

***Khdrbs3* Cas9-KO Strategy**

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Design Date:2020-2-14

Project Overview

Project Name

Khdrbs3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Khdrbs3* gene. The schematic diagram is as follows:



- The *Khdrbs3* gene has 6 transcripts. According to the structure of *Khdrbs3* gene, exon4-exon5 of *Khdrbs3-201* (ENSMUST00000022954.6) transcript is recommended as the knockout region. The region contains 287bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Khdrbs3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable and fertile with no detectable spatial memory deficits. Males sire slightly smaller litters than control males.
- The *Khdrbs3* gene is located on the Chr15. 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)

Khdrbs3 KH domain containing, RNA binding, signal transduction associated 3 [*Mus musculus* (house mouse)]

Gene ID: 13992, updated on 12-Aug-2019

Summary

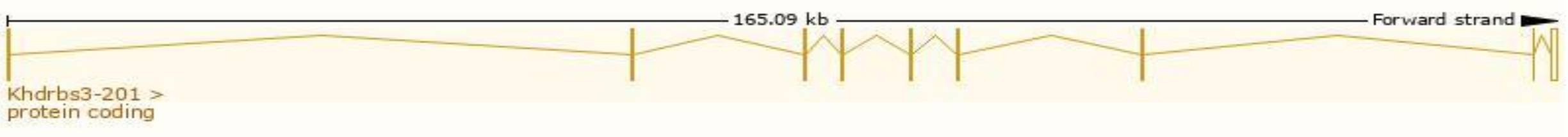
Official Symbol	Khdrbs3 provided by MGI
Official Full Name	KH domain containing, RNA binding, signal transduction associated 3 provided by MGI
Primary source	MGI:MGI:1313312
See related	Ensembl:ENSMUSG00000022332
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Etle; Salp; SIm2; SLM-2; T-STAR
Expression	Broad expression in CNS E18 (RPKM 36.8), cortex adult (RPKM 31.0) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

