

Plaur Cas9-KO Strategy

Designer:

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Project Overview



Project Name

Plaur

Project type

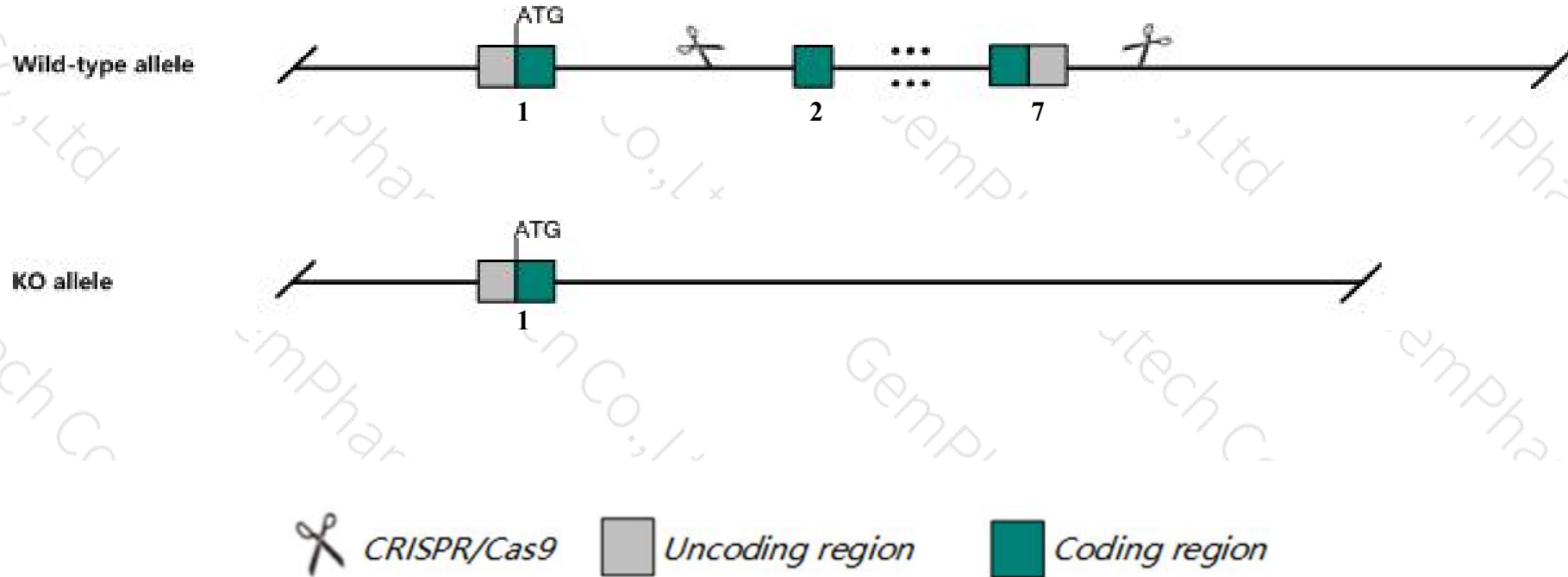
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Plaur* gene has 6 transcripts. According to the structure of *Plaur* gene, exon2-exon7 of *Plaur-201* (ENSMUST0000002284.10) transcript is recommended as the knockout region. The region contains 926bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plaur* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a null allele exhibit chronic inflammation, macrophage dysfunction, and reduced angiogenesis. Homozygotes for another null allele show neutrophil dysfunction, increased anxiety, loss of GABAergic neurons, myoclonus, and susceptibility to bacterial infection and PTZ -induced seizures.
- The *Plaur* 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)

Plaur plasminogen activator, urokinase receptor [Mus musculus (house mouse)]

