Slc26a6 Cas9-CKO Strategy

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Project Overview

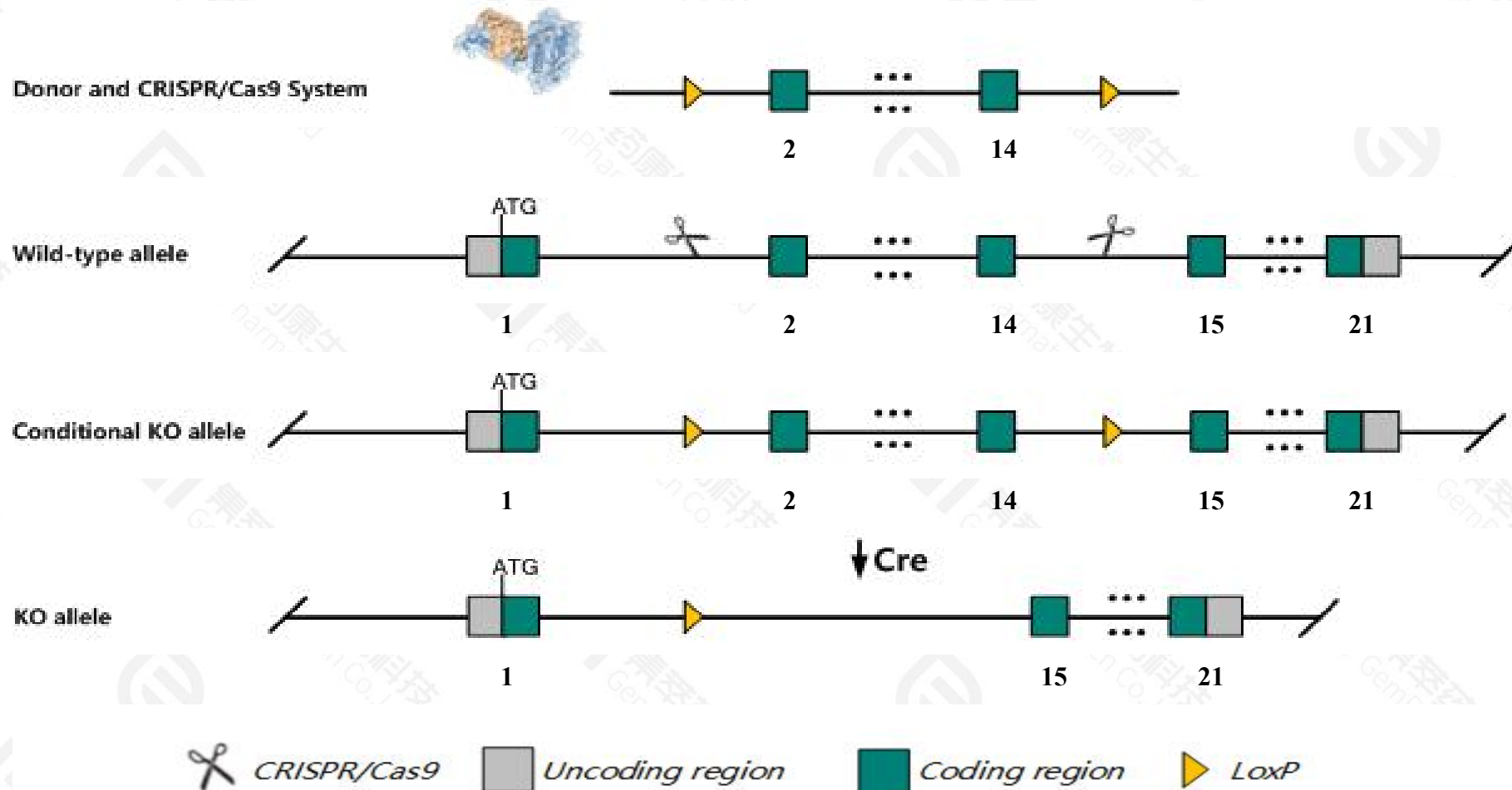|	
Project Name	*Slc26a6*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc26a6* gene. The schematic diagram is as follows:

Technical routes

➢ The *Slc26a6* gene has 9 transcripts. According to the structure of *Slc26a6* gene, exon2-exon14 of *Slc26a6-201*(ENSMUST00000188557.8) transcript is recommended as the knockout region.The region contains Ens 1580bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc26a6* 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,homozygous null mice display abnormal proximal tubule and duodenal anion exchange, but are otherwise normal.

