

I11r12 Cas9-CKO Strategy

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Design Date: 2025-4-14

Overview

Target Gene Name

- Il1rl2

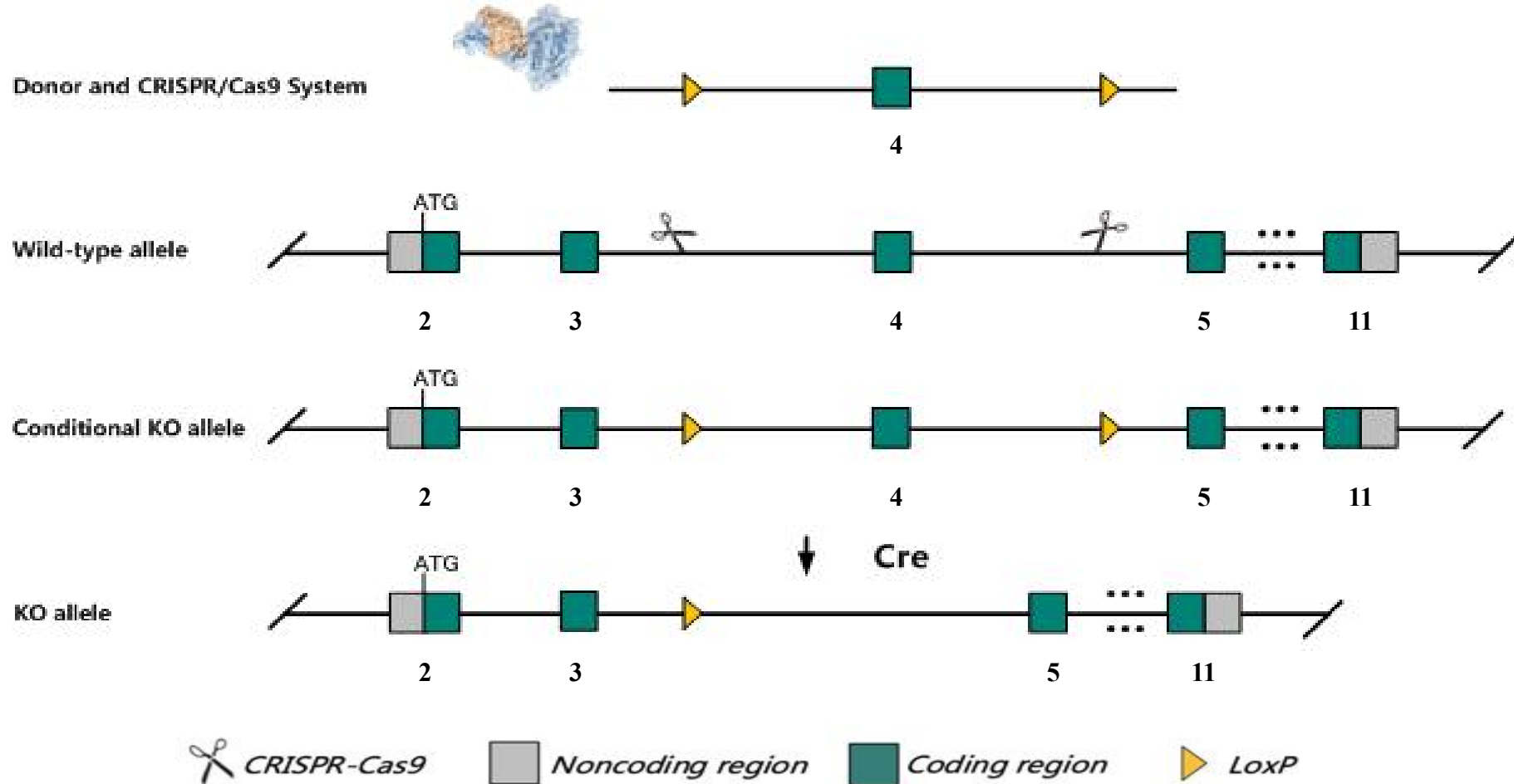
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Illrl2* gene.

Technical Information

- The *Il1rl2* gene has 4 transcripts. According to the structure of *Il1rl2* gene, exon4 of *Il1rl2-204* (ENSMUST00000194296.6) transcript is recommended as the knockout region. The region contains 199bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Il1rl2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

Il1rl2 interleukin 1 receptor-like 2 [Mus musculus (house mouse)]

Gene ID: 107527, updated on 18-May-2023

Summary

Official Symbol	Il1rl2 <small>provided by MGI</small>
Official Full Name	interleukin 1 receptor-like 2 <small>provided by MGI</small>
Primary source	MGI:MGI:1913107
See related	Ensembl:ENSMUSG00000070942
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	IL-1Rrp2
Summary	Predicted to enable cytokine receptor activity. Acts upstream of or within positive regulation of T cell differentiation; positive regulation of interleukin-6 production; and regulation of inflammatory response. Predicted to be located in membrane. Predicted to be integral component of membrane. Orthologous to human IL1RL2 (interleukin 1 receptor like 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in mammary gland adult (RPKM 3.8), subcutaneous fat pad adult (RPKM 2.3) and 21 other tissues See more
Orthologs	human all

