Rfc2 Cas9-KO Strategy

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Project Overview

Project Name	*Rfc2*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rfc2* gene. The schematic diagram is as follows:

➢ The *Rfc2* gene has 6 transcripts. According to the structure of *Rfc2* gene, exon2-exon8 of *Rfc2-201* (ENSMUST00000023867.7) transcript is recommended as the knockout region.The region contains 646bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rfc2* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

➢ The *Rfc2* gene is located on the Chr5. 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）

Rfc2   replication factor C (activator 1) 2 [*Mus musculus* (house mouse)]

Gene ID: 19718, updated on 13-Mar-2020

▲ Summary

Official Symbol	Rfc2 provided by MGI
Official Full Name	replication factor C (activator 1) 2 provided by MGI
Primary source	MGI:MGI:1341868
See related	Ensembl:ENSMUSG00000023104
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	40kDa; Recc2; AI326953; 2610008M13Rik
Expression	Ubiquitous expression in testis adult (RPKM 104.6), liver E14 (RPKM 51.0) and 27 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 5 G2; 5 74.68 cM

See Rfc2 in Genome Data Viewer

Exon count: 11

| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (134582690..134598328)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (135058560..135074198)

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rfc2-201	ENSMUST00000023867.7	4995	349aa	Protein coding	CCDS19722	Q4KL82 Q9WUK4	TSL:1 GENCODE basic APPRIS P1
Rfc2-203	ENSMUST00000201258.3	671	43aa	Nonsense mediated decay	-	A0A0J9YV68	CDS 5' incomplete TSL:3
Rfc2-206	ENSMUST00000202761.3	655	No protein	Processed transcript	-	-	TSL:3
Rfc2-205	ENSMUST00000201674.1	967	No protein	Retained intron	-	-	TSL:2
Rfc2-204	ENSMUST00000201464.1	831	No protein	Retained intron	-	-	TSL:2
Rfc2-202	ENSMUST00000200767.1	738	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Rfc2-201* transcript,The transcription is shown below
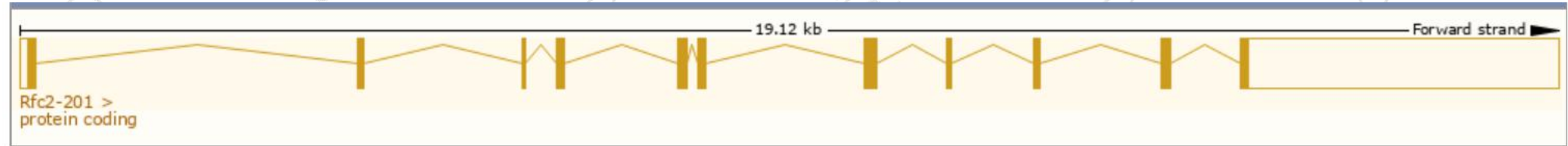
Genomic location distribution
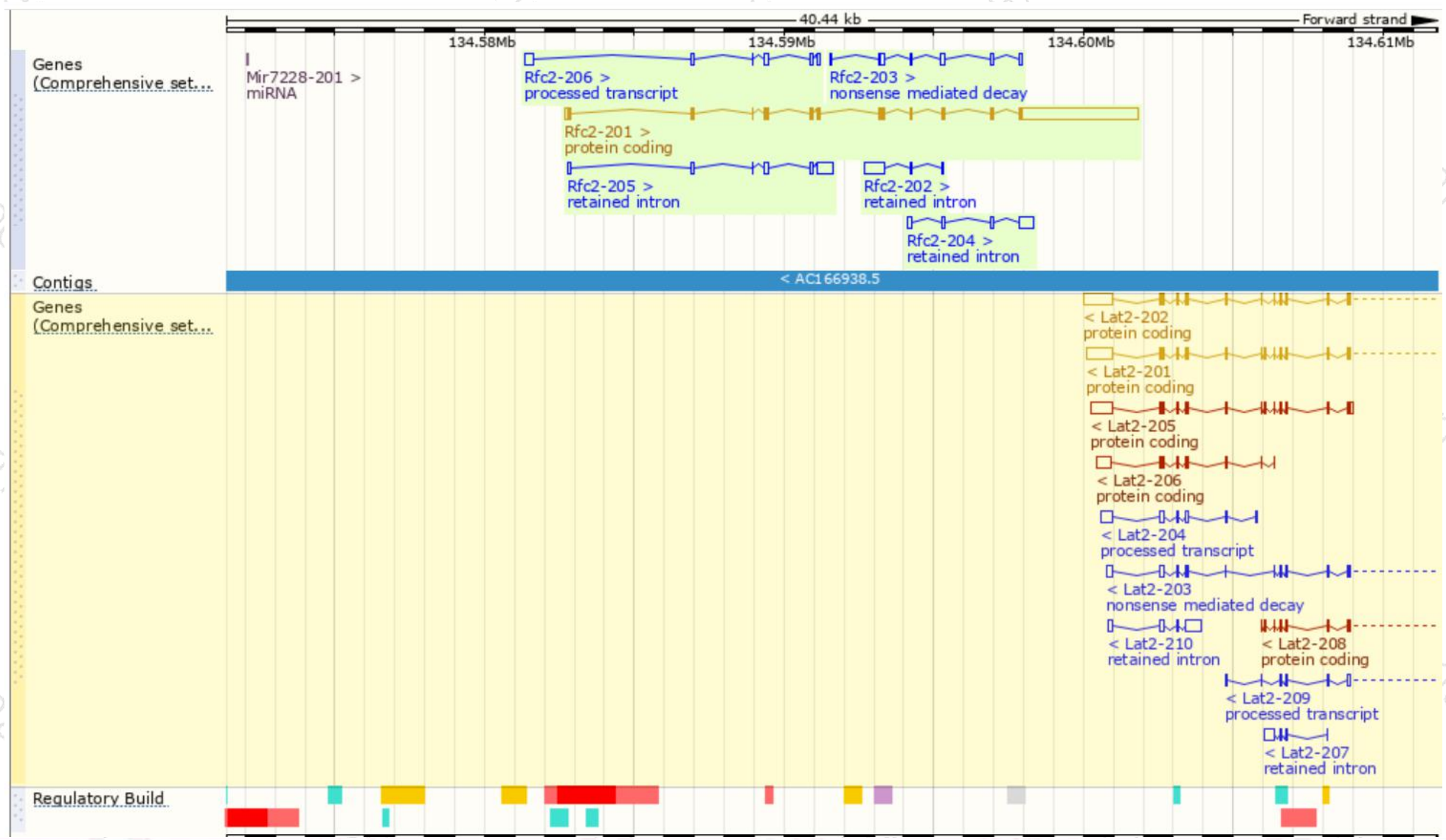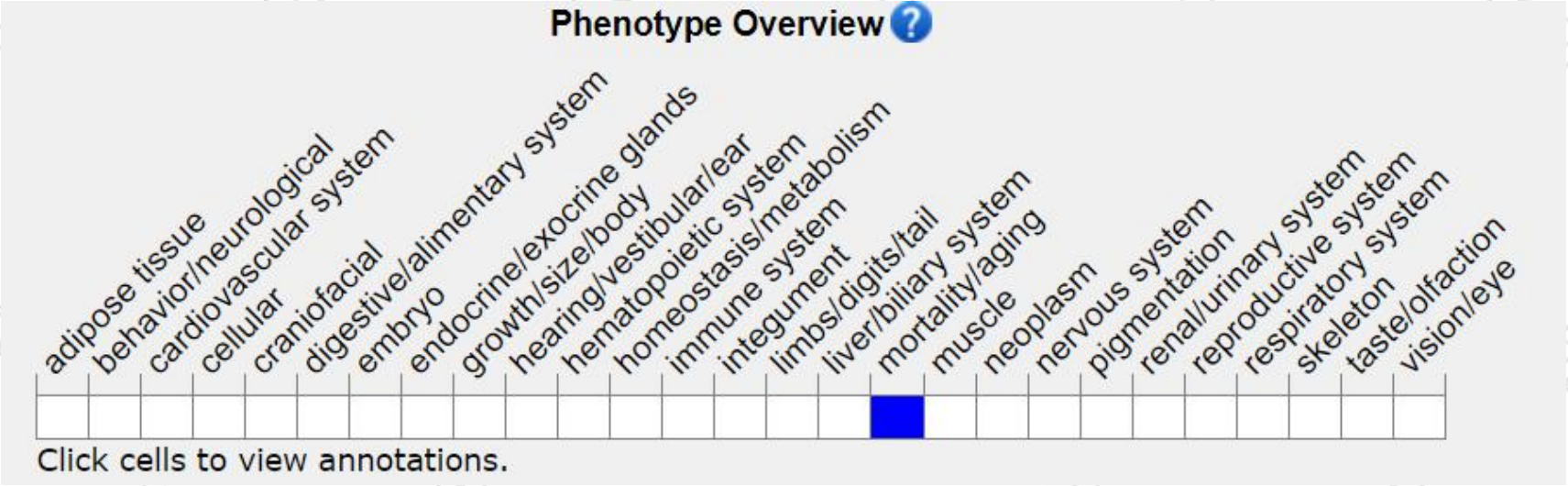
Protein domain

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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