

Vt1a Cas9-CKO Strategy

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Project Overview

Project Name

Vt1a

Project type

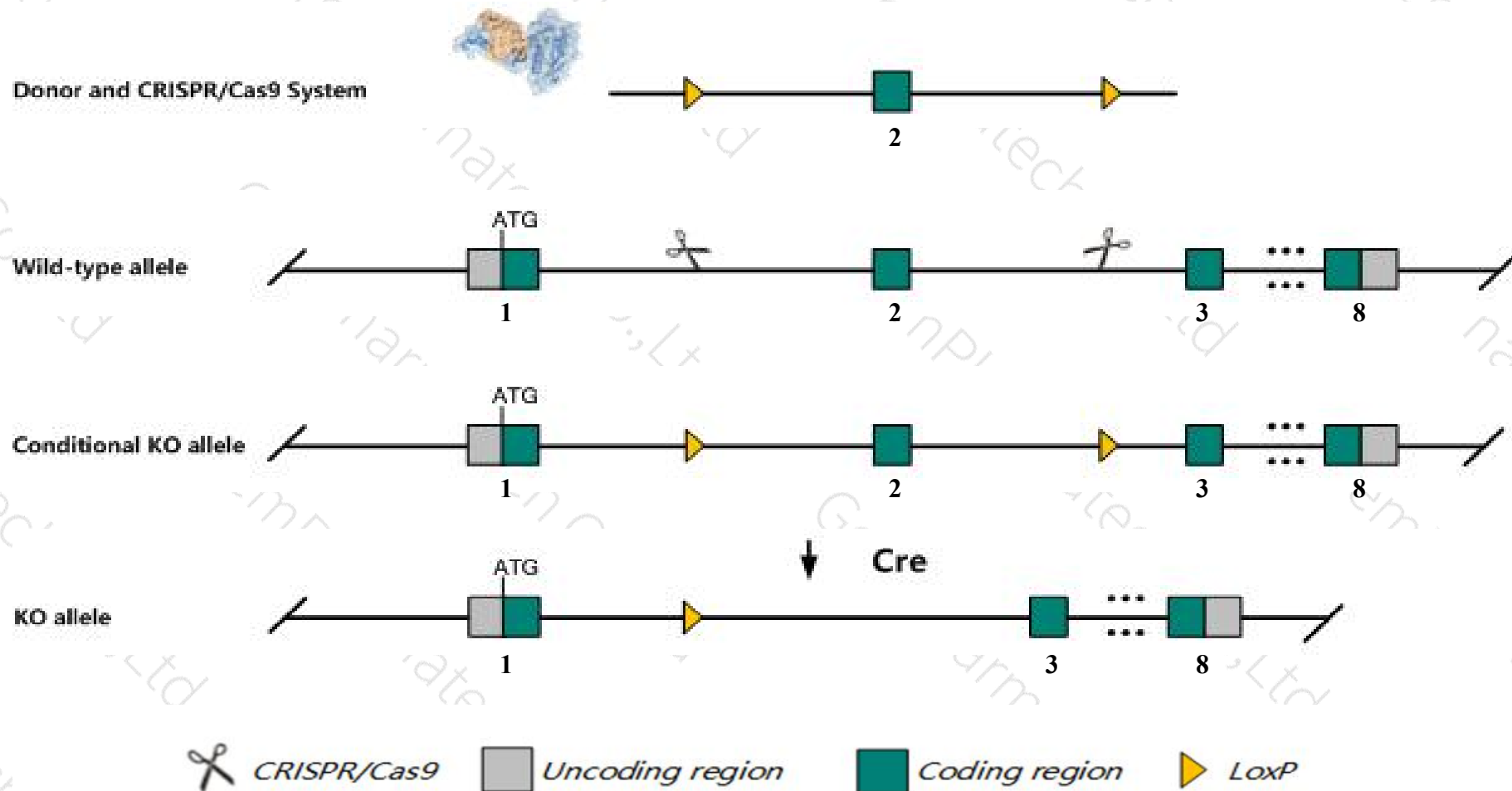
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Vtla* gene has 7 transcripts. According to the structure of *Vtla* gene, exon2 of *Vtla-201* (ENSMUST00000095950.2) transcript is recommended as the knockout region. The region contains 59bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vtla* 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 are viable and fertile.
- Transcript *Vt1a*-203 may not be affected.
- The floxed region is near to the N-terminal of *Zdhhc6* gene, this strategy may influence the regulatory function of the N-terminal of *Zdhhc6* gene.
- The *Vt1a* gene is located on the Chr19. 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)

