

Stat2 Cas9-KO Strategy

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Project Overview

Project Name

Stat2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stat2* gene. The schematic diagram is as follows:



- The *Stat2* gene has 8 transcripts. According to the structure of *Stat2* gene, exon2-exon8 of *Stat2-201* (ENSMUST00000085708.2) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stat2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Immune response is impaired in homozygous null mice.
- The *Stat2* gene is located on the Chr10. 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)

Stat2 signal transducer and activator of transcription 2 [Mus musculus (house mouse)]

Gene ID: 20847, updated on 19-Feb-2019

Summary



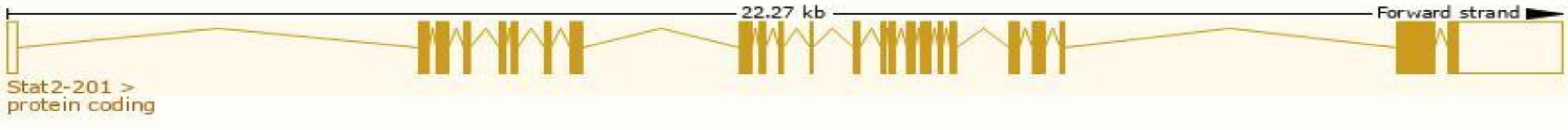
Official Symbol	Stat2 provided by MGI
Official Full Name	signal transducer and activator of transcription 2 provided by MGI
Primary source	MGI:MGI:103039
See related	Ensembl:ENSMUSG00000040033
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1600010G07Rik, AW496480
Expression	Ubiquitous expression in cerebellum adult (RPKM 14.3), thymus adult (RPKM 11.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

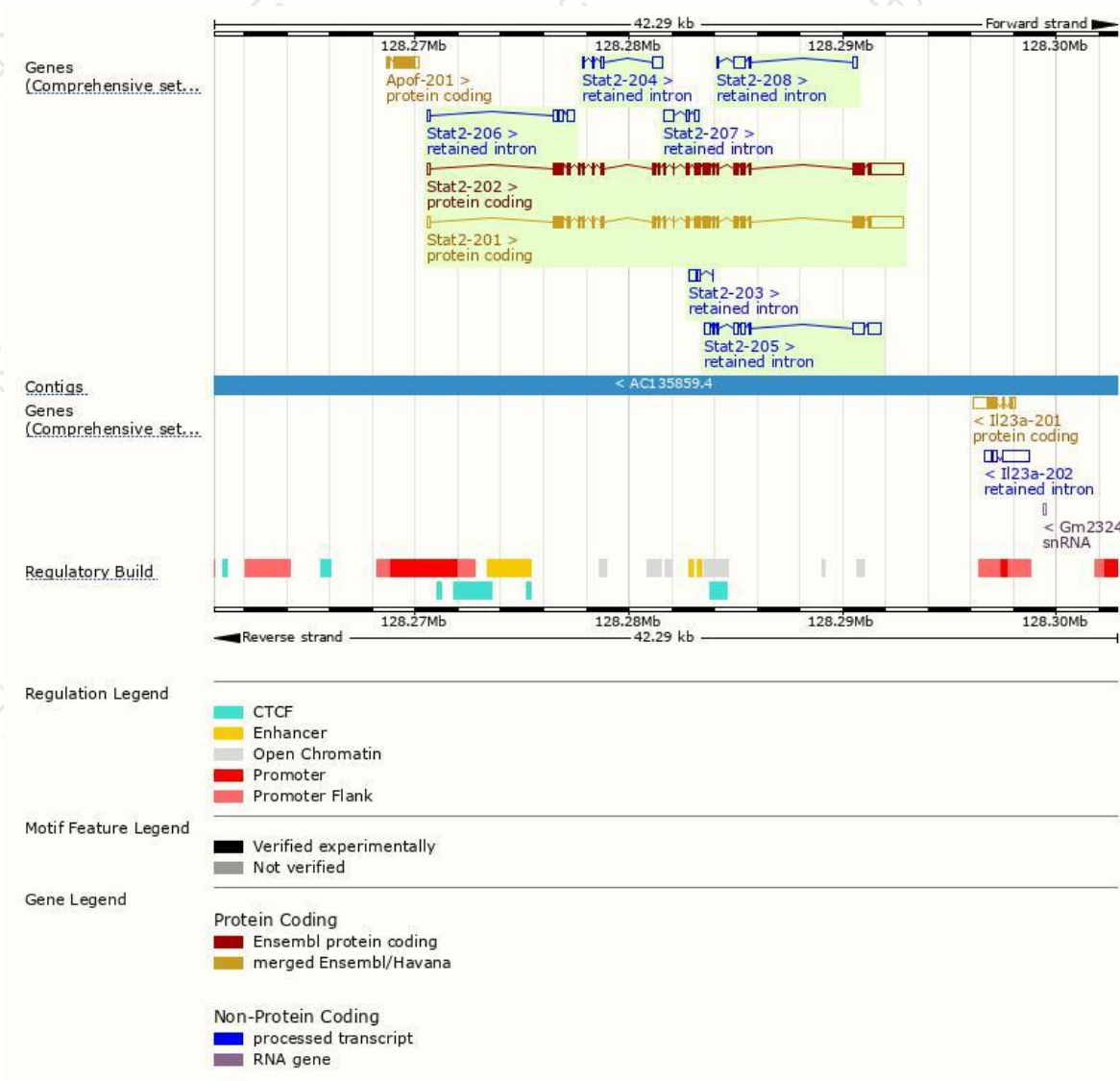
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stat2-201	ENSMUST00000085708.2	4394	922aa	Protein coding	CCDS24269	Q9QXJ2	TSL:1 GENCODE basic APPRIS P2
Stat2-202	ENSMUST00000105238.9	4397	923aa	Protein coding	-	E9QJX9	TSL:1 GENCODE basic APPRIS ALT2
Stat2-205	ENSMUST00000218862.1	1873	No protein	Retained intron	-	-	TSL:5
Stat2-208	ENSMUST00000220277.1	861	No protein	Retained intron	-	-	TSL:3
Stat2-204	ENSMUST00000217852.1	799	No protein	Retained intron	-	-	TSL:3
Stat2-207	ENSMUST00000220142.1	747	No protein	Retained intron	-	-	TSL:3
Stat2-206	ENSMUST00000218863.1	736	No protein	Retained intron	-	-	TSL:2
Stat2-203	ENSMUST00000217727.1	459	No protein	Retained intron	-	-	TSL:3

