

***Fstl1* Cas9-CKO Strategy**

Designer:

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Design Date:

2019-8-6

Project Overview

Project Name

Fstl1

Project type

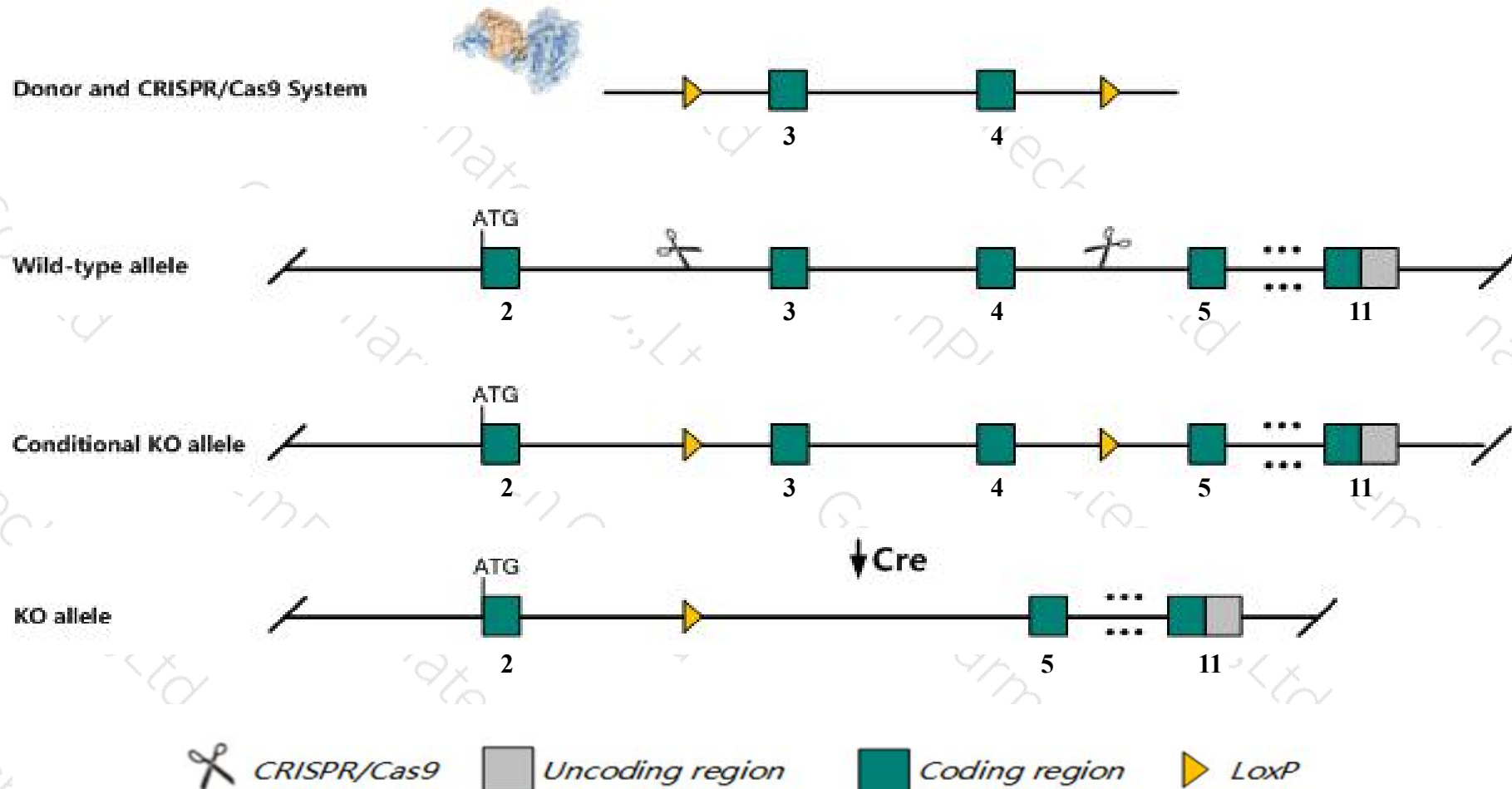
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fstll1* gene. The schematic diagram is as follows:



