Slc16a2 Cas9-KO Strategy

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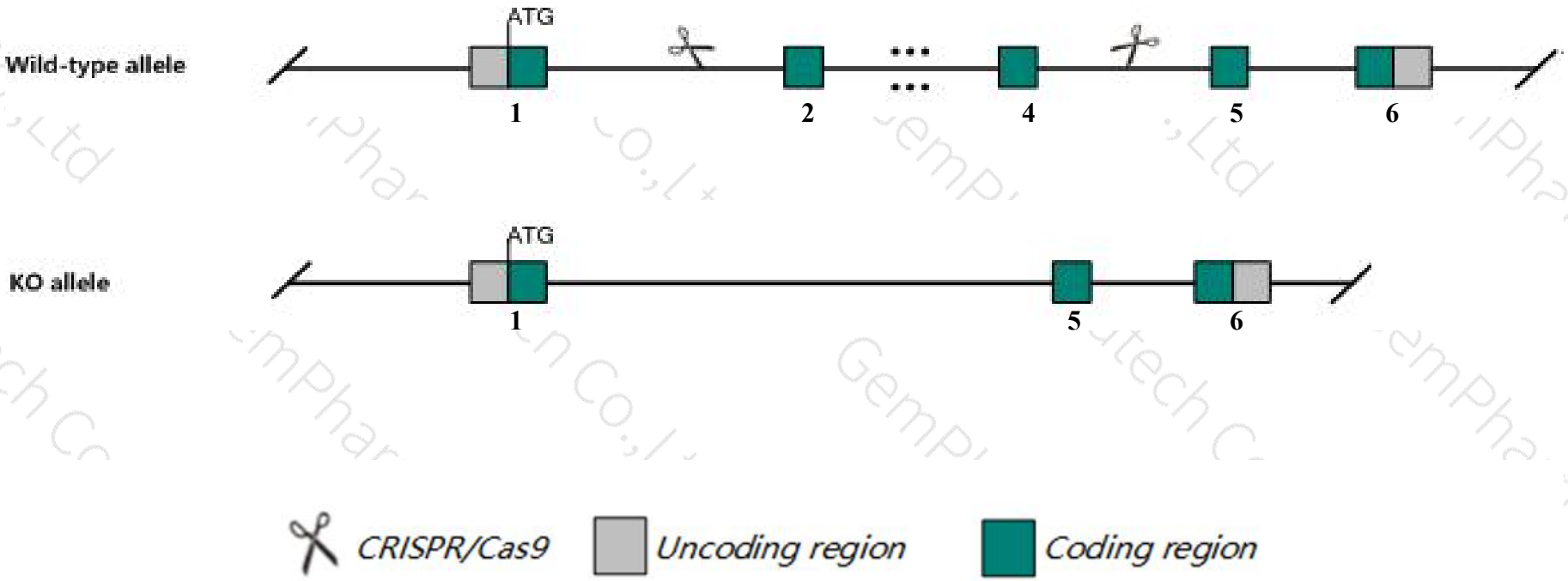
Project Overview

Project Name	***Slc16a2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc16a2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc16a2* gene has 3 transcripts. According to the structure of *Slc16a2* gene, exon2-exon4 of *Slc16a2-201* (ENSMUST00000042664.9) transcript is recommended as the knockout region.The region contains 740bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc16a2* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ According to the existing MGI data,Homo- and hemizygous inactivation of this gene leads to abnormal thyroid hormone metabolism with no apparent neurological phenotype. Males hemizygous for a knock-out allele also show altered deiodinase enzymatic activities, reduced serum cholesterol and increased serum alkaline phosphatase levels.

➢ The *Slc16a2* gene is located on the ChrX. 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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Slc16a2 solute carrier family 16 (monocarboxylic acid transporters), member 2 [Mus musculus (house mouse)]

Gene ID: 20502, updated on 31-Jan-2019

Summary

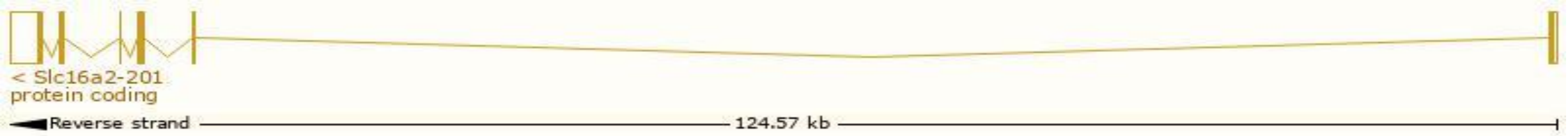
Official Symbol	Slc16a2 provided by MGI
Official Full Name	solute carrier family 16 (monocarboxylic acid transporters), member 2 provided by MGI
Primary source	MGI:MGI:1203732
See related	Ensembl:ENSMUSG00000033965
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW105741, Mct8, Xpct
Expression	Broad expression in kidney adult (RPKM 54.4), liver adult (RPKM 41.5) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

