

Il13ra2 Cas9-KO Strategy

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Project Overview



Project Name

Il13ra2

Project type

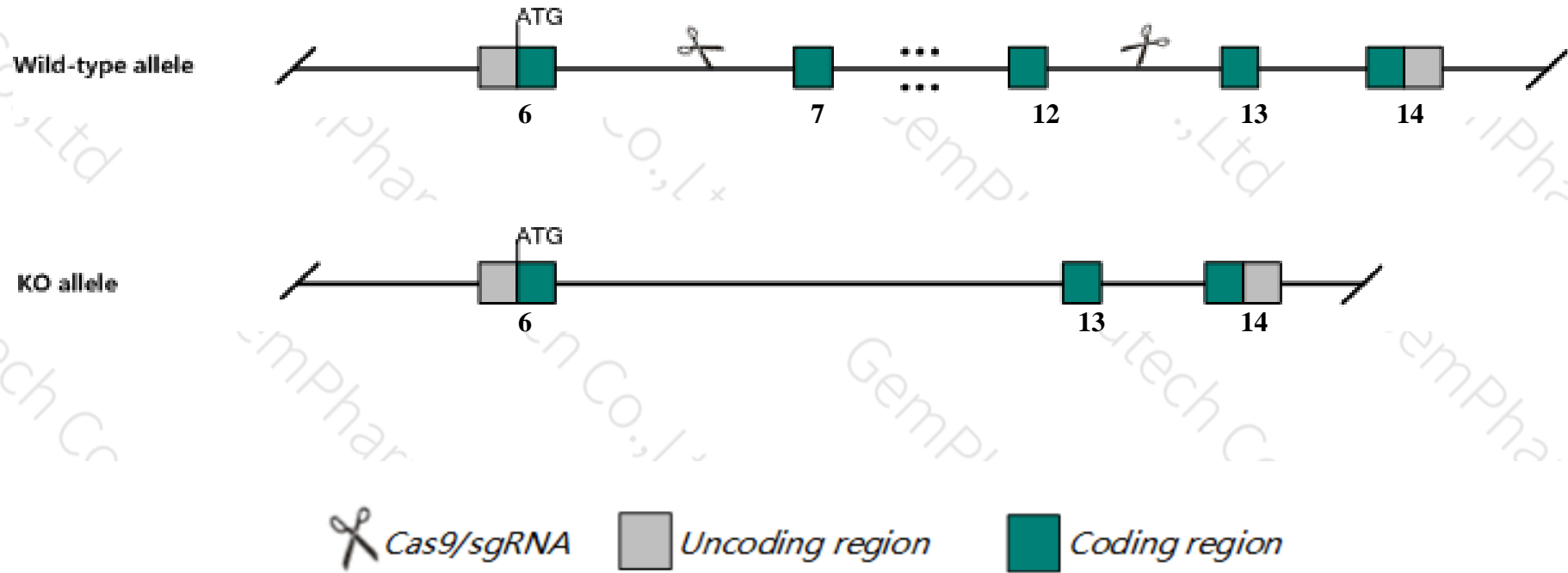
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Il13ra2* gene. The schematic diagram is as follows:



- The *Il13ra2* gene has 2 transcripts. According to the structure of *Il13ra2* gene, exon7-exon12 of *Il13ra2-201* (ENSMUST00000033646.8) 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 *Il13ra2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Null mice display a phenotype consistent with attenuated IL13 responsiveness, including abnormal serum protein concentrations, increased frequency of bone marrow macrophage progenitor cells, and abnormal response of tissue macrophage to LPS.
- The *Il13ra2* 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)

Il13ra2 interleukin 13 receptor, alpha 2 [*Mus musculus* (house mouse)]

Gene ID: 16165, updated on 12-Aug-2019

Summary

Official Symbol Il13ra2 provided by [MGI](#)

Official Full Name interleukin 13 receptor, alpha 2 provided by [MGI](#)

Primary source [MGI:MGI:1277954](#)

See related [Ensembl:ENSMUSG00000031289](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as CD213a2; IL-13R-alpha-2

