Slc23a2 Cas9-CKO Strategy

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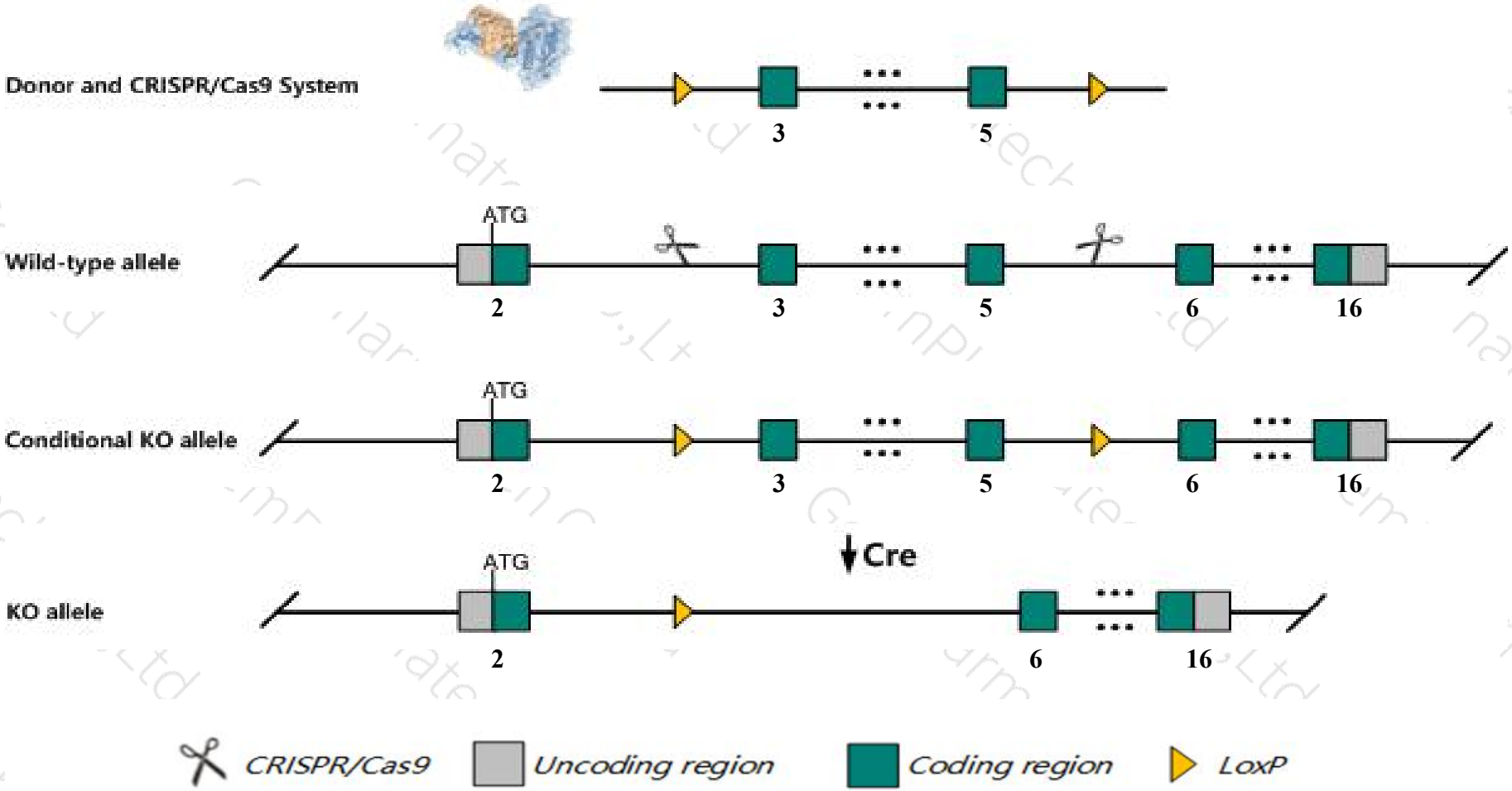
Project Overview

Project Name	***Slc23a2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc23a2* gene. The schematic diagram is as follows:



Technical routes

- The *Slc23a2* gene has 7 transcripts. According to the structure of *Slc23a2* gene, exon3-exon5 of *Slc23a2-201* (ENSMUST00000028815.14) transcript is recommended as the knockout region.The region contains 374bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc23a2* 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,Mice homozygous for disruptions in this gene die within minutes of birth from respiratory distress.

