Plxnb1 Cas9-KO Strategy

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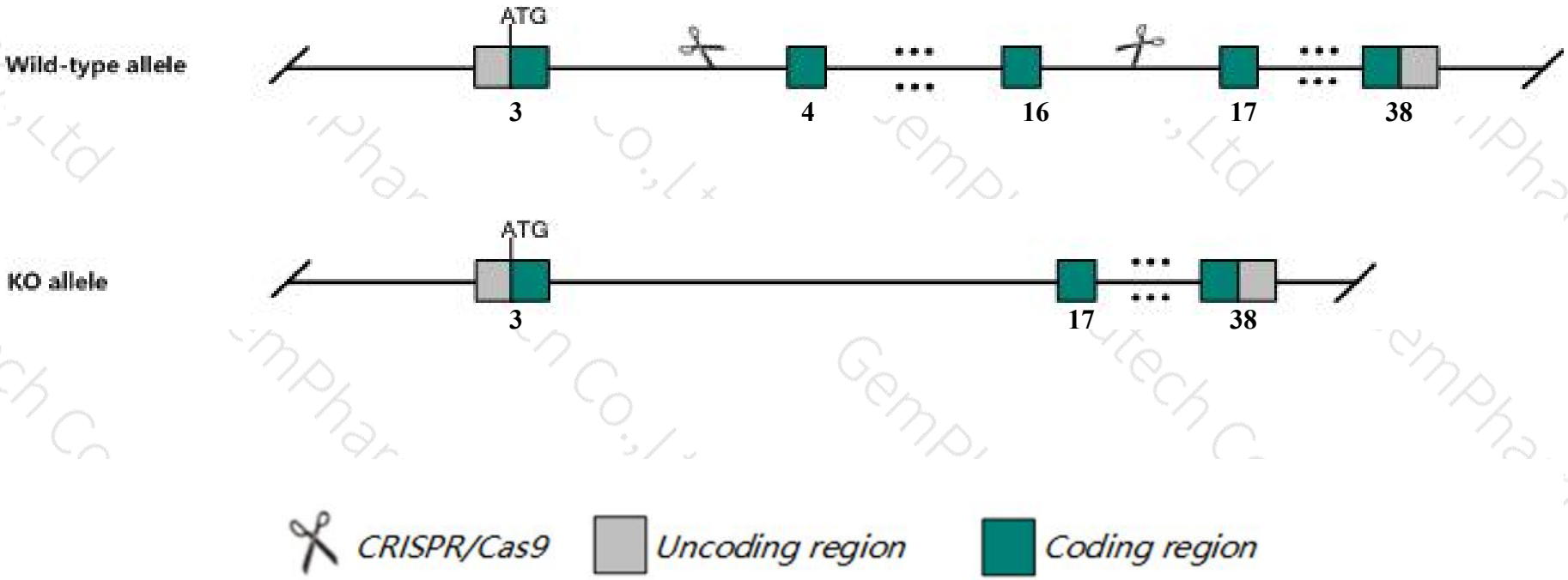
Project Overview

Project Name	***Plxnb1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plxnb1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Plxnb1* gene has 7 transcripts. According to the structure of *Plxnb1* gene, exon4-exon16 of *Plxnb1-201* (ENSMUST00000072093.12) transcript is recommended as the knockout region.The region contains 2261bp coding sequenc Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Plxnb1* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

- According to the existing MGI data,Homozygous null mutants are viable and fertile and show no apparent defects in development, adult histology or basic functional parameters. However, a transitory renal phenotype, characterized by increased ureteric branching and enlarged kidneys, is noted over early stages of renal development.
- The knockou region is near to the N-terminal of *Gm7628* gene,this strategy may influence the regulatory function of the N-terminal of *Gm7628* gene.
- The effect on transcript *Plxnb1*-202&203&205 is unknown.
- The N-terminal of *Plxnb1* gene will remain 376aa,it may remain the partial function of *Plxnb1* gene.
- The *Plxnb1* gene is located on the Chr9. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Plxnb1 plexin B1 [*Mus musculus* (house mouse)]

