

Socs1 Cas9-KO Strategy

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Project Overview

Project Name

Socs1

Project type

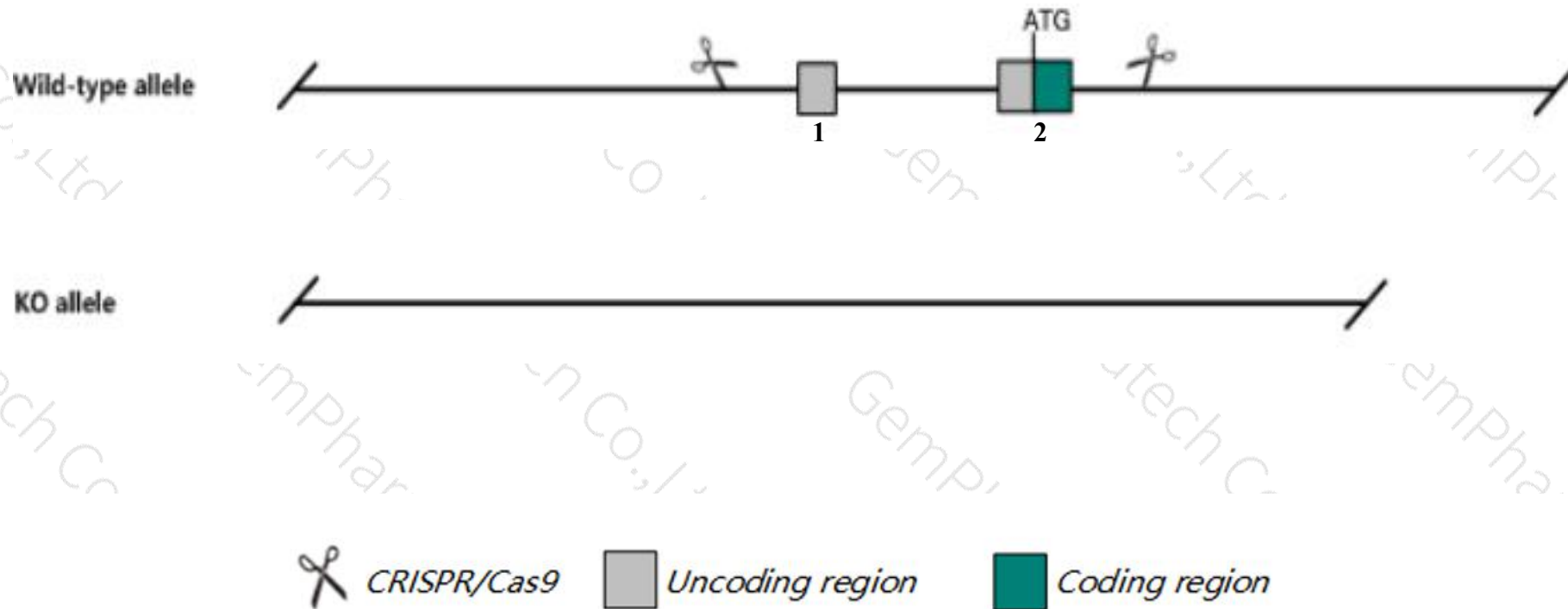
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Socs1* gene. The schematic diagram is as follows:



Technical routes

- The *Socs1* gene has 2 transcripts. According to the structure of *Socs1* gene, exon1-exon2 of *Socs1*-202(ENSMUST00000229866.1) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Socs1* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, homozygotes for targeted null mutations exhibit retarded growth, hyperresponsiveness to endogenous interferon gamma, hepatitis with fatty degeneration, lymphopenia due to excess apoptosis, monocytic organ infiltration, and lethality by 3 weeks of age.
- This strategy may affect the 5-terminal regulation of *Socs1* gene and the 3-terminal regulation of *Tnp2* gene.
- The *Socs1* gene is located on the Chr16. 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)