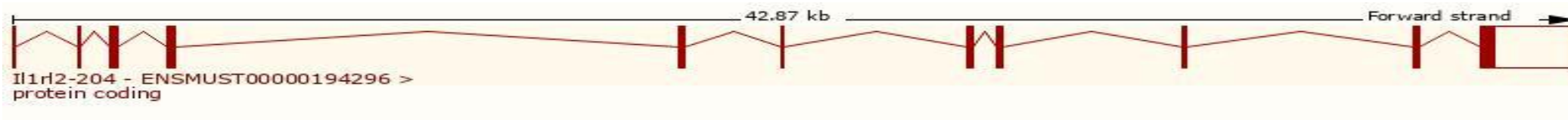
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 4 transcripts, all transcripts are shown below:

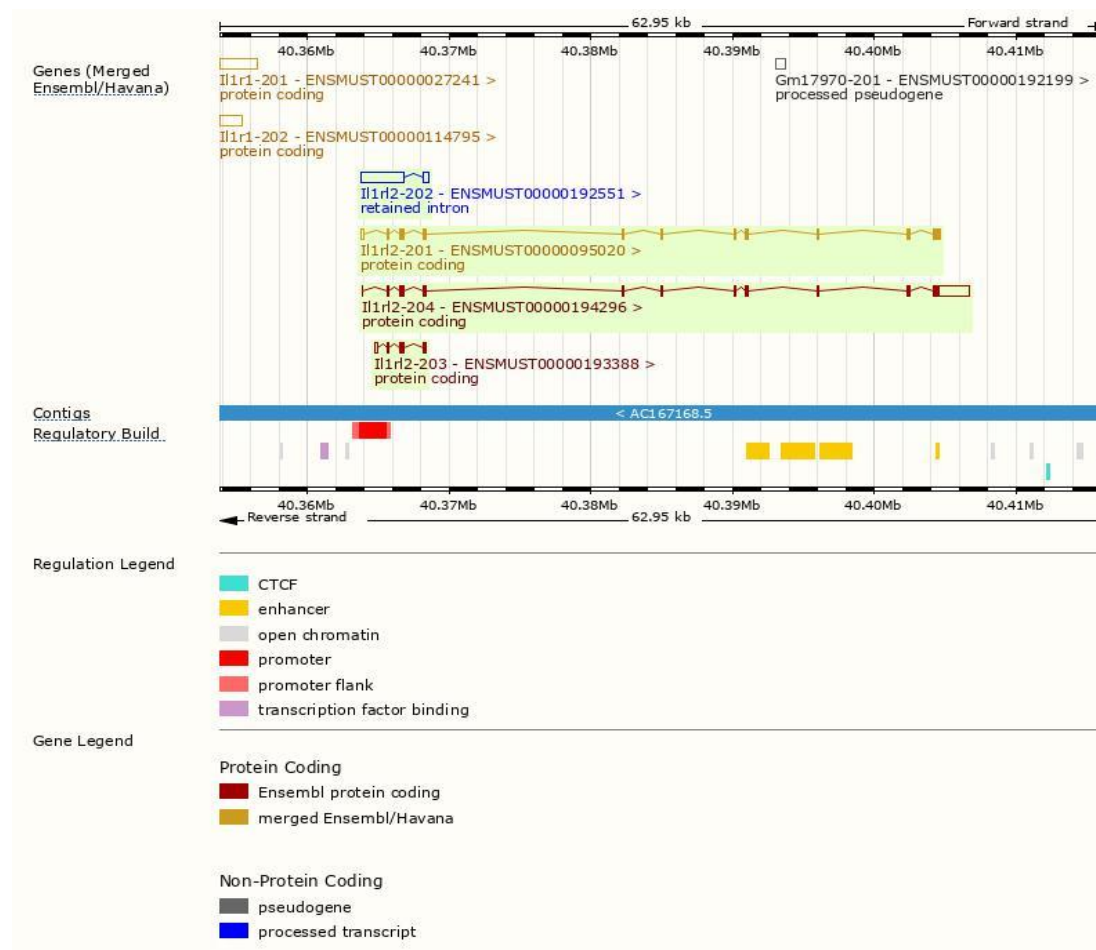
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000194296.6	Il1rl2-204	3908	574aa	Protein coding	CCDS14910	Q149G7 Q9ERS7	Ensembl Canonical Gencode Basic APPRIS P1 TSL:1
ENSMUST00000095020.9	Il1rl2-201	1950	574aa	Protein coding	CCDS14910	Q149G7 Q9ERS7	Gencode Basic APPRIS P1 TSL:1
ENSMUST00000193388.2	Il1rl2-203	693	166aa	Protein coding		A0A0A6YWD7	TSL:1 CDS 3' incomplete
ENSMUST00000192551.2	Il1rl2-202	3468	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Il1rl2-204* transcript, the transcription is shown below:

