

Jak3 **Cas9-KO Strategy**

Designer:

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2019-7-17

Project Overview

Project Name

Jak3

Project type

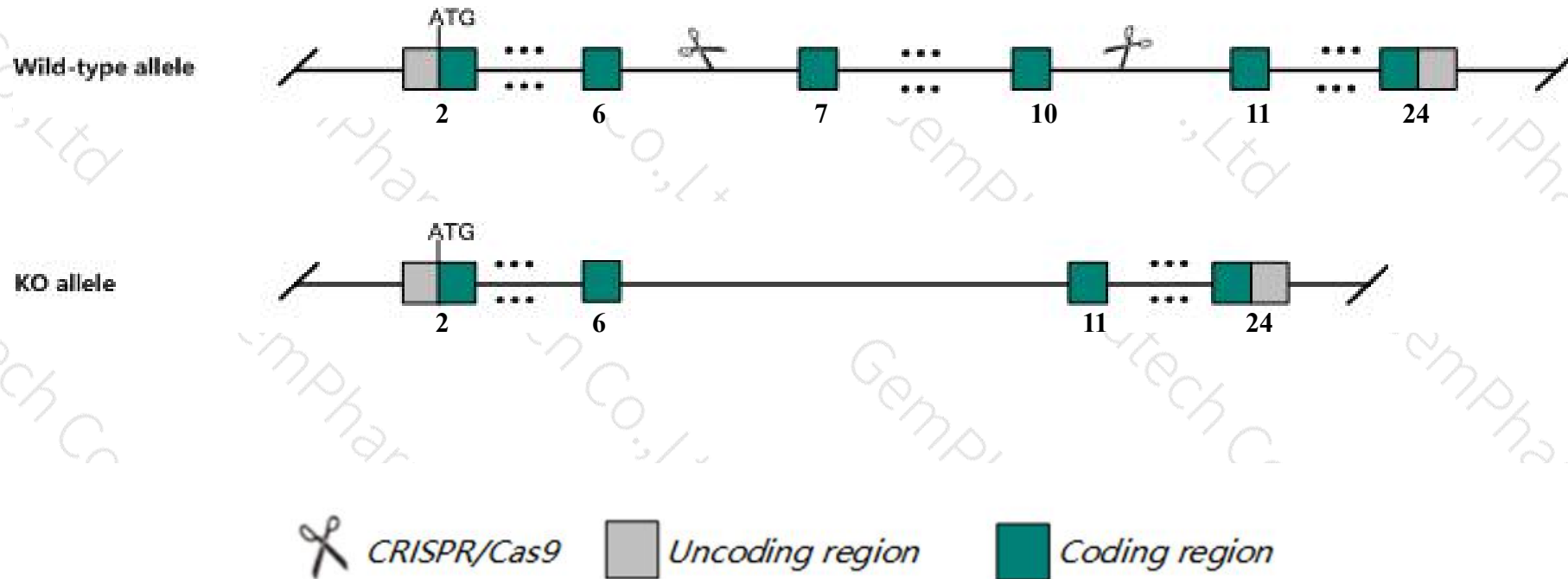
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Jak3* gene. The schematic diagram is as follows:



- The *Jak3* gene has 5 transcripts. According to the structure of *Jak3* gene, exon7-exon10 of *Jak3-201* (ENSMUST00000051995.13) transcript is recommended as the knockout region. The region contains 580bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Jak3* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit impaired B cell development, small thymus and T cell proliferate. Point mutation homozygotes develop autoimmune inflammatory bowel disease, decreased susceptibility to malaria infection and/or increased susceptibility to bacterial infection.
- The *Jak3* gene is located on the Chr8. 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)

Jak3 Janus kinase 3 [Mus musculus (house mouse)]