Gene ID: 18793, updated on 31-Jan-2019

Summary



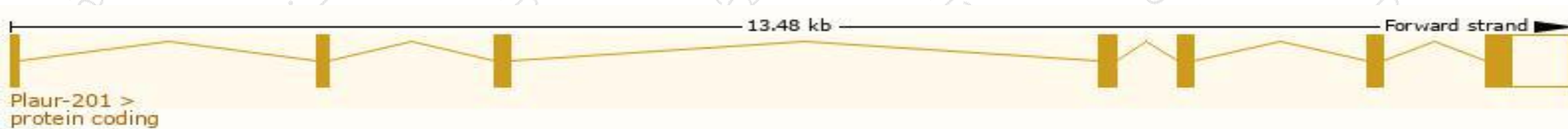
Official Symbol	Plaur provided by MGI
Official Full Name	plasminogen activator, urokinase receptor provided by MGI
Primary source	MGI:MGI:97612
See related	Ensembl:ENSMUSG00000046223
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cd87, u-PAR, uPAR
Expression	Broad expression in lung adult (RPKM 24.3), spleen adult (RPKM 16.2) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

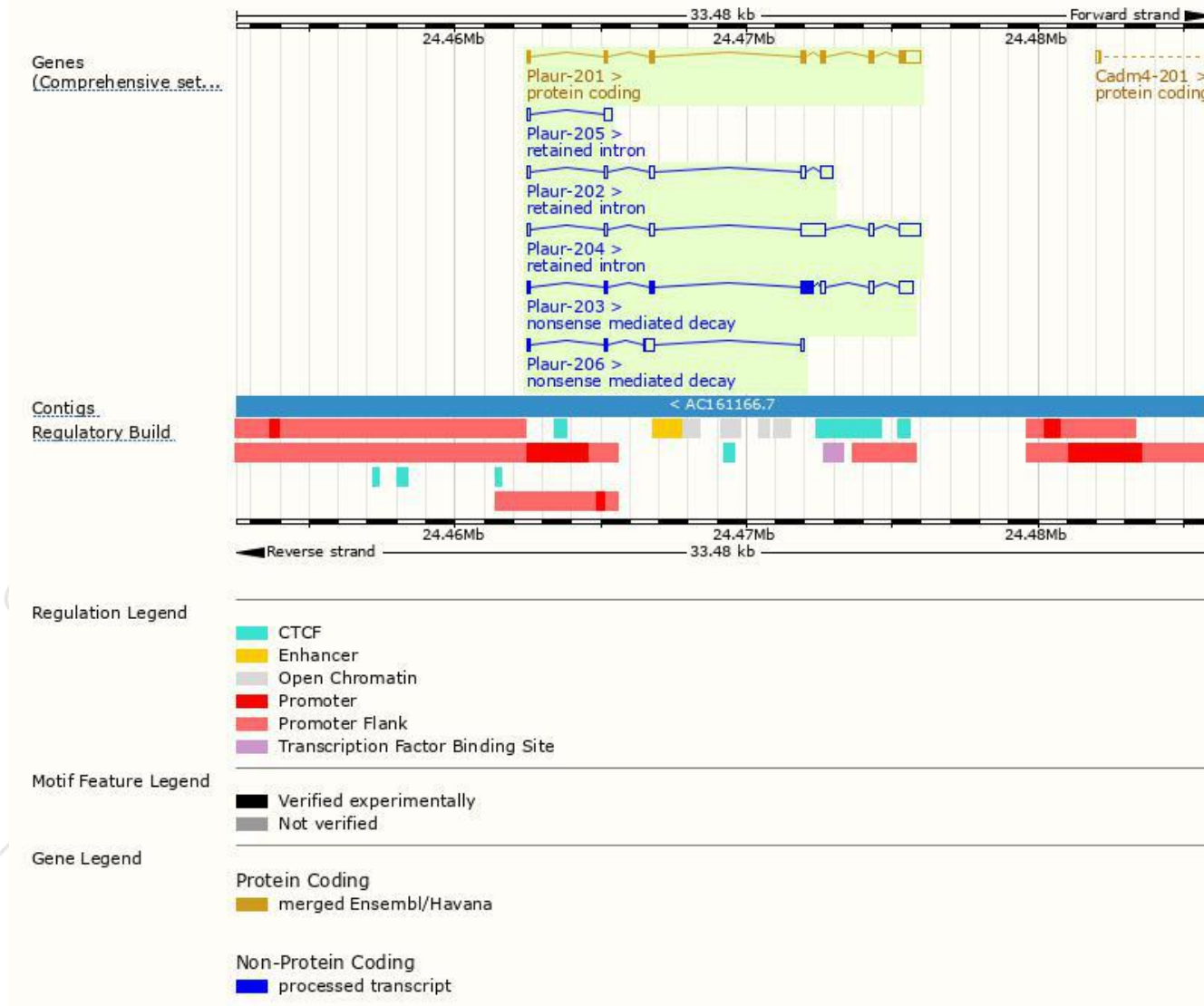
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plaur-201	ENSMUST00000002284.10	1506	327aa	Protein coding	CCDS20950	P35456 Q545X5	TSL:1 GENCODE basic APPRIS P1
Plaur-203	ENSMUST00000206514.1	1456	222aa	Nonsense mediated decay	-	A0A0U1RNN0	TSL:1
Plaur-206	ENSMUST00000206935.1	604	74aa	Nonsense mediated decay	-	A0A0U1RNF3	TSL:3
Plaur-204	ENSMUST00000206636.1	2009	No protein	Retained intron	-	-	TSL:2
Plaur-202	ENSMUST00000205877.1	872	No protein	Retained intron	-	-	TSL:2
Plaur-205	ENSMUST00000206693.1	347	No protein	Retained intron	-	-	TSL:3

