

Was Cas9-KO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

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Project Overview

Project Name

Was

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Was* gene has 2 transcripts. According to the structure of *Was* gene, exon1-exon11 of *Was-201* (ENSMUST00000033505.6) 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 *Was* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous mutant females and hemizygous mutant males exhibit reduced numbers of peripheral blood lymphocytes and platelets, but increased numbers of neutrophils.
- The 5 terminal regulation of Gm6787 may be affected.
- The *Was* gene is located on the ChrX. 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)

Was Wiskott-Aldrich syndrome [*Mus musculus* (house mouse)]

Gene ID: 22376, updated on 5-Nov-2019

Summary

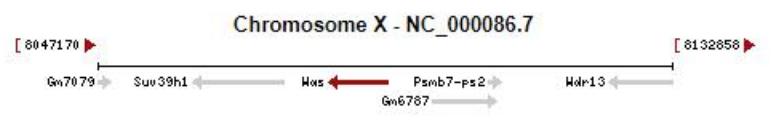
Official Symbol Was provided by [MGI](#)
Official Full Name Wiskott-Aldrich syndrome provided by [MGI](#)
Primary source [MGI:MGI:105059](#)
See related [Ensembl:ENSMUSG00000031165](#)
Gene type protein coding
RefSeq status VALIDATED
Organism [Mus musculus](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as Wasp; U42471
Expression Biased expression in thymus adult (RPKM 28.4), spleen adult (RPKM 26.0) and 11 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: X A1.1; X 3.65 cM [See Was in Genome Data Viewer](#)

Exon count: 12

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	X	NC_000086.7 (8081466..8090491, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	X	NC_000086.6 (7658592..7667617, complement)

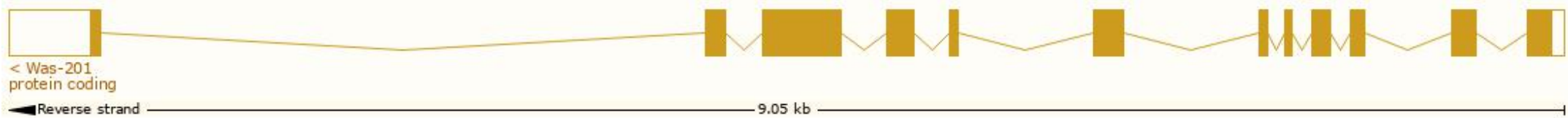


Transcript information (Ensembl)