➢The knockout region is near to the N-terminal of *Gm14052* gene,this strategy may influence the regulatory function of the N-terminal of *Gm14052* gene.

➢Transcript *Slc23a2*-205&206&207 may not be affected.

➢ The *Slc23a2* 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）

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Slc23a2 solute carrier family 23 (nucleobase transporters), member 2 [*Mus musculus* (house mouse)]

Gene ID: 54338, updated on 10-Oct-2019

Summary

Official Symbol	Slc23a2 provided by MGI
Official Full Name	solute carrier family 23 (nucleobase transporters), member 2 provided by MGI
Primary source	MGI:MGI:1859682
See related	Ensembl:ENSMUSG00000027340
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	NBTL1; SVCT2; YSPL2; YSPL3; Slc23a1; AI844736; mKIAA0238
Expression	Ubiquitous expression in lung adult (RPKM 24.3), cortex adult (RPKM 20.2) and 26 other tissues See more
Orthologs	human all

Genomic context

Location: 2; 2 F2

See Slc23a2 in Genome Data Viewer

Exon count: 21

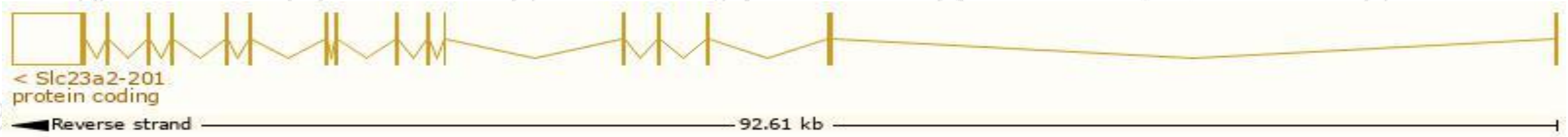
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (132052496..132145320, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (131878232..131970844, complement)