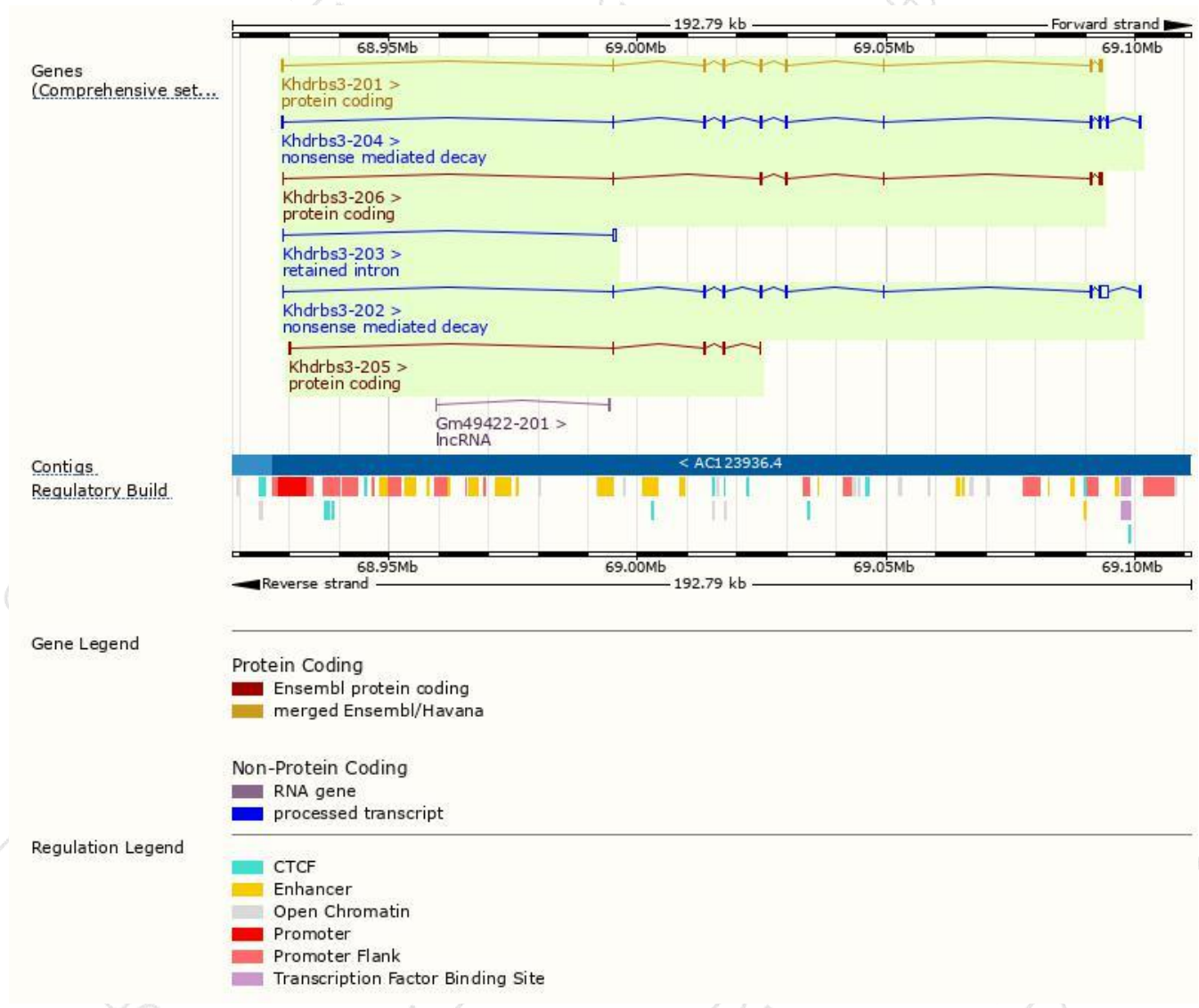
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Khdrbs3-201	ENSMUST00000022954.6	1887	346aa	Protein coding	CCDS27513	Q9R226	TSL:1 GENCODE basic APPRIS P1
Khdrbs3-206	ENSMUST00000230847.1	1344	258aa	Protein coding	-	A0A2R8VJR4	GENCODE basic
Khdrbs3-205	ENSMUST00000230073.1	501	126aa	Protein coding	-	A0A2R8VHM1	CDS 3' incomplete
Khdrbs3-202	ENSMUST00000229234.1	2861	346aa	Nonsense mediated decay	CCDS27513	Q9R226	
Khdrbs3-204	ENSMUST00000229683.1	1740	346aa	Nonsense mediated decay	CCDS27513	Q9R226	
Khdrbs3-203	ENSMUST00000229534.1	688	No protein	Retained intron	-	-	

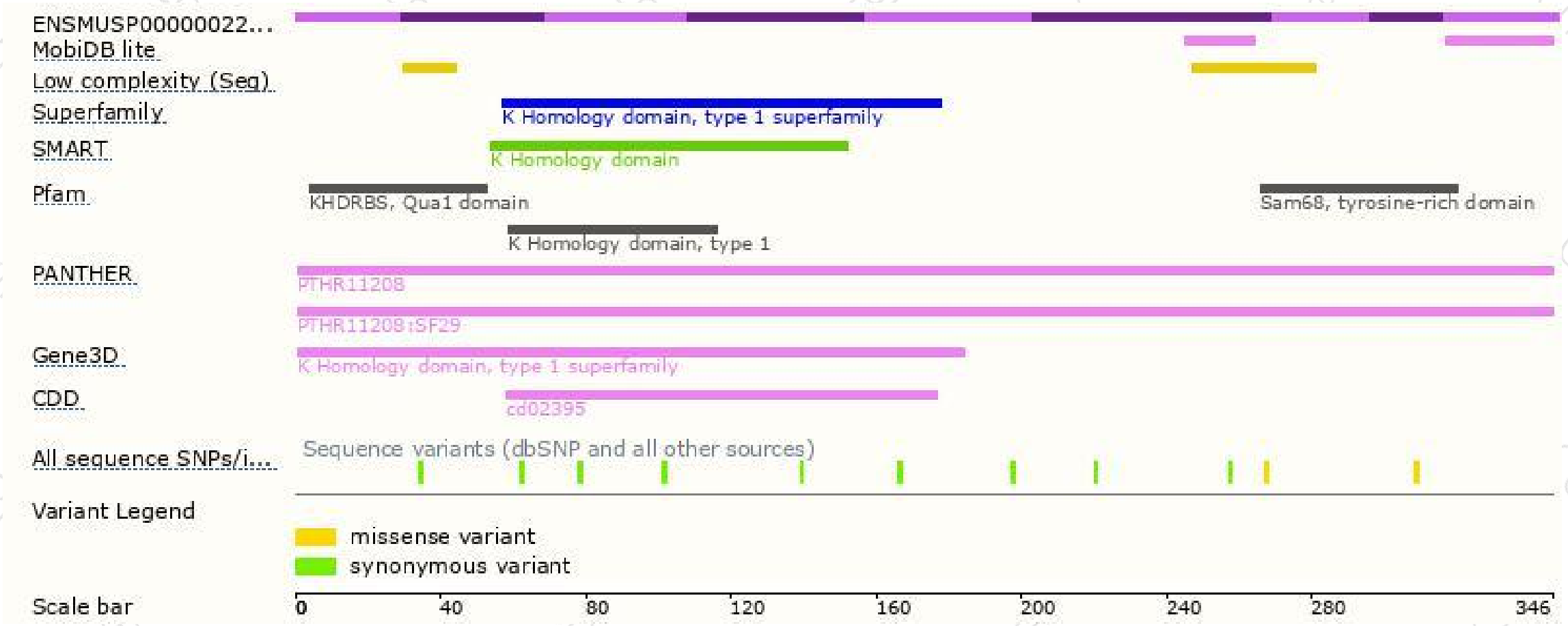
The strategy is based on the design of *Khdrbs3-201* transcript,The transcription is shown below