Technical routes

- The *Fstl1* gene has 6 transcripts. According to the structure of *Fstl1* gene, exon3-exon4 of *Fstl1-201* (ENSMUST00000114763.2) transcript is recommended as the knockout region. The region contains 235bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fstl1* 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 neonatal lethality, soft and enlarged trachea, cyanosis, primary atelectasis, lung epithelial cell hyperplasia, over-expanded bronchiole, impaired pneumocyte differentiation and maturation, and decreased surfactant production.
- The *Fstl1* gene is located on the Chr16. 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)

Fstl1 follistatin-like 1 [Mus musculus (house mouse)]

Gene ID: 14314, updated on 9-Apr-2019

Summary



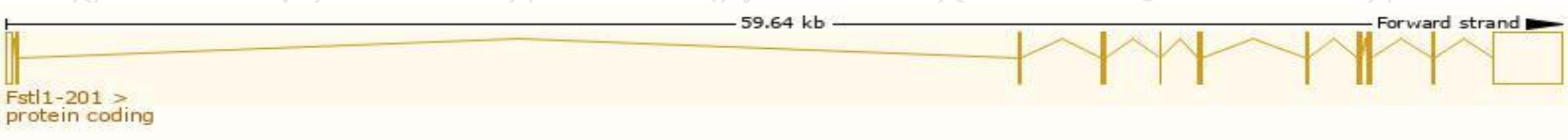
Official Symbol	Fstl1 provided by MGI
Official Full Name	follistatin-like 1 provided by MGI
Primary source	MGI:MGI:102793
See related	Ensembl:ENSMUSG00000022816
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI316791, AW107808, Fstl, TSC-36
Expression	Biased expression in limb E14.5 (RPKM 177.9), bladder adult (RPKM 102.9) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

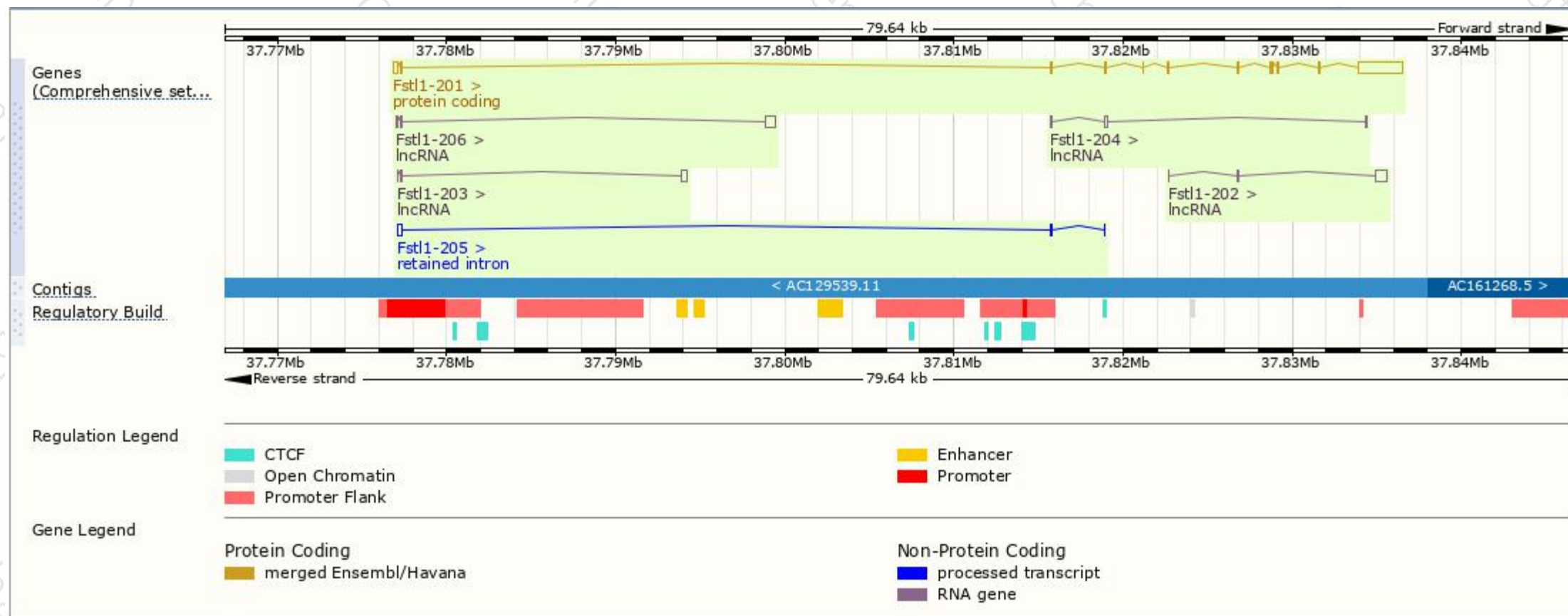
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fstl1-201	ENSMUST00000114763.2	3789	306aa	Protein coding	CCDS37339	Q62356	TSL:1 GENCODE basic APPRIS P1
Fstl1-205	ENSMUST00000135668.7	343	No protein	Retained intron	-	-	TSL:3
Fstl1-202	ENSMUST00000123077.1	884	No protein	lncRNA	-	-	TSL:5
Fstl1-206	ENSMUST00000152579.7	777	No protein	lncRNA	-	-	TSL:1
Fstl1-203	ENSMUST00000125279.1	486	No protein	lncRNA	-	-	TSL:2
Fstl1-204	ENSMUST00000127495.1	298	No protein	lncRNA	-	-	TSL:5

