Slc5a2 Cas9-CKO Strategy

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Reviewer: Huimin Su
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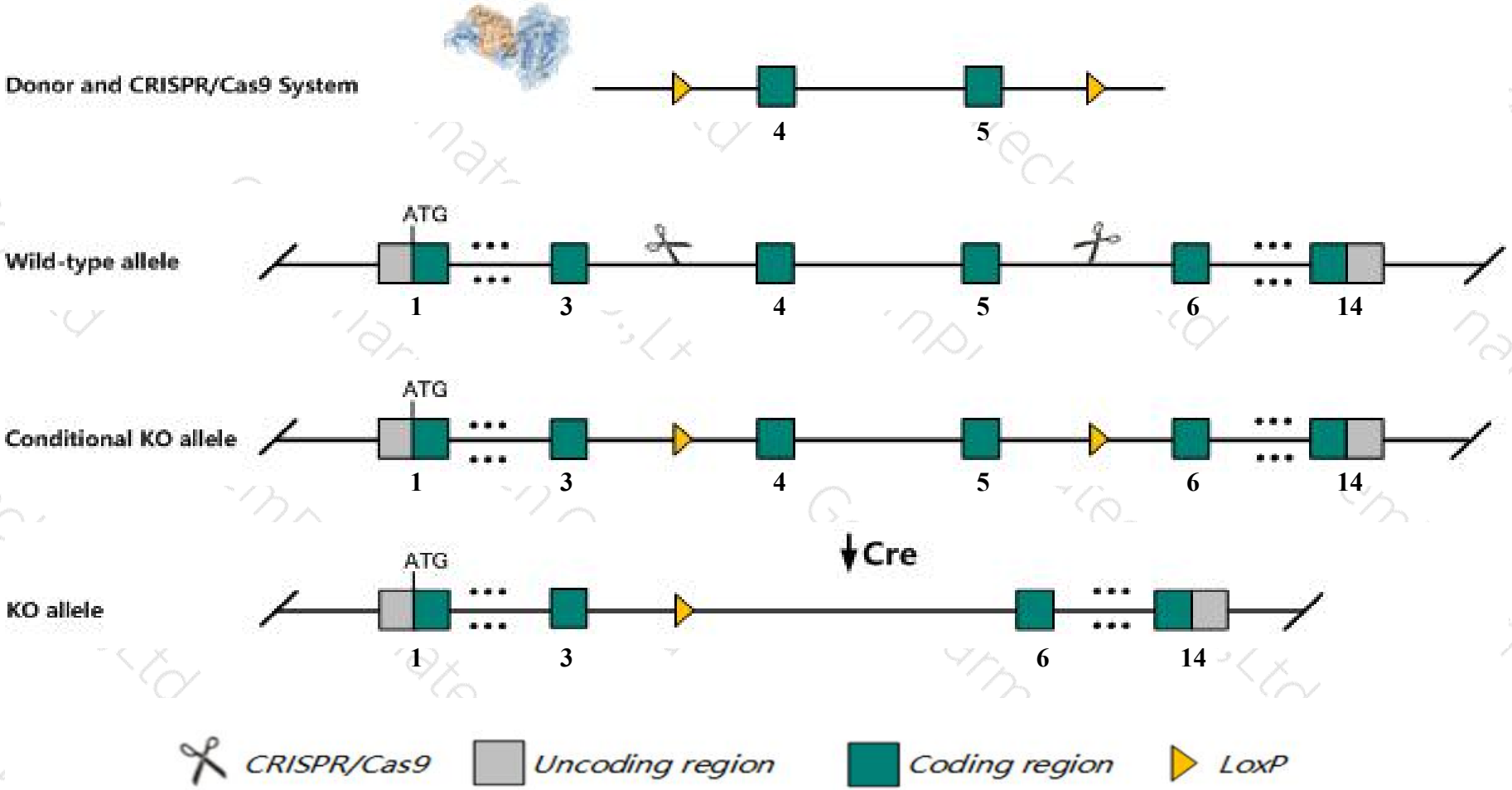
Project Overview

Project Name	***Slc5a2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc5a2* gene. The schematic diagram is as follows:



Technical routes

- The *Slc5a2* gene has 12 transcripts. According to the structure of *Slc5a2* gene, exon4-exon5 of *Slc5a2-202* (ENSMUST00000118169.7) transcript is recommended as the knockout region.The region contains 271bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc5a2* 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 a null allele exhibit increased urine glucose, increased eating and drinking behaviors, increased circulating renin activity, decreased urine osmolality, decreased serum aldosterone levels, polyuria, and decreased glucose renal reabsorption.

