

Csf1r Cas9-KO Strategy

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Project Overview



Project Name

Csf1r

Project type

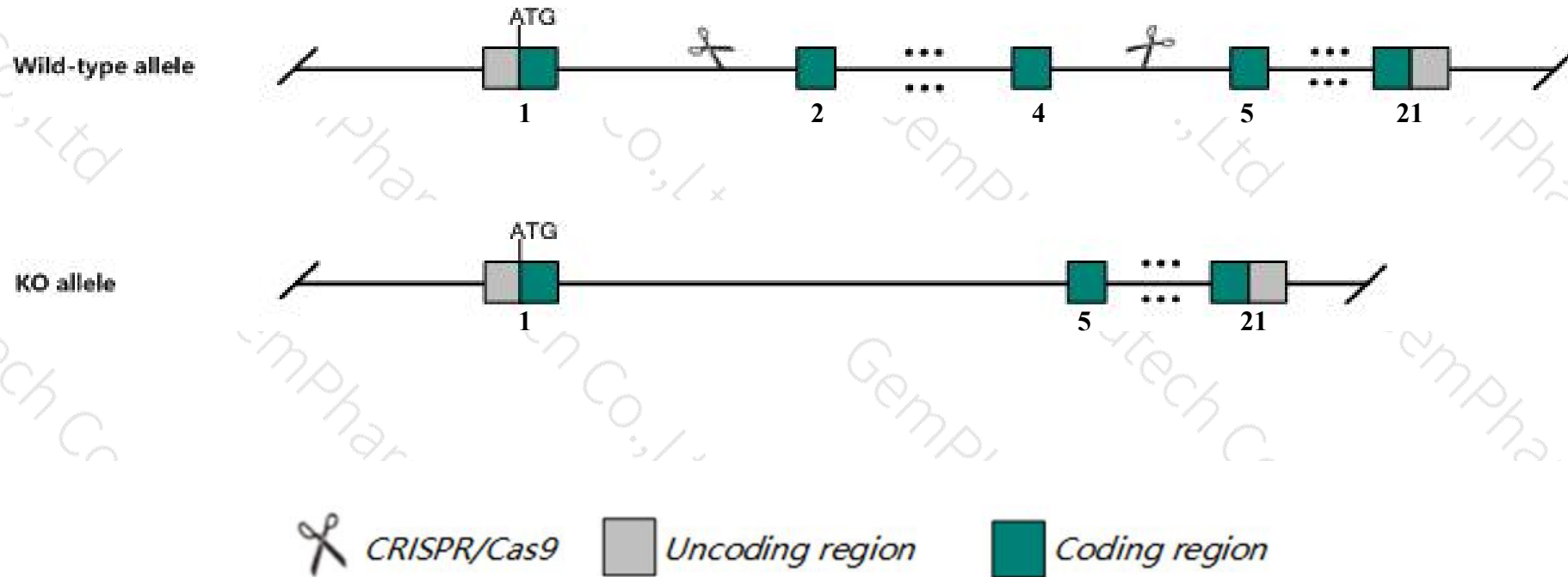
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Csflr* gene has 6 transcripts. According to the structure of *Csflr* gene, exon2-exon4 of *Csflr-202* (ENSMUST00000115268.3) transcript is recommended as the knockout region. The region contains 680bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Csflr* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a targeted null mutation exhibit skeletal, sensory, and reproductive abnormalities associated with severe deficiencies in osteoclasts, macrophages, and brain microglia.
- The *Csf1r* gene is located on the Chr18. 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)

Csf1r colony stimulating factor 1 receptor [Mus musculus (house mouse)]