Transcript information（Ensembl）

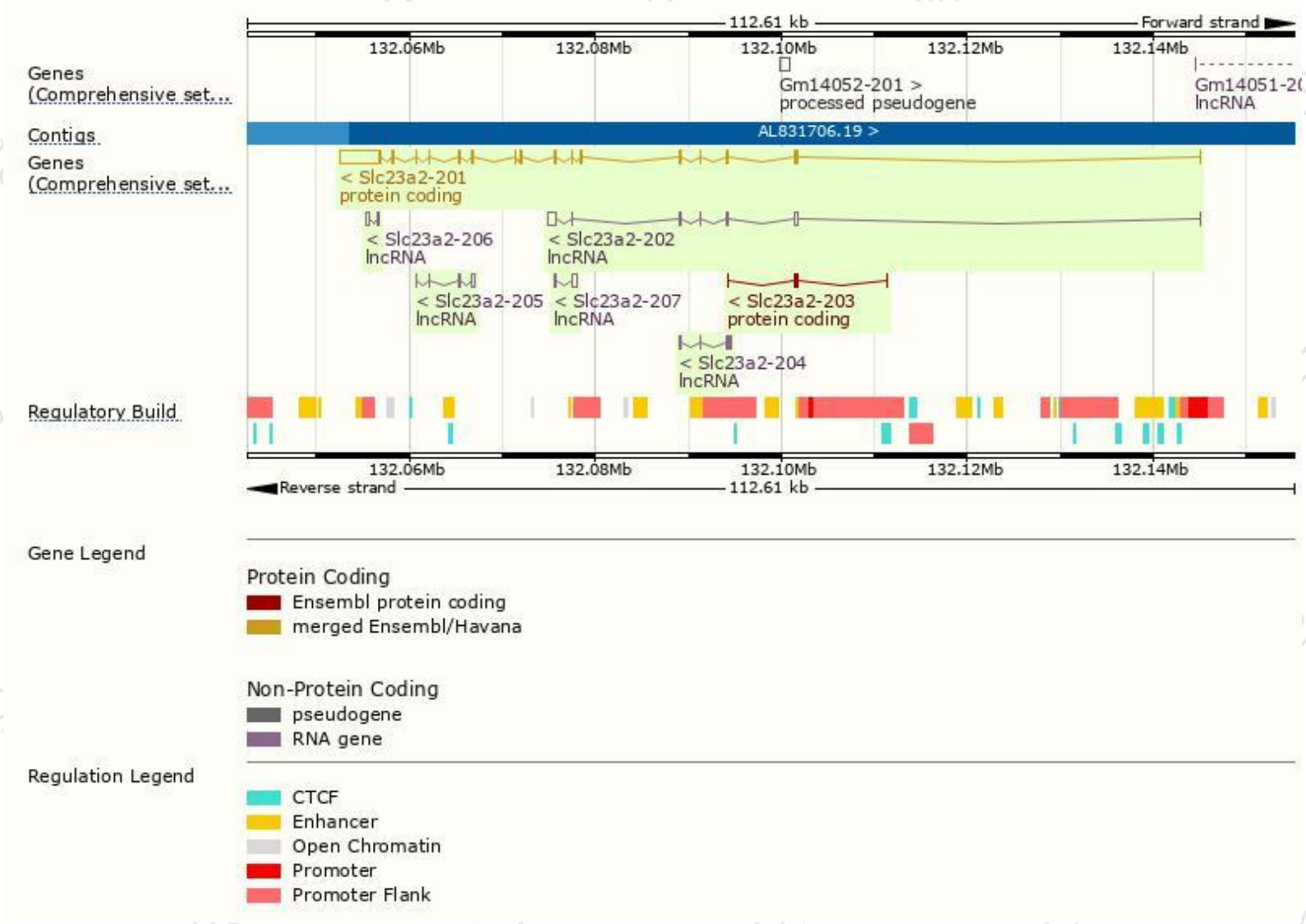
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc23a2-201	ENSMUST00000028815.14	6364	648aa	Protein coding	CCDS16769	Q9EPR4	TSL:1 GENCODE basic APPRIS P1
Slc23a2-203	ENSMUST00000128899.1	379	41aa	Protein coding	-	A2ANL1	CDS 3' incomplete TSL:5
Slc23a2-202	ENSMUST00000127724.7	1638	No protein	lncRNA	-	-	TSL:1
Slc23a2-207	ENSMUST00000154009.1	655	No protein	lncRNA	-	-	TSL:2
Slc23a2-205	ENSMUST00000137910.1	652	No protein	lncRNA	-	-	TSL:2
Slc23a2-204	ENSMUST00000133407.1	486	No protein	lncRNA	-	-	TSL:2
Slc23a2-206	ENSMUST00000148749.1	400	No protein	lncRNA	-	-	TSL:3