➢ The *Slc5a2* gene is located on the Chr7. 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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Slc5a2 solute carrier family 5 (sodium/glucose cotransporter), member 2 [Mus musculus (house mouse)]

Gene ID: 246787, updated on 31-Jan-2019

Summary

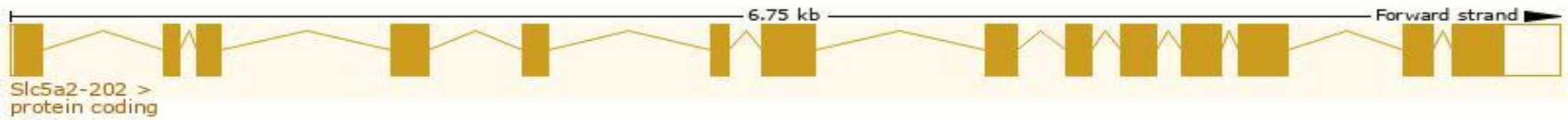
Official Symbol	Slc5a2 provided by MGI
Official Full Name	solute carrier family 5 (sodium/glucose cotransporter), member 2 provided byMGI
Primary source	MGI:MGI:2181411
See related	Ensembl:ENSMUSG00000030781
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Sglt2
Expression	Biased expression in kidney adult (RPKM 372.3) and adrenal adult (RPKM 11.1)See more
Orthologs	human all

Transcript information（Ensembl）

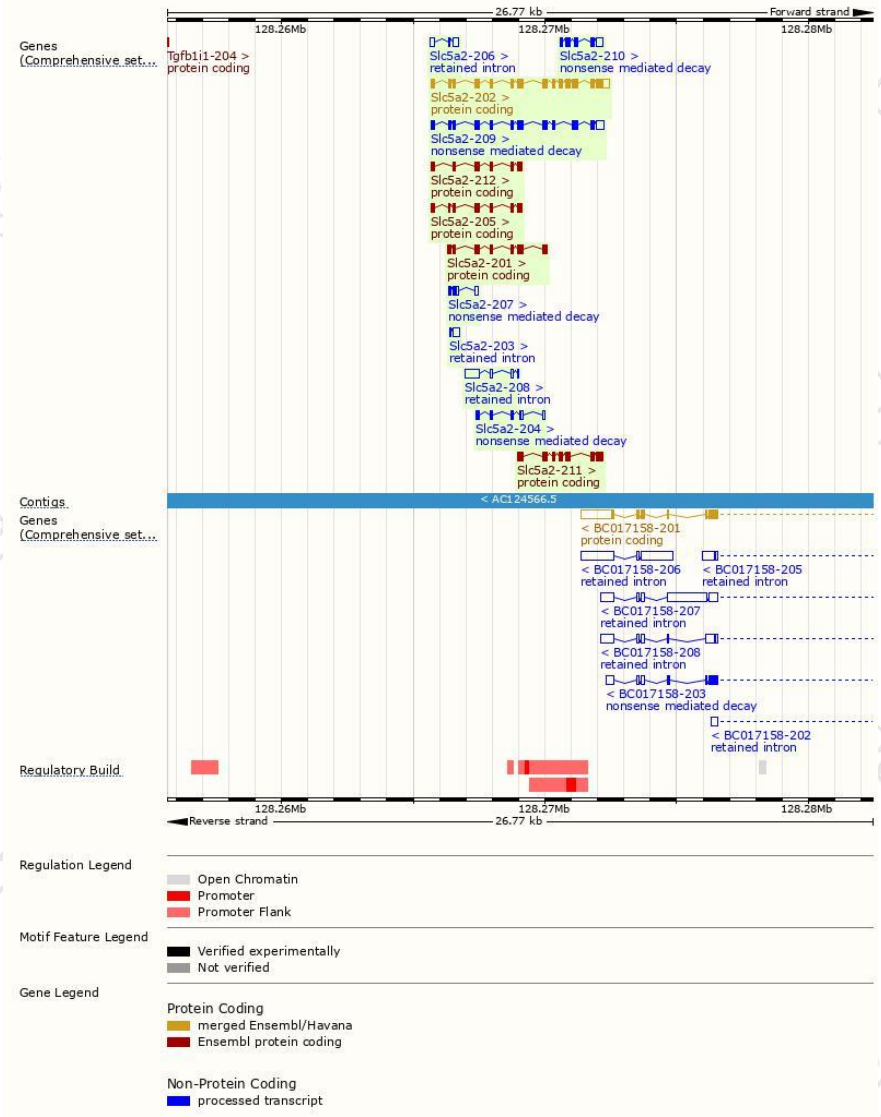
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc5a2-202	ENSMUST00000118169.7	2277	670aa	Protein coding	CCDS21894	Q923I7	TSL:1 GENCODE basic APPRIS P1
Slc5a2-211	ENSMUST00000206716.1	1148	382aa	Protein coding	-	A0A0U1RNI5	CDS 5' incomplete TSL:5
Slc5a2-201	ENSMUST00000033045.10	940	297aa	Protein coding	-	A0A0U1RP15	CDS 3' incomplete TSL:2
Slc5a2-205	ENSMUST00000142841.7	830	276aa	Protein coding	-	D3Z0A1	CDS 3' incomplete TSL:3
Slc5a2-212	ENSMUST00000206909.1	778	254aa	Protein coding	-	A0A0U1RNX5	CDS 3' incomplete TSL:5
Slc5a2-209	ENSMUST00000205720.1	1745	466aa	Nonsense mediated decay	-	A0A0U1RNI8	TSL:5
Slc5a2-210	ENSMUST00000206703.1	756	154aa	Nonsense mediated decay	-	A0A0U1RNL6	CDS 5' incomplete TSL:5
Slc5a2-204	ENSMUST00000137038.2	510	115aa	Nonsense mediated decay	-	F6TFB9	CDS 5' incomplete TSL:3
Slc5a2-207	ENSMUST00000153418.1	438	64aa	Nonsense mediated decay	-	A0A0U1RNT9	TSL:3
Slc5a2-208	ENSMUST00000171335.1	771	No protein	Retained intron	-	-	TSL:5
Slc5a2-206	ENSMUST00000146735.1	445	No protein	Retained intron	-	-	TSL:3
Slc5a2-203	ENSMUST00000136345.1	329	No protein	Retained intron	-	-	TSL:3

