

Rps6ka5 Cas9-KO Strategy

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Project Overview

Project Name

Rps6ka5

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rps6ka5* gene. The schematic diagram is as follows:



- The *Rps6ka5* gene has 9 transcripts. According to the structure of *Rps6ka5* gene, exon2-exon5 of *Rps6ka5-201* (ENSMUST00000043599.6) transcript is recommended as the knockout region. The region contains 515bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rps6ka5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a mutant allele exhibit altered response to cocaine including decreased hyperlocomotor activity and sensitization at a lower dose. Mice homozygous for a kinase dead allele exhibit altered experience-dependent synaptic plasticity.
- Transcript *Rps6ka5*-204 may not be affected .
- *Gm48585* and *Gm48586* gene will be deleted together in the strategy.
- The *Rps6ka5* gene is located on the Chr12. 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)

Rps6ka5 ribosomal protein S6 kinase, polypeptide 5 [Mus musculus (house mouse)]

Gene ID: 73086, updated on 31-Jan-2019

Summary



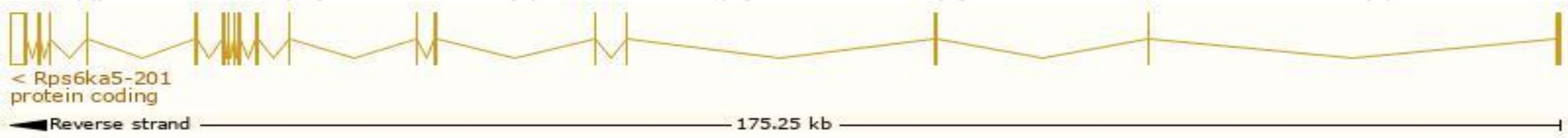
Official Symbol	Rps6ka5 provided by MGI
Official Full Name	ribosomal protein S6 kinase, polypeptide 5 provided by MGI
Primary source	MGI:MGI:1920336
See related	Ensembl:ENSMUSG000000021180
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110005L17Rik, 6330404E13Rik, AI854034, MSK1, MSPK1, RLPK, RLSK, S6K-alpha-5
Expression	Broad expression in cerebellum adult (RPKM 5.5), CNS E18 (RPKM 4.9) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