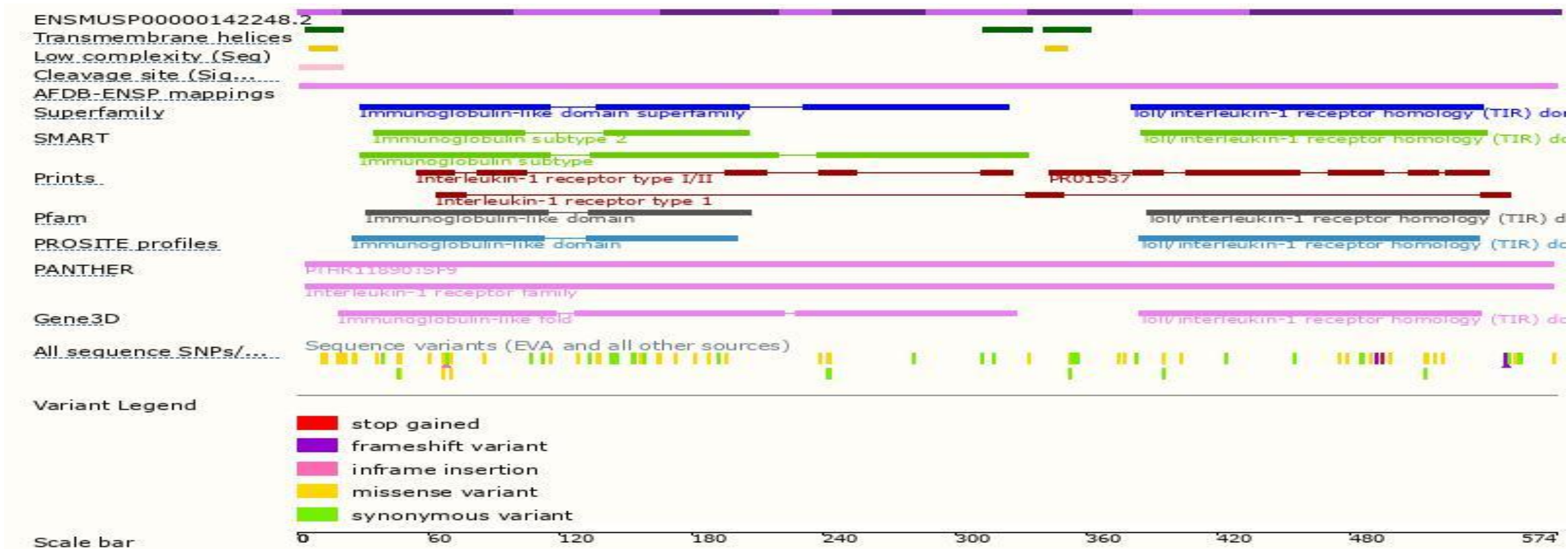


Source: <https://www.ensembl.org>

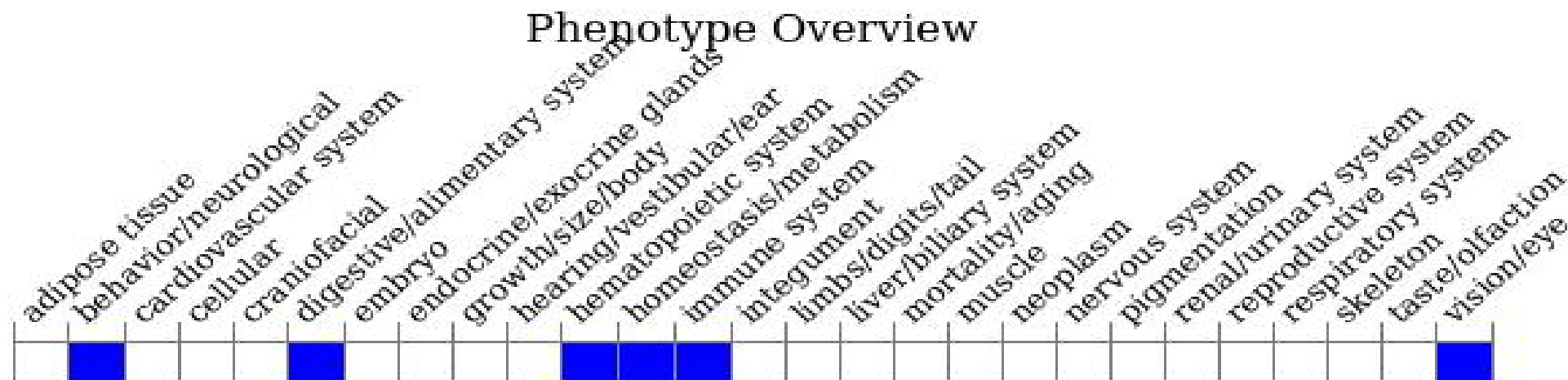
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Mice homozygous for a reporter allele are viable and overtly normal and have normal skin in an unchallenged context.

Important Information

- According to the MGI data, mice homozygous for a reporter allele are viable and overtly normal and have normal skin in an unchallenged context.
- The effect on *Il1rl2*-203 is unknown.
- *Il1rl2* is located on Chr1. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.