

Il15ra Cas9-KO Strategy

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Project Overview

Project Name

Il15ra

Project type

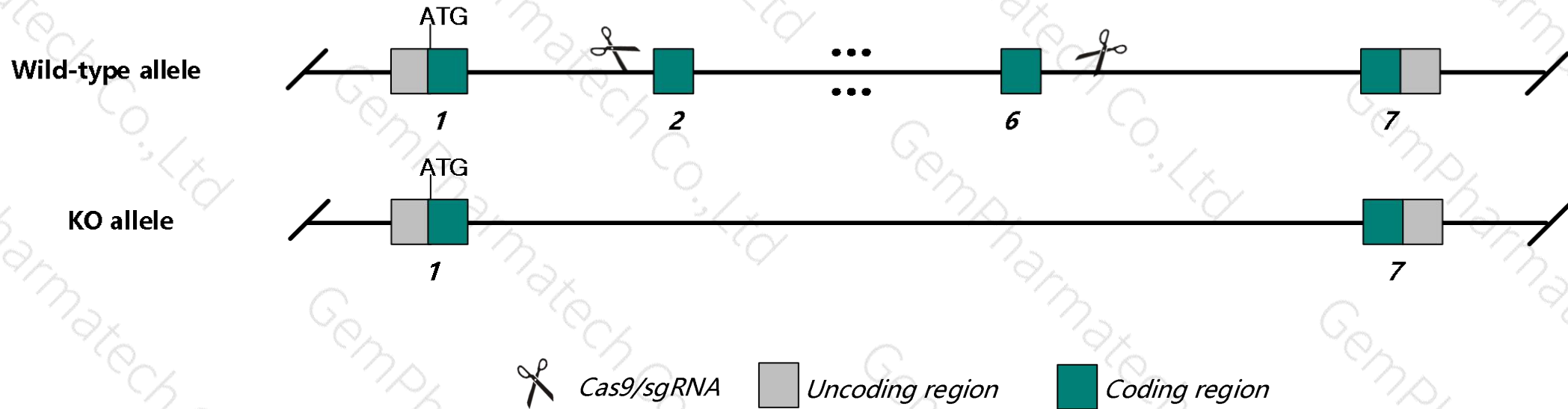
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Il15ra* gene. The schematic diagram is as follows:



- The *Il15ra* gene has 18 transcripts. According to the structure of *Il15ra* gene, exon2-exon6 of *Il15ra-201* (ENSMUST00000078834.11) transcript is recommended as the knockout region. The region contains 595bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Il15ra* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mutation of this gene results in absence of NK cell production in spleen and bone marrow.
- The *Il15ra* gene is located on the Chr2. 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)

Il15ra interleukin 15 receptor, alpha chain [Mus musculus (house mouse)]

Gene ID: 16169, updated on 31-Jan-2019

Summary



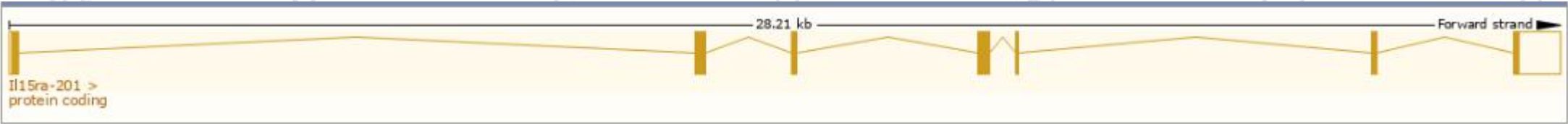
Official Symbol	Il15ra provided by MGI
Official Full Name	interleukin 15 receptor, alpha chain provided by MGI
Primary source	MGI:MGI:104644
See related	Ensembl:ENSMUSG00000023206
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA690181, IL-15RA
Expression	Broad expression in mammary gland adult (RPKM 8.1), liver E18 (RPKM 7.6) and 23 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

