

***Foxs1* Cas9-CKO Strategy**

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Design Date: 2019-7-31

Project Overview

Project Name

Foxs1

Project type

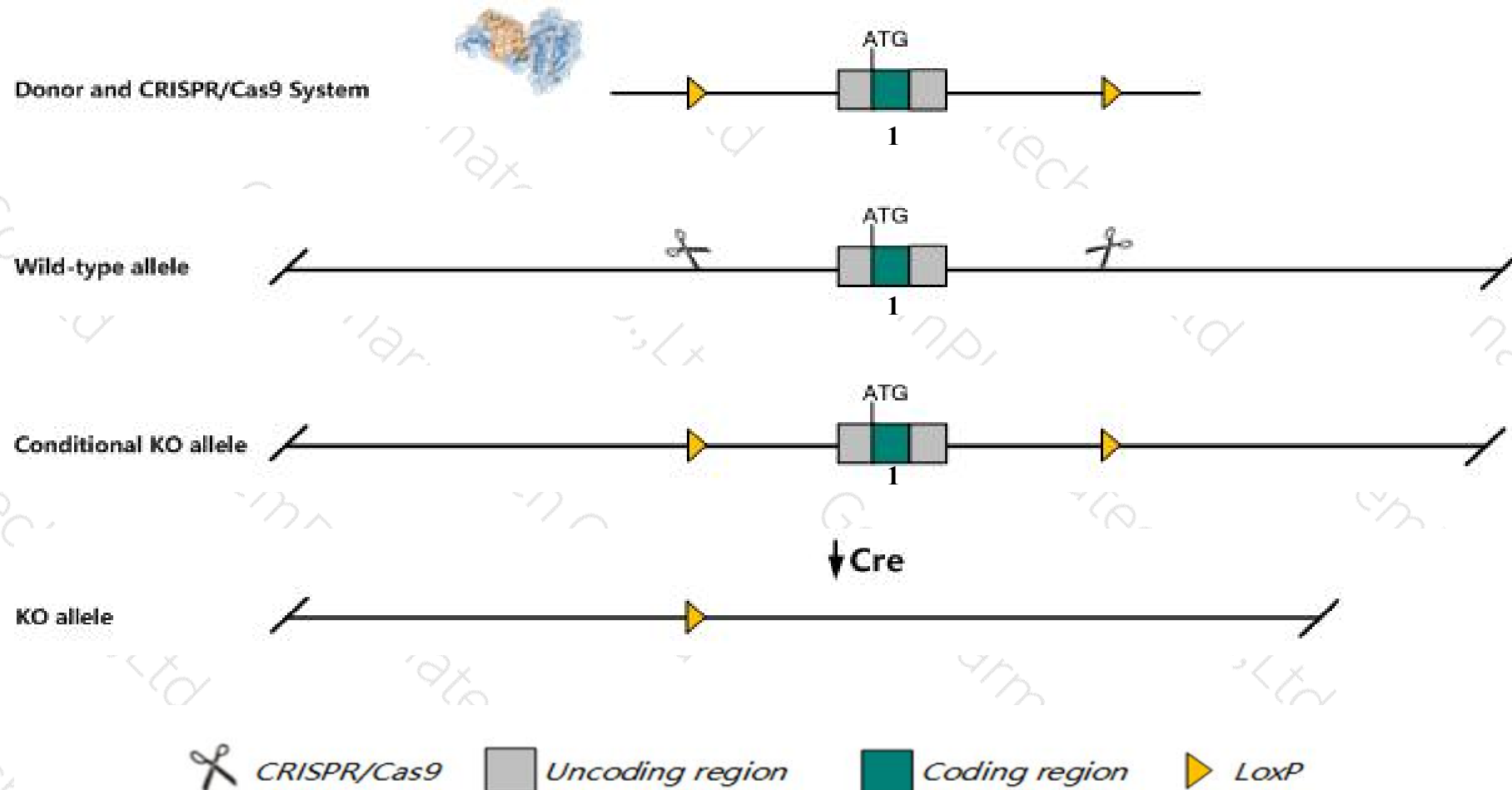
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxs1* gene. The schematic diagram is as follows:



- The *Foxs1* gene has 1 transcript. According to the structure of *Foxs1* gene, exon1 of *Foxs1-201* (ENSMUST00000099200.2) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Foxs1* 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, Homozygotes for one reporter allele display enhanced rotarod performance and increased male resistance to diet-induced obesity. Homozygotes for another reporter allele show impaired testicular vasculature, including blood accumulation in fetal testis and marked apoptosis of periendothelial cells.
- The *Foxs1* gene is located on the Chr2. 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)

Foxs1 forkhead box S1 [Mus musculus (house mouse)]

Gene ID: 14239, updated on 31-Jan-2019

Summary



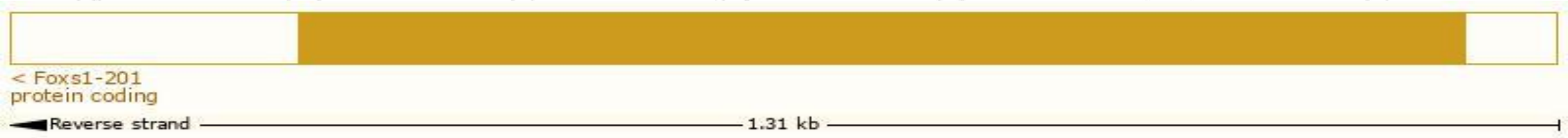
Official Symbol	Foxs1 provided by MGI
Official Full Name	forkhead box S1 provided by MGI
Primary source	MGI:MGI:95546
See related	Ensembl:ENSMUSG00000074676
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FREAC10, Fkh3, Fkh18
Orthologs	human all

Transcript information (Ensembl)

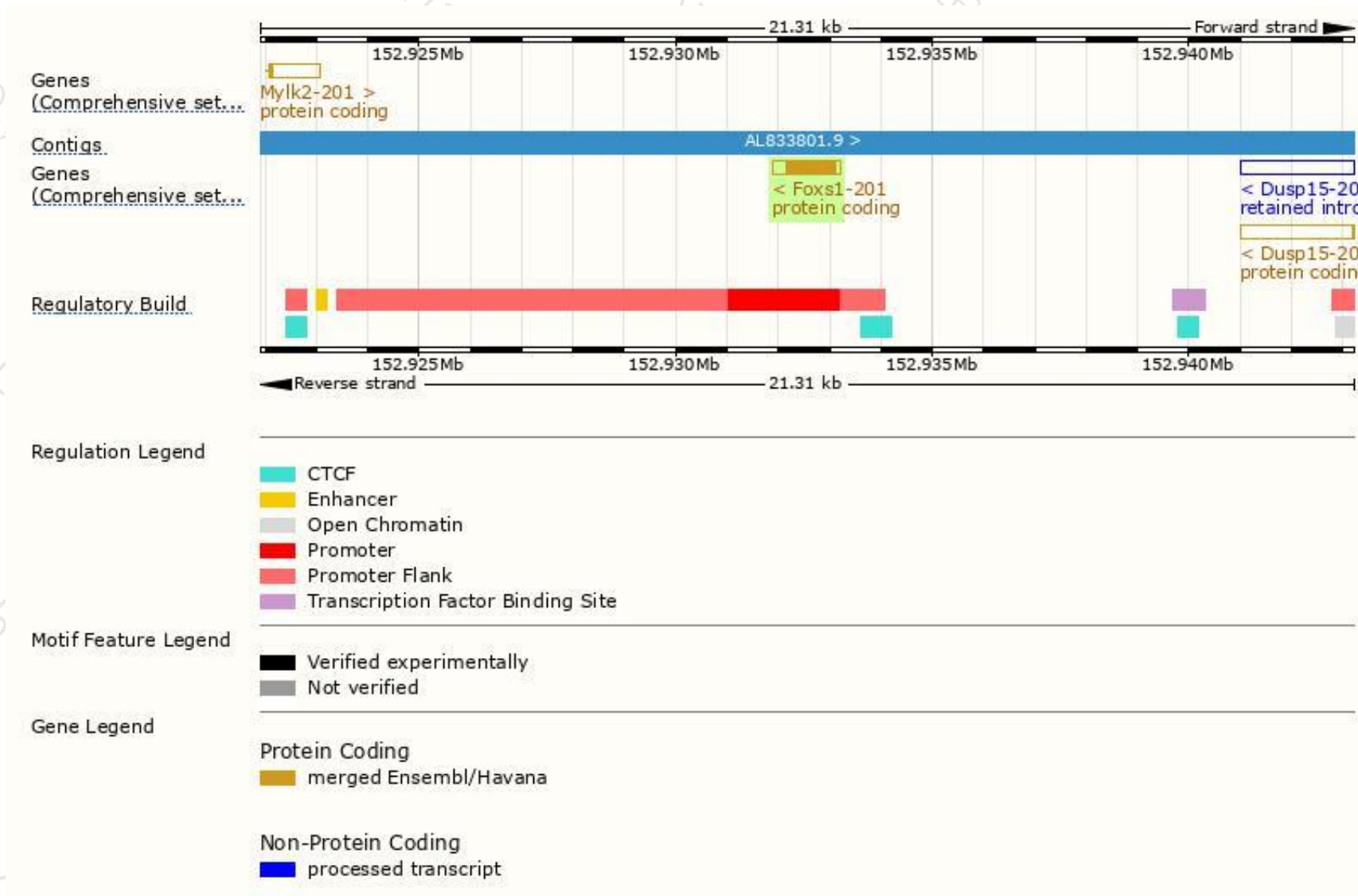
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxs1-201	ENSMUST00000099200.2	1311	329aa	Protein coding	CCDS16901	Q4VA05 Q61574	TSL:NA GENCODE basic APPRIS P1