Vti1a vesicle transport through interaction with t-SNAREs 1A [*Mus musculus* (house mouse)]

Gene ID: 53611, updated on 26-Nov-2019

Summary

- Official Symbol** Vti1a provided by [MGI](#)
- Official Full Name** vesicle transport through interaction with t-SNAREs 1A provided by [MGI](#)
- Primary source** [MGI:MGI:1855699](#)
- See related** [Ensembl:ENSMUSG00000024983](#)
- 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** Vti1; MVti1; MVti1a; Vti1-rp2; 1110014F16Rik; 1110018K19Rik; 4921537J05Rik
- Expression** Ubiquitous expression in cortex adult (RPKM 1.7), frontal lobe adult (RPKM 1.7) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 19; 19 D2 See Vti1a in [Genome Data Viewer](#)

Exon count: 16

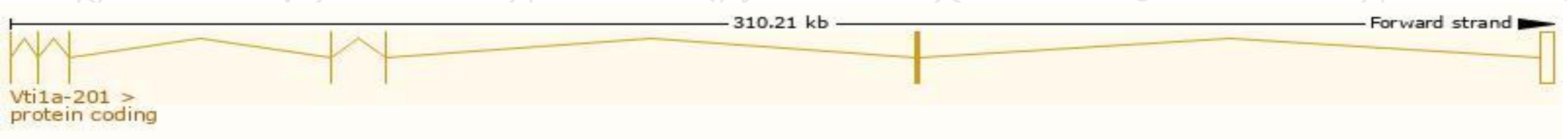
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (55316030..55627461)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (55390841..55701051)

Transcript information (Ensembl)

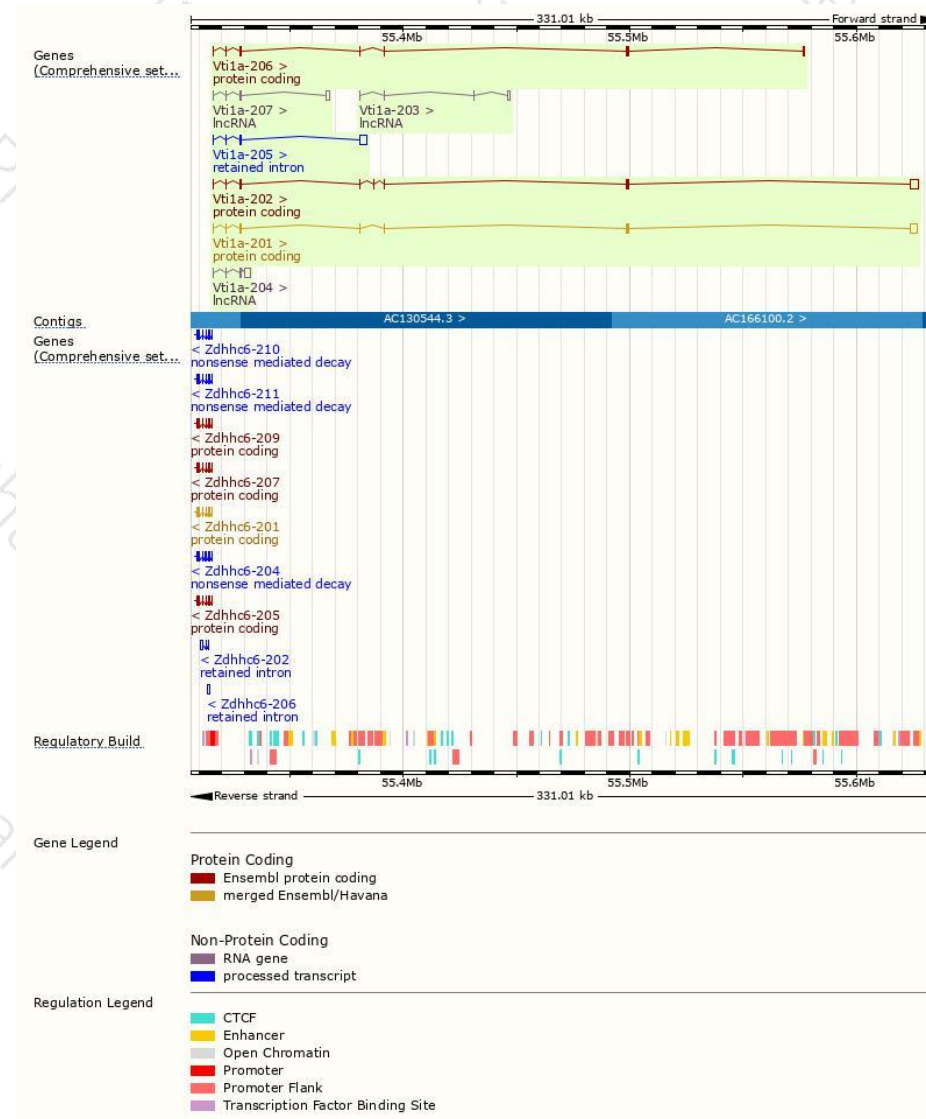
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vti1a-201	ENSMUST00000095950.2	3405	217aa	Protein coding	CCDS29910	Q89116	TSL:1 GENCODE basic APPRIS P2
Vti1a-202	ENSMUST00000223690.1	4175	224aa	Protein coding	-	Q5FWJ7	GENCODE basic APPRIS ALT1
Vti1a-206	ENSMUST00000225529.1	1244	197aa	Protein coding	-	A0A286YDF2	GENCODE basic
Vti1a-205	ENSMUST00000225392.1	3370	No protein	Retained intron	-	-	
Vti1a-204	ENSMUST00000225051.1	2919	No protein	lncRNA	-	-	
Vti1a-207	ENSMUST00000226069.1	1599	No protein	lncRNA	-	-	
Vti1a-203	ENSMUST00000224396.1	955	No protein	lncRNA	-	-	