➢ The *Slc26a6* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Slc26a6 solute carrier family 26, member 6 [Mus musculus (house mouse)]

Gene ID: 171429, updated on 7-Mar-2021

Summary

|	
Official Symbol	Slc26a6 provided by MGI
Official Full Name	solute carrier family 26, member 6 provided by MGI
Primary source	MGI:MGI:2159728
See related	Ensembl:ENSMUSG00000023259
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	B930010B04Rik, CFEX, Pa, Pat-1, Pat1
Expression	Annotation category: partial on reference assembly See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc26a6-209	ENSMUST00000239562.1	2659	735aa	Protein coding	-		GENCODE basic , APPRIS ALT2 ,
Slc26a6-201	ENSMUST00000188557.8	2552	758aa	Protein coding	-		TSL:1 , GENCODE basic , APPRIS P5 ,
Slc26a6-207	ENSMUST00000193874.3	2514	239aa	Nonsense mediated decay	-		TSL:5 ,
Slc26a6-203	ENSMUST00000192559.7	1799	262aa	Nonsense mediated decay	-		TSL:1 ,
Slc26a6-206	ENSMUST00000193825.2	349	No protein	Processed transcript	-		TSL:2 ,
Slc26a6-202	ENSMUST00000192507.7	4943	No protein	Retained intron	-		TSL:1 ,
Slc26a6-205	ENSMUST00000193463.6	4566	No protein	Retained intron	-		TSL:2 ,
Slc26a6-204	ENSMUST00000193291.7	3046	No protein	Retained intron	-		TSL:1 ,