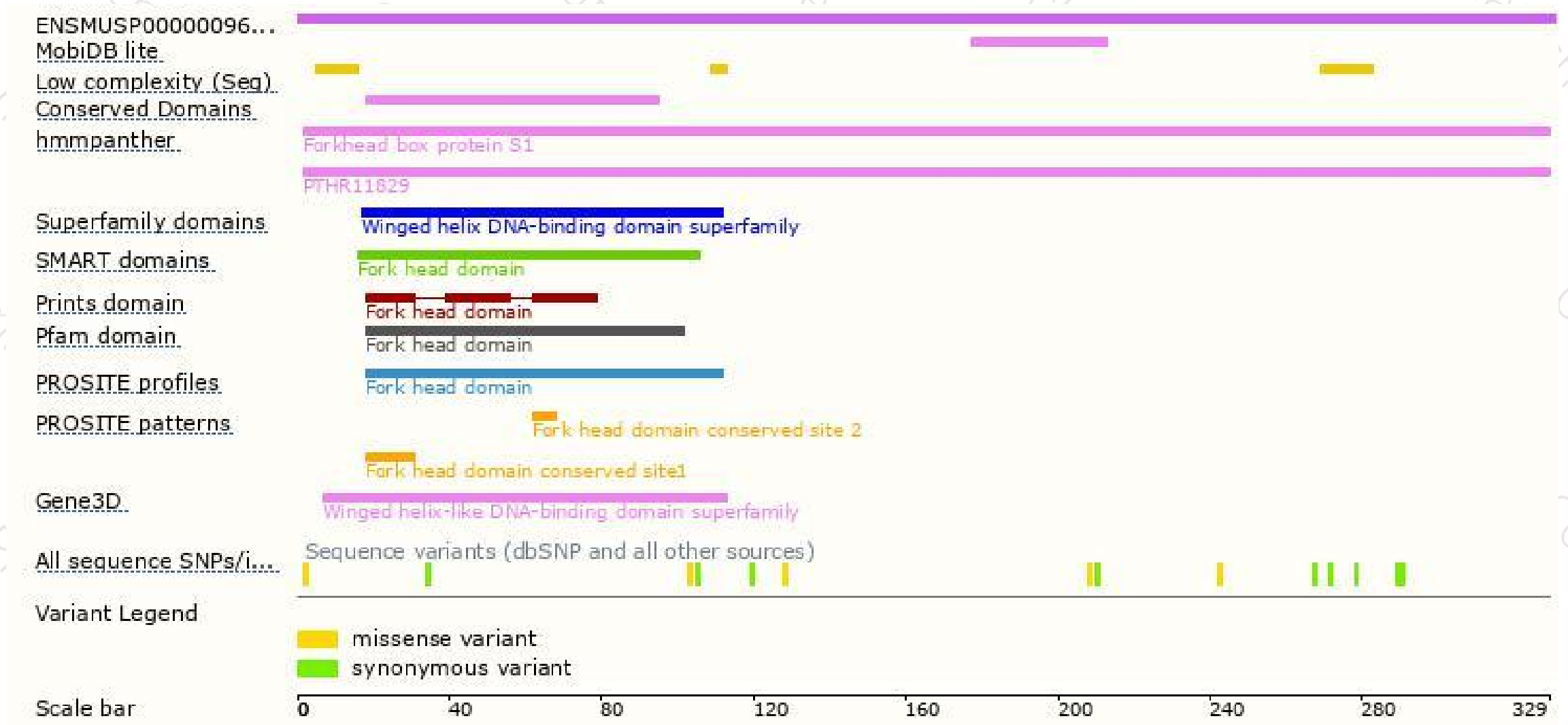
The strategy is based on the design of *Foxs1-201* transcript, The transcription is shown below