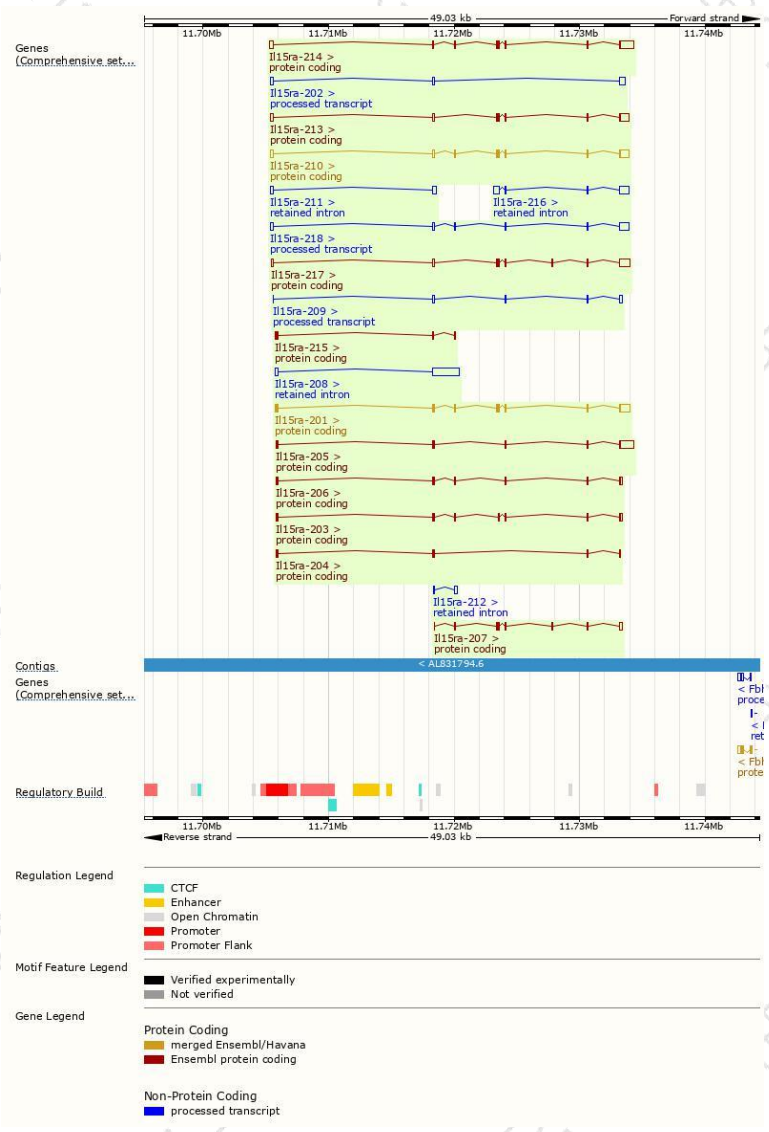
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
II15ra-201	ENSMUST00000078834.11	1600	263aa	Protein coding	CCDS15686	Q60819	TSL:5 GENCODE basic APPRIS P3
II15ra-202	ENSMUST00000091456.11	921	No protein	lncRNA	-	-	TSL:3
II15ra-203	ENSMUST00000114831.8	882	230aa	Protein coding	CCDS70977	Q60819	TSL:1 GENCODE basic APPRIS ALT2
II15ra-204	ENSMUST00000114832.2	468	155aa	Protein coding	-	Q60819	TSL:5 GENCODE basic
II15ra-205	ENSMUST00000114833.9	1607	166aa	Protein coding	CCDS70979	Q60819	TSL:1 GENCODE basic
II15ra-206	ENSMUST00000114834.9	784	197aa	Protein coding	CCDS70978	Q60819	TSL:1 GENCODE basic APPRIS ALT2
II15ra-207	ENSMUST00000123600.4	767	155aa	Protein coding	-	E9QA82	CDS 5' incomplete TSL:1
II15ra-208	ENSMUST00000124448.1	2315	No protein	Retained intron	-	-	TSL:2
II15ra-209	ENSMUST00000126394.7	583	No protein	lncRNA	-	-	TSL:1
II15ra-210	ENSMUST00000128156.8	1624	123aa	Protein coding	CCDS15687	Q501M1 Q60819	TSL:1 GENCODE basic
II15ra-211	ENSMUST00000130245.1	507	No protein	Retained intron	-	-	TSL:2
II15ra-212	ENSMUST00000133975.1	406	No protein	Retained intron	-	-	TSL:3
II15ra-213	ENSMUST00000135341.7	1545	123aa	Protein coding	CCDS15687	Q501M1 Q60819	TSL:3 GENCODE basic
II15ra-214	ENSMUST00000138349.7	1936	123aa	Protein coding	CCDS15687	Q501M1 Q60819	TSL:1 GENCODE basic
II15ra-215	ENSMUST00000138856.1	405	89aa	Protein coding	-	A2AP38	CDS 3' incomplete TSL:2
II15ra-216	ENSMUST00000139774.2	1375	No protein	Retained intron	-	-	TSL:1
II15ra-217	ENSMUST00000148748.7	1542	103aa	Protein coding	CCDS70980	Q810T6	TSL:1 GENCODE basic
II15ra-218	ENSMUST00000191662.5	1408	No protein	lncRNA	-	-	TSL:1

