Exosc3 Cas9-KO Strategy

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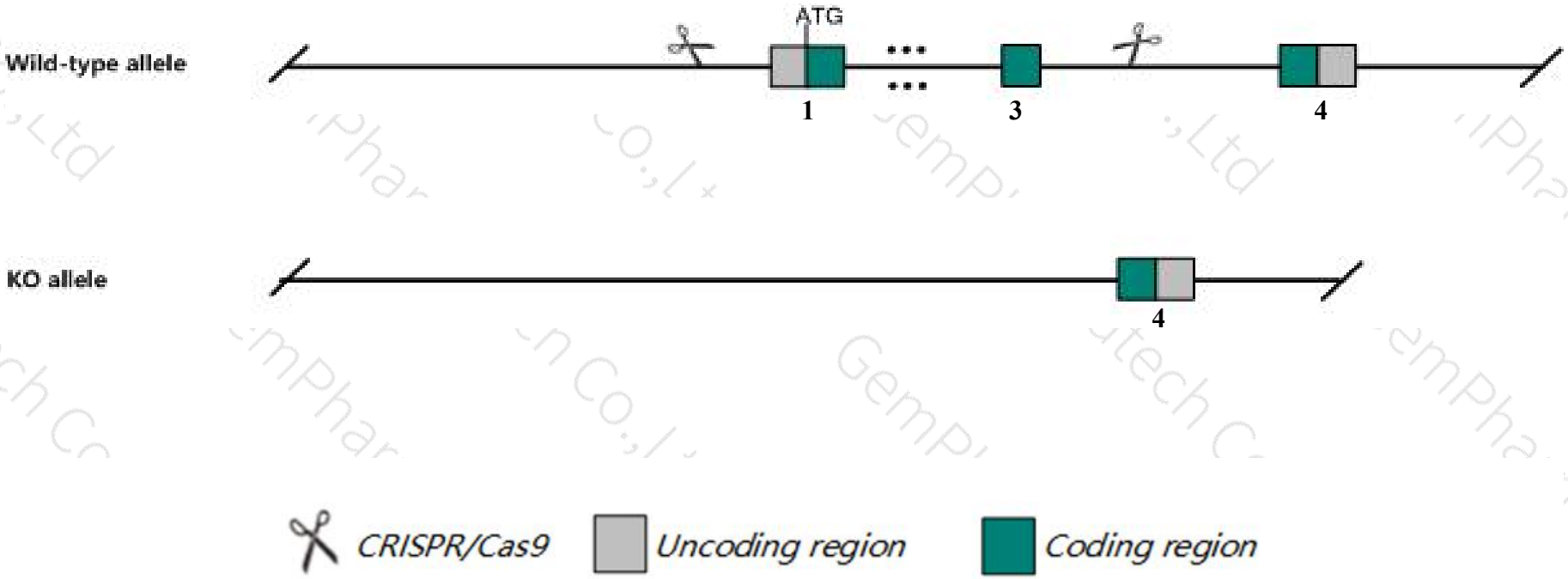
Project Overview

Project Name	***Exosc3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Exosc3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Exosc3* gene has 4 transcripts. According to the structure of *Exosc3* gene, exon1-exon3 of *Exosc3-201* (ENSMUST00000030003.9) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Exosc3* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

- According to the existing MGI data,Mice homozygous for a conditional ready allele appear phenotypically normal.
- The knockout region is near to the C-terminal of *Trmt10b* gene,this strategy may influence the regulatory function of the C-terminal of *Trmt10b* gene.
- The *Exosc3* gene is located on the Chr4. 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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Exosc3 exosome component 3 [*Mus musculus* (house mouse)]

Gene ID: 66362, updated on 12-Aug-2019

Summary

Official Symbol	Exosc3 provided by MGI
Official Full Name	exosome component 3 provided by MGI
Primary source	MGI:MGI:1913612
See related	Ensembl:ENSMUSG00000028322
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	Rrp40; AI593501; 2310005D06Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 24.3), liver E14 (RPKM 19.9) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 4; 4 B1

See Exosc3 in Genome Data Viewer

Exon count: 4

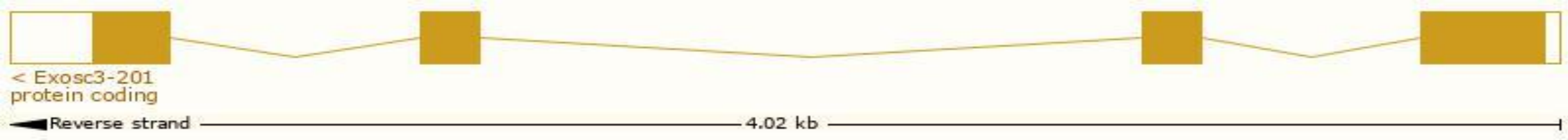
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (45316613..45320616, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (45329501..45333475, complement)

