

Csf1 Cas9-KO Strategy

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Project Overview



Project Name

Csf1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Csf1* gene. The schematic diagram is as follows:



- The *Csf1* gene has 7 transcripts. According to the structure of *Csf1* gene, exon2-exon5 of *Csf1-201* (ENSMUST00000014743.9) transcript is recommended as the knockout region. The region contains 505bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Csf1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygotes for a spontaneous mutation exhibit lack of incisors, a broad domed skull, short thick limb bones with reduced marrow cavities, impaired hearing and vision, and reduced fertility in females.
- The *Csf1* gene is located on the Chr3. 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)

Csf1 colony stimulating factor 1 (macrophage) [Mus musculus (house mouse)]

Gene ID: 12977, updated on 9-Apr-2019

Summary



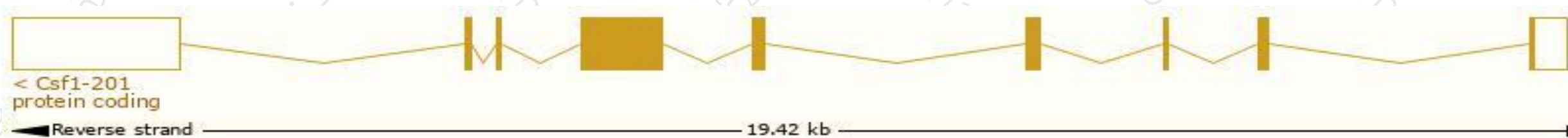
Official Symbol	Csf1 provided by MGI
Official Full Name	colony stimulating factor 1 (macrophage) provided by MGI
Primary source	MGI:MGI:1339753
See related	Ensembl:ENSMUSG00000014599
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C87615, Csfm, MCSF, op
Expression	Ubiquitous expression in spleen adult (RPKM 14.8), mammary gland adult (RPKM 13.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

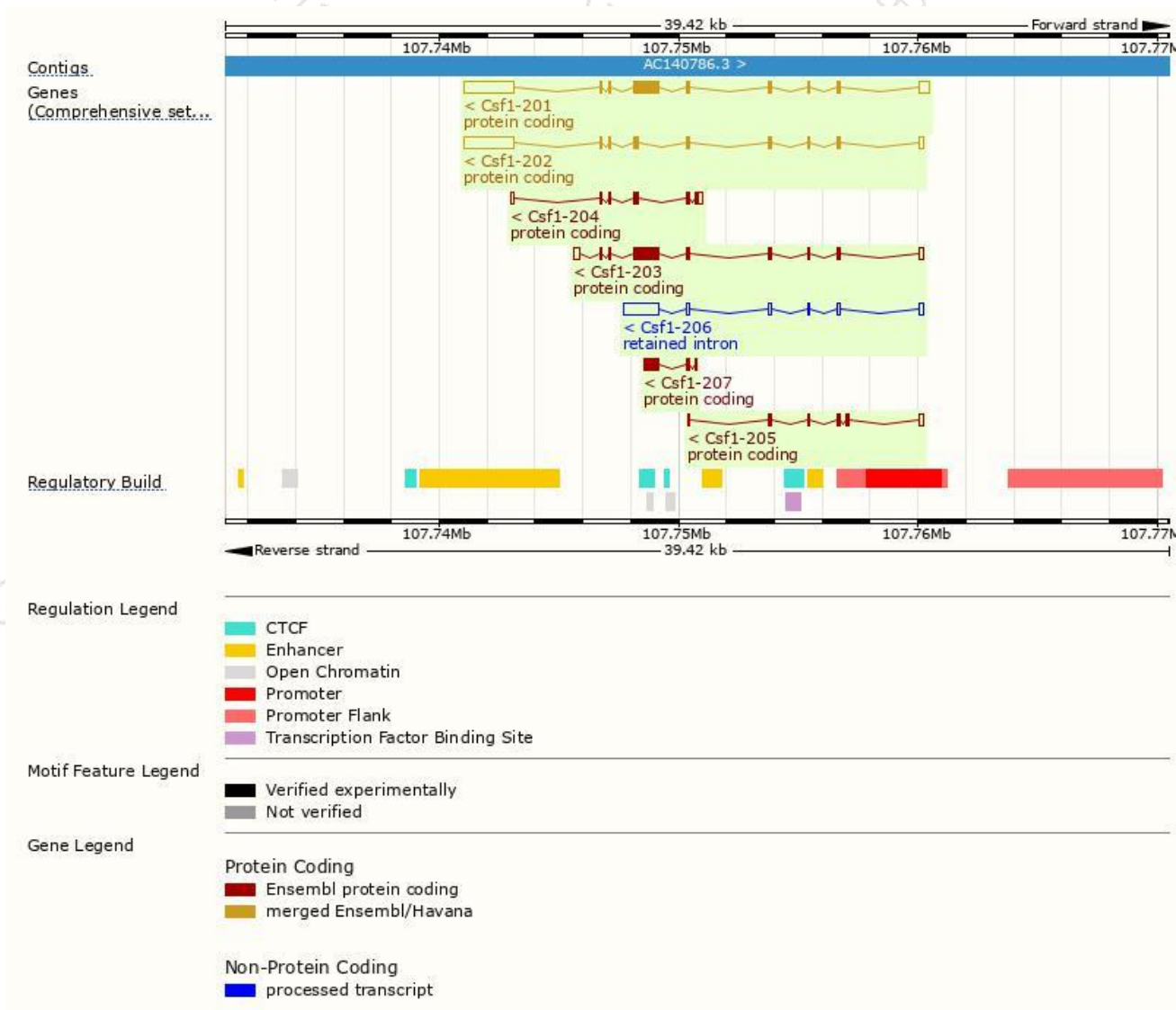
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Csf1-201	ENSMUST00000014743.9	4176	552aa	Protein coding	CCDS17740	P07141	TSL:1 GENCODE basic APPRIS P3
Csf1-202	ENSMUST00000118593.7	3058	257aa	Protein coding	CCDS51044	P07141	TSL:1 GENCODE basic APPRIS ALT2
Csf1-203	ENSMUST00000120243.7	2097	552aa	Protein coding	CCDS17740	P07141	TSL:1 GENCODE basic APPRIS P3
Csf1-207	ENSMUST00000156820.1	836	278aa	Protein coding	-	F6RNW8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Csf1-204	ENSMUST00000120654.7	821	163aa	Protein coding	-	D3YTW1	TSL:3 GENCODE basic
Csf1-205	ENSMUST00000153114.1	773	182aa	Protein coding	-	D3Z090	CDS 3' incomplete TSL:2
Csf1-206	ENSMUST00000155557.1	2160	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Csf1-201* transcript, The transcription is shown below



