

Glis3 Cas9-CKO Strategy

Designer:

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Project Overview

Project Name

Glis3

Project type

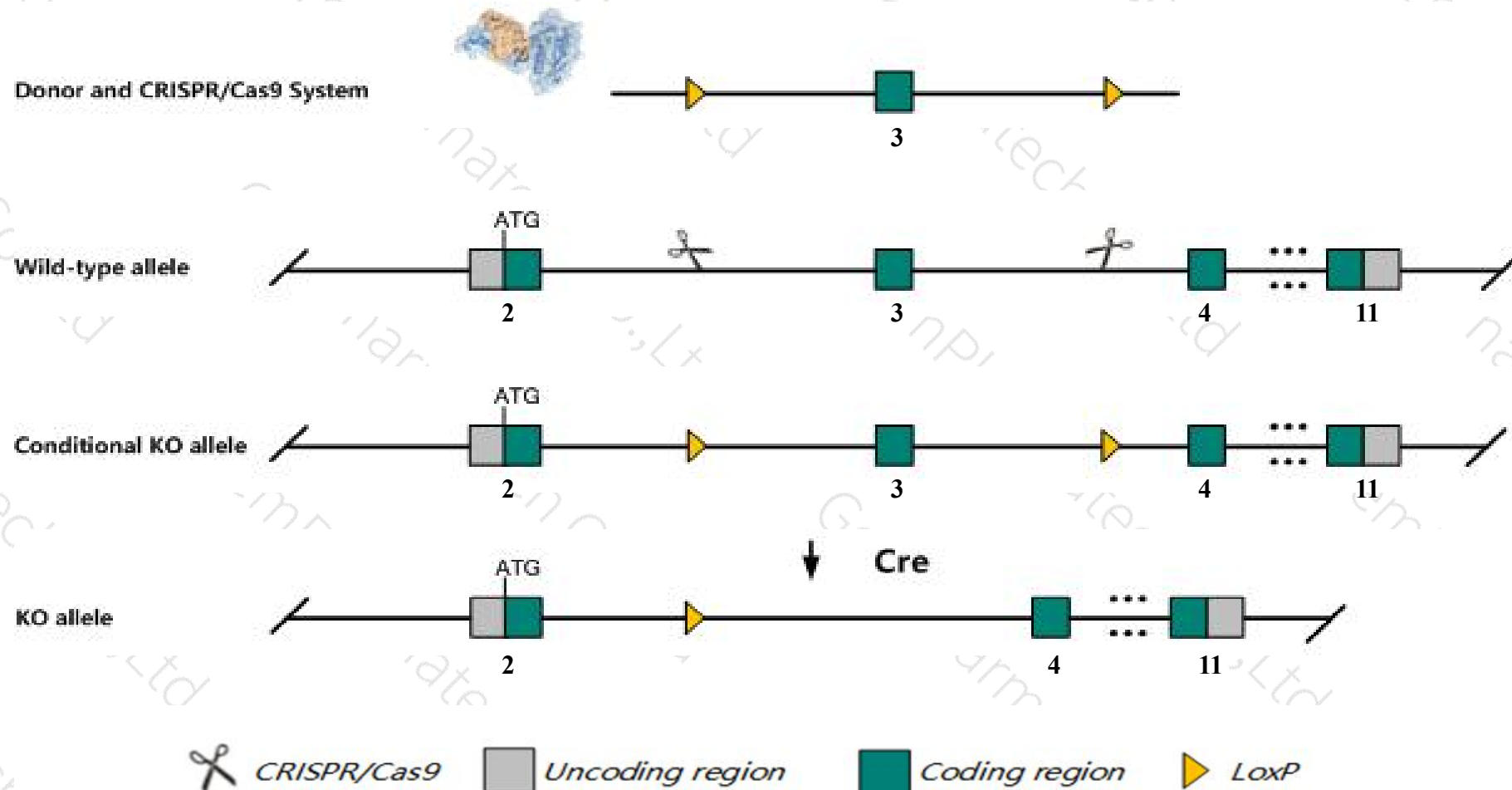
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Glis3* gene. The schematic diagram is as follows:



- The *Glis3* gene has 10 transcripts. According to the structure of *Glis3* gene, exon3 of *Glis3-209* (ENSMUST00000162022.7) transcript is recommended as the knockout region. The region contains 208bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Glis3* 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 knock-out alleles exhibit postnatal lethality associated with neonatal diabetes and polycystic kidney disease.
- The *Glis3* 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)

