

# ***Il12a*** Cas9-CKO Strategy

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# Project Overview

**Project Name**

***Il12a***

**Project type**