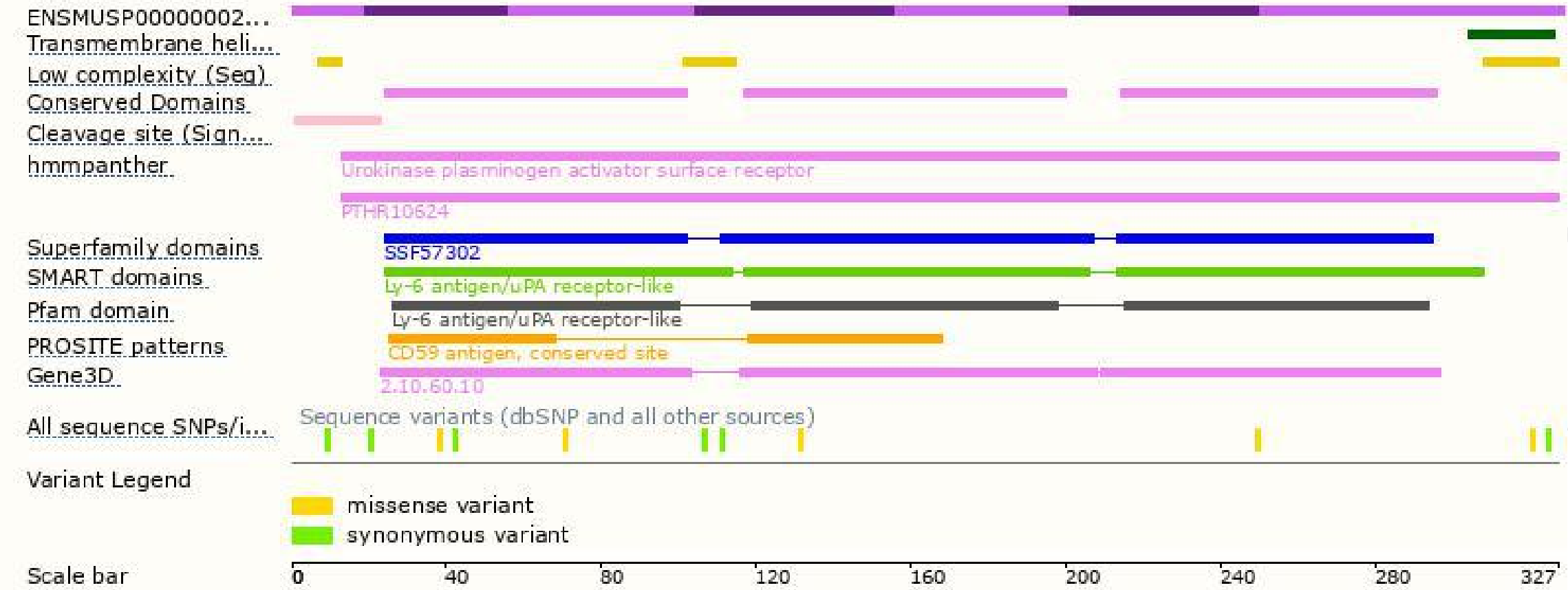
The strategy is based on the design of *Plaur-201* transcript, The transcription is shown below