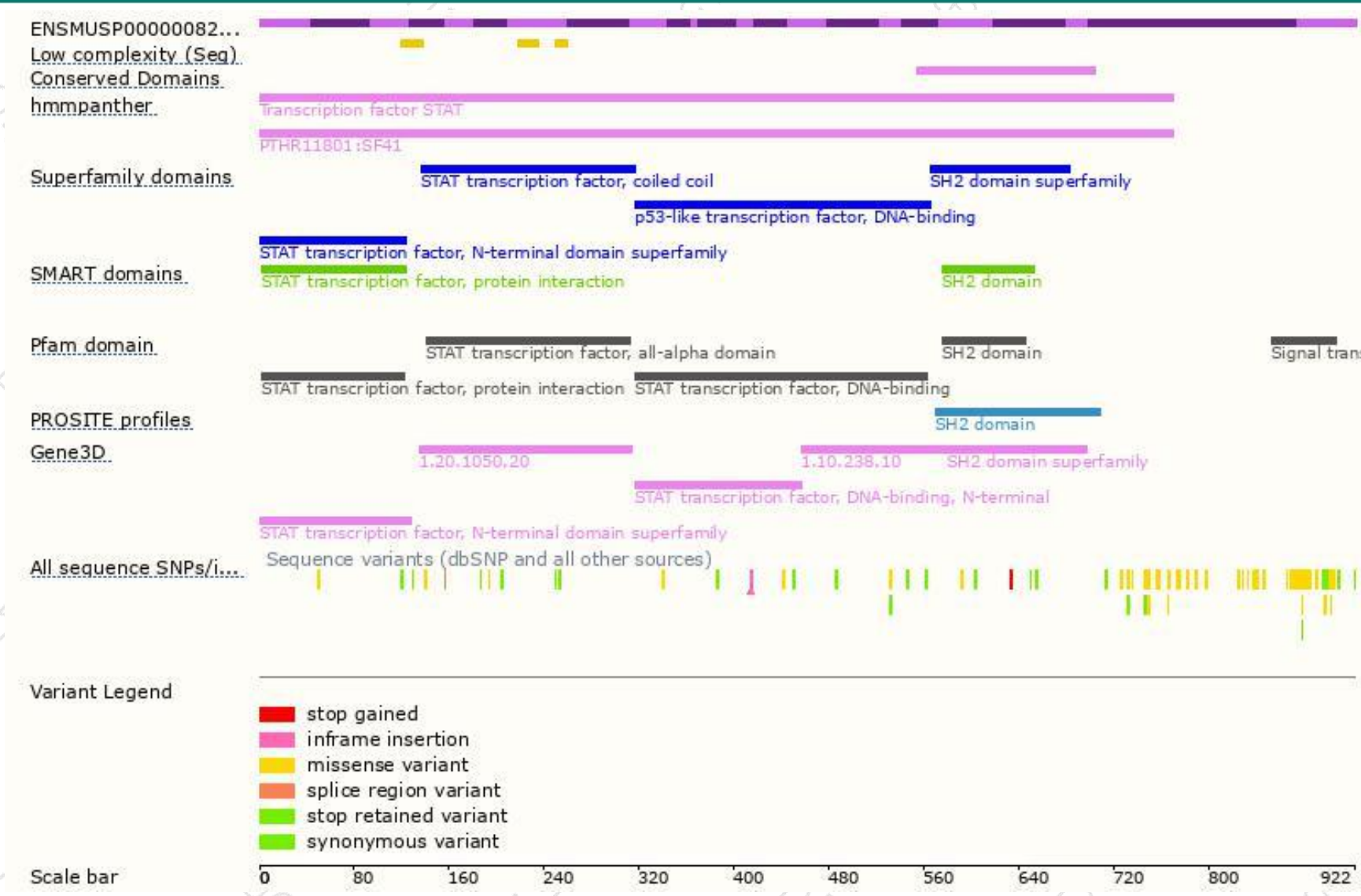
The strategy is based on the design of *Stat2-201* transcript,The transcription is shown below