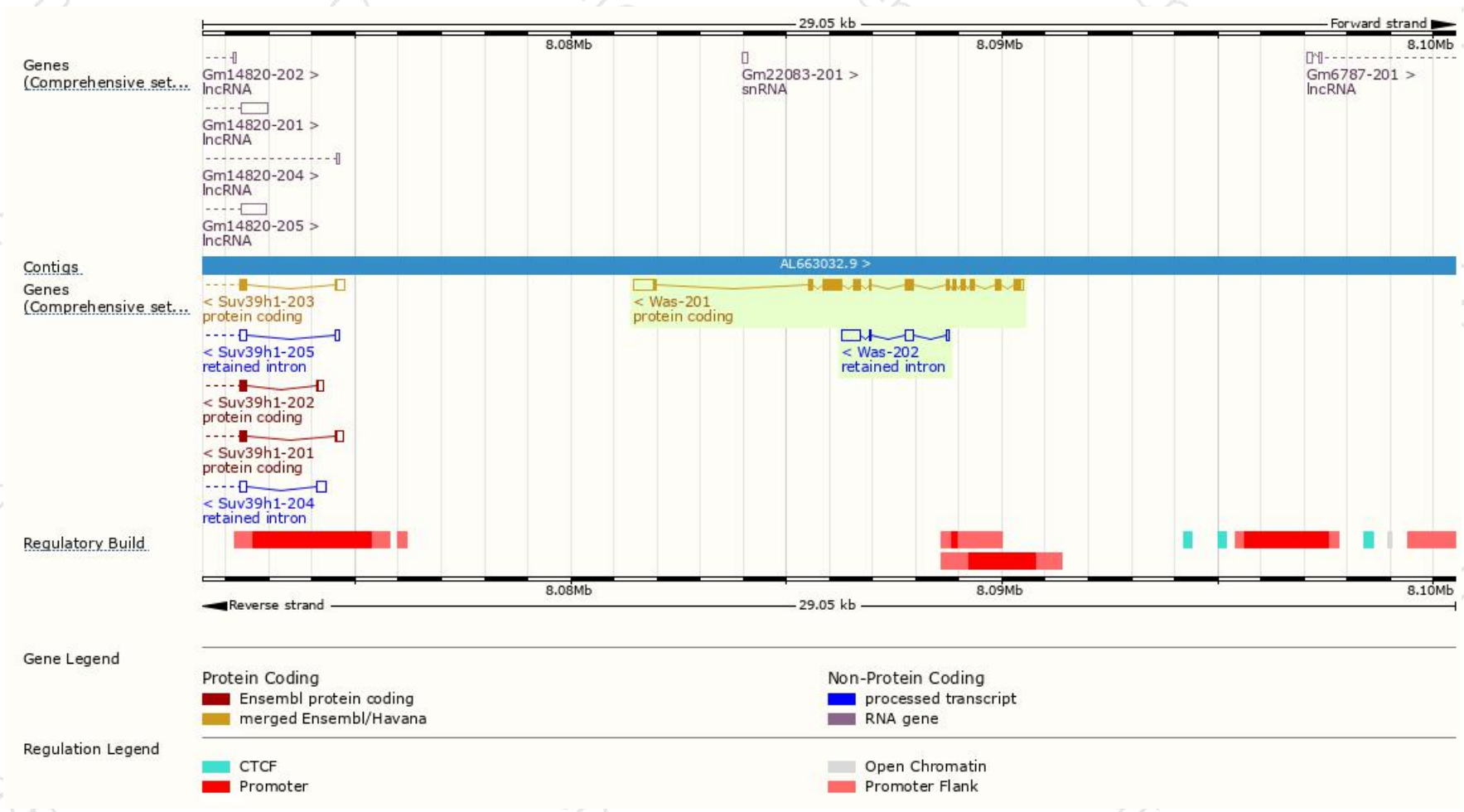
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Was-201	ENSMUST00000033505.6	2114	520aa	Protein coding	CCDS29984	P70315 Q53WY0	TSL:1 GENCODE basic APPRIS P1
Was-202	ENSMUST00000146029.1	707	No protein	Retained intron	-	-	TSL:5

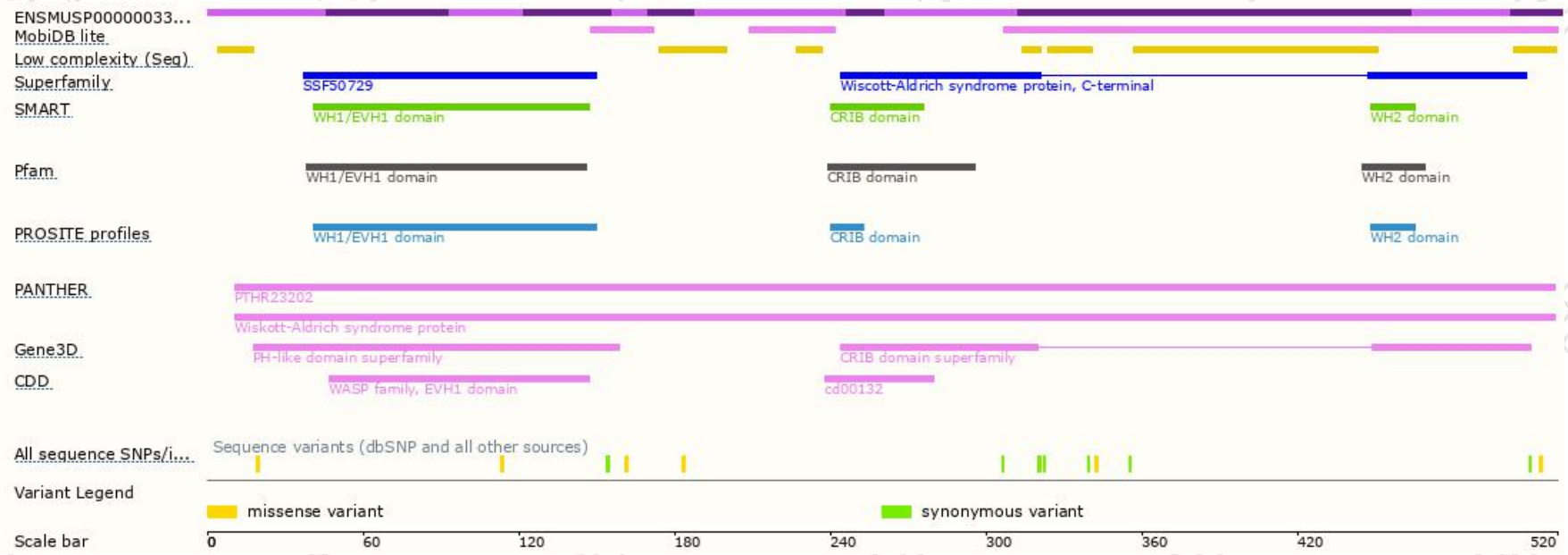
The strategy is based on the design of *Was-201* transcript,The transcription is shown below