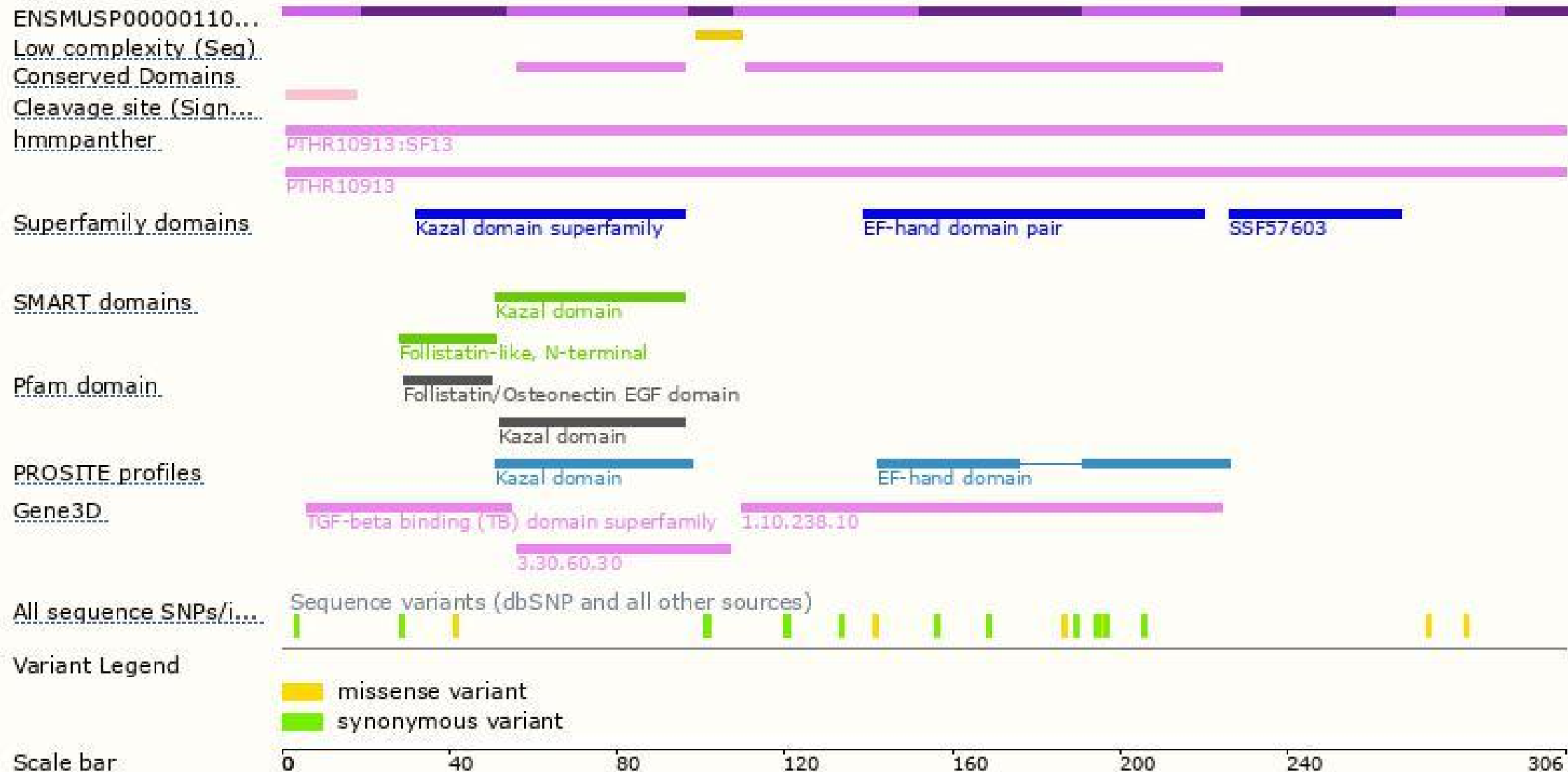
The strategy is based on the design of *Fstl1-201* transcript,The transcription is shown below