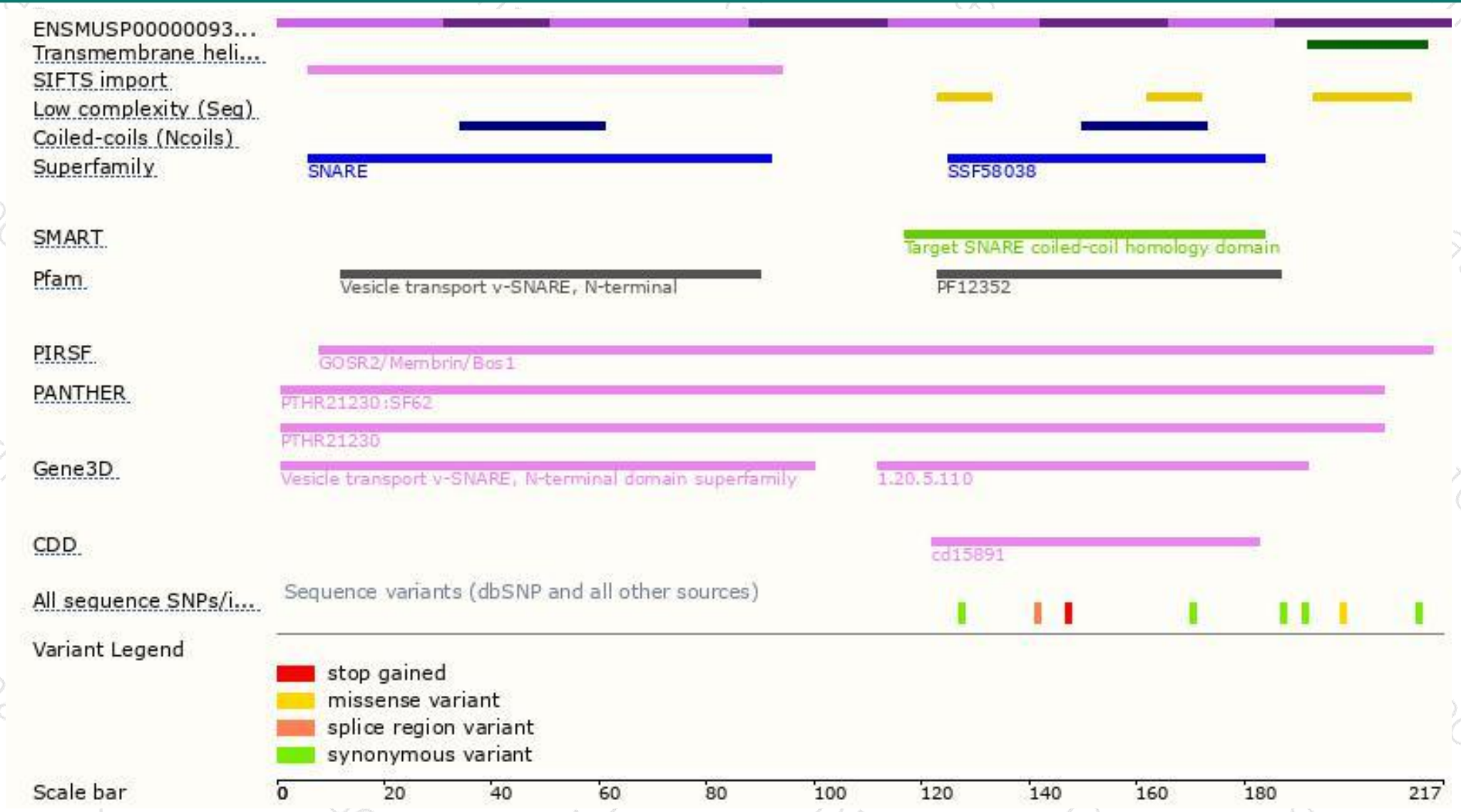
The strategy is based on the design of *Vti1a-201* transcript,The transcription is shown below