Summary This gene encodes a receptor protein that binds to interleukin 13 (IL-13) with very high affinity. The encoded protein acts as a decoy receptor, and does not elicit any signal upon the binding of IL-13. Mice lacking the encoded protein exhibit increased levels of serum immunoglobulins, immune-dependent production of interferon gamma and, increased bone marrow macrophage progenitor frequency. Macrophages lacking the encoded protein release less nitric oxide and IL-12 in response to lipopolysaccharide. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Apr 2015]

Expression Biased expression in bladder adult (RPKM 1.3), frontal lobe adult (RPKM 0.3) and 2 other tissues [See more](#)

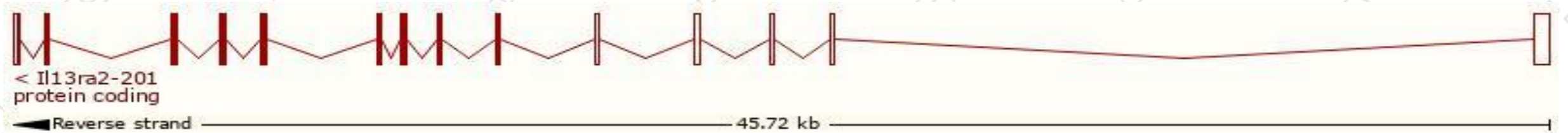
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

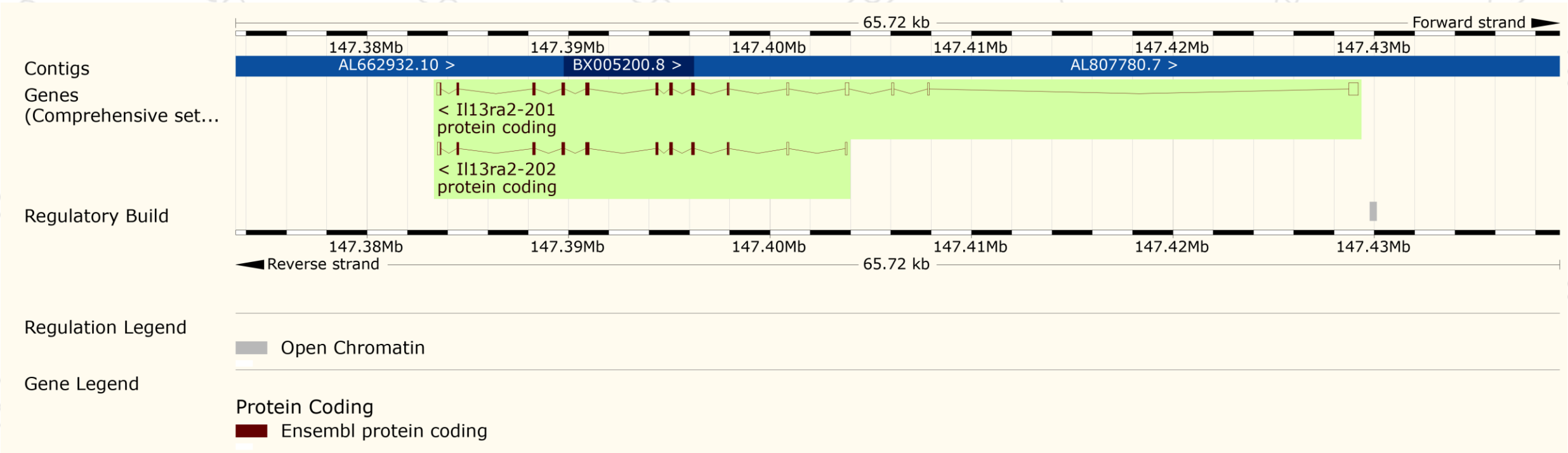
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Il13ra2-201	ENSMUST00000033646.8	2281	383aa	Protein coding	CCDS30460	O88786	TSL:1 GENCODE basic APPRIS P1
Il13ra2-202	ENSMUST00000112827.1	1536	383aa	Protein coding	CCDS30460	O88786	TSL:1 GENCODE basic APPRIS P1

