

Isg20 Cas9-KO Strategy

Designer: Yanhua Shen

Reviewer: Daohua Xu

Design Date: 2021-05-25

Project Overview

Project Name

Isg20

Project type

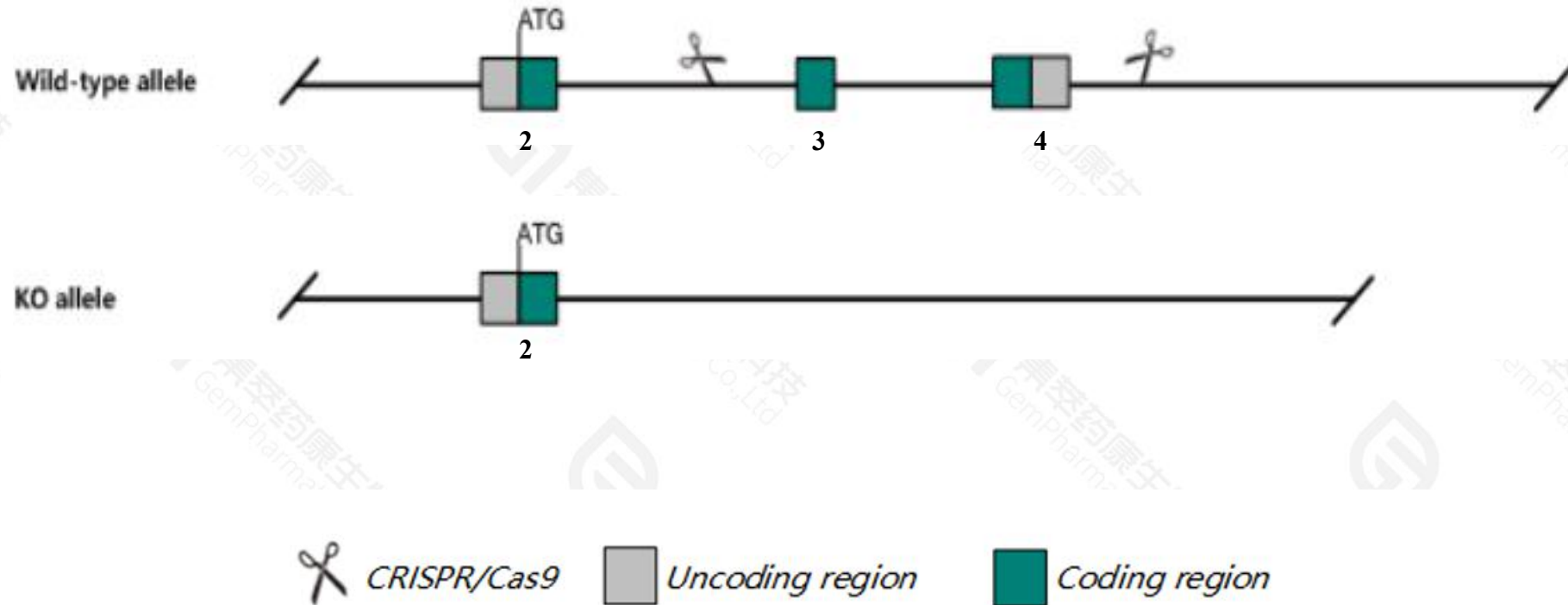
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Isg20* gene. The schematic diagram is as follows:



- The *Isg20* gene has 6 transcripts. According to the structure of *Isg20* gene, exon3-exon4 of *Isg20*-204(ENSMUST00000121645.8) transcript is recommended as the knockout region. The region contains most 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 *Isg20* 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.

- The *Isg20* gene is located on the Chr7. 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.

Isg20 interferon-stimulated protein [Mus musculus (house mouse)]

Gene ID: 57444, updated on 17-Dec-2020

Summary



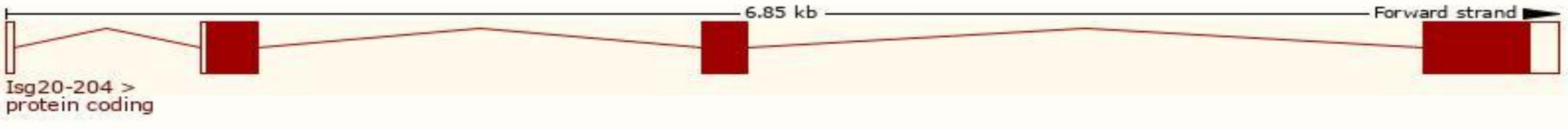
Official Symbol	Isg20 provided by MGI
Official Full Name	interferon-stimulated protein provided by MGI
Primary source	MGI:MGI:1928895
See related	Ensembl:ENSMUSG00000039236
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1600023I01Rik, 2010107M23Rik, 20kD, 20kDa, Dn, DnaQL, HEM45
Expression	Broad expression in genital fat pad adult (RPKM 49.6), testis adult (RPKM 49.3) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

