

Il9r Cas9-KO Strategy

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Project Overview

Project Name

Il9r

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Il9r* gene. The schematic diagram is as follows:



- The *Il9r* gene has 5 transcripts. According to the structure of *Il9r* gene, exon2-exon7 of *Il9r*-205 (ENSMUST00000145401.7) transcript is recommended as the knockout region. The region contains 859bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Il9r* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mice are more susceptible to experimental autoimmune encephalomyelitis, a defect partially attributable to defective regulatory T cell function.
- The *Il9r* gene is located on the Chr11. 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)

Il9r interleukin 9 receptor [Mus musculus (house mouse)]

Gene ID: 16199, updated on 19-Feb-2019

Summary



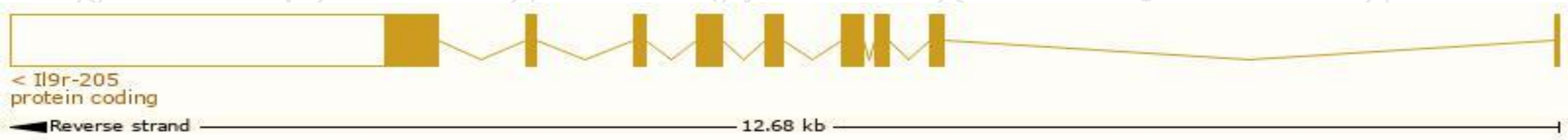
Official Symbol	Il9r provided by MGI
Official Full Name	interleukin 9 receptor provided by MGI
Primary source	MGI:MGI:96564
See related	Ensembl:ENSMUSG00000020279
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in spleen adult (RPKM 4.9), thymus adult (RPKM 1.8) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

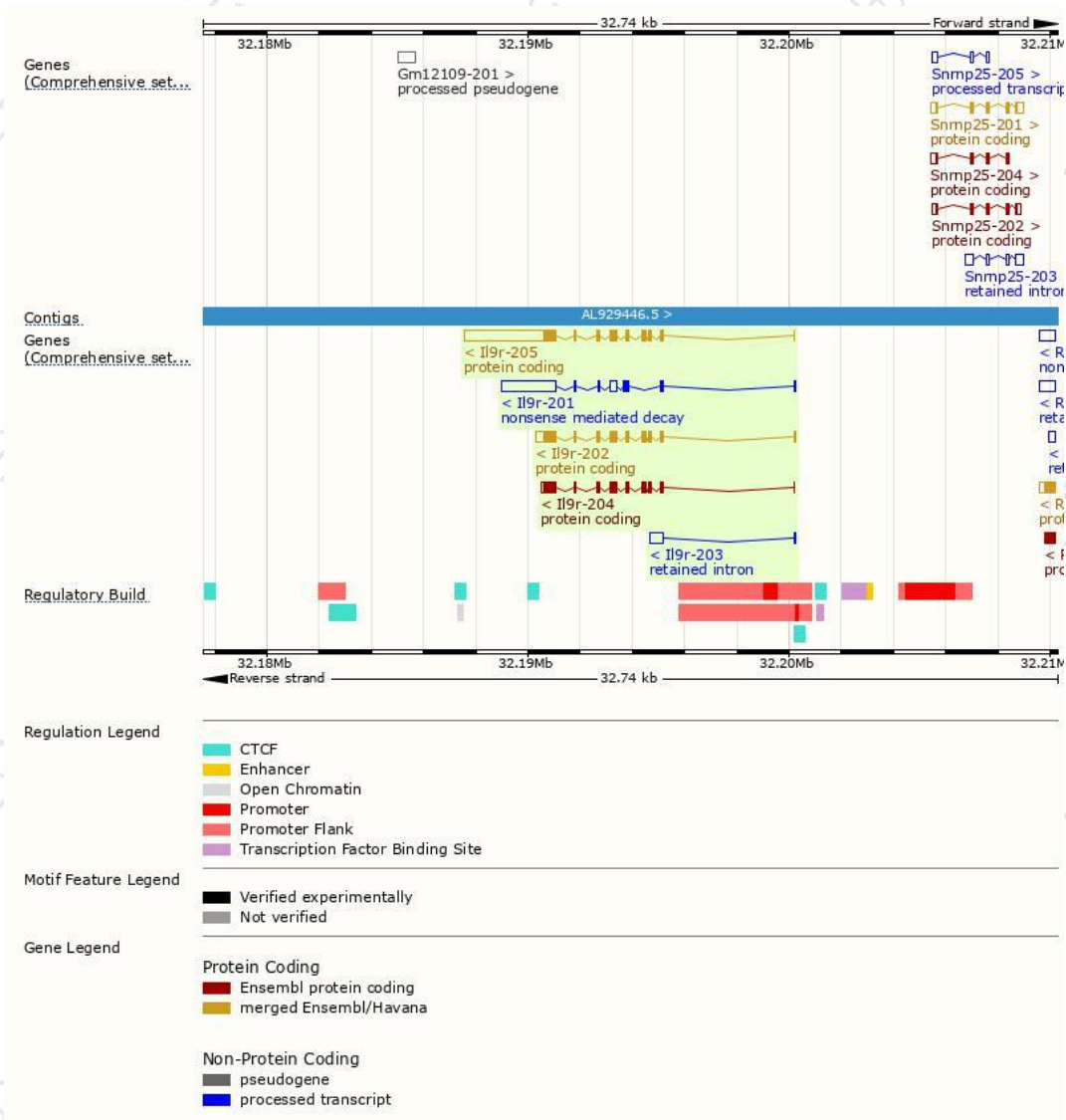
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
II9r-205	ENSMUST00000145401.7	4482	468aa	Protein coding	CCDS24517	Q01114 Q78PA5	TSL:1 GENCODE basic APPRIS P3
II9r-202	ENSMUST00000128311.7	1757	469aa	Protein coding	CCDS48765	A2AVE0	TSL:1 GENCODE basic APPRIS ALT2
II9r-204	ENSMUST00000142396.1	1542	474aa	Protein coding	-	B7ZD65	TSL:1 GENCODE basic APPRIS ALT2
II9r-201	ENSMUST00000020518.10	2798	98aa	Nonsense mediated decay	-	F8WJ69	TSL:5
II9r-203	ENSMUST00000131979.1	605	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *II9r-205* transcript,The transcription is shown below