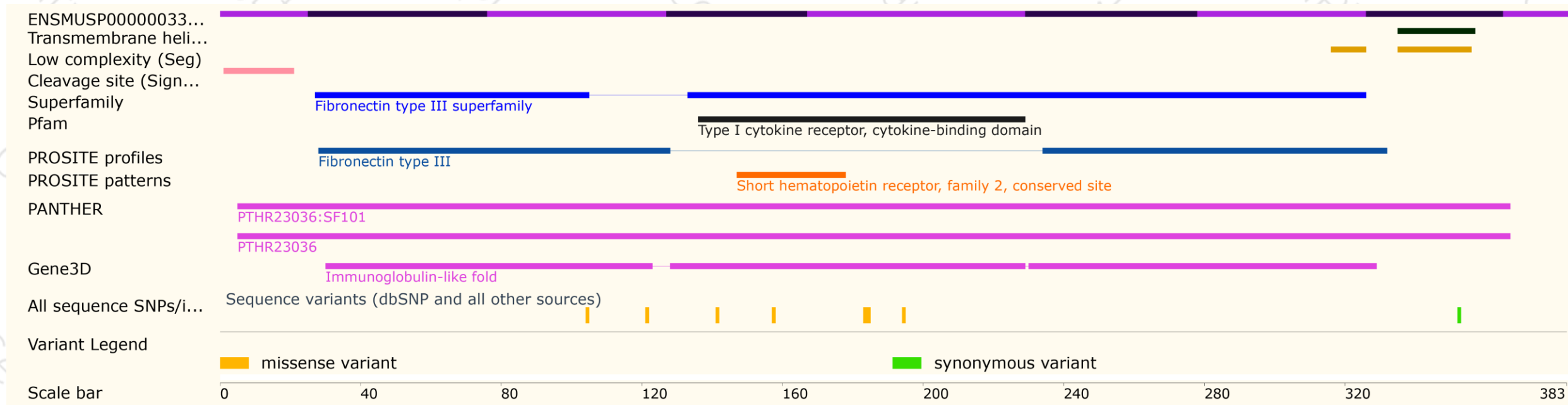
The strategy is based on the design of *Il13ra2-201* transcript, The transcription is shown below



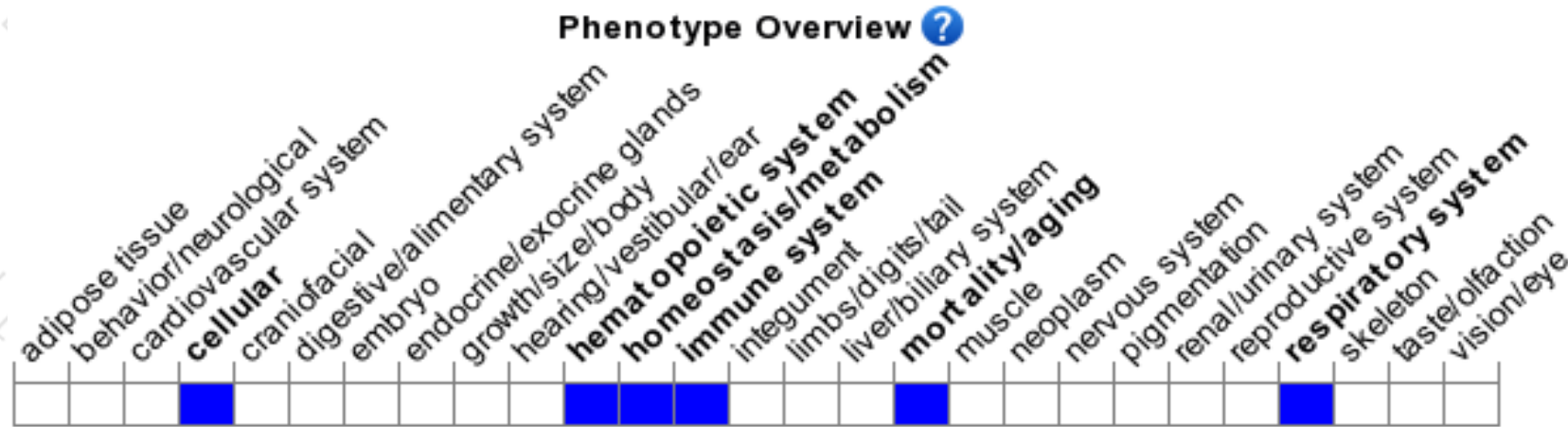
Genomic location distribution



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, Null mice display a phenotype consistent with attenuated IL13 responsiveness, including abnormal serum protein concentrations, increased frequency of bone marrow macrophage progenitor cells, and abnormal response of tissue macrophage to LPS.

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

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