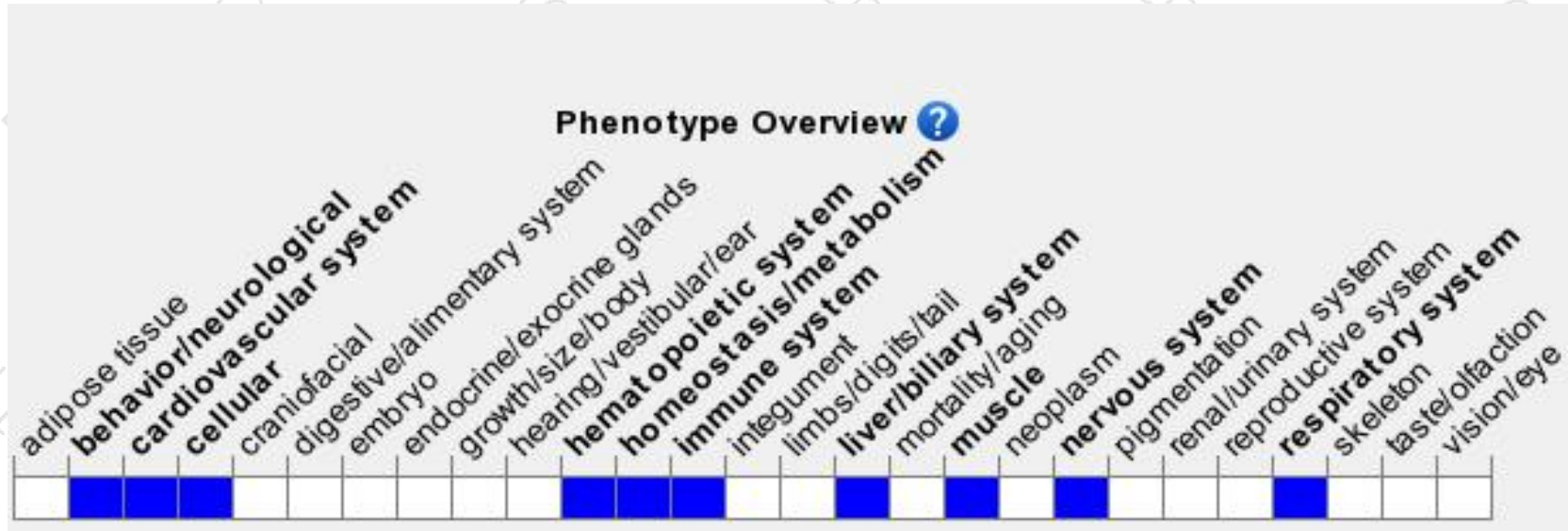
Genomic location distribution



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, Homozygotes for a null allele exhibit chronic inflammation, macrophage dysfunction, and reduced angiogenesis. Homozygotes for another null allele show neutrophil dysfunction, increased anxiety, 1 GABAergic neurons, myoclonus, and susceptibility to bacterial infection and PTZ -induced seizures.

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

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