Gene ID: 16453, updated on 9-Apr-2019

Summary



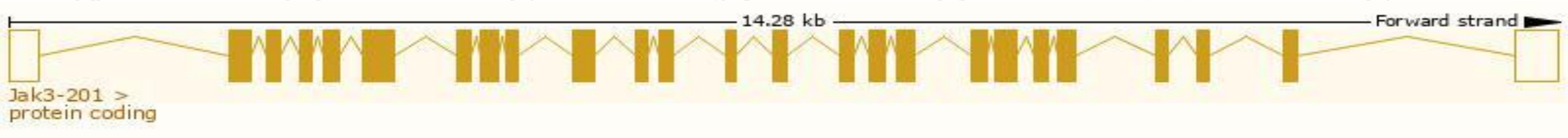
Official Symbol	Jak3 provided by MGI
Official Full Name	Janus kinase 3 provided by MGI
Primary source	MGI:MGI:99928
See related	Ensembl:ENSMUSG000000031805
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	fae, wil
Expression	Biased expression in testis adult (RPKM 193.9), spleen adult (RPKM 34.5) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

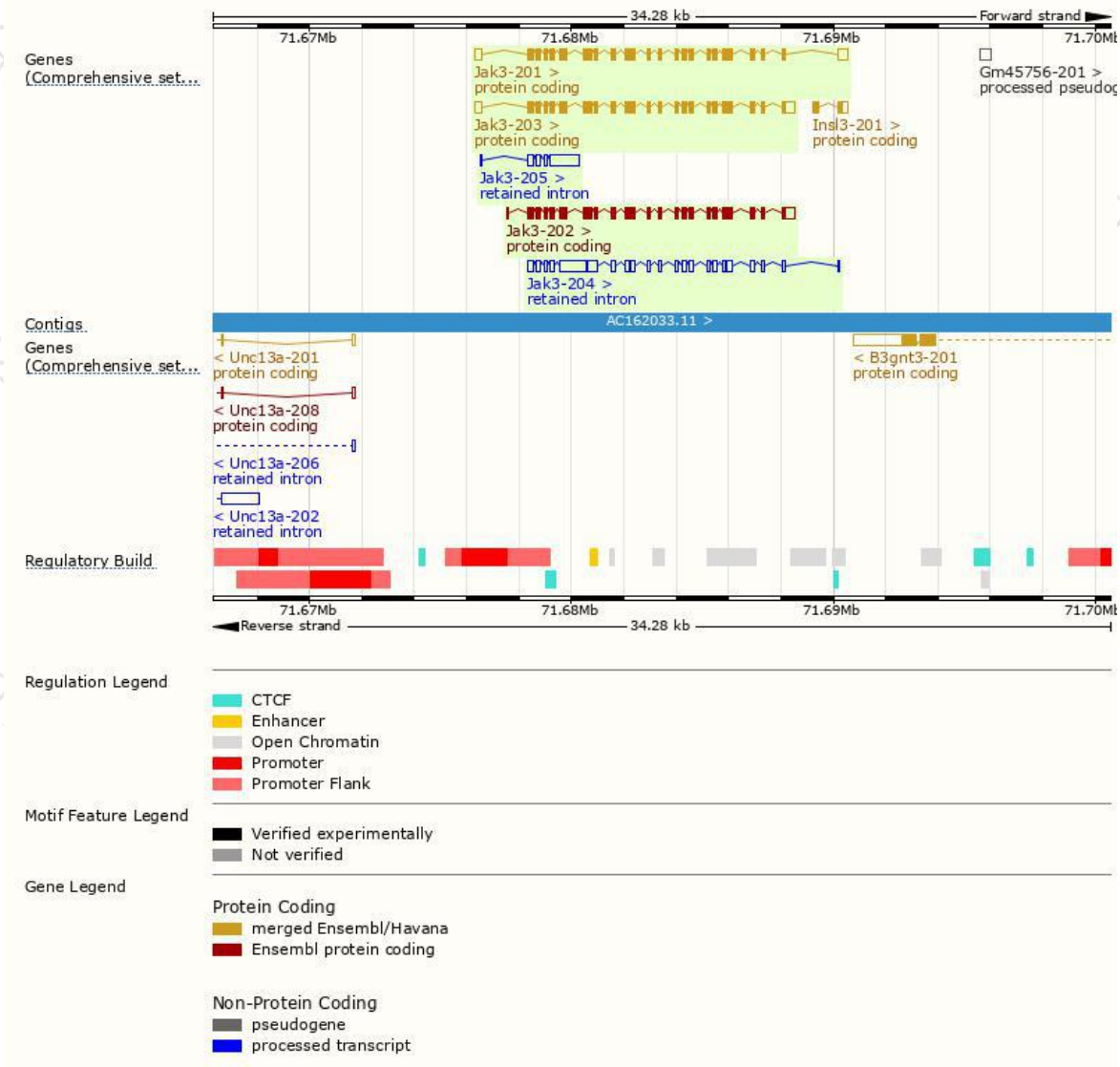
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jak3-201	ENSMUST00000051995.13	4019	1100aa	Protein coding	CCDS22403	A0A0R4J0R7	TSL:1 GENCODE basic APPRIS P1
Jak3-203	ENSMUST00000110013.9	4009	1100aa	Protein coding	CCDS22403	A0A0R4J0R7	TSL:1 GENCODE basic APPRIS P1
Jak3-202	ENSMUST00000110012.1	3774	1100aa	Protein coding	CCDS22403	A0A0R4J0R7	TSL:5 GENCODE basic APPRIS P1
Jak3-204	ENSMUST00000130624.1	4049	No protein	Retained intron	-	-	TSL:5
Jak3-205	ENSMUST00000133263.7	1566	No protein	Retained intron	-	-	TSL:2