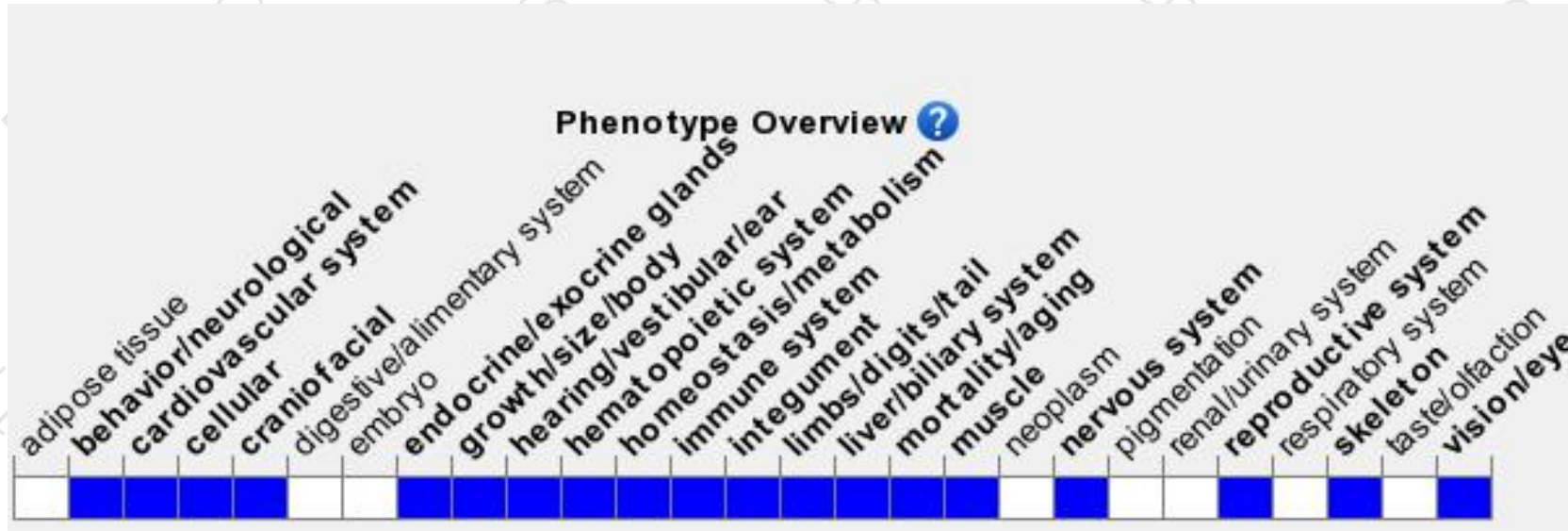
Genomic location distribution



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 spontaneous mutation exhibit lack of incisors, a broad domed skull, short thick limb bones with reduced marrow cavities, impaired hearing and vision, and reduced fertility in females.

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

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