and 28 other tissues [See more](#)

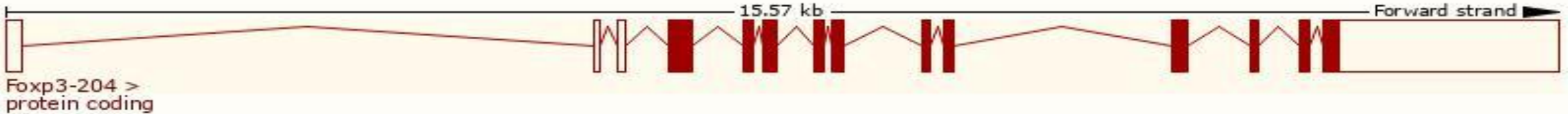
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

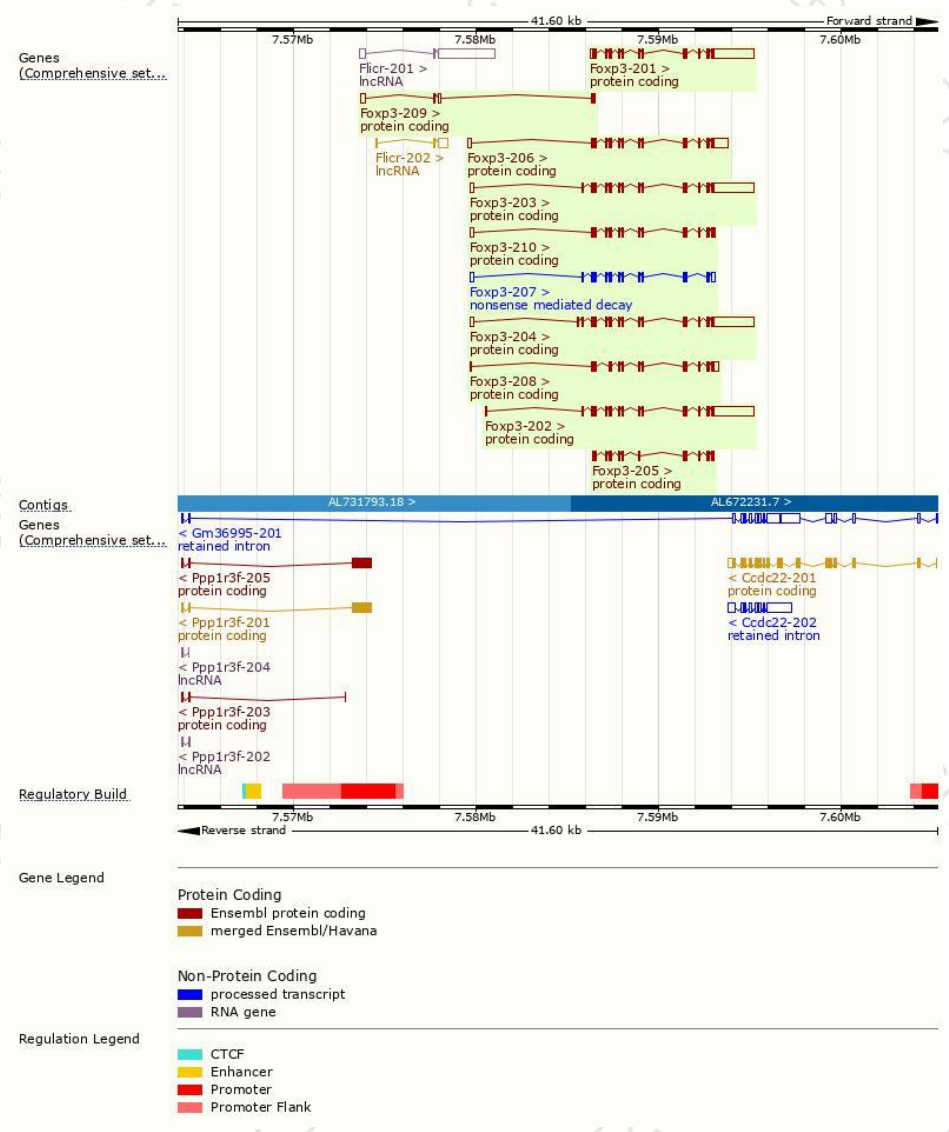
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxp3-204	ENSMUST00000115740.8	3834	429aa	Protein coding	CCDS29965	Q53Z59 Q99JB6	TSL:1 GENCODE basic APPRIS P1
Foxp3-203	ENSMUST00000115739.8	3763	429aa	Protein coding	CCDS29965	Q53Z59 Q99JB6	TSL:1 GENCODE basic APPRIS P1
Foxp3-202	ENSMUST00000115738.7	3681	429aa	Protein coding	CCDS29965	Q53Z59 Q99JB6	TSL:1 GENCODE basic APPRIS P1
Foxp3-201	ENSMUST00000045566.6	3572	429aa	Protein coding	CCDS29965	Q53Z59 Q99JB6	TSL:5 GENCODE basic APPRIS P1
Foxp3-206	ENSMUST00000234363.1	2226	429aa	Protein coding	CCDS29965	Q53Z59	GENCODE basic APPRIS P1
Foxp3-210	ENSMUST00000235116.1	1551	429aa	Protein coding	CCDS29965	Q53Z59	GENCODE basic APPRIS P1
Foxp3-208	ENSMUST00000234574.1	1477	394aa	Protein coding	-	-	GENCODE basic
Foxp3-205	ENSMUST00000234015.1	1214	402aa	Protein coding	-	-	GENCODE basic
Foxp3-209	ENSMUST00000234896.1	662	54aa	Protein coding	-	-	CDS 3' incomplete
Foxp3-207	ENSMUST00000234479.1	1557	335aa	Nonsense mediated decay	-	-	

