

Selp Cas9-KO Strategy

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Project Overview

Project Name

Selp

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Selp* gene has 5 transcripts. According to the structure of *Selp* gene, exon2-exon5 of *Selp*-205 (ENSMUST00000162746.1) transcript is recommended as the knockout region. The region contains 772bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Selp* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit mildly attenuated inflammatory responses, increased numbers of circulating neutrophils, lack of leukocyte rolling in mesenteric venules, and increased survival after *Plasmodium berghei* infection.
- The *Selp* gene is located on the Chr1. 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)

Selp selectin, platelet [*Mus musculus* (house mouse)]

Gene ID: 20344, updated on 13-Aug-2019

Summary

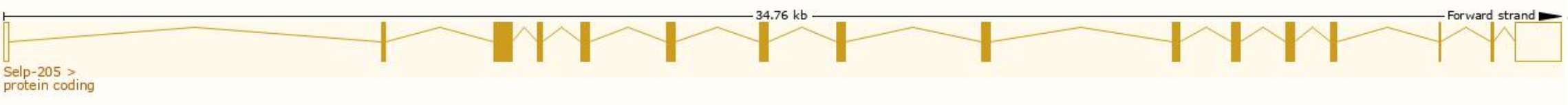
Official Symbol	Selp provided by MGI
Official Full Name	selectin, platelet provided by MGI
Primary source	MGI:MGI:98280
See related	Ensembl:ENSMUSG00000026580
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Grmp; CD62P; LECAM3; PADGEM; GMP-140
Expression	Broad expression in subcutaneous fat pad adult (RPKM 2.1), bladder adult (RPKM 1.8) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Selp-205	ENSMUST00000162746.1	3438	768aa	Protein coding	CCDS48422	Q01102	TSL:1 GENCODE basic APPRIS P1
Selp-203	ENSMUST00000161152.7	917	46aa	Nonsense mediated decay	-	F6TL88	CDS 5' incomplete TSL:1
Selp-202	ENSMUST00000161020.7	1392	No protein	Retained intron	-	-	TSL:1
Selp-204	ENSMUST00000162102.1	778	No protein	Retained intron	-	-	TSL:5
Selp-201	ENSMUST00000160000.1	339	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Selp-205* transcript,The transcription is shown below



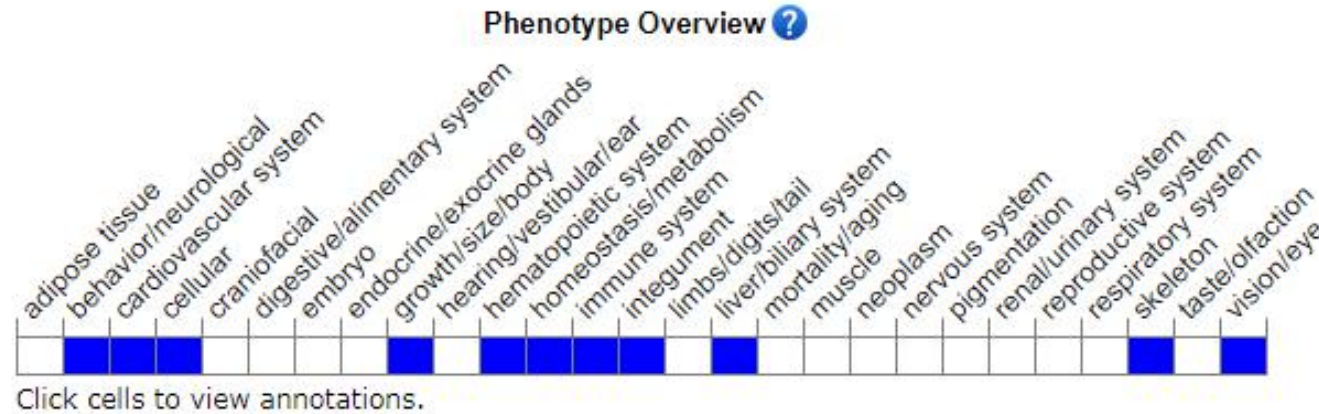
Genomic location distribution



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 targeted null mutations exhibit mildly attenuated inflammatory responses, increased numbers of circulating neutrophils, lack of leukocyte rolling in mesenteric venules, and increased survival after *Plasmodium berghei* infection.

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

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