Gene ID: 12978, updated on 23-Mar-2019

Summary



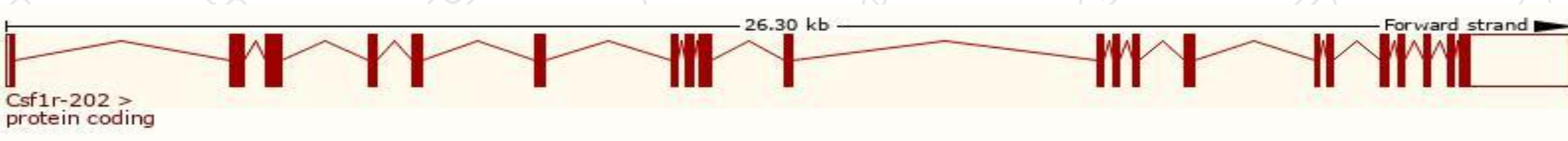
Official Symbol	Csf1r provided by MGI
Official Full Name	colony stimulating factor 1 receptor provided by MGI
Primary source	MGI:MGI:1339758
See related	Ensembl:ENSMUSG00000024621
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323359, CD115, CSF-1R, Csfmr, Fim-2, Fim2, Fms, M-CSF-R, M-CSFR
Expression	Broad expression in spleen adult (RPKM 69.7), placenta adult (RPKM 34.8) and 23 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

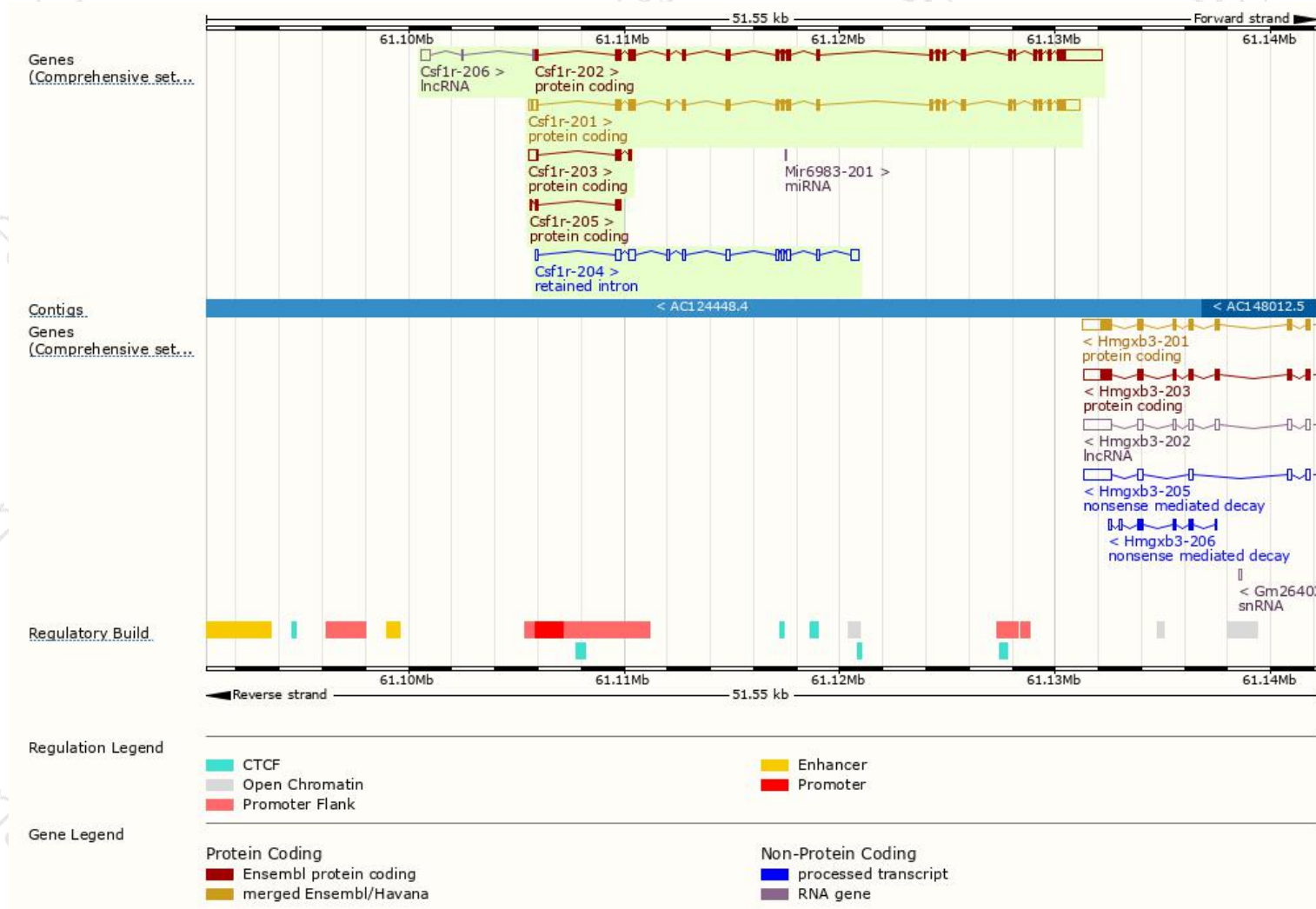
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Csf1r-202	ENSMUST00000115268.3	4701	977aa	Protein coding	CCDS29280	P09581 Q0P635	TSL:1 GENCODE basic APPRIS P1
Csf1r-201	ENSMUST00000025523.12	3870	977aa	Protein coding	CCDS29280	P09581 Q0P635	TSL:1 GENCODE basic APPRIS P1
Csf1r-203	ENSMUST00000235447.1	776	139aa	Protein coding	-	-	CDS 3' incomplete
Csf1r-205	ENSMUST00000237706.1	416	103aa	Protein coding	-	-	CDS 3' incomplete
Csf1r-206	ENSMUST00000237873.1	465	No protein	Processed transcript	-	-	
Csf1r-204	ENSMUST00000237485.1	2035	No protein	Retained intron	-	-	