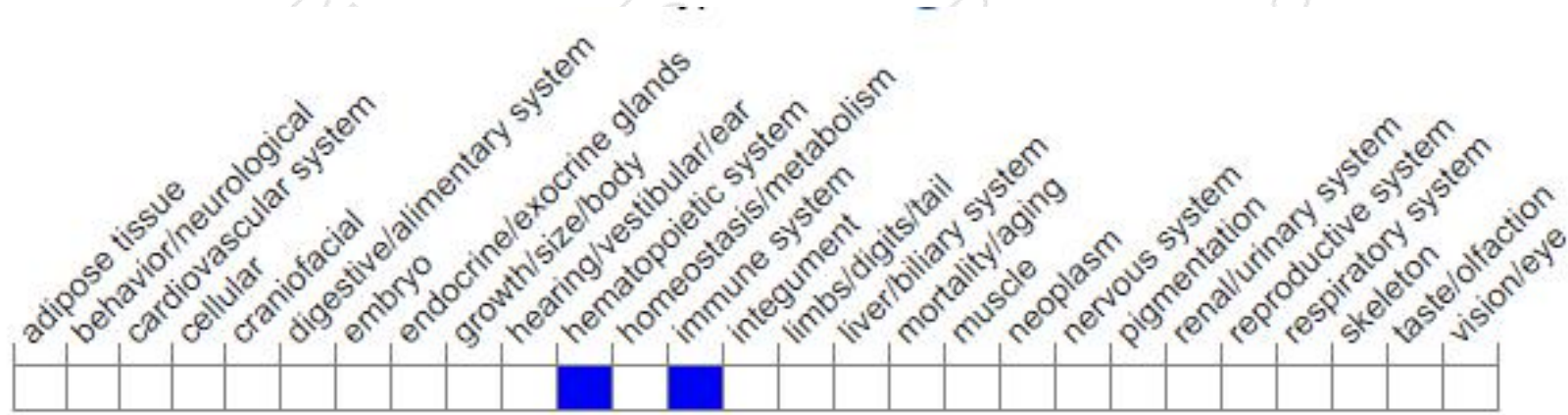
Genomic location distribution



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 null mice are more susceptible to experimental autoimmune encephalomyelitis, a defect partially attributable to defective regulatory T cell function.

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

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