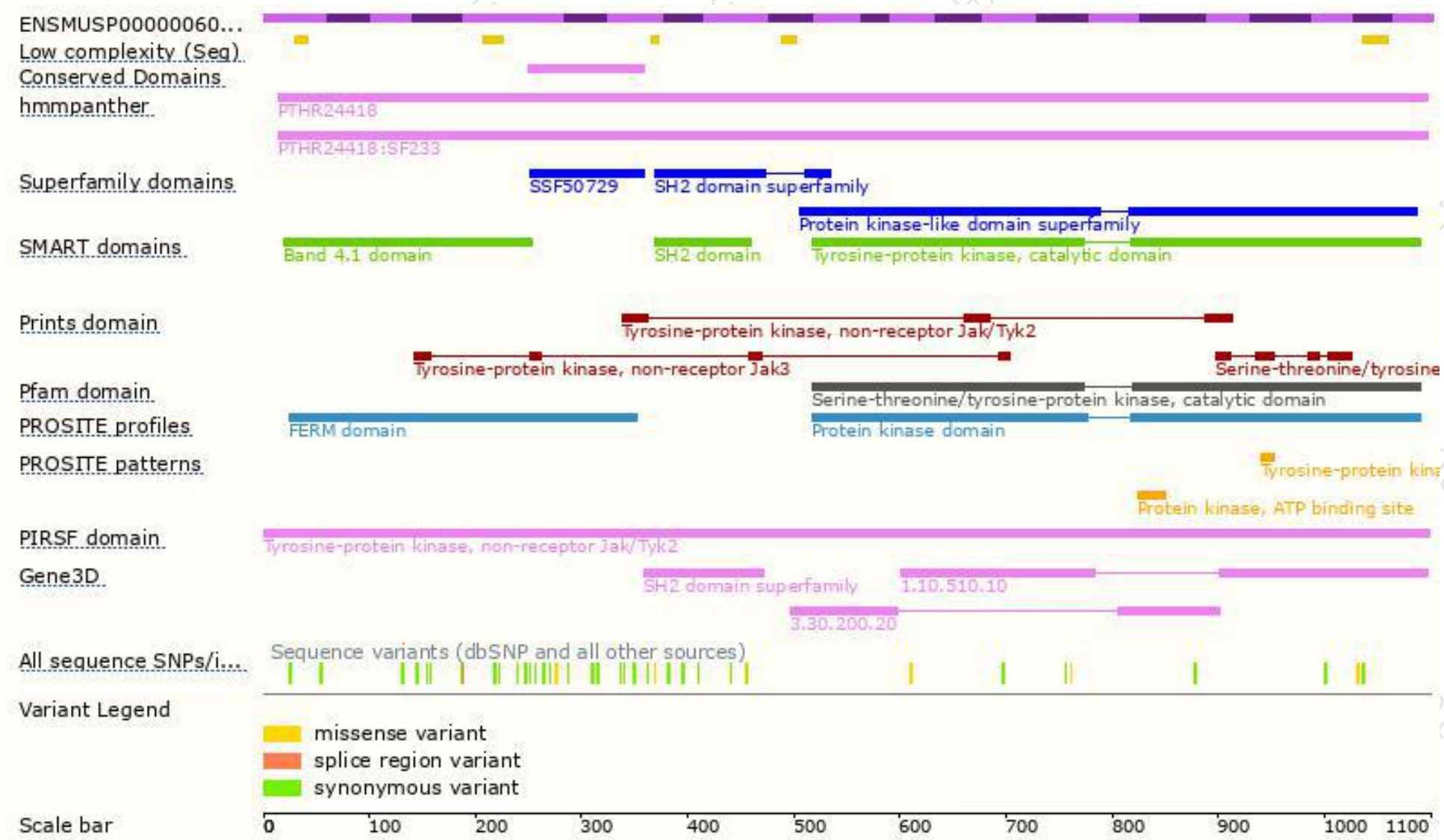
The strategy is based on the design of *Jak3-201* transcript,The transcription is shown below