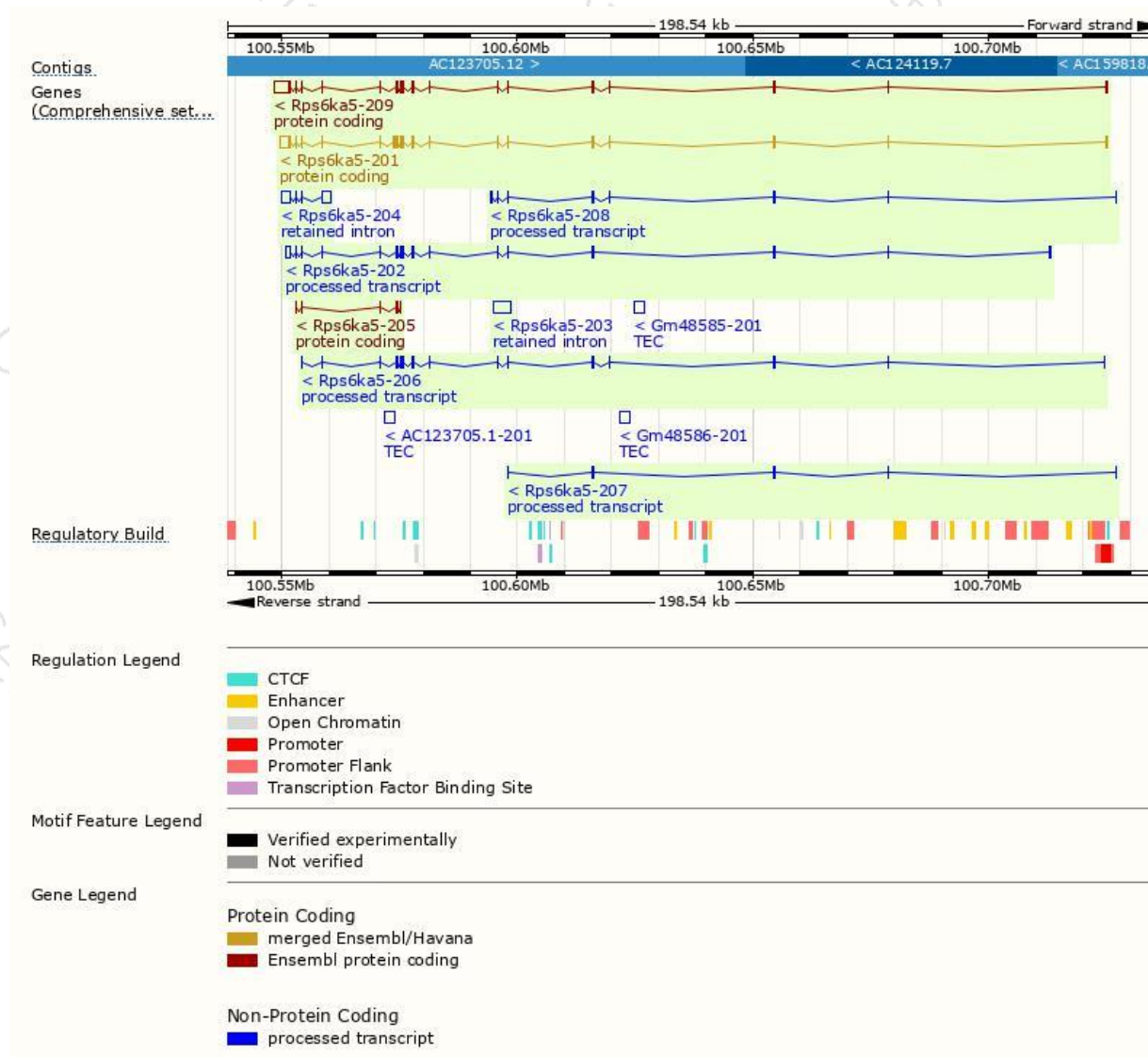
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rps6ka5-201	ENSMUST00000043599.6	4406	863aa	Protein coding	CCDS26107	Q8C050	TSL:1 GENCODE basic APPRIS P2
Rps6ka5-209	ENSMUST00000222731.1	5642	798aa	Protein coding	-	Q8C050	TSL:1 GENCODE basic APPRIS ALT2
Rps6ka5-205	ENSMUST00000221356.1	620	207aa	Protein coding	-	A0A1Y7VL39	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Rps6ka5-202	ENSMUST00000221246.1	2915	No protein	Processed transcript	-	-	TSL:1
Rps6ka5-206	ENSMUST00000221379.1	1833	No protein	Processed transcript	-	-	TSL:1
Rps6ka5-208	ENSMUST00000222403.1	1039	No protein	Processed transcript	-	-	TSL:2
Rps6ka5-207	ENSMUST00000222347.1	519	No protein	Processed transcript	-	-	TSL:5
Rps6ka5-204	ENSMUST00000221323.1	4197	No protein	Retained intron	-	-	TSL:1
Rps6ka5-203	ENSMUST00000221307.1	3730	No protein	Retained intron	-	-	TSL:NA