Transcript information（Ensembl）

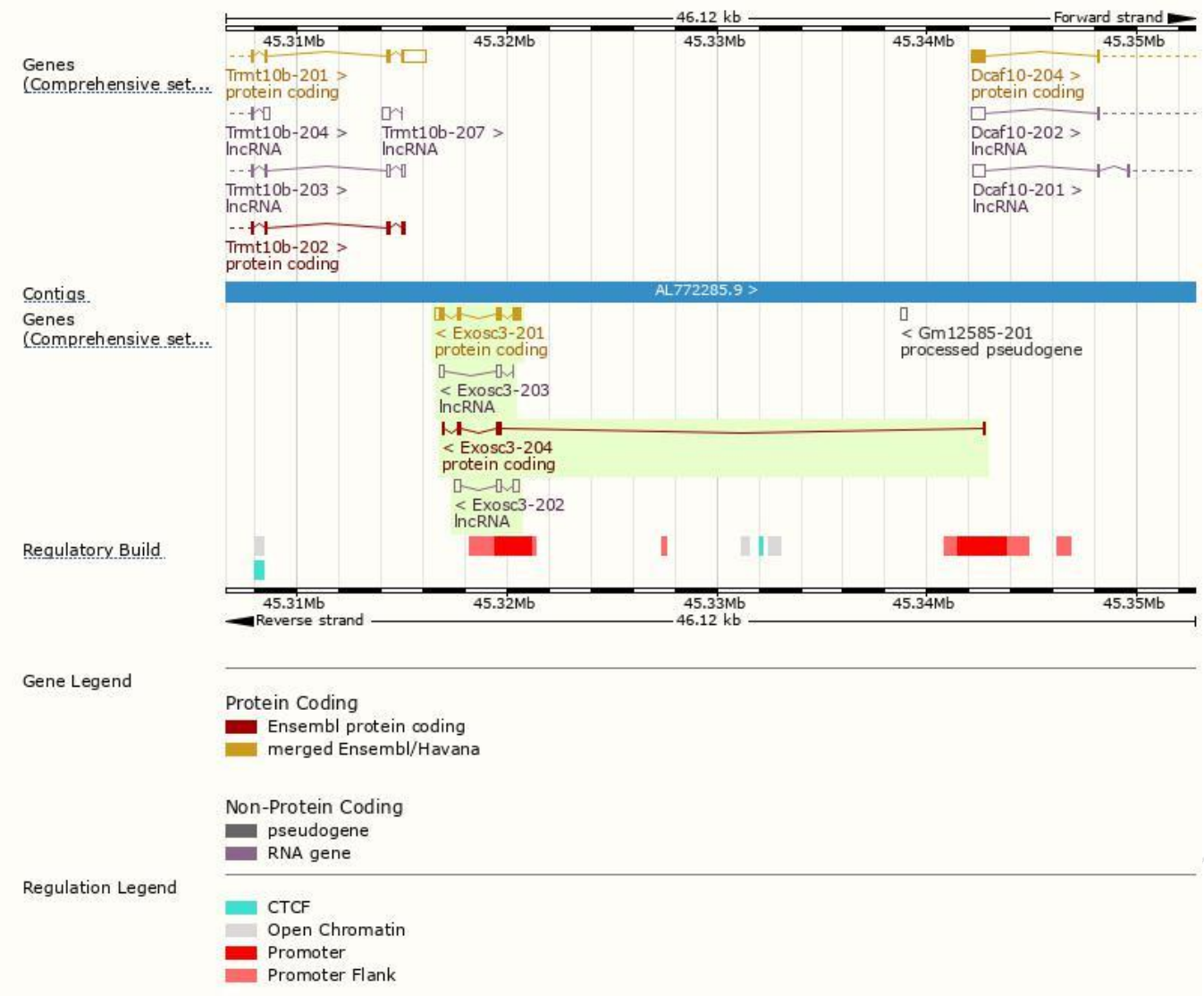
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Exosc3-201	ENSMUST00000030003.9	1077	274aa	Protein coding	CCDS18136	Q7TQK4	TSL:1 GENCODE basic APPRIS P1
Exosc3-204	ENSMUST00000152056.1	435	145aa	Protein coding	-	F6TGV1	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
Exosc3-202	ENSMUST00000130843.1	825	No protein	lncRNA	-	-	TSL:1
Exosc3-203	ENSMUST00000143111.7	451	No protein	lncRNA	-	-	TSL:5