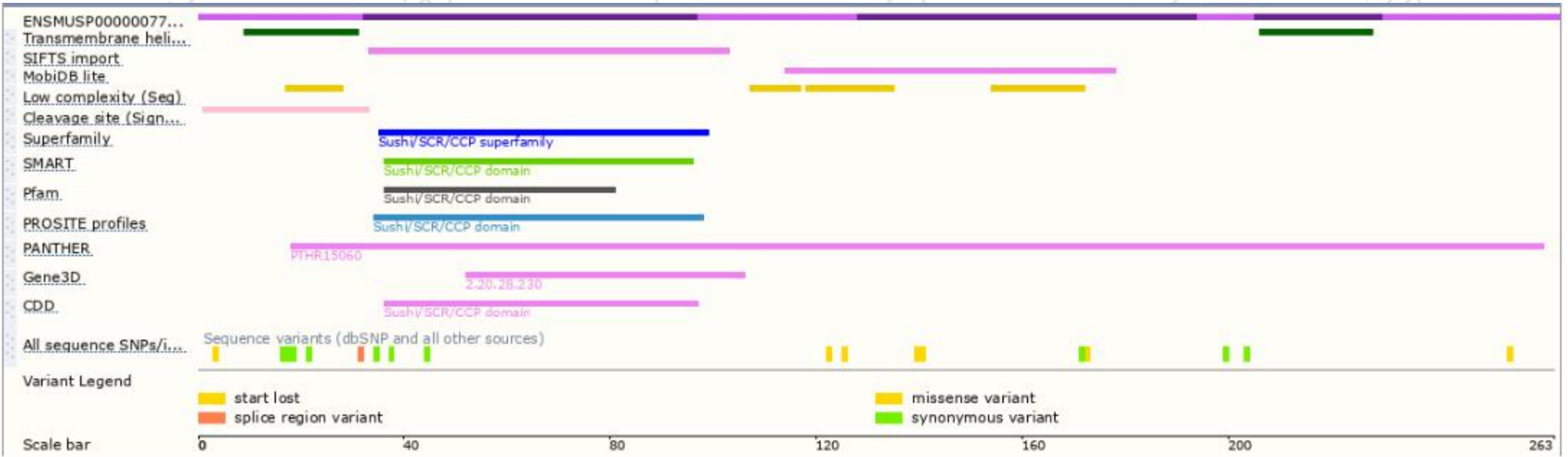
The strategy is based on the design of *II15ra-201* transcript,The transcription is shown below



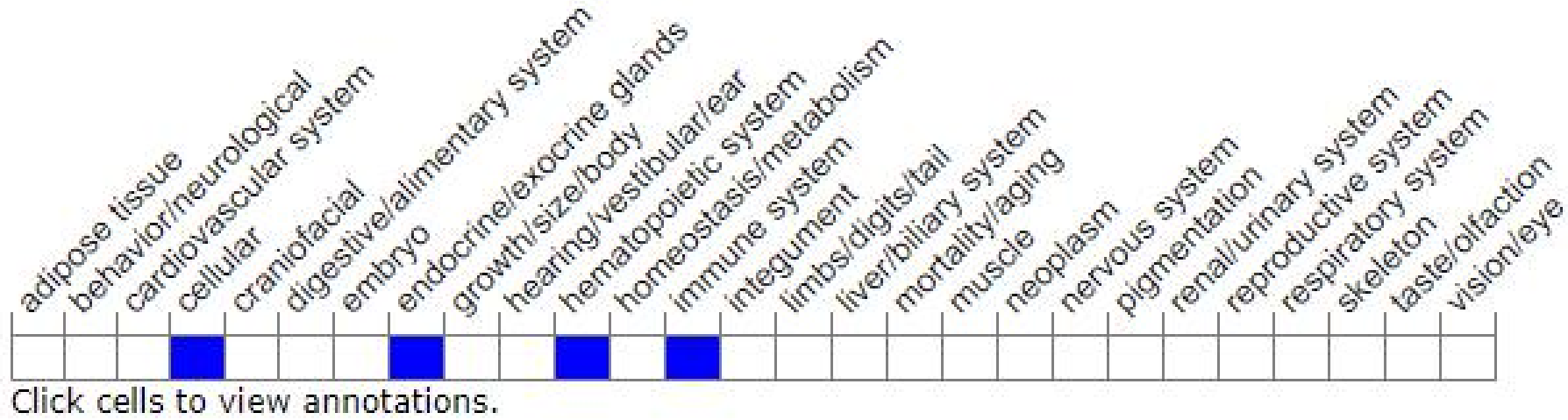
Genomic location distribution



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, Mutation of this gene results in absence of NK cell production in spleen and bone marrow.

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

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