Gene ID: 235611, updated on 12-Aug-2019

Summary

Official Symbol	Plxnb1 provided by MGI
Official Full Name	plexin B1 provided by MGI
Primary source	MGI:MGI:2154238
See related	Ensembl:ENSMUSG00000053646
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	AU042020; mKIAA0407; 2900002G15Rik
Expression	Broad expression in adrenal adult (RPKM 35.3), ovary adult (RPKM 25.4) and 25 other tissues See more
Orthologs	human all

Genomic context

Location: 9; 9 F2

See Plxnb1 in Genome Data Viewer

Exon count: 43

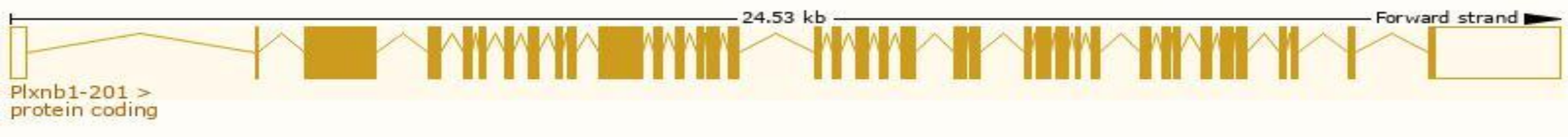
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (109093849..109119915)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (108997950..109022429)

Transcript information（Ensembl）

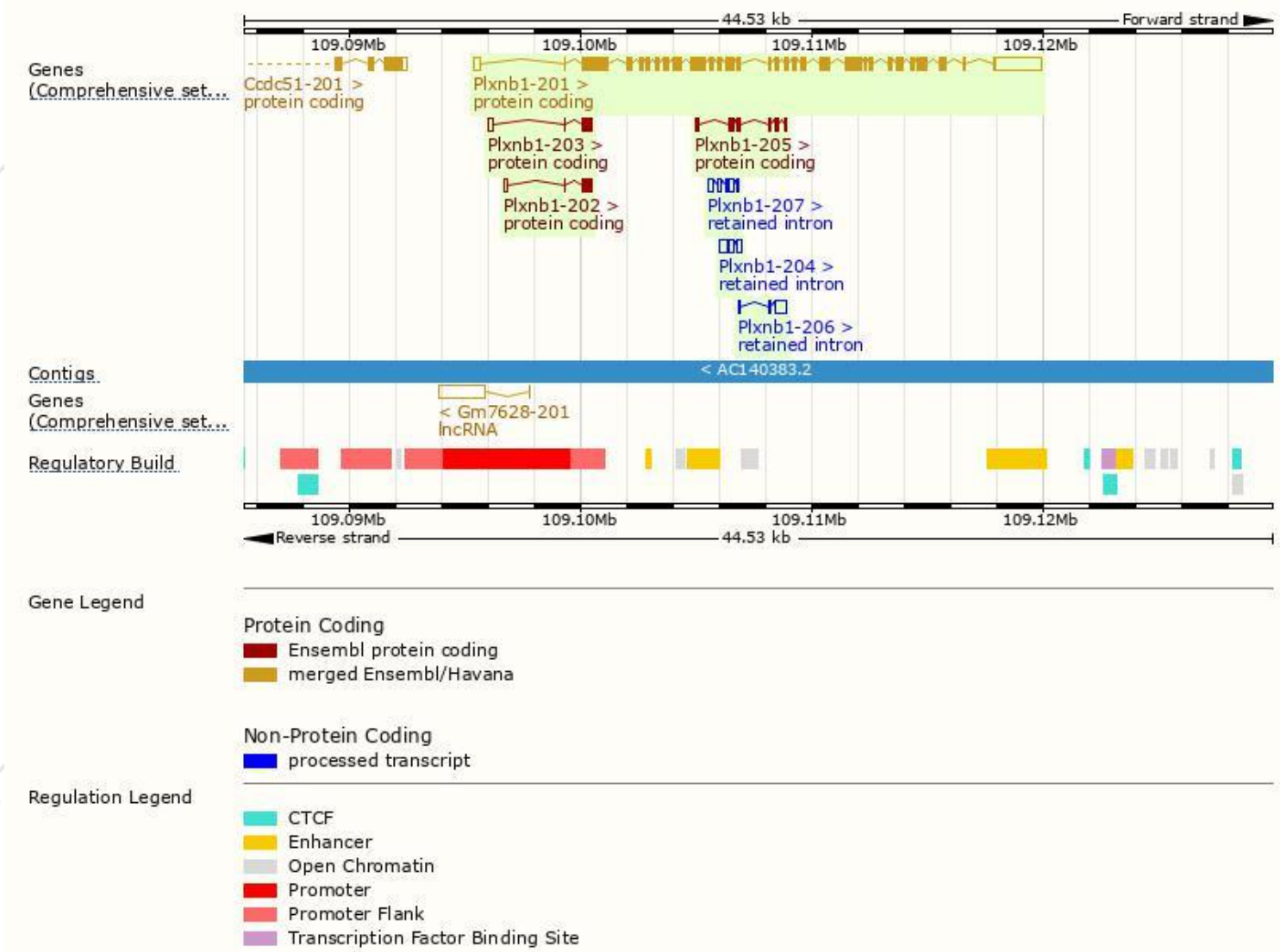
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plxnb1-201	ENSMUST00000072093.12	8649	2119aa	Protein coding	CCDS23546	Q8CJH3	TSL:1 GENCODE basic APPRIS P1
Plxnb1-205	ENSMUST00000192988.2	799	266aa	Protein coding	-	A0A0G2JDM9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Plxnb1-203	ENSMUST00000131462.7	731	140aa	Protein coding	-	D3YUD0	CDS 3' incomplete TSL:2
Plxnb1-202	ENSMUST00000130366.1	585	140aa	Protein coding	-	D3YUD0	CDS 3' incomplete TSL:3
Plxnb1-204	ENSMUST00000192117.1	737	No protein	Retained intron	-	-	TSL:3
Plxnb1-206	ENSMUST00000194734.1	729	No protein	Retained intron	-	-	TSL:3
Plxnb1-207	ENSMUST00000195364.5	651	No protein	Retained intron	-	-	TSL:5

