U2af2 Cas9-KO Strategy

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Project Overview

Project Name	*U2af2*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *U2af2* gene. The schematic diagram is as follows:

➢ The *U2af2* gene has 9 transcripts. According to the structure of *U2af2* gene, exon2-exon6 of *U2af2-201* (ENSMUST00000005041.14) transcript is recommended as the knockout region.The region contains 554bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *U2af2* gene. The brief process is as follows: CRISPR/Cas9 system we

Notice

➢ The *U2af2* gene is located on the Chr7. 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）

U2af2 U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 [*Mus musculus* (house mouse)]

Gene ID: 22185, updated on 9-Feb-2020

▲ Summary

|	
Official Symbol	U2af2 provided by MGI
Official Full Name	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 provided by MGI
Primary source	MGI:MGI:98886
See related	Ensembl:ENSMUSG00000030435
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	65kDa
Expression	Ubiquitous expression in CNS E11.5 (RPKM 88.3), CNS E14 (RPKM 83.6) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 7; 7 A1

See U2af2 in Genome Data Viewer

Exon count: 14

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (5060885..5079945)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (5013784..5031541)

Chromosome 7 - NC_000073.6

[5038519 ▶   [5116911 ▶

Zfp580   U2af2   Rfp14

Gm15510   Epn1

Ccdc106
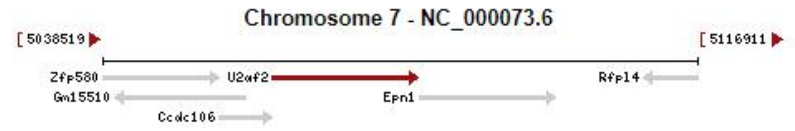
Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
U2af2-201	ENSMUST00000005041.14	2183	471aa	Protein coding	CCDS85208	Q80XR5	TSL:1	GENCODE basic	APPRIS ALT1
U2af2-209	ENSMUST00000209099.1	2088	475aa	Protein coding	CCDS57476	P26369	TSL:1	GENCODE basic	APPRIS P3
U2af2-202	ENSMUST00000165399.1	1810	307aa	Protein coding	-	Q3KQM4	TSL:5	GENCODE basic	
U2af2-204	ENSMUST00000207498.1	1455	95aa	Nonsense mediated decay	-	A0A140LJK3	CDS 5' incomplete	TSL:5	
U2af2-203	ENSMUST00000207097.1	626	111aa	Nonsense mediated decay	-	A0A140LJ08	TSL:3		
U2af2-206	ENSMUST00000207926.1	2412	No protein	Retained intron	-	-	TSL:2		
U2af2-207	ENSMUST00000207960.1	904	No protein	Retained intron	-	-	TSL:2		
U2af2-208	ENSMUST00000208419.1	684	No protein	Retained intron	-	-	TSL:2		
U2af2-205	ENSMUST00000207523.1	486	No protein	Retained intron	-	-	TSL:2		

The strategy is based on the design of *U2af2-209* transcript,The transcription is shown below