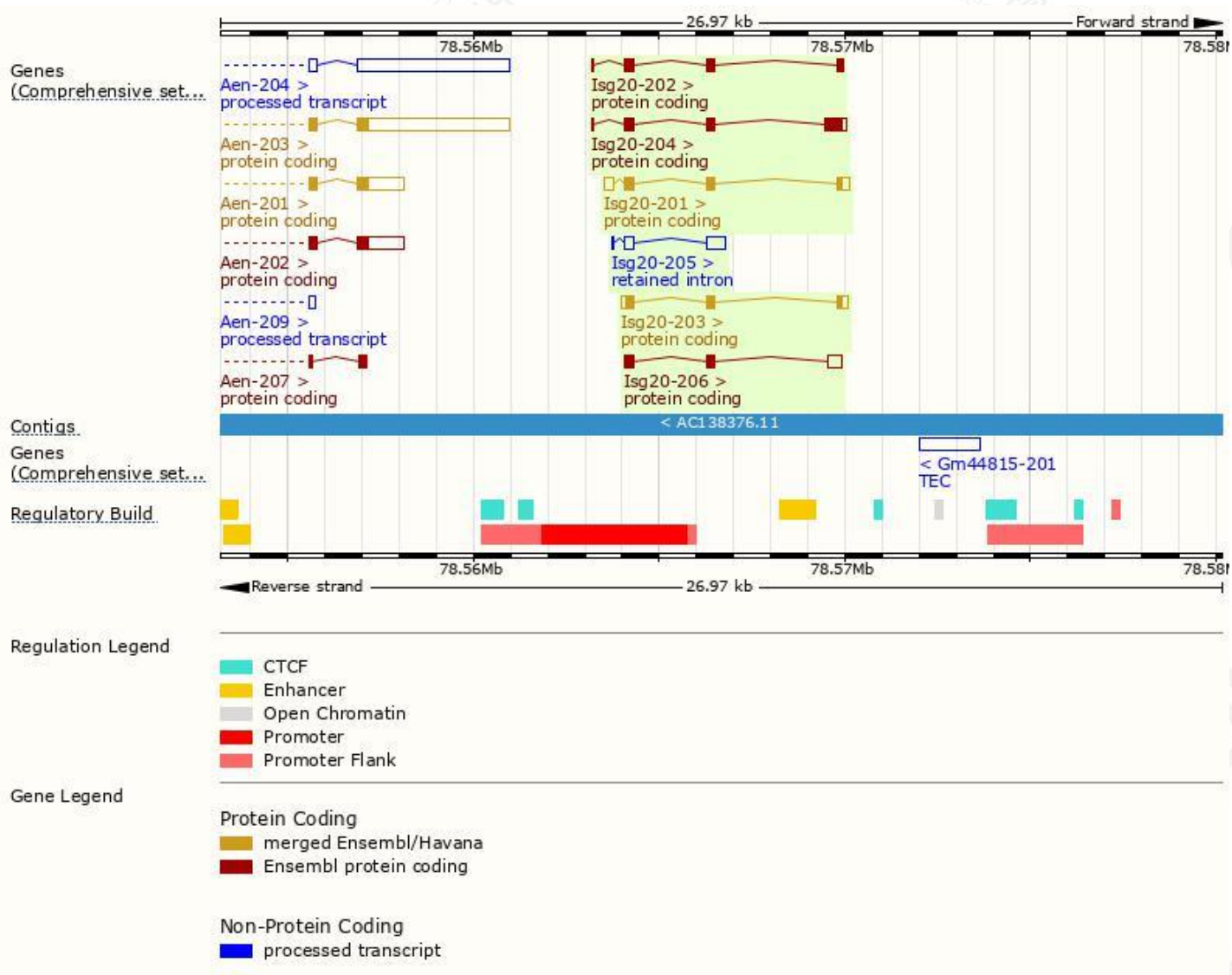
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Isg20-204	ENSMUST00000121645.8	1087	300aa	Protein coding	CCDS71982		TSL:1 , GENCODE basic ,
Isg20-201	ENSMUST00000038142.15	1083	181aa	Protein coding	CCDS21376		TSL:1 , GENCODE basic , APPRIS P1 ,
Isg20-203	ENSMUST00000120331.4	845	181aa	Protein coding	CCDS21376		TSL:1 , GENCODE basic , APPRIS P1 ,
Isg20-202	ENSMUST00000118867.8	697	181aa	Protein coding	CCDS21376		TSL:3 , GENCODE basic , APPRIS P1 ,
Isg20-206	ENSMUST00000205981.2	834	145aa	Protein coding	-		TSL:3 , GENCODE basic ,
Isg20-205	ENSMUST00000133042.2	801	No protein	Retained intron	-		TSL:2 ,