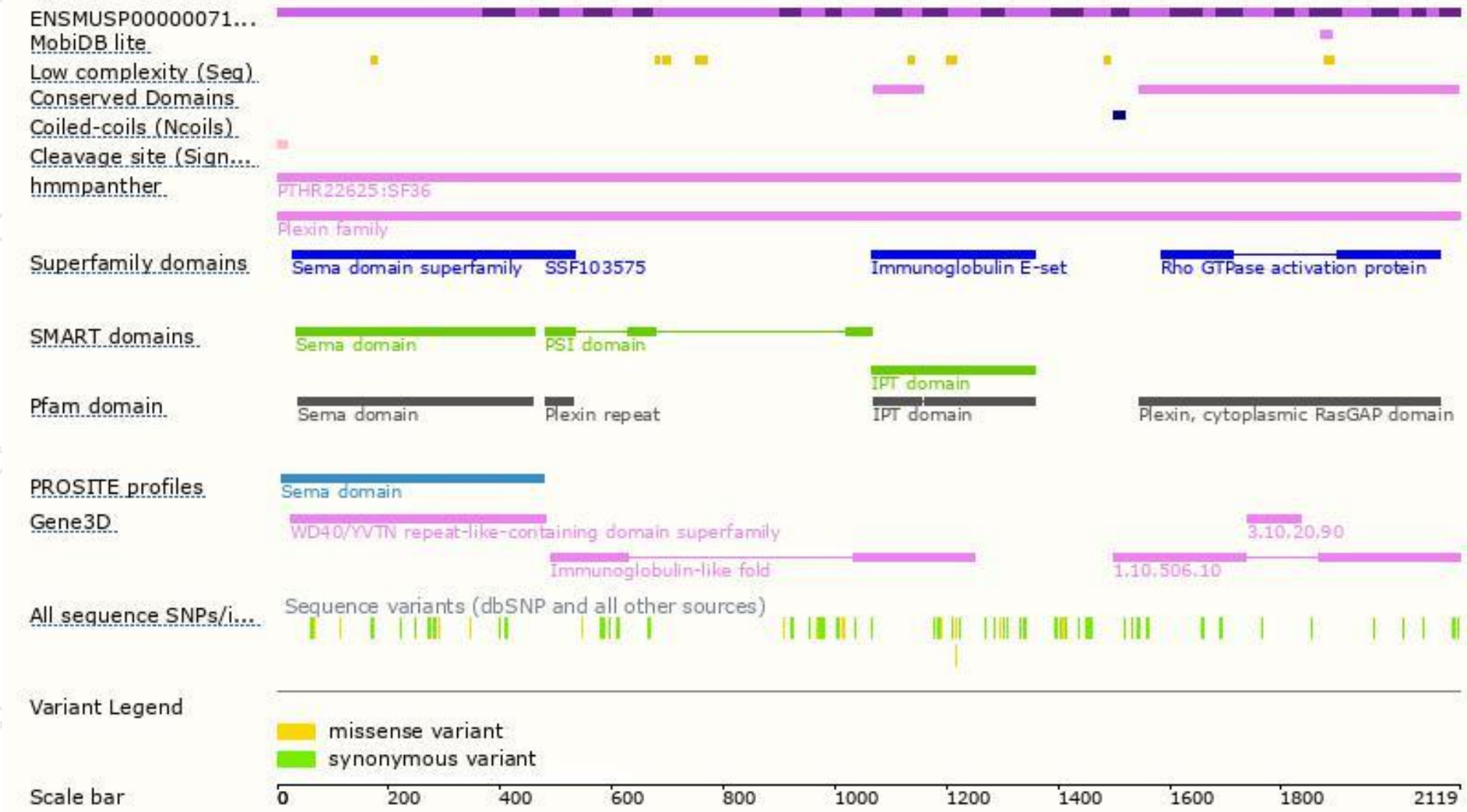
The strategy is based on the design of *Plxnb1-201* transcript,The transcription is shown below