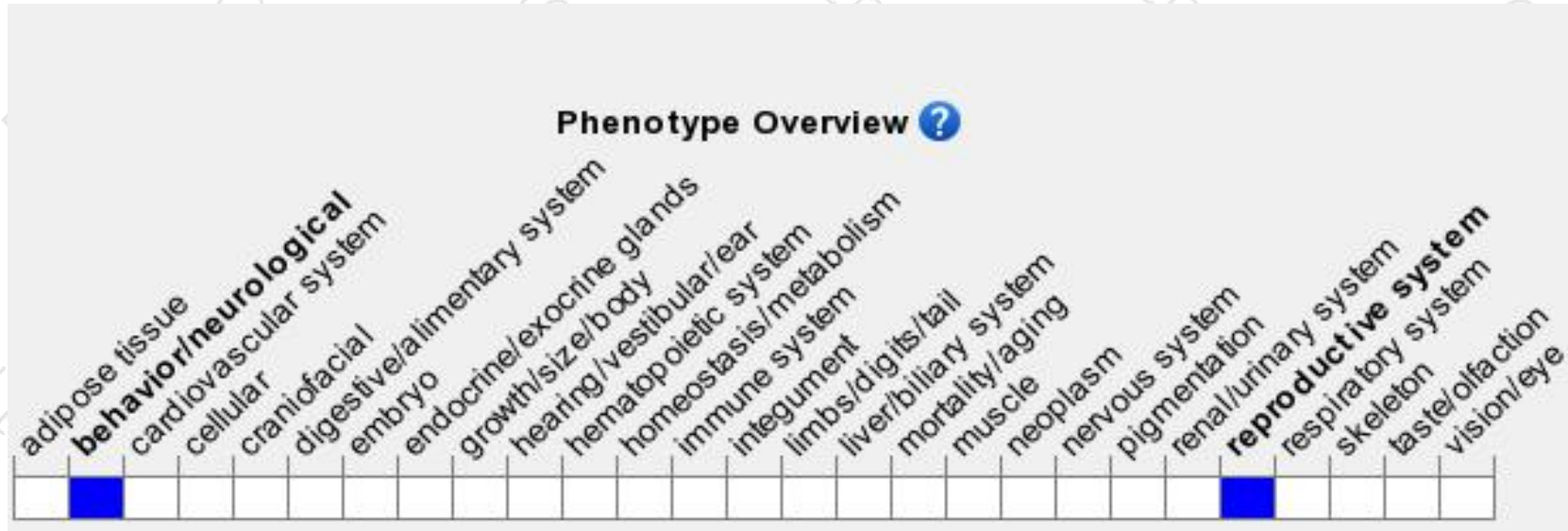
Genomic location distribution



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 knock-out allele are viable and fertile with no detectable spatial memory deficits. Males sire slightly smaller litters than control males.

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

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