Socs1 suppressor of cytokine signaling 1 [Mus musculus (house mouse)]

Gene ID: 12703, updated on 13-Mar-2020

Summary



Official Symbol Socs1 provided by [MGI](#)

Official Full Name suppressor of cytokine signaling 1 provided by [MGI](#)

Primary source [MGI:MGI:1354910](#)

See related [Ensembl:ENSMUSG00000038037](#)

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 Cish1, Cish7, JAB, SOCS-1, SSI-1

Expression Biased expression in thymus adult (RPKM 221.8), adrenal adult (RPKM 34.5) and 7 other tissues [See more](#)

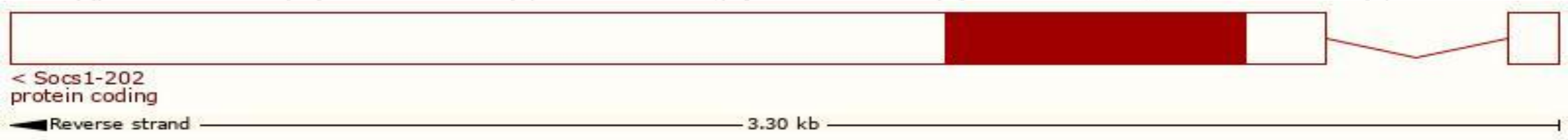
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

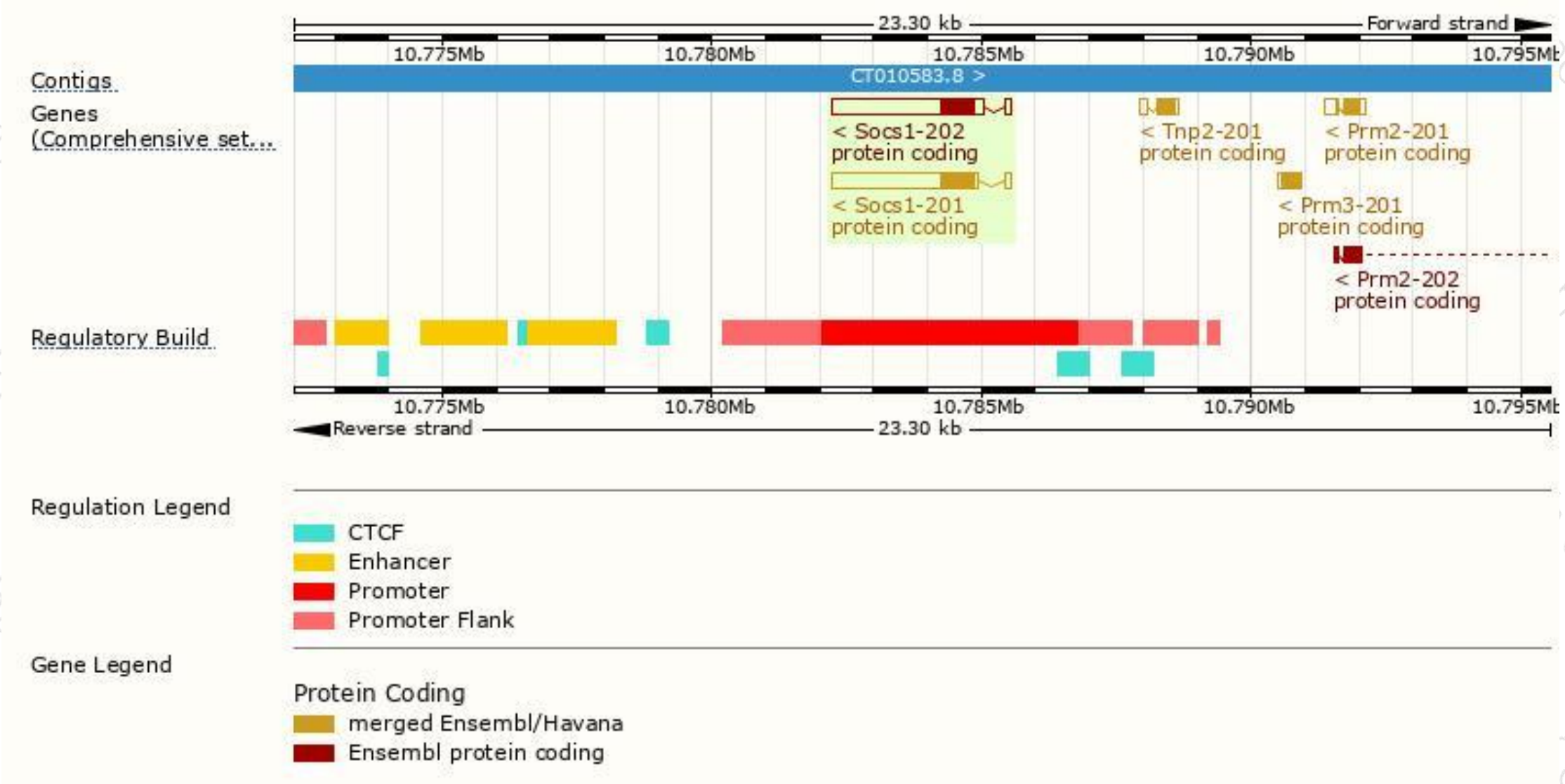
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Socs1-202	ENSMUST00000229866.1	2908	212aa	Protein coding	CCDS27952	Q35716	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Socs1-201	ENSMUST00000038099.5	2785	212aa	Protein coding	CCDS27952	Q35716	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

