Dkc1 Cas9-CKO Strategy

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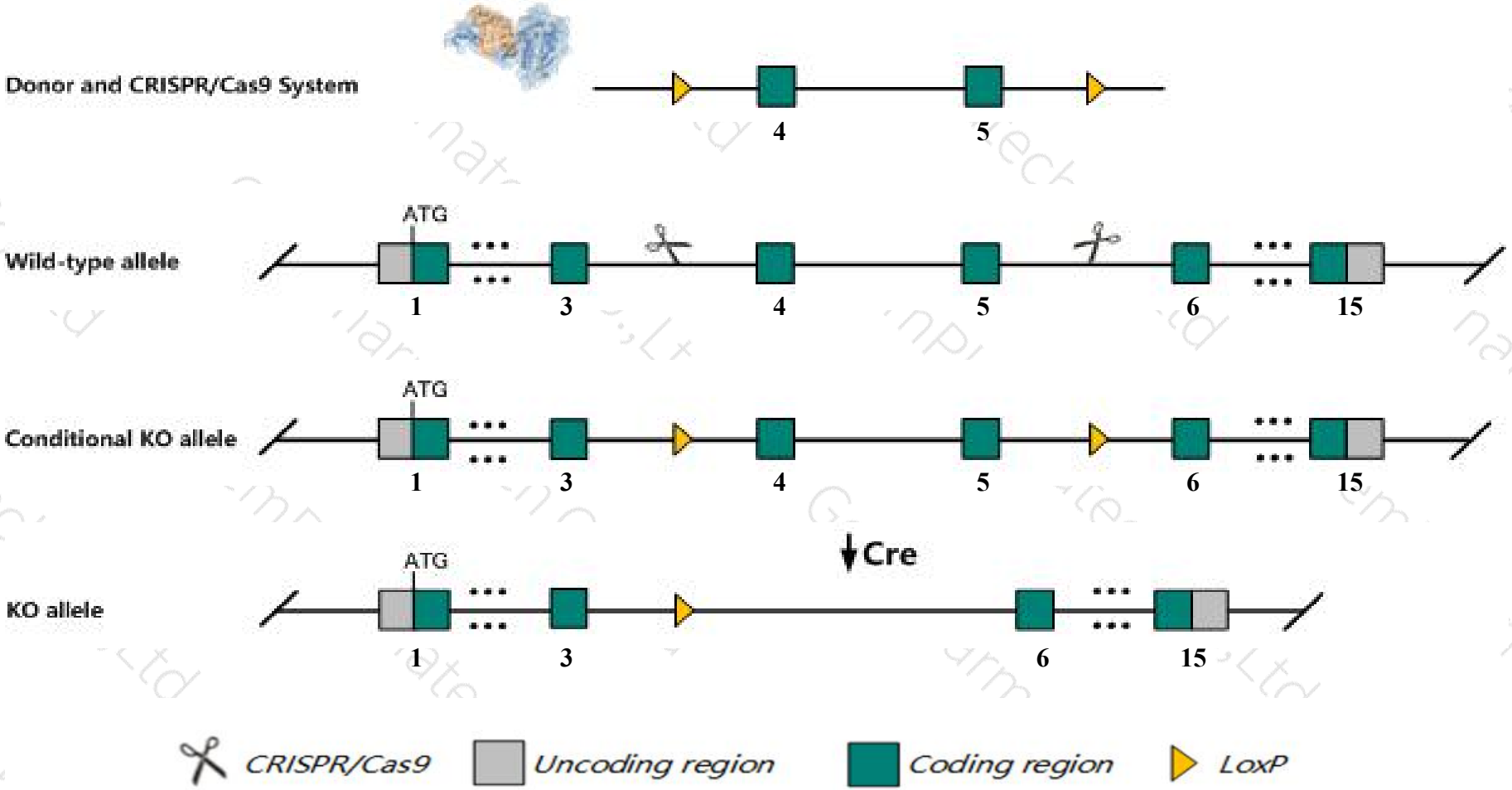
Project Overview

Project Name	***Dkc1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dkc1* gene. The schematic diagram is as follows:



Technical routes

- The *Dkc1* gene has 12 transcripts. According to the structure of *Dkc1* gene, exon4-exon5 of *Dkc1-201* (ENSMUST00000033776.14) transcript is recommended as the knockout region.The region contains 277bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Dkc1* 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.