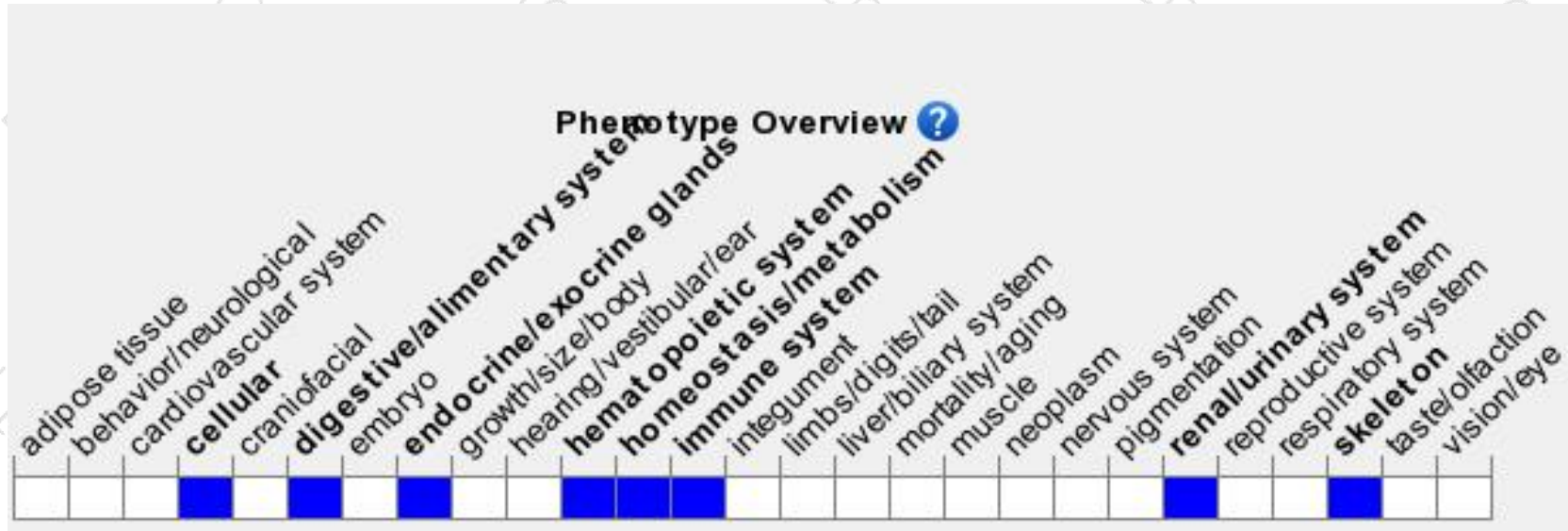
Genomic location distribution



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, Homozygous mutant females and hemizygous mutant males exhibit reduced numbers of peripheral blood lymphocytes and platelets, but increased numbers of neutrophils.

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

Tel: 400-9660890