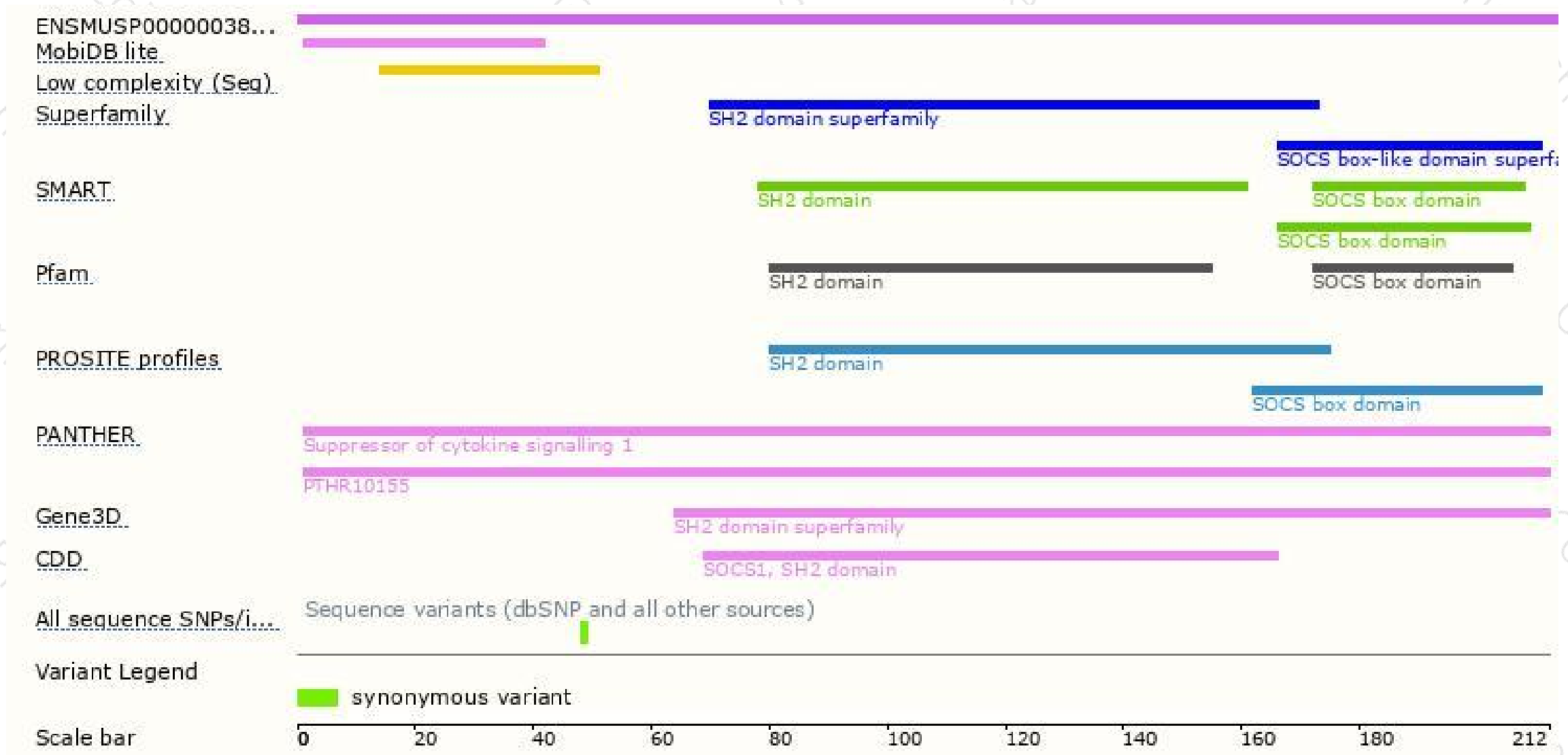
The strategy is based on the design of *Socs1-202* transcript,the transcription is shown below:



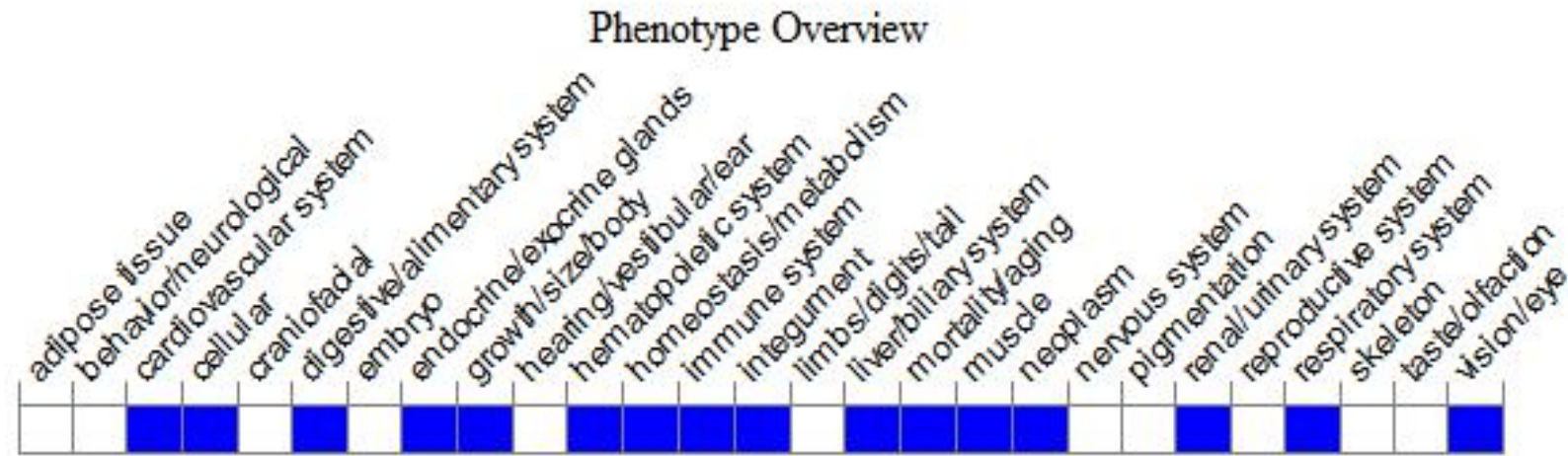
Genomic location distribution



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/>).

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

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