Notice

- According to the existing MGI data,Early generation male mice hemizygous for a hypomorphic allele exhibit bone marrow failure, dyskeratosis, extramedullary hematopoieis, splenomegaly, lung and kidney abnormalities, increased tumor incidence, and altered ribosome function; decreased telomere length is noted only in later generations.

- The *Dkc1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Dkc1 dyskeratosis congenita 1, dyskerin [*Mus musculus* (house mouse)]

Gene ID: 245474, updated on 12-Aug-2019

Summary

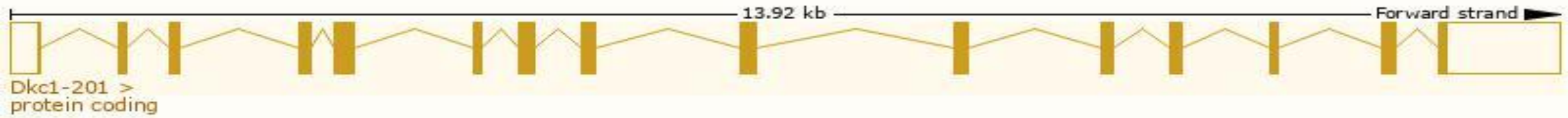
Official Symbol	Dkc1 provided by MGI
Official Full Name	dyskeratosis congenita 1, dyskerin provided by MGI
Primary source	MGI:MGI:1861727
See related	Ensembl:ENSMUSG00000031403
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC068171
Expression	Broad expression in liver E14 (RPKM 19.1), CNS E11.5 (RPKM 18.3) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

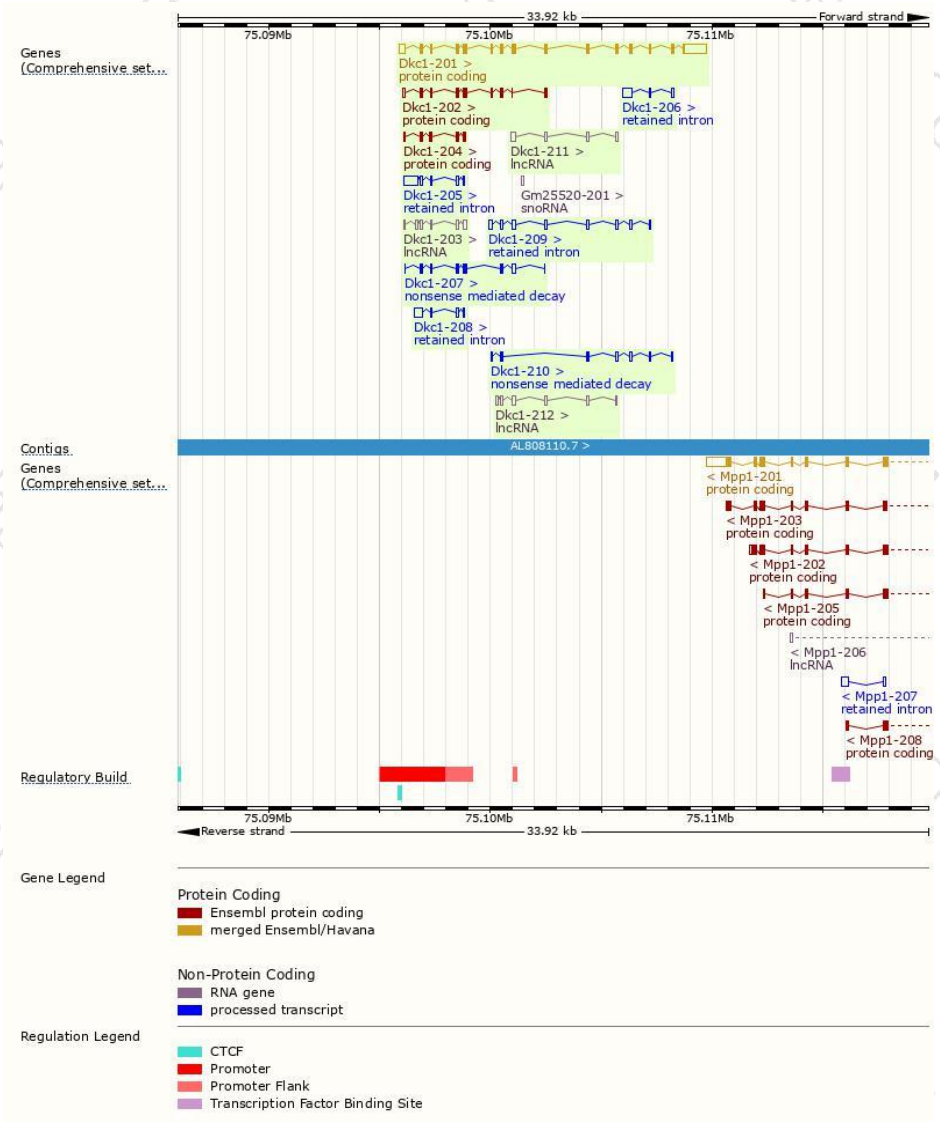
The gene has 12 transcripts,all transcripts are shown below:

Name ▲	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dkc1-201	ENSMUST00000033776.14	2804	509aa	Protein coding	CCDS41029	Q9ESX5	TSL:1 GENCODE basic APPRIS P1
Dkc1-202	ENSMUST00000131155.7	839	260aa	Protein coding	-	B7ZCL7	CDS 3' incomplete TSL:5
Dkc1-203	ENSMUST00000131867.7	541	No protein	lncRNA	-	-	TSL:3
Dkc1-204	ENSMUST00000132000.7	462	145aa	Protein coding	-	A2AN81	CDS 3' incomplete TSL:3
Dkc1-205	ENSMUST00000135389.7	898	No protein	Retained intron	-	-	TSL:3
Dkc1-206	ENSMUST00000137286.1	610	No protein	Retained intron	-	-	TSL:2
Dkc1-207	ENSMUST00000140609.7	754	184aa	Nonsense mediated decay	-	F6YUI5	CDS 5' incomplete TSL:5
Dkc1-208	ENSMUST00000145222.1	592	No protein	Retained intron	-	-	TSL:2
Dkc1-209	ENSMUST00000151327.7	963	No protein	Retained intron	-	-	TSL:5
Dkc1-210	ENSMUST00000153844.7	657	74aa	Nonsense mediated decay	-	F6S1S5	CDS 5' incomplete TSL:5
Dkc1-211	ENSMUST00000154422.1	551	No protein	lncRNA	-	-	TSL:2
Dkc1-212	ENSMUST00000154936.7	668	No protein	lncRNA	-	-	TSL:3

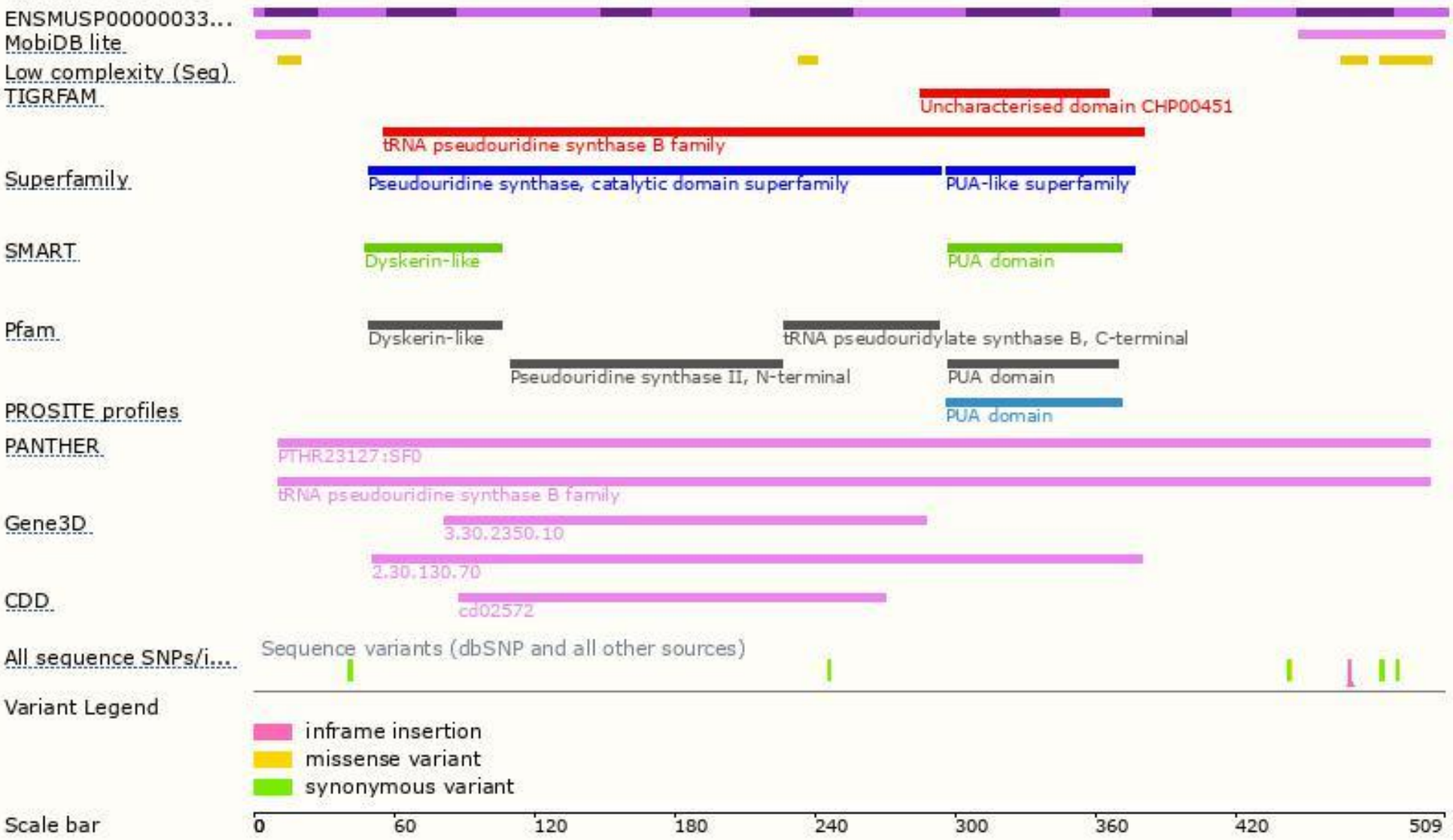
The strategy is based on the design of *Dkc1-201* transcript,The transcription is shown below