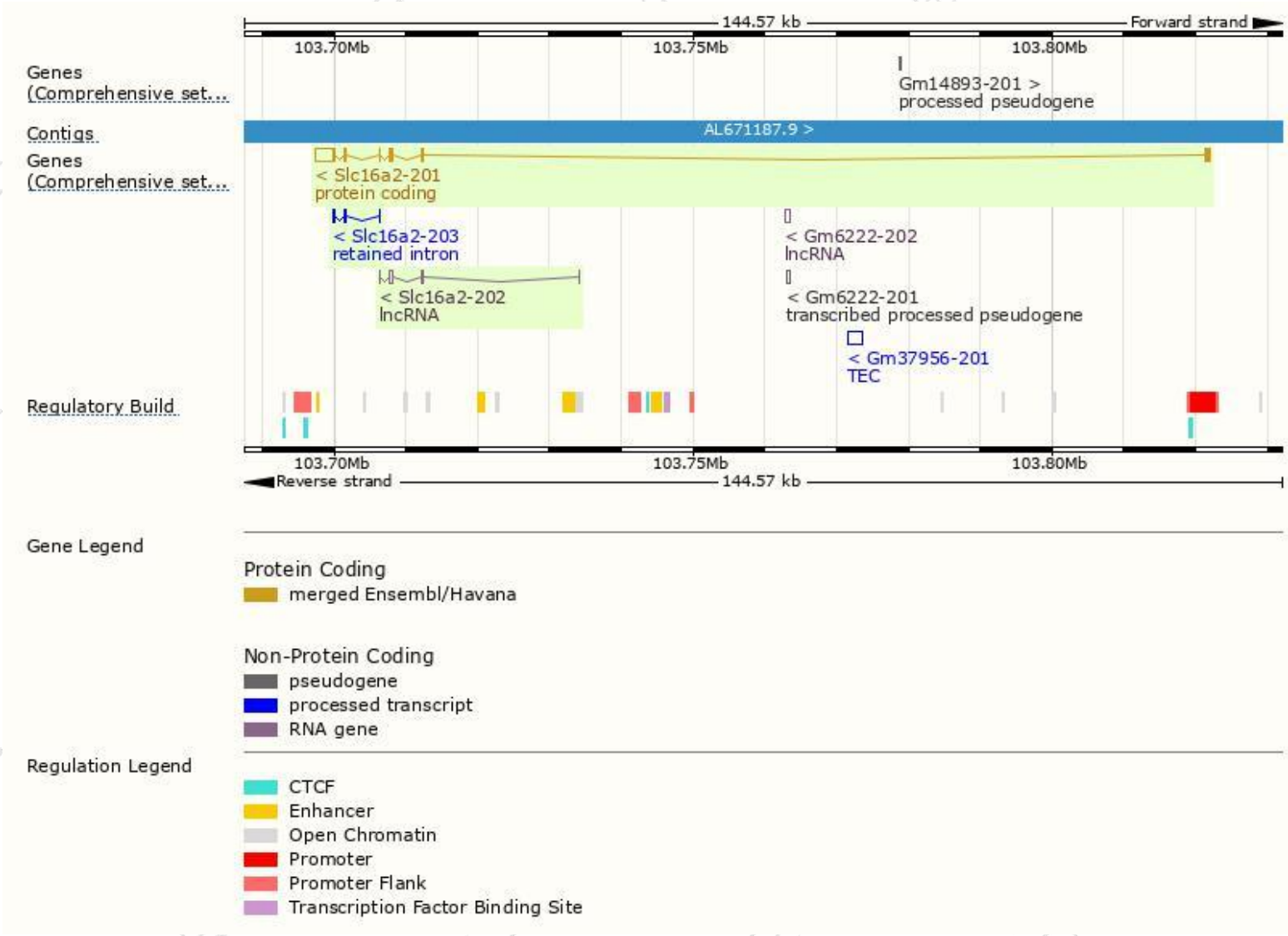
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc16a2-201	ENSMUST00000042664.9	4152	545aa	Protein coding	CCDS30330	O70324 Q05BA2	TSL:1 GENCODE basic APPRIS P1
Slc16a2-203	ENSMUST00000171837.1	549	No protein	Retained intron	-	-	TSL:2
Slc16a2-202	ENSMUST00000148684.2	660	No protein	lncRNA	-	-	TSL:5