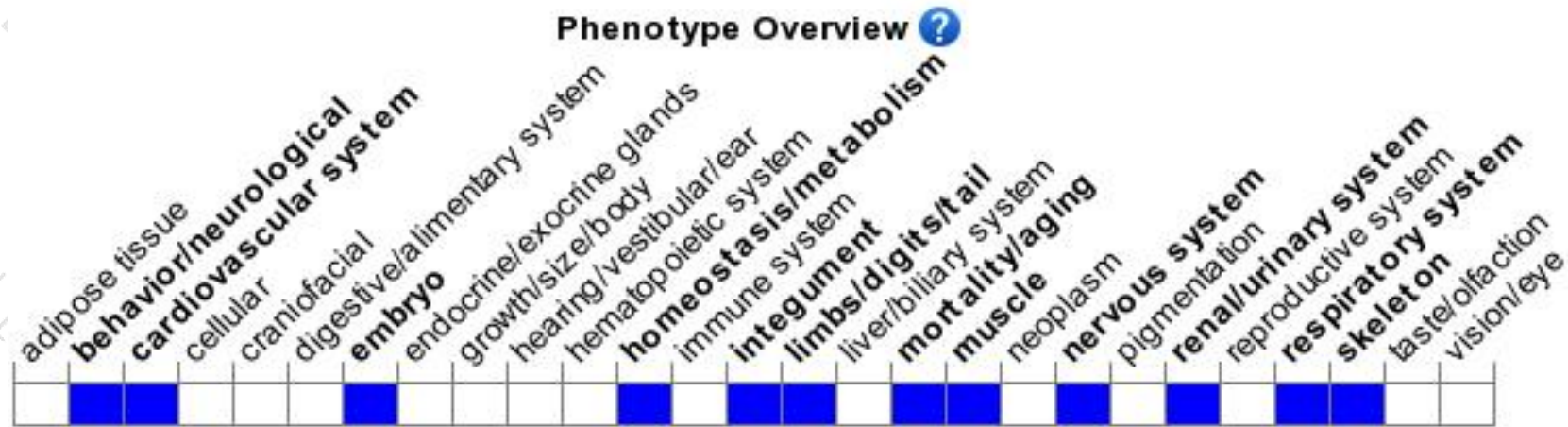
Genomic location distribution



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 neonatal lethality, soft and enlarged trachea, cyanosis, primary atelectasis, lung epithelial cell hyperplasia, over-expanded bronchiole, impaired pneumocyte differentiation and maturation, and decreased surfactant production.

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

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