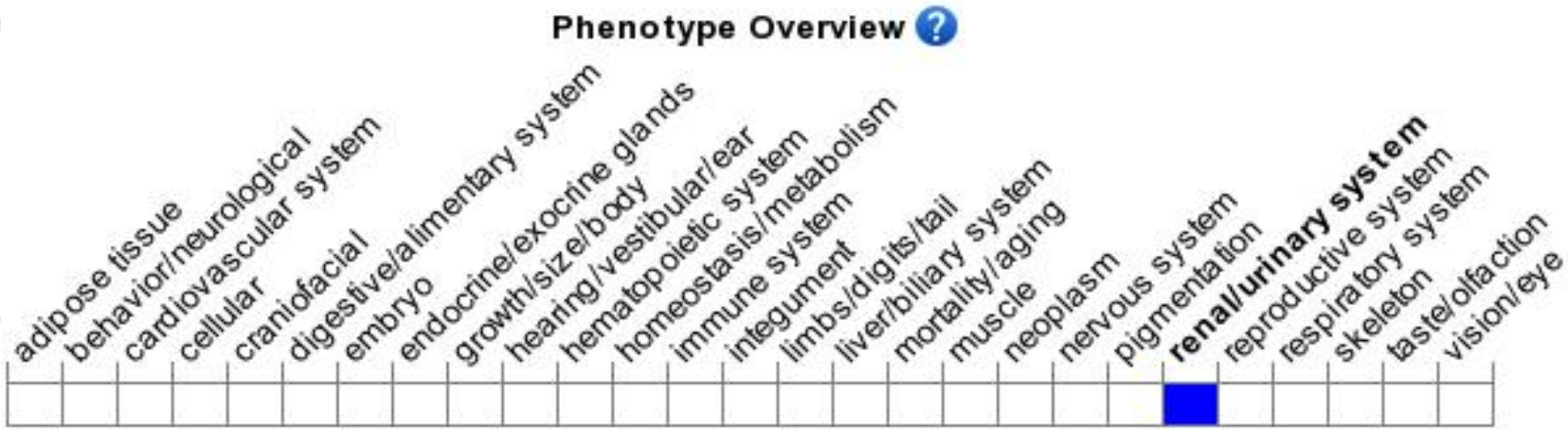
Genomic location distribution



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,Homozygous null mutants are viable and fertile and show no apparent defects in development, adult histology or basic functional parameters. However, a transitory renal phenotype, characterized by increased ureteric branching and enlarged kidneys, is noted over early stages of renal development.

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

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