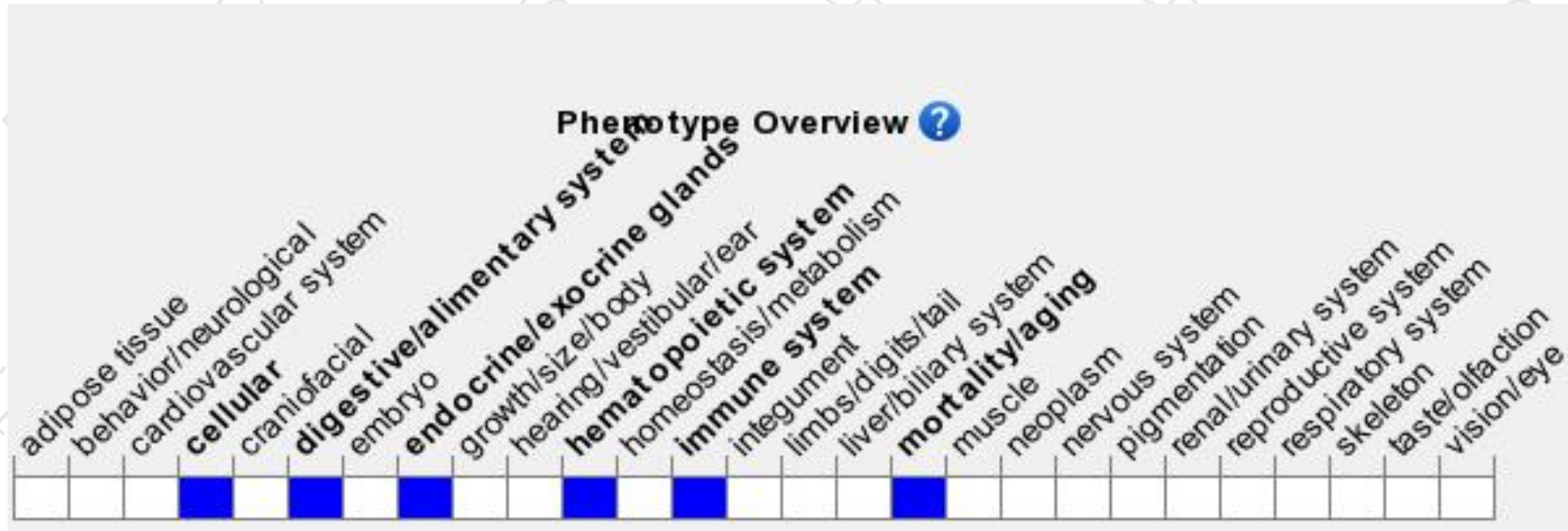
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit impaired B cell development, small thymic and T cell proliferate. Point mutation homozygotes develop autoimmune inflammatory bowel disease, decreased susceptibility to malaria infection and/or increased susceptibility to bacterial infection.

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

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