Slc26a6-208	ENSMUST00000195646.7	2643	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Slc26a6-201* transcript,the transcription is shown below:
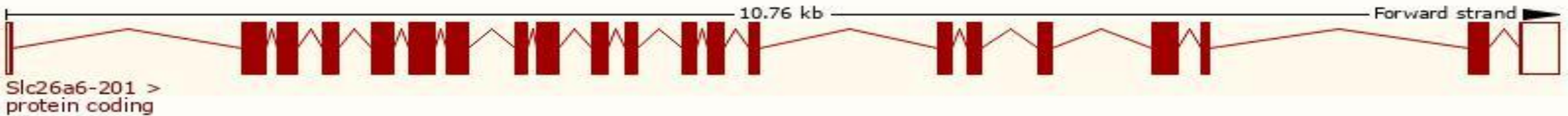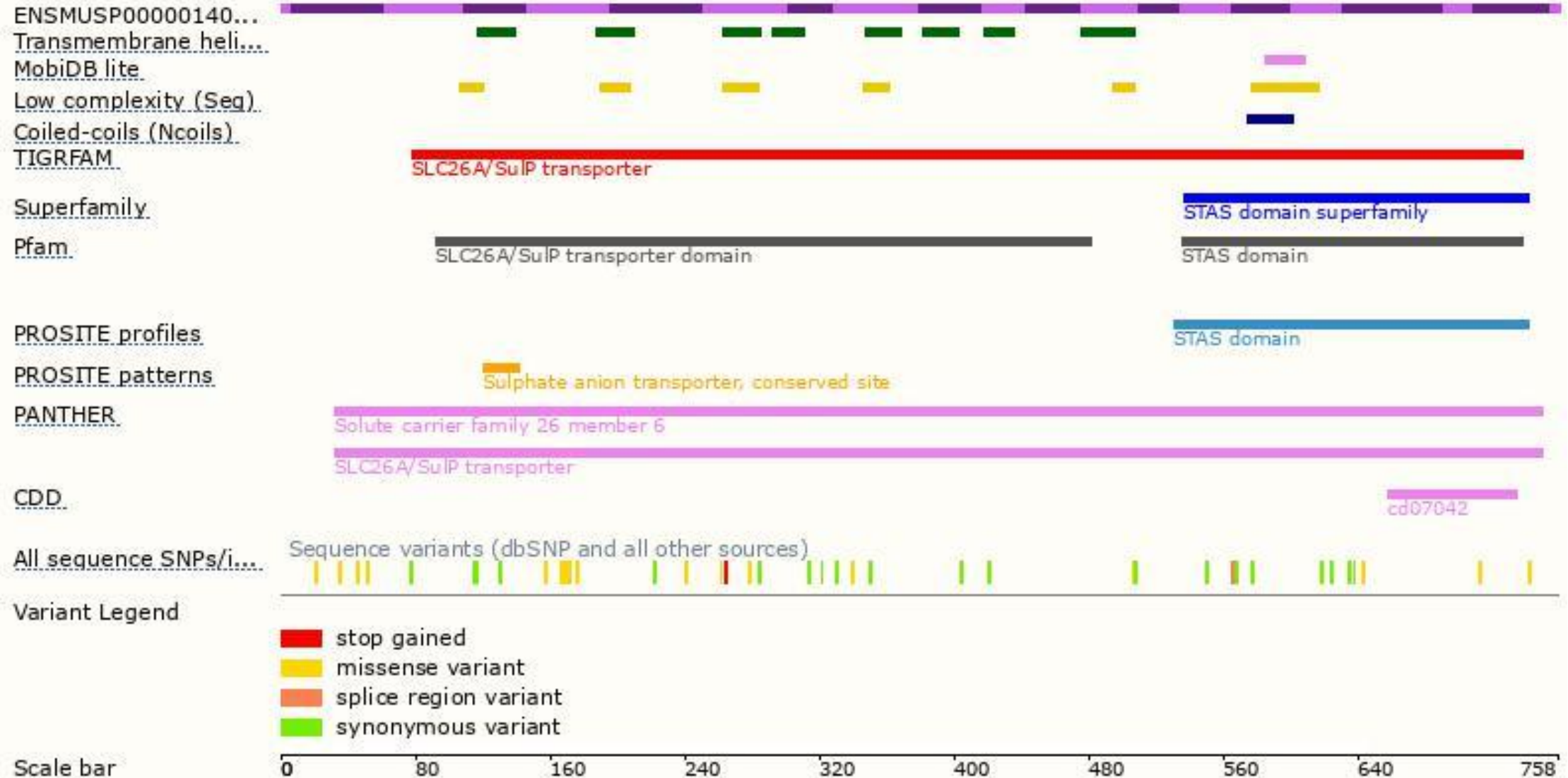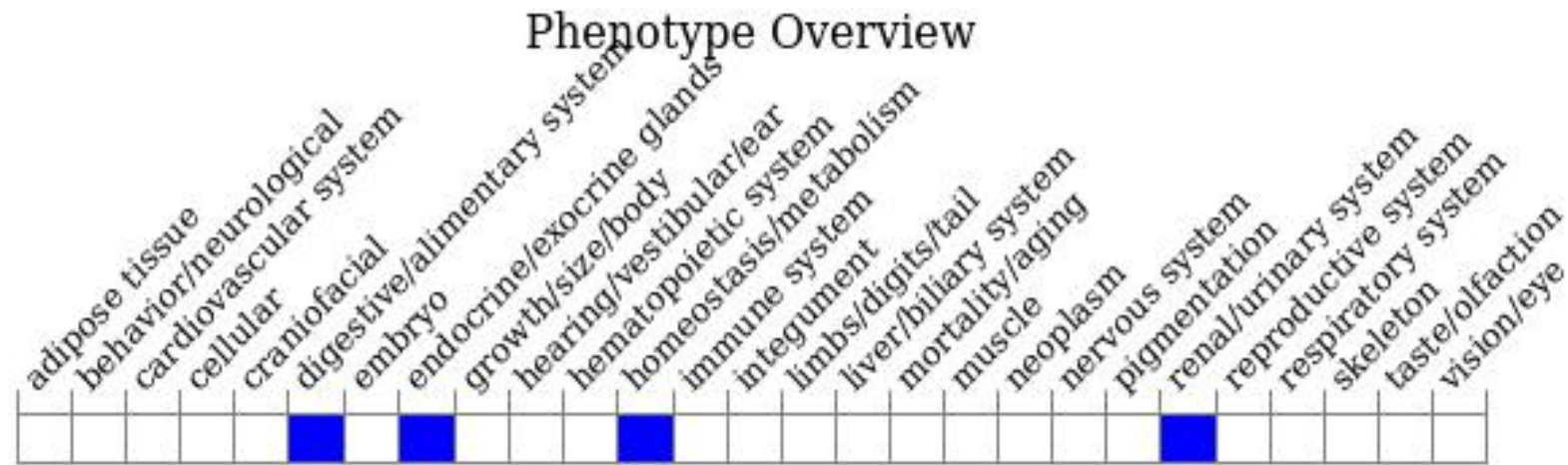
Genomic location distribution
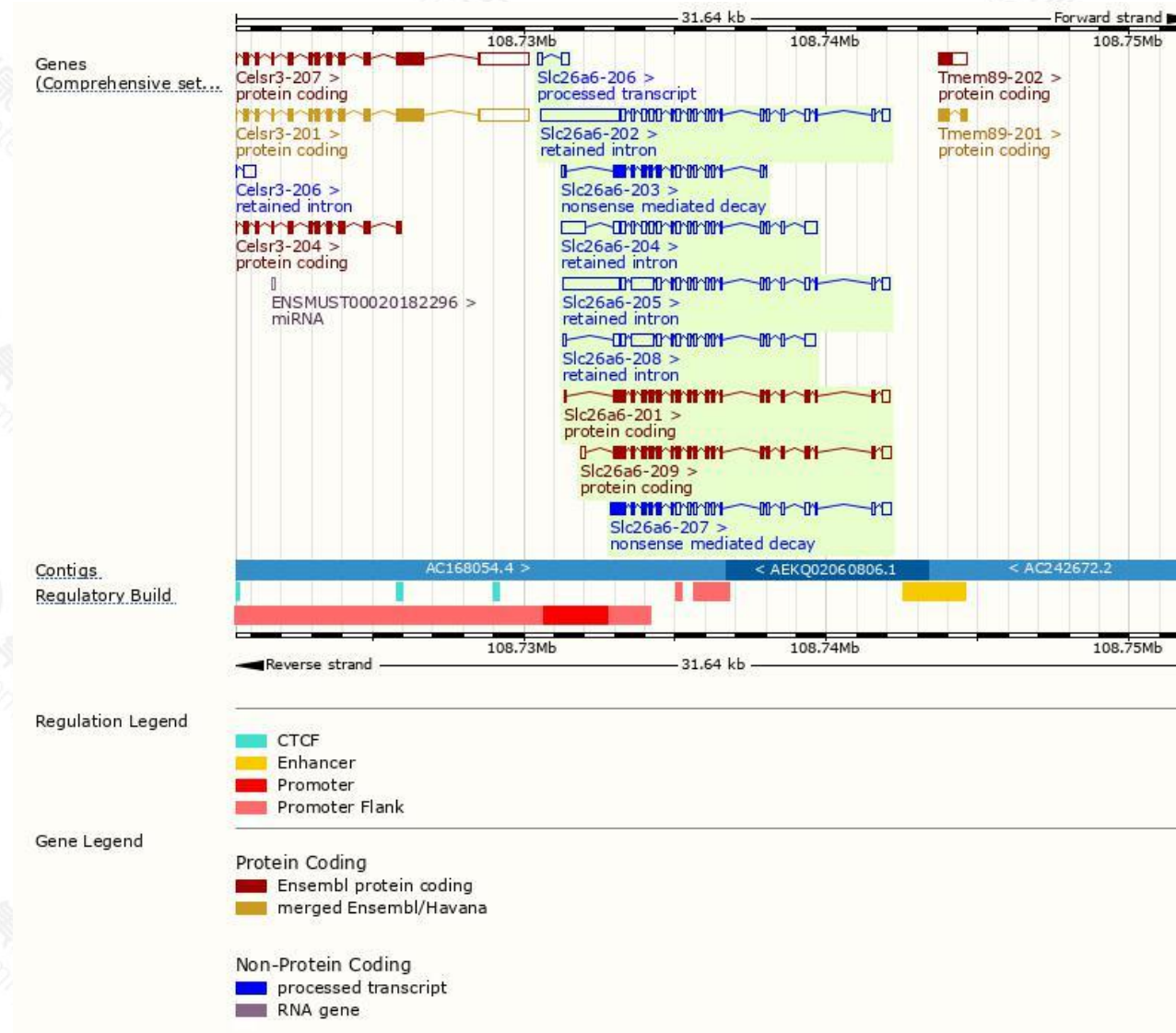
Protein domain

Mouse phenotype description(MGI)

Phenotype Overview

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 mice display abnormal proximal tubule and duodenal anion exchange, but are otherwise normal.

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