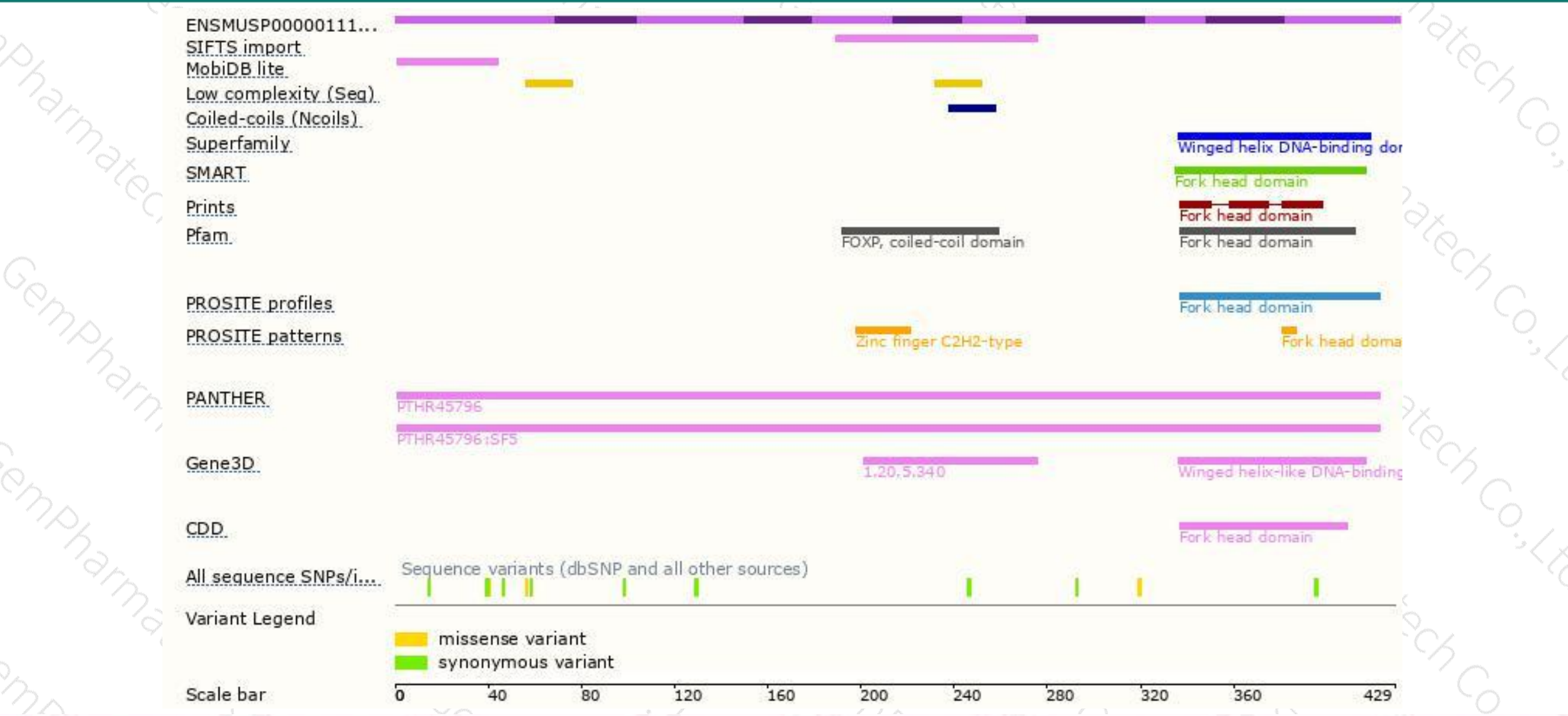
The strategy is based on the design of *Foxp3-204* transcript,The transcription is shown below