Glis3 GLIS family zinc finger 3 [Mus musculus (house mouse)]

Gene ID: 226075, updated on 2-Mar-2019

Summary



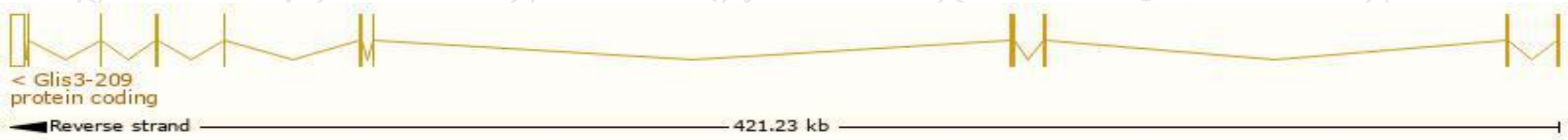
Official Symbol	Glis3 provided by MGI
Official Full Name	GLIS family zinc finger 3 provided by MGI
Primary source	MGI:MGI:2444289
See related	Ensembl:ENSMUSG00000052942
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4833409N03Rik, E330013K21Rik
Summary	This gene is a member of the GLI-similar zinc finger protein family and encodes a nuclear protein which contains multiple C2H2-type zinc finger domains. This protein functions as both a repressor and activator of transcription and is specifically involved in the transcriptional regulation of insulin. It is thought to enhance GLI-RE-dependent transcription by binding to the GLI-RE consensus sequence (GACCACCCAC). Mutations in a similar gene in human have been associated with neonatal diabetes and congenital hypothyroidism (NDH). Alternatively spliced transcript variants have been identified. [provided by RefSeq, Mar 2015]
Expression	Broad expression in kidney adult (RPKM 6.0), ovary adult (RPKM 1.9) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

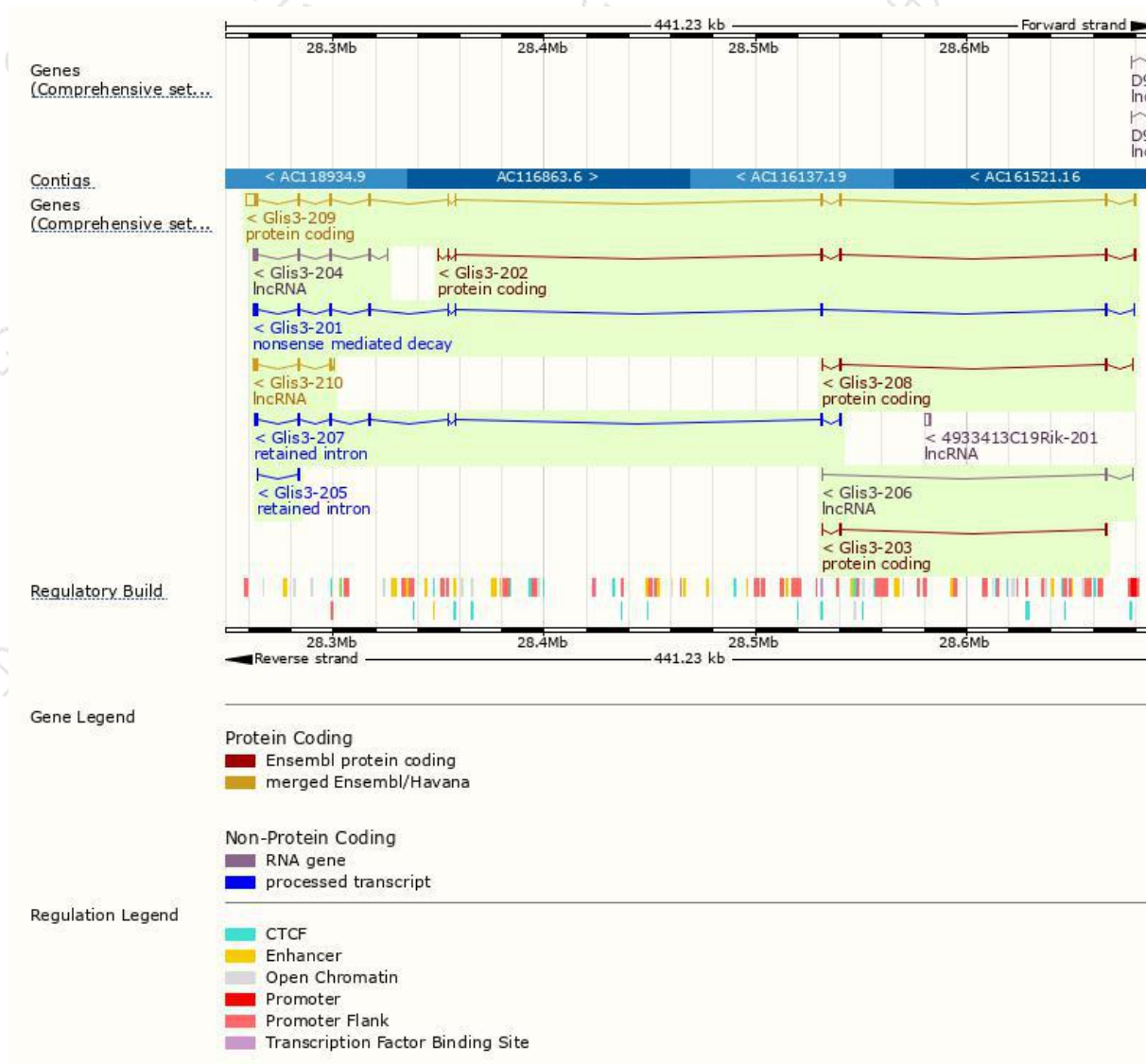
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Glis3-209	ENSMUST00000162022.7	7514	935aa	Protein coding	CCDS37947	Q0GE24	TSL:1 GENCODE basic APPRIS P2
Glis3-202	ENSMUST00000112612.8	3016	671aa	Protein coding	-	Q6XP49	TSL:1 GENCODE basic APPRIS ALT2
Glis3-203	ENSMUST00000159178.1	1281	245aa	Protein coding	-	E0CX93	CDS 3' incomplete TSL:5
Glis3-208	ENSMUST00000161328.7	948	245aa	Protein coding	-	E0CX93	CDS 3' incomplete TSL:5
Glis3-201	ENSMUST00000065113.13	3382	142aa	Nonsense mediated decay	-	E0CYJ3	TSL:1
Glis3-207	ENSMUST00000161026.1	2438	No protein	Retained intron	-	-	TSL:1
Glis3-205	ENSMUST00000159639.1	349	No protein	Retained intron	-	-	TSL:3
Glis3-204	ENSMUST00000159520.7	1569	No protein	lncRNA	-	-	TSL:1
Glis3-210	ENSMUST00000162873.7	1323	No protein	lncRNA	-	-	TSL:1
Glis3-206	ENSMUST00000160376.7	740	No protein	lncRNA	-	-	TSL:5