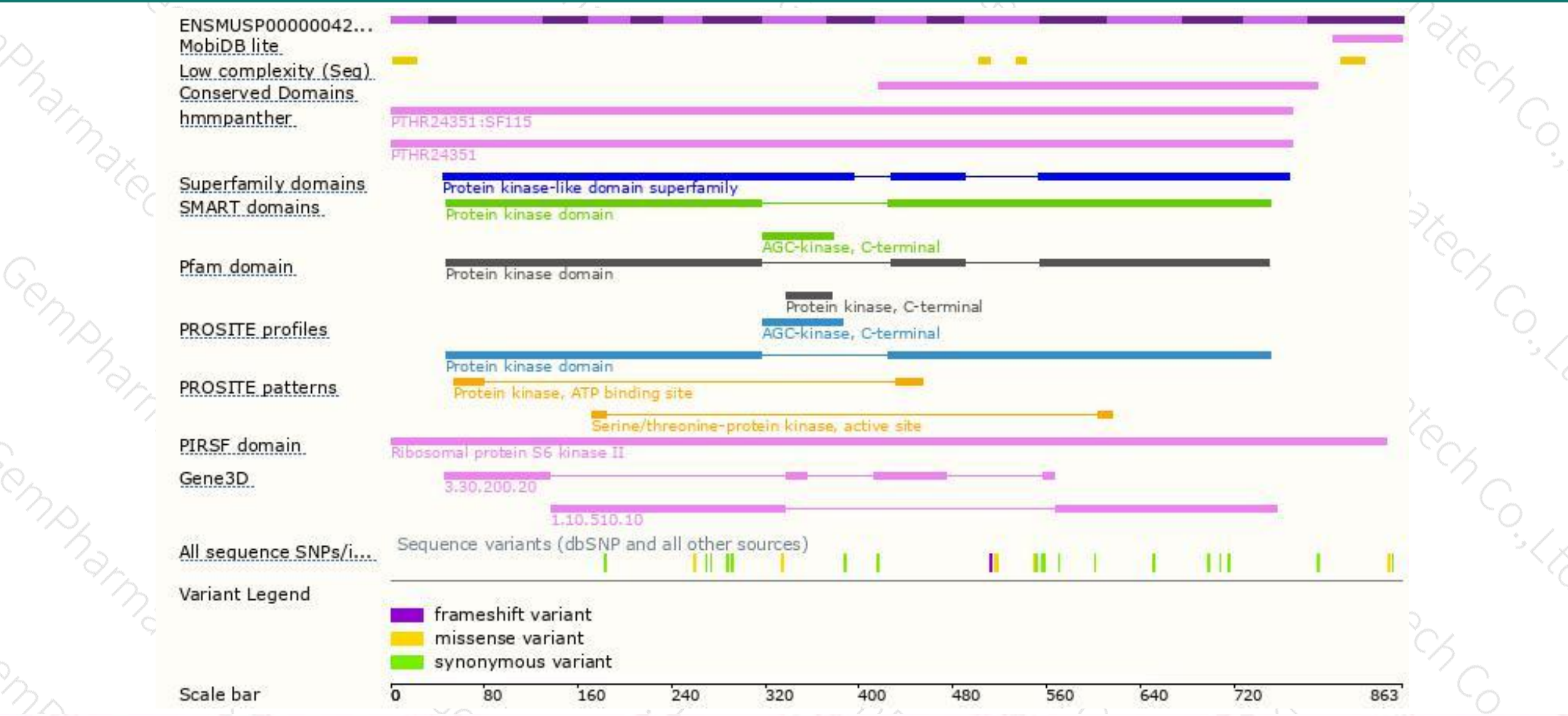
The strategy is based on the design of *Rps6ka5-201* transcript,The transcription is shown below



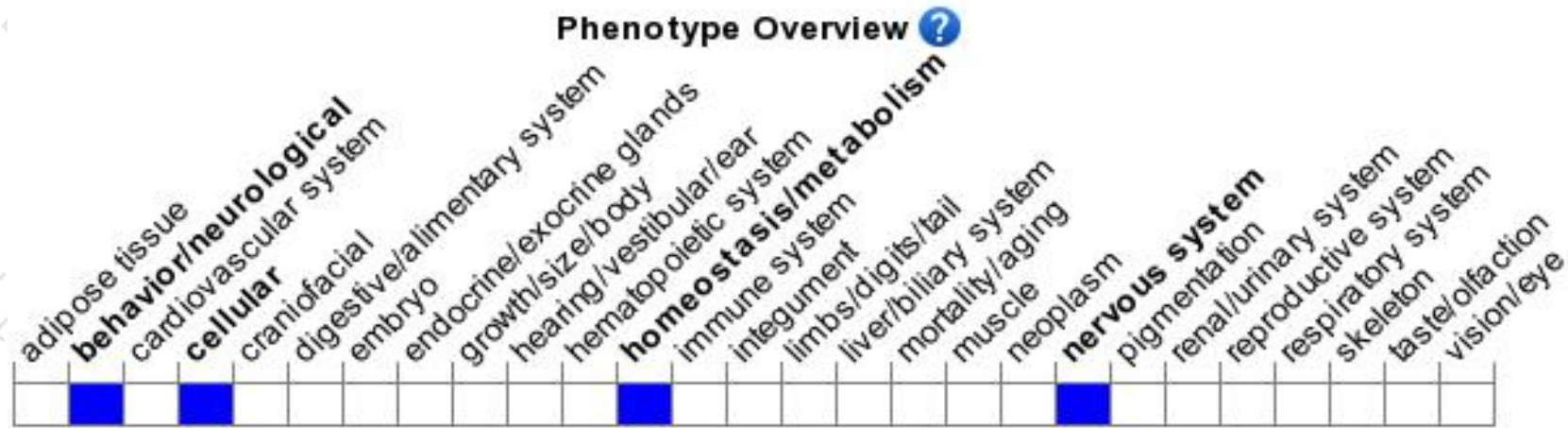
Genomic location distribution



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 mutant allele exhibit altered response to cocaine including decreased hyperlocomotor activity and sensitization at a lower dose. Mice homozygous for a kinase dead allele exhibit altered experience-dependent synaptic plasticity.

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

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