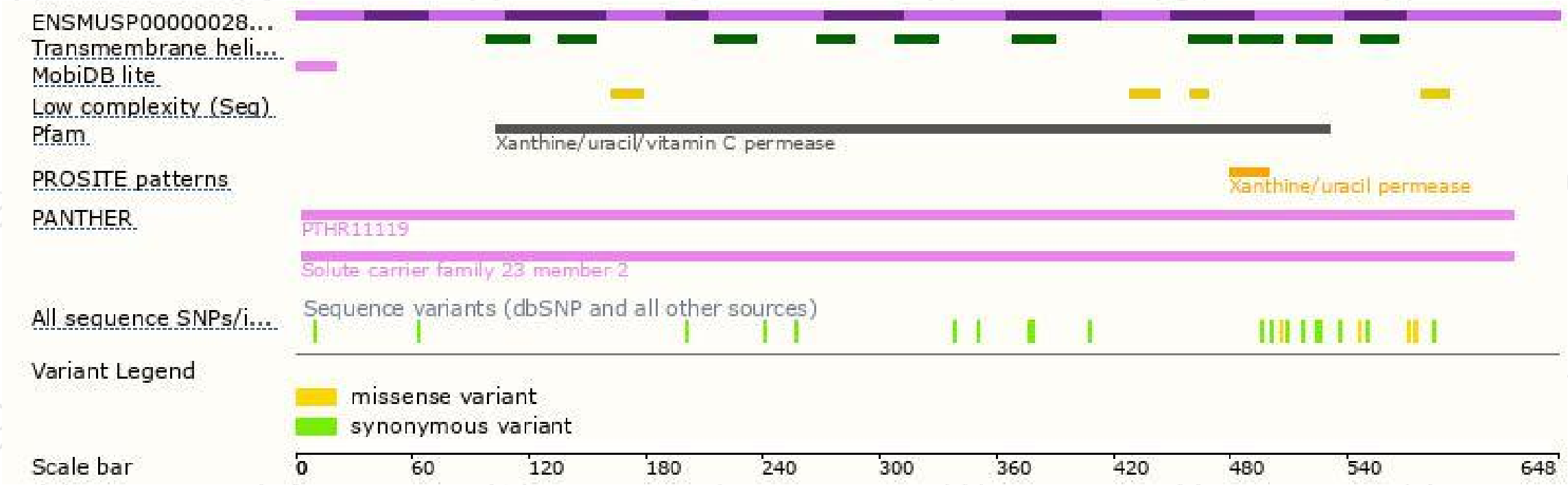
The strategy is based on the design of *Slc23a2-201* transcript,The transcription is shown below



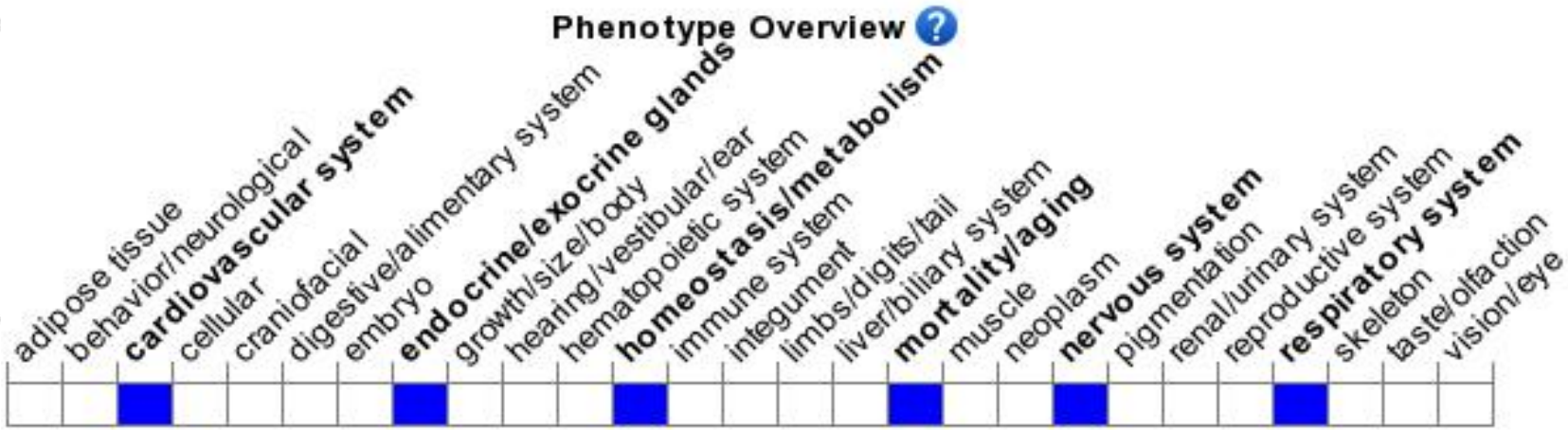
Genomic location distribution



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 disruptions in this gene die within minutes of birth from respiratory distress.

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

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