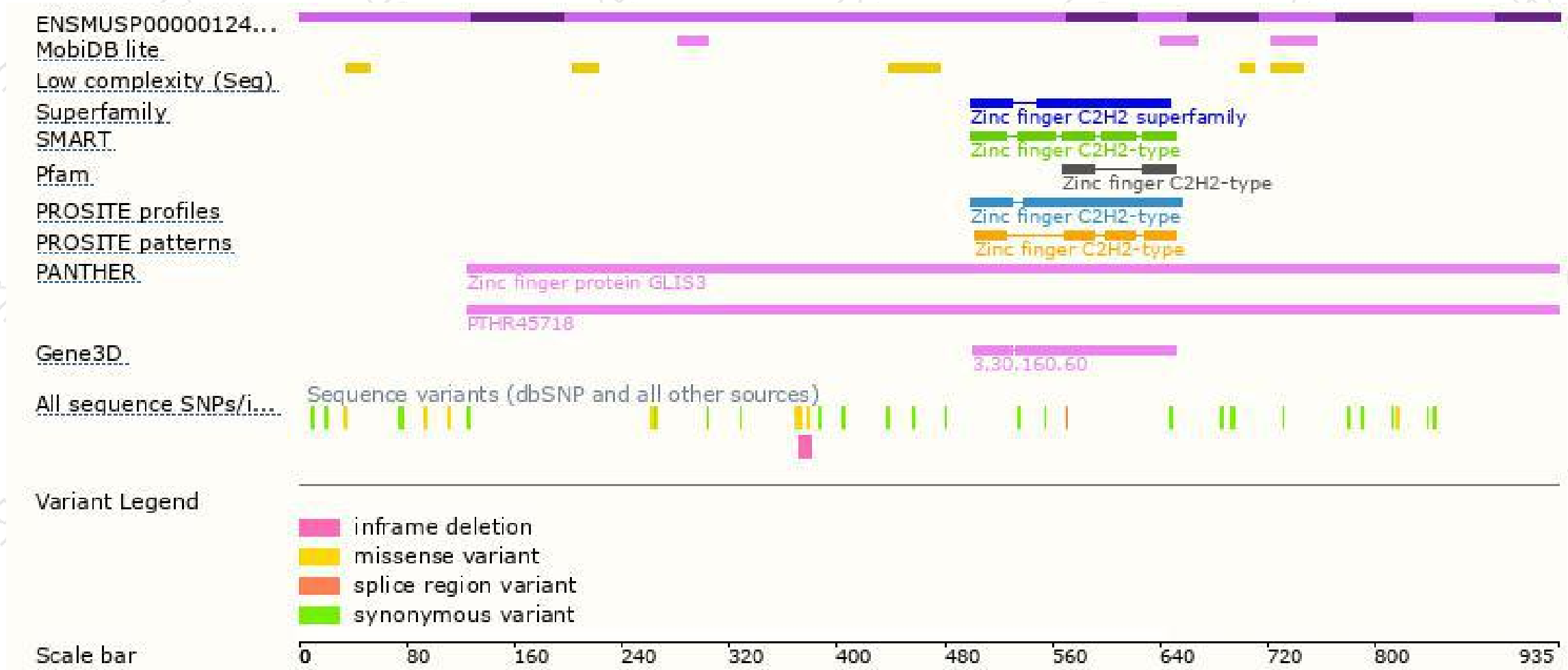
The strategy is based on the design of *Glis3-209* transcript,The transcription is shown below