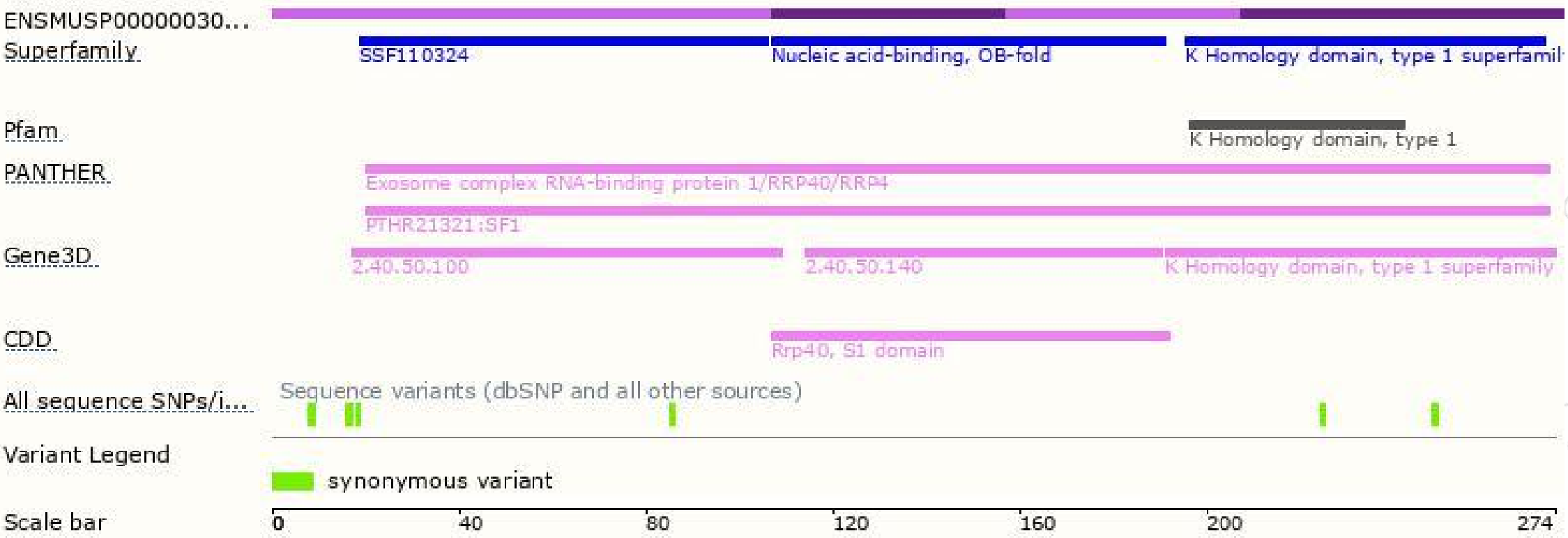
The strategy is based on the design of *Exosc3-201* transcript,The transcription is shown below



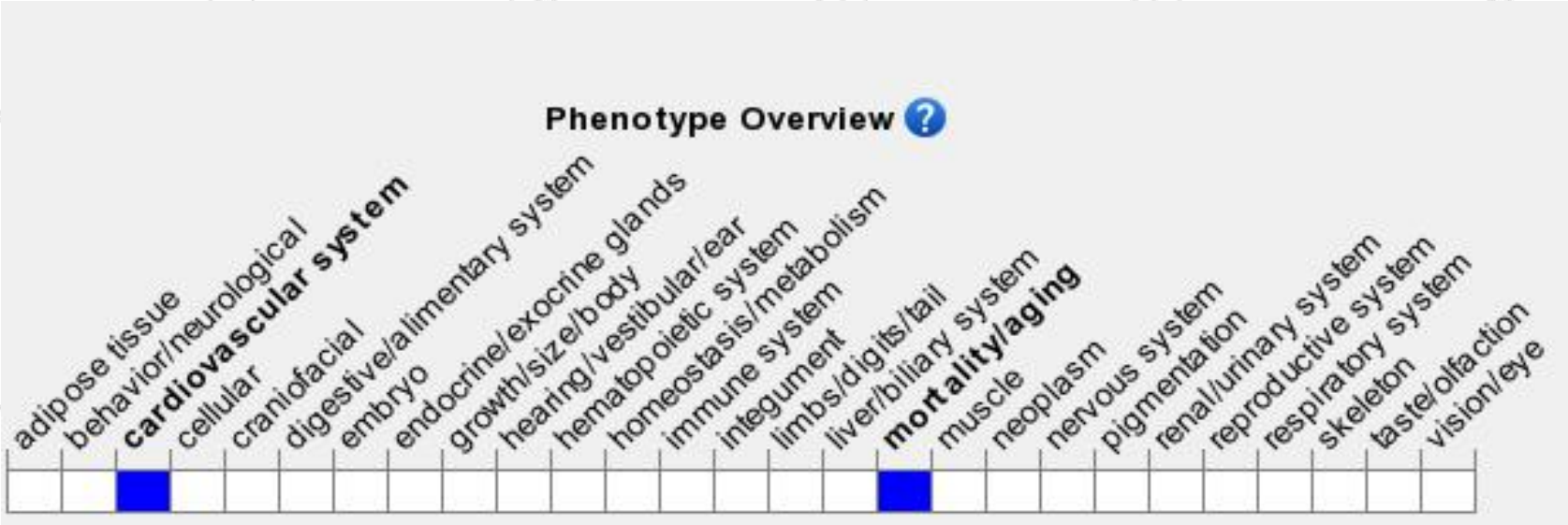
Genomic location distribution



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,Mice homozygous for a conditional ready allele appear phenotypically normal.

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

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