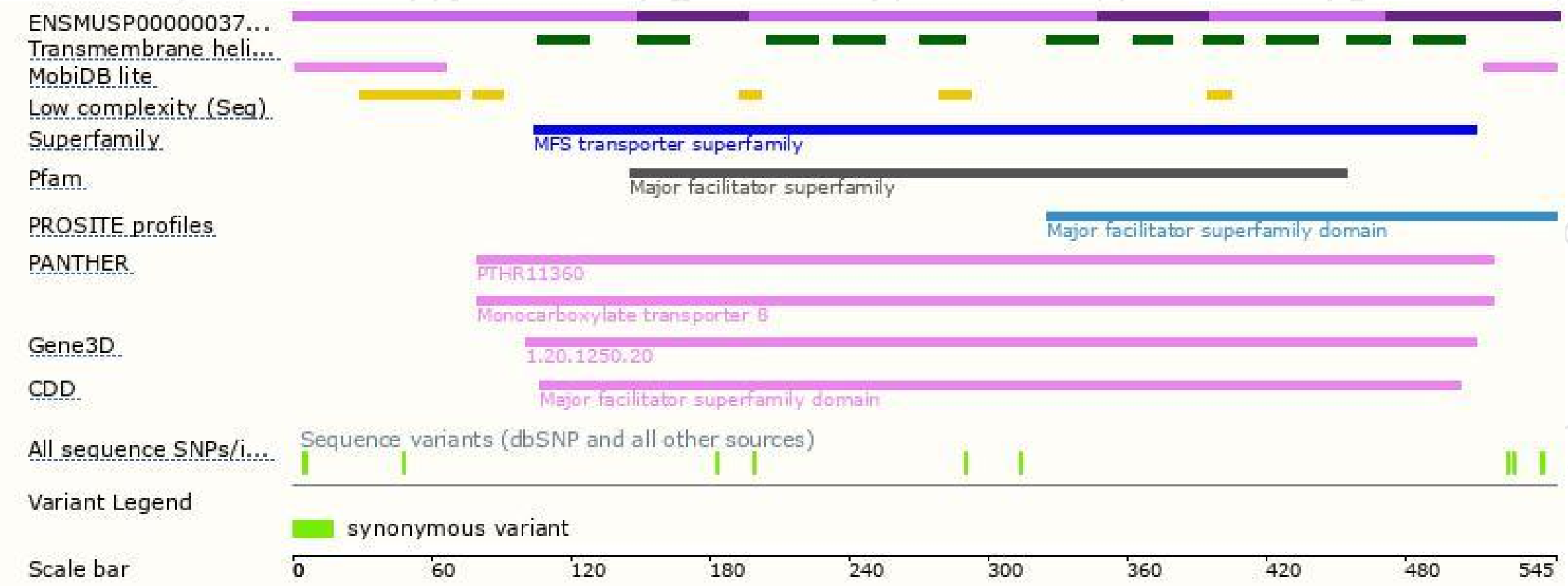
The strategy is based on the design of *Slc16a2-201* transcript,The transcription is shown below



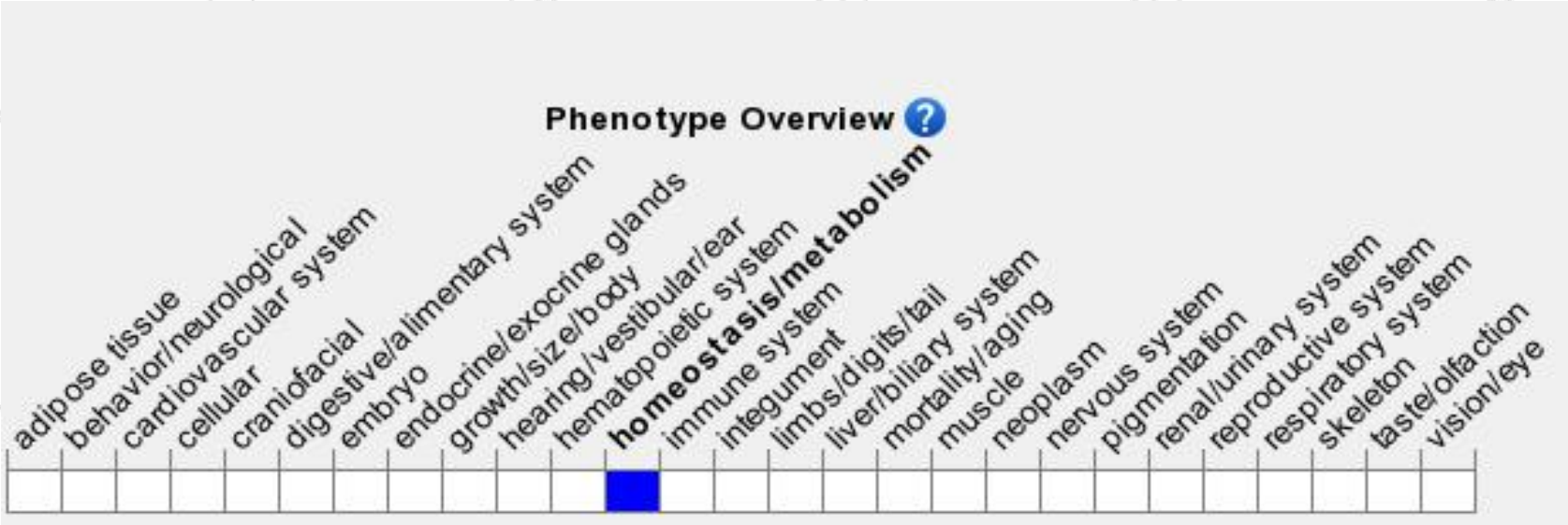
Genomic location distribution



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/).

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

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