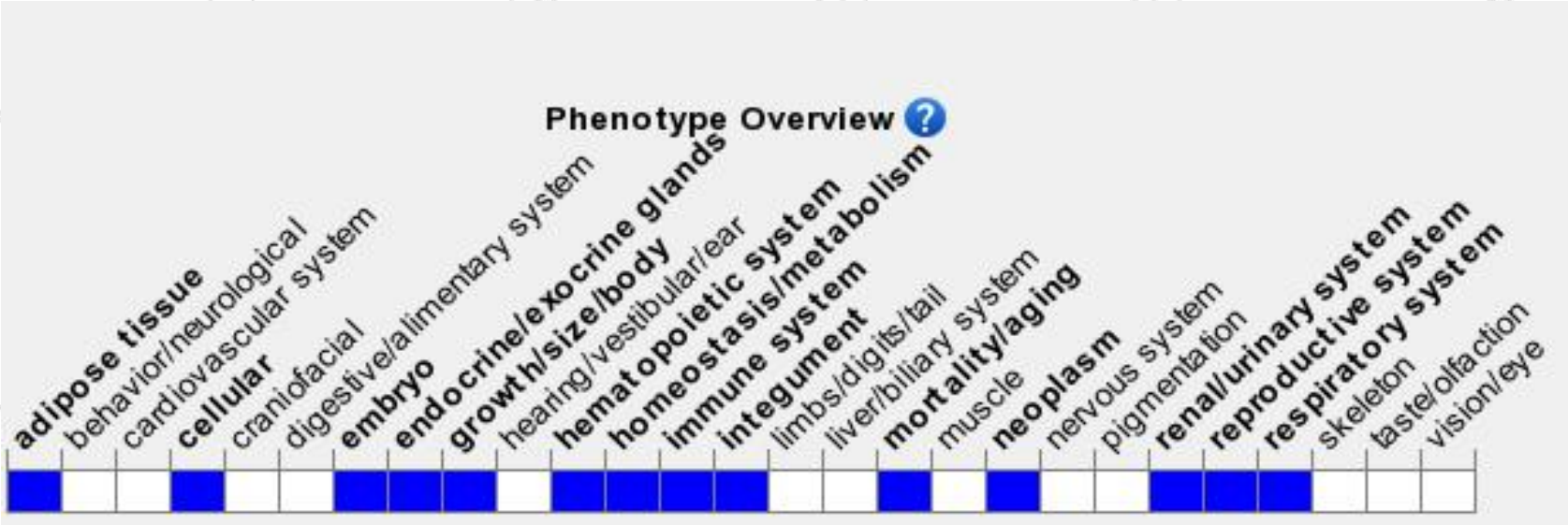
Genomic location distribution



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/).

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

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