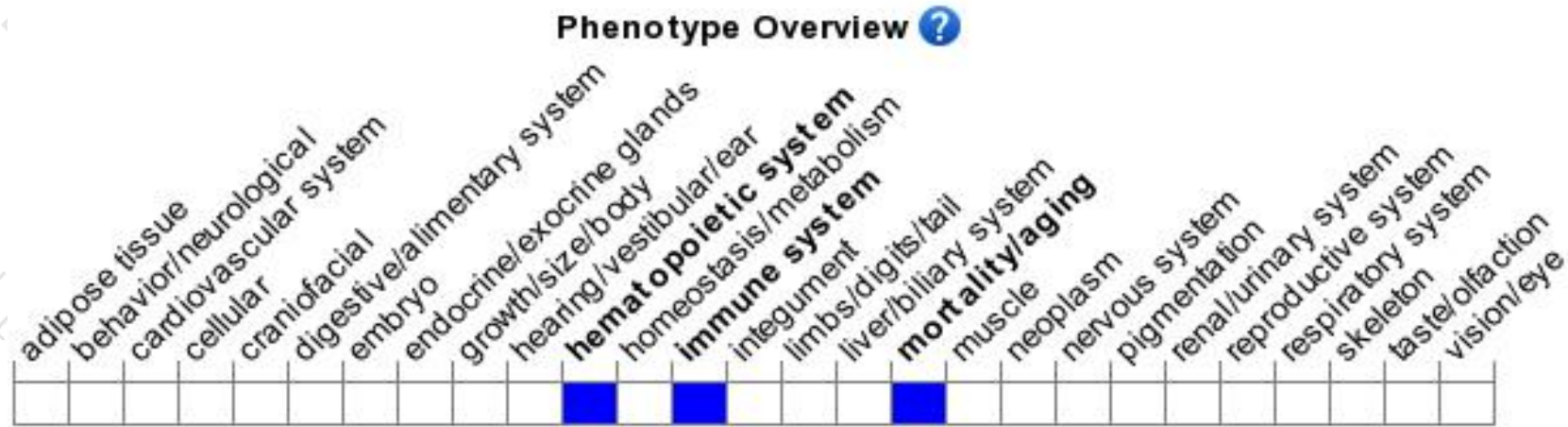
Genomic location distribution



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, Immune response is impaired in homozygous null mice.

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

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