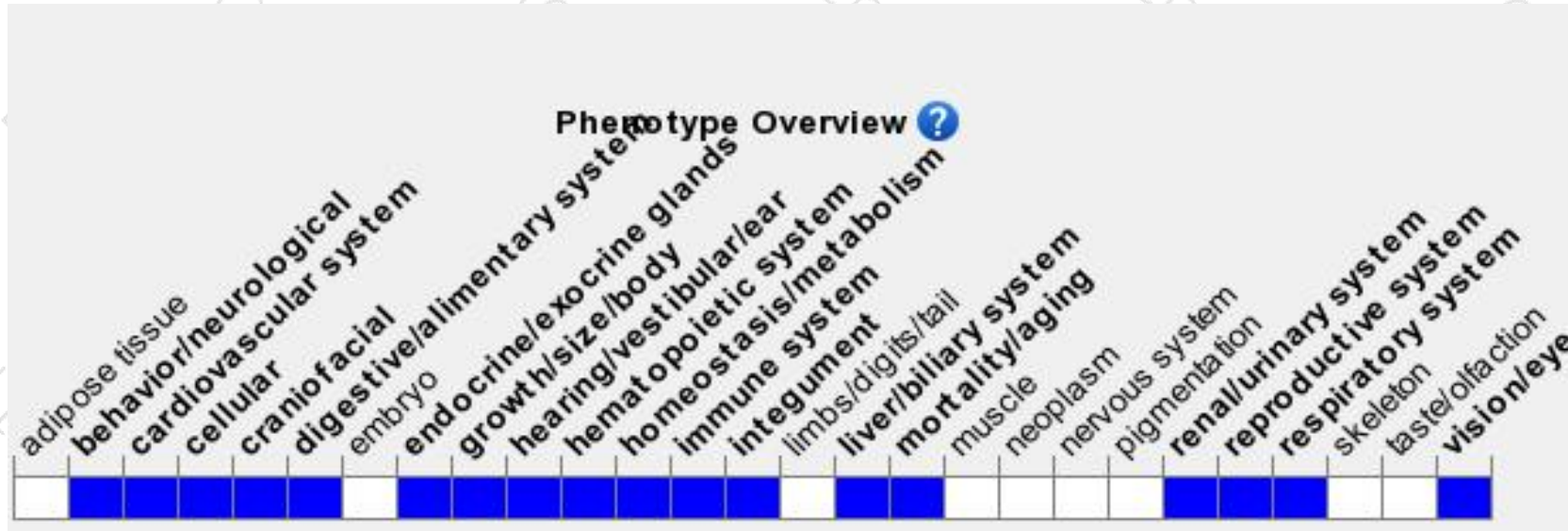
Genomic location distribution



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/>).

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

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