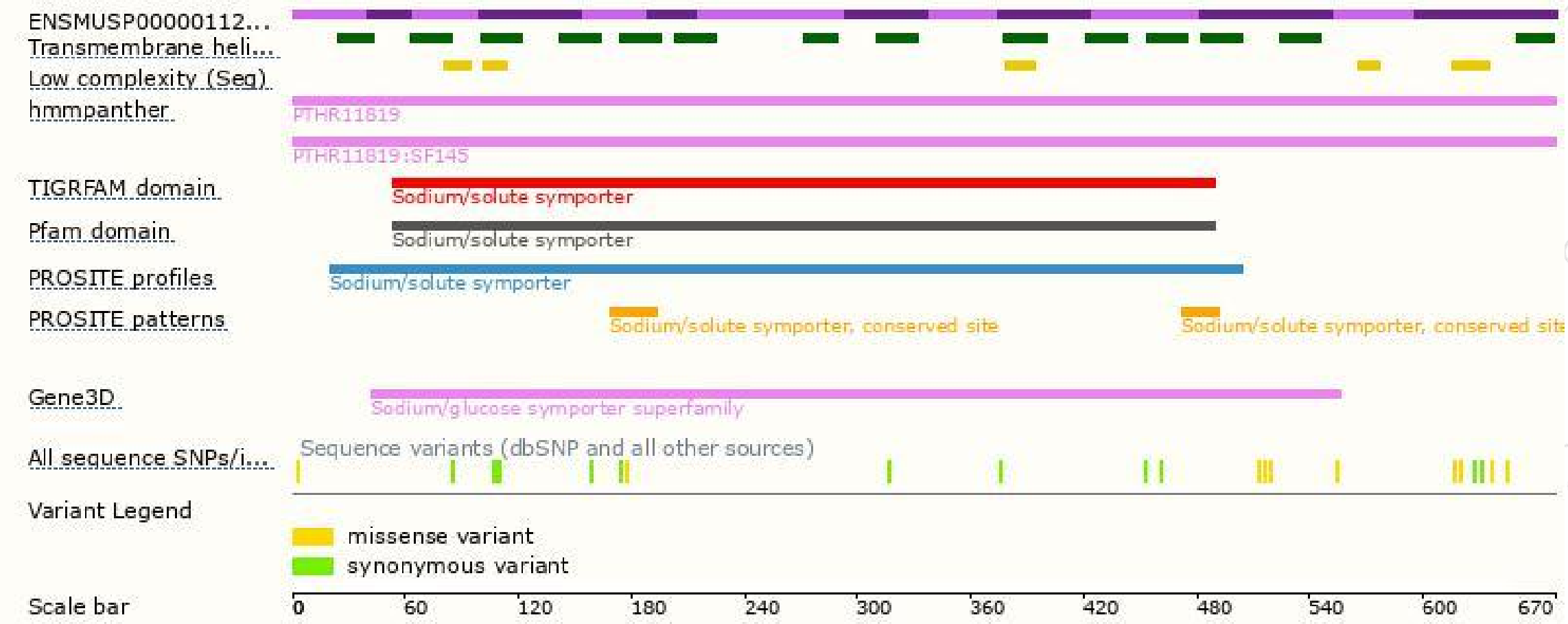
The strategy is based on the design of *Slc5a2-202* transcript,The transcription is shown below