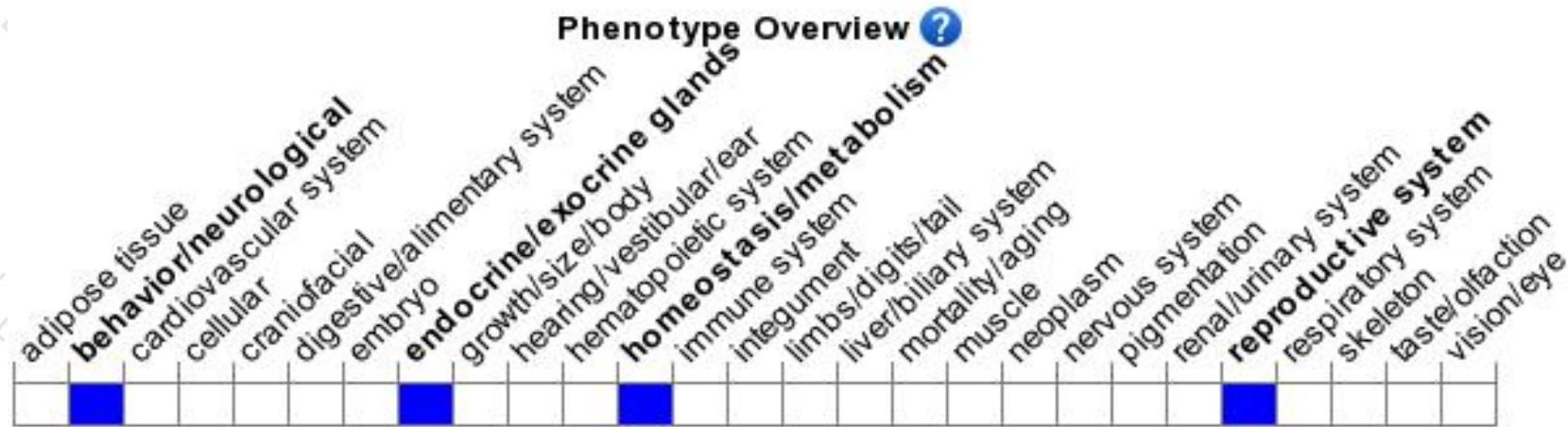
Genomic location distribution



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 are viable and fertile.

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

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