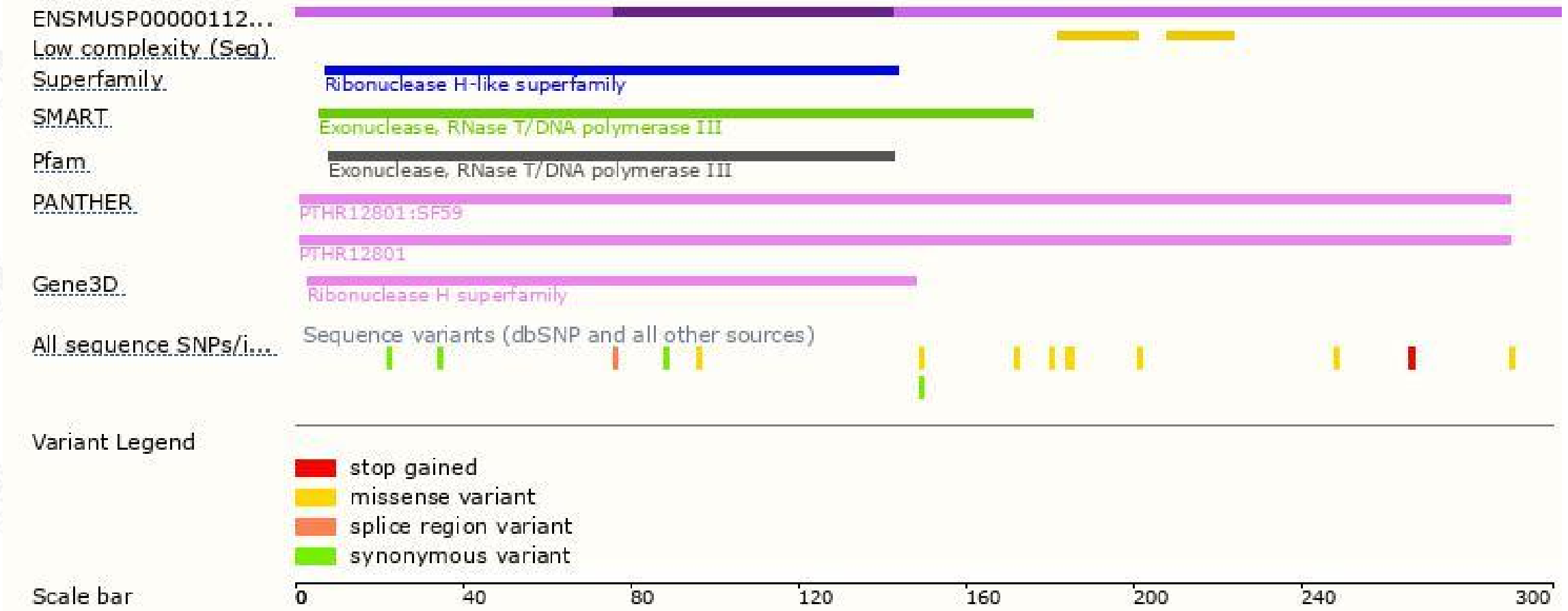
The strategy is based on the design of *Isg20-204* transcript,the transcription is shown below:



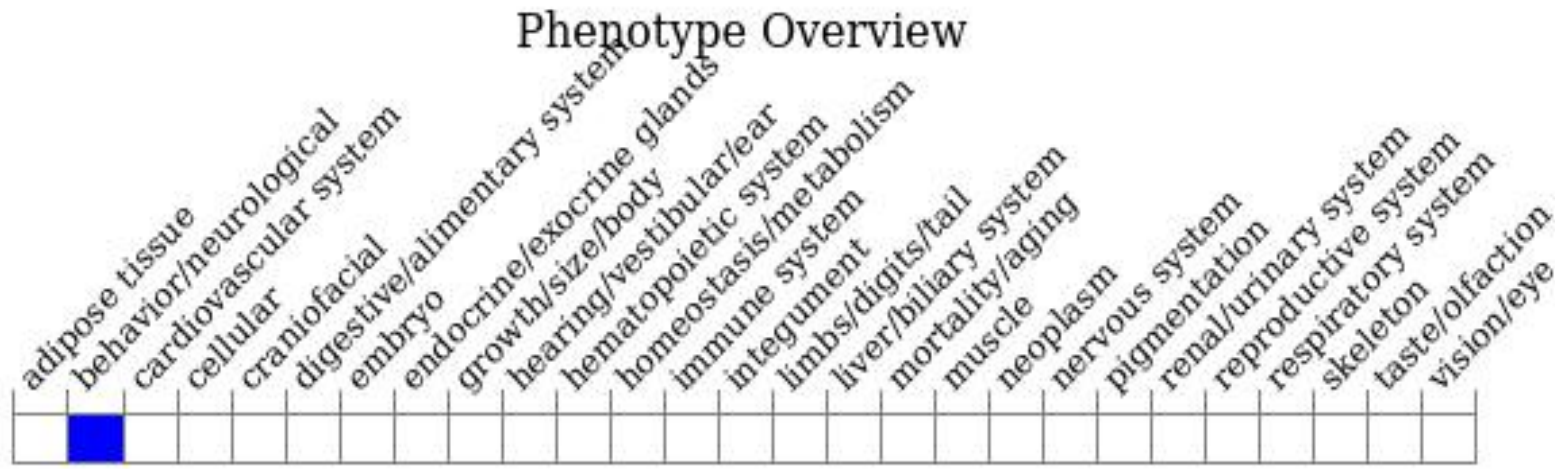
Genomic location distribution



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/>).

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