17.69 kb

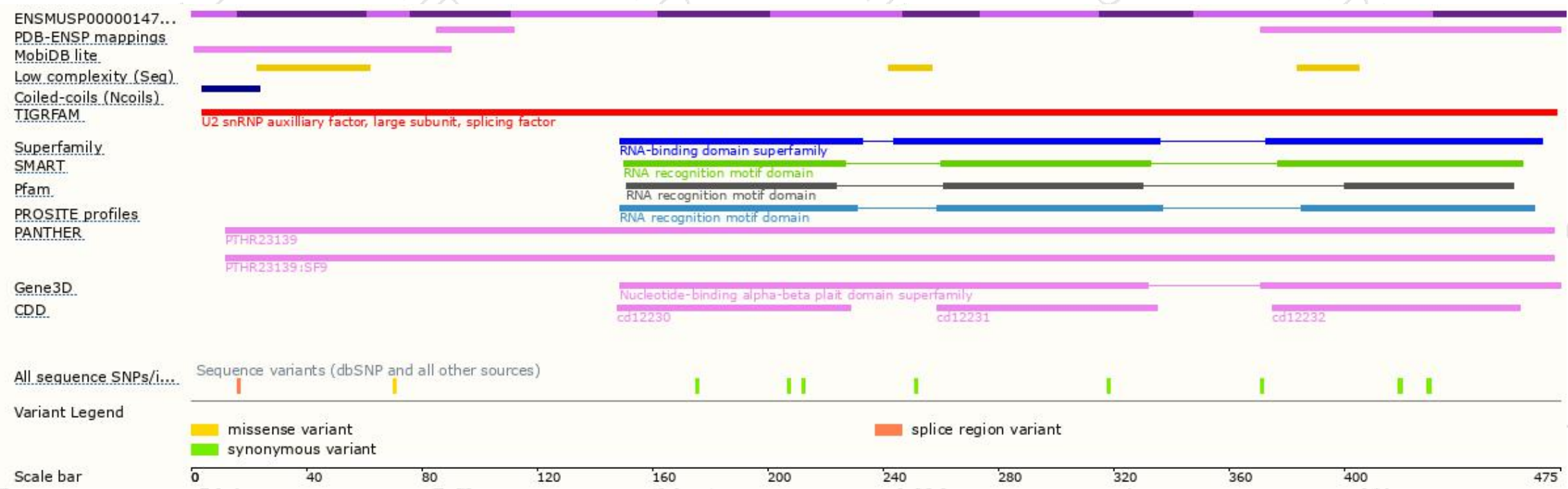Forward strand

U2af2-209 >
protein coding
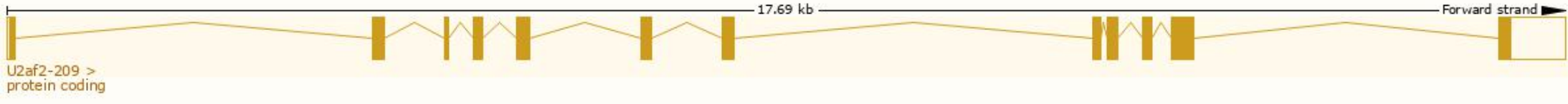
Genomic location distribution
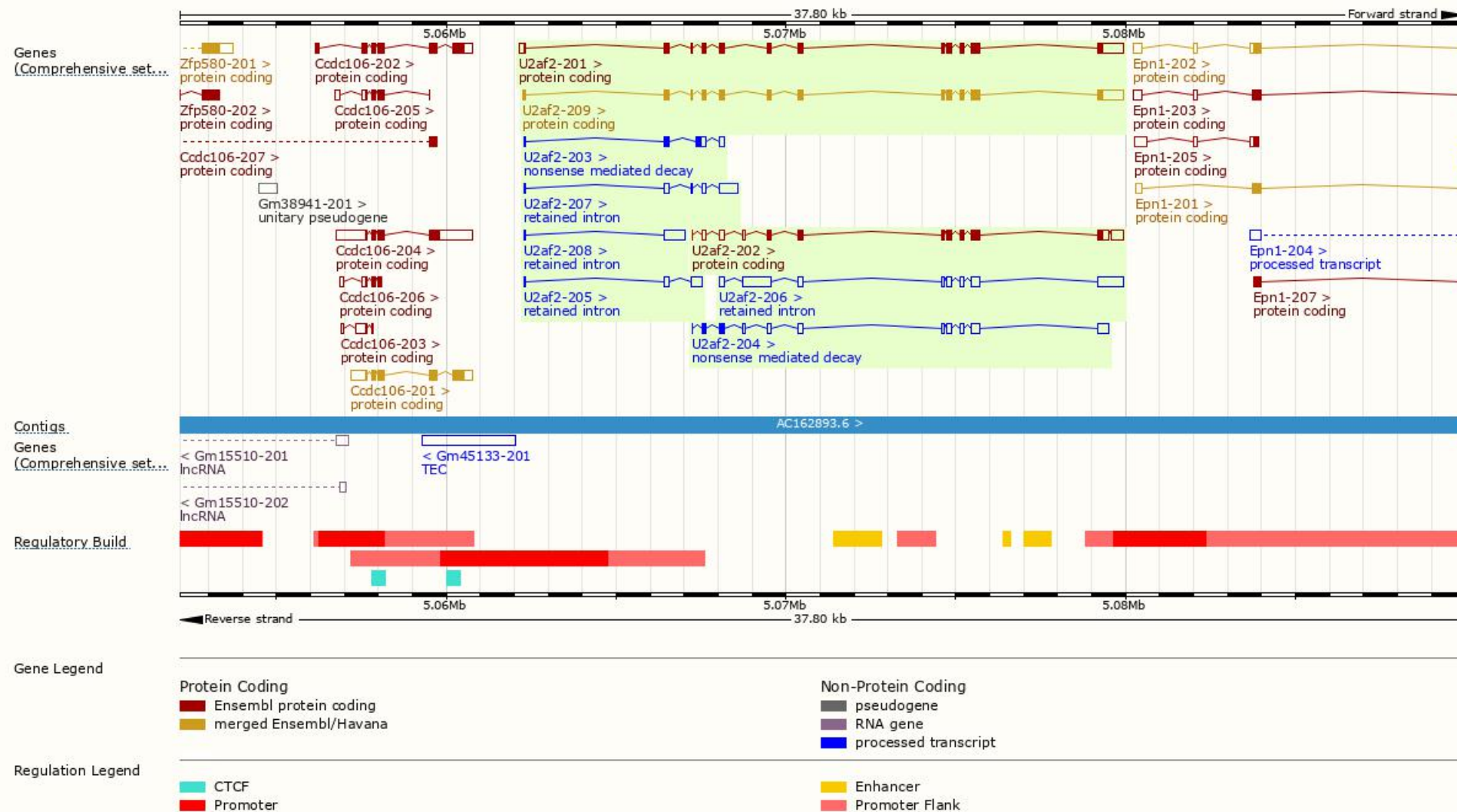
Protein domain

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