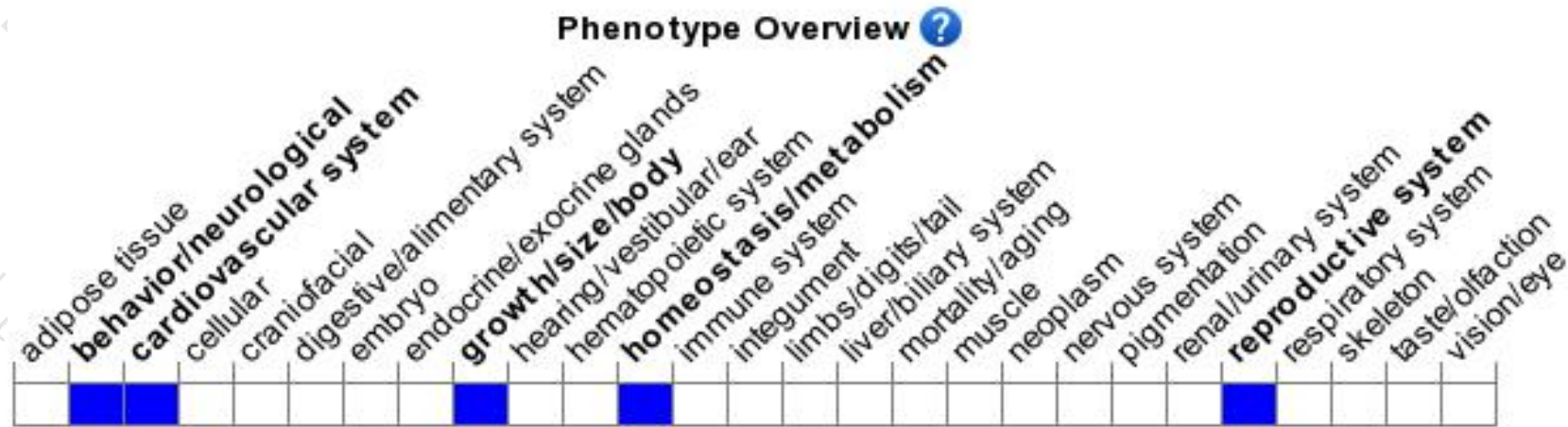
Genomic location distribution



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, Homozygotes for one reporter allele display enhanced rotarod performance and increased male resistance to diet-induced obesity. Homozygotes for another reporter allele show impaired testicular vasculature, including blood accumulation in fetal testis and marked apoptosis of periendothelial cells.

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

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