The strategy is based on the design of *Csf1r-202* transcript, The transcription is shown below



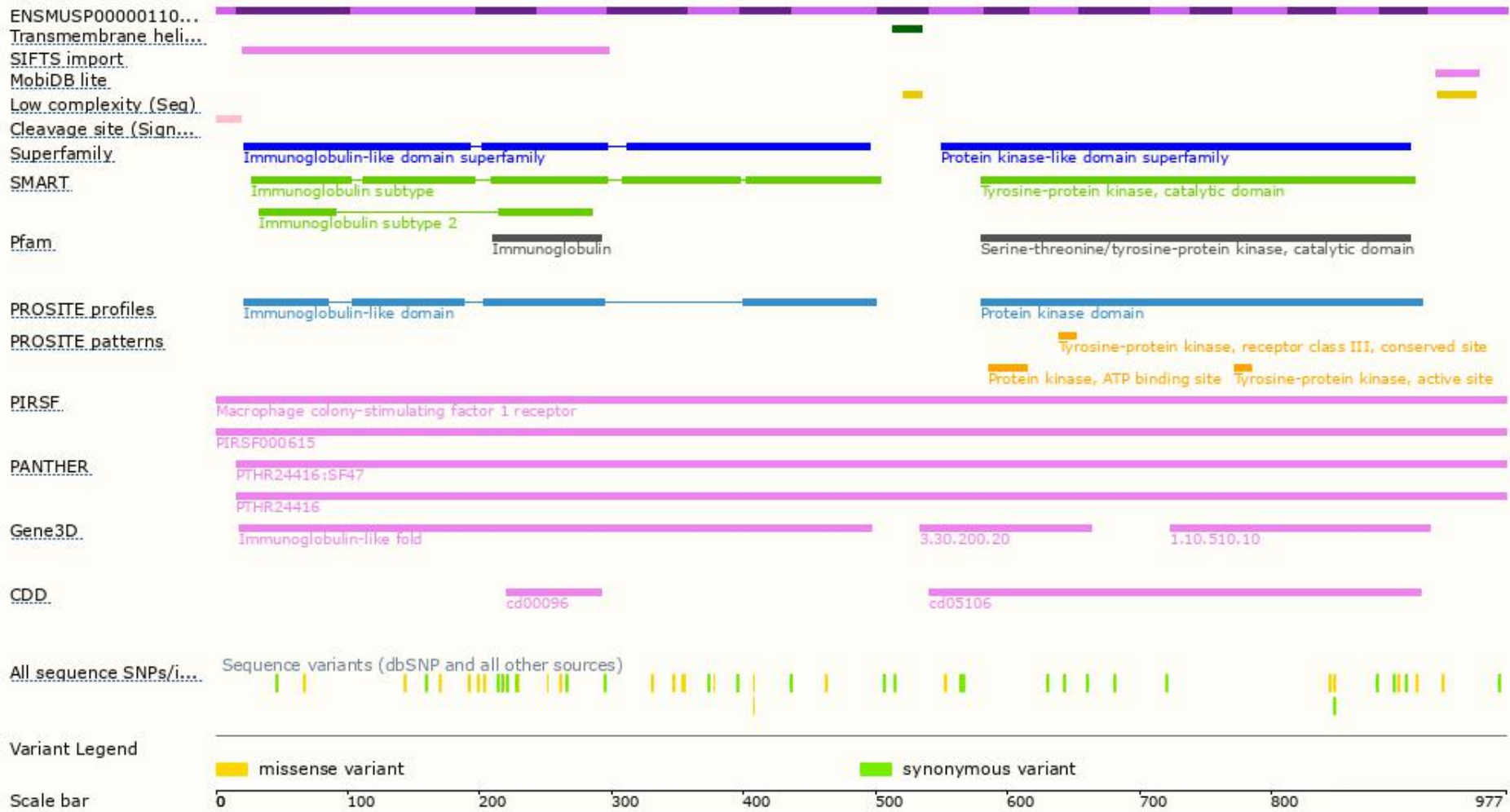
Genomic location distribution



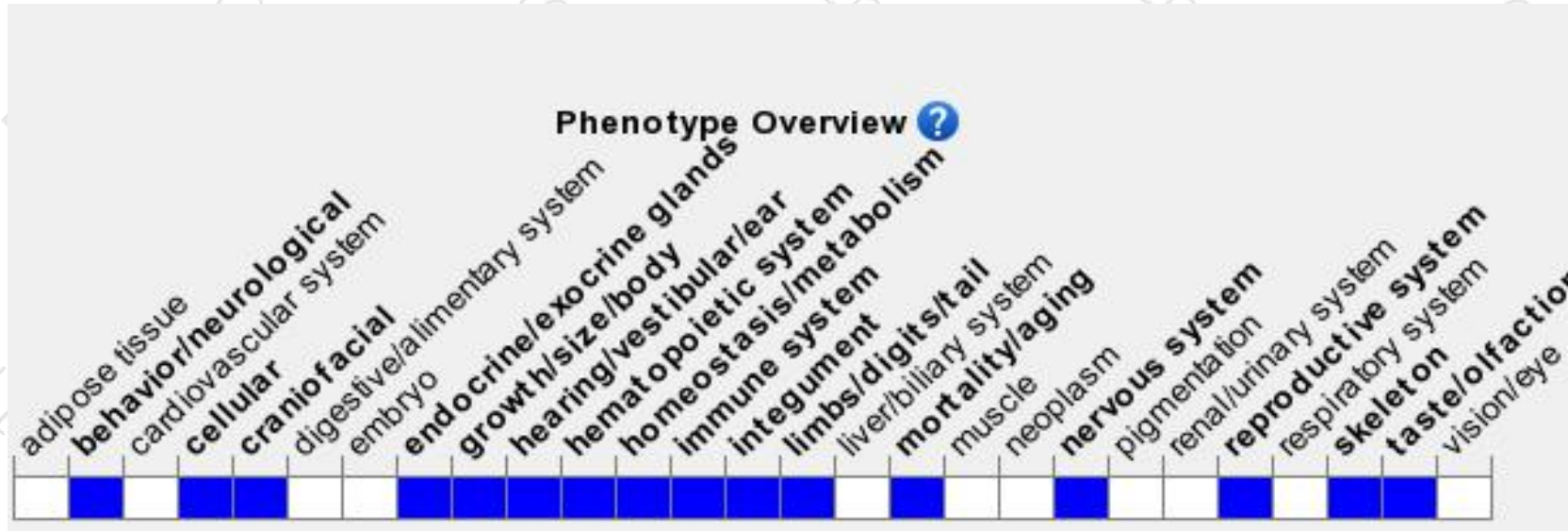
Protein domain



集萃药康
GemPharmatech



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 targeted null mutation exhibit skeletal, sensory, and reproductive abnormalities associated with severe deficiencies in osteoclasts, macrophages, and brain microglia.

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

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