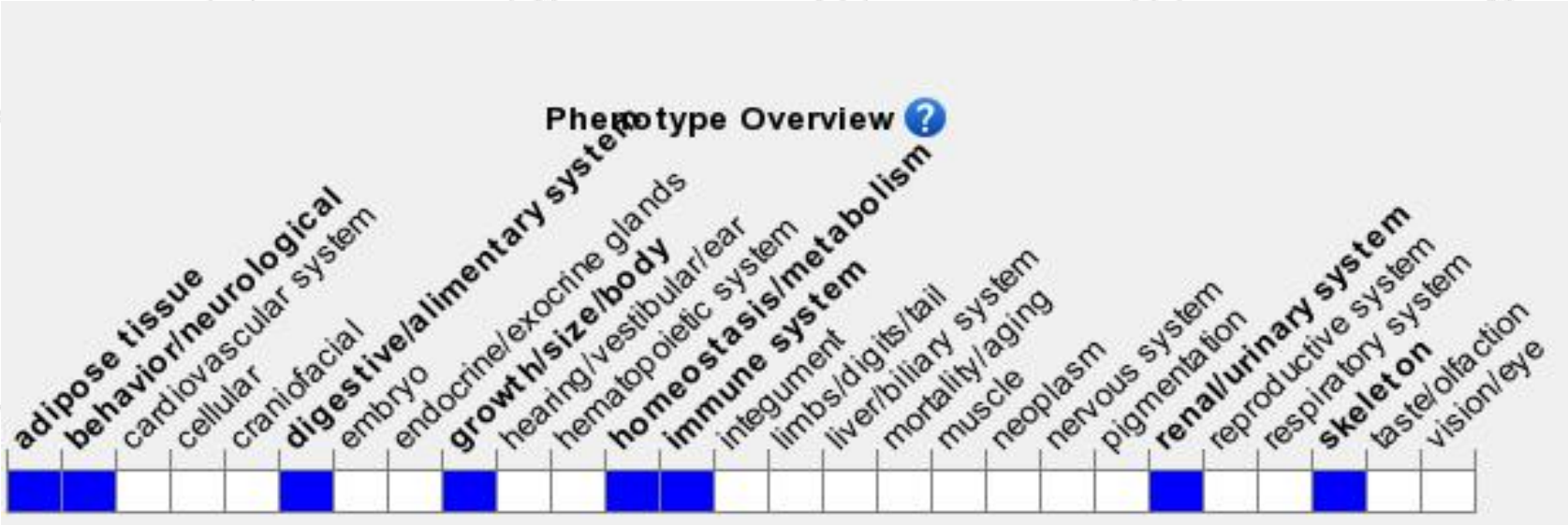
Genomic location distribution



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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