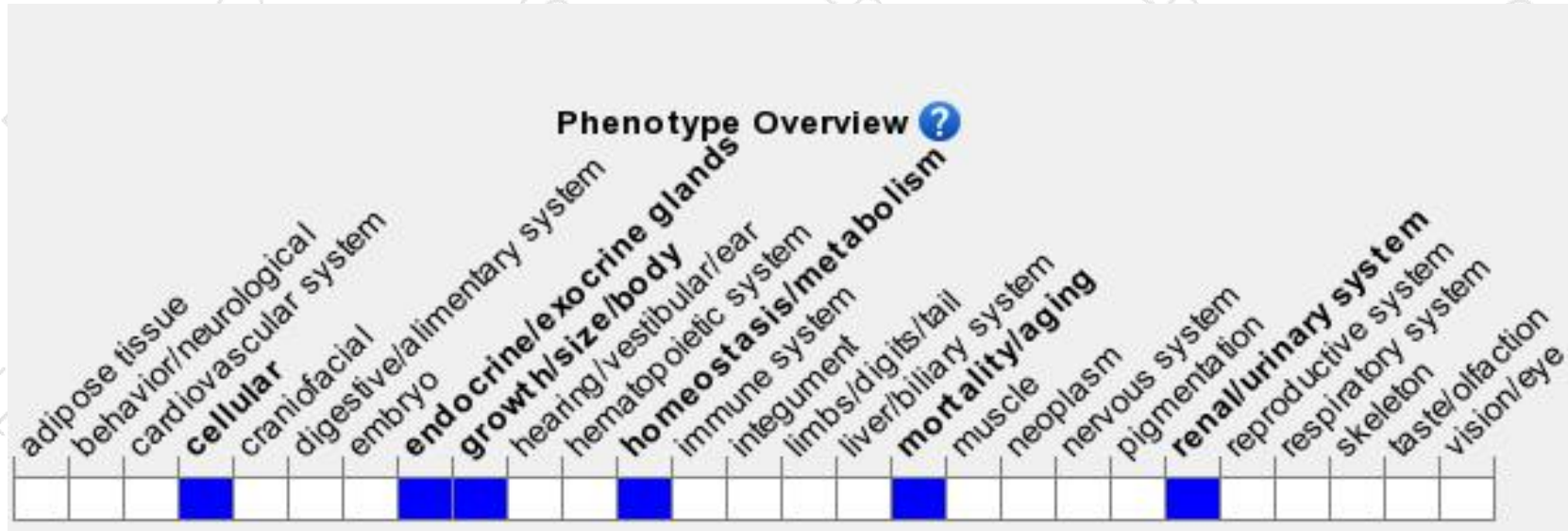
Genomic location distribution



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 knock-out alleles exhibit postnatal lethality associated with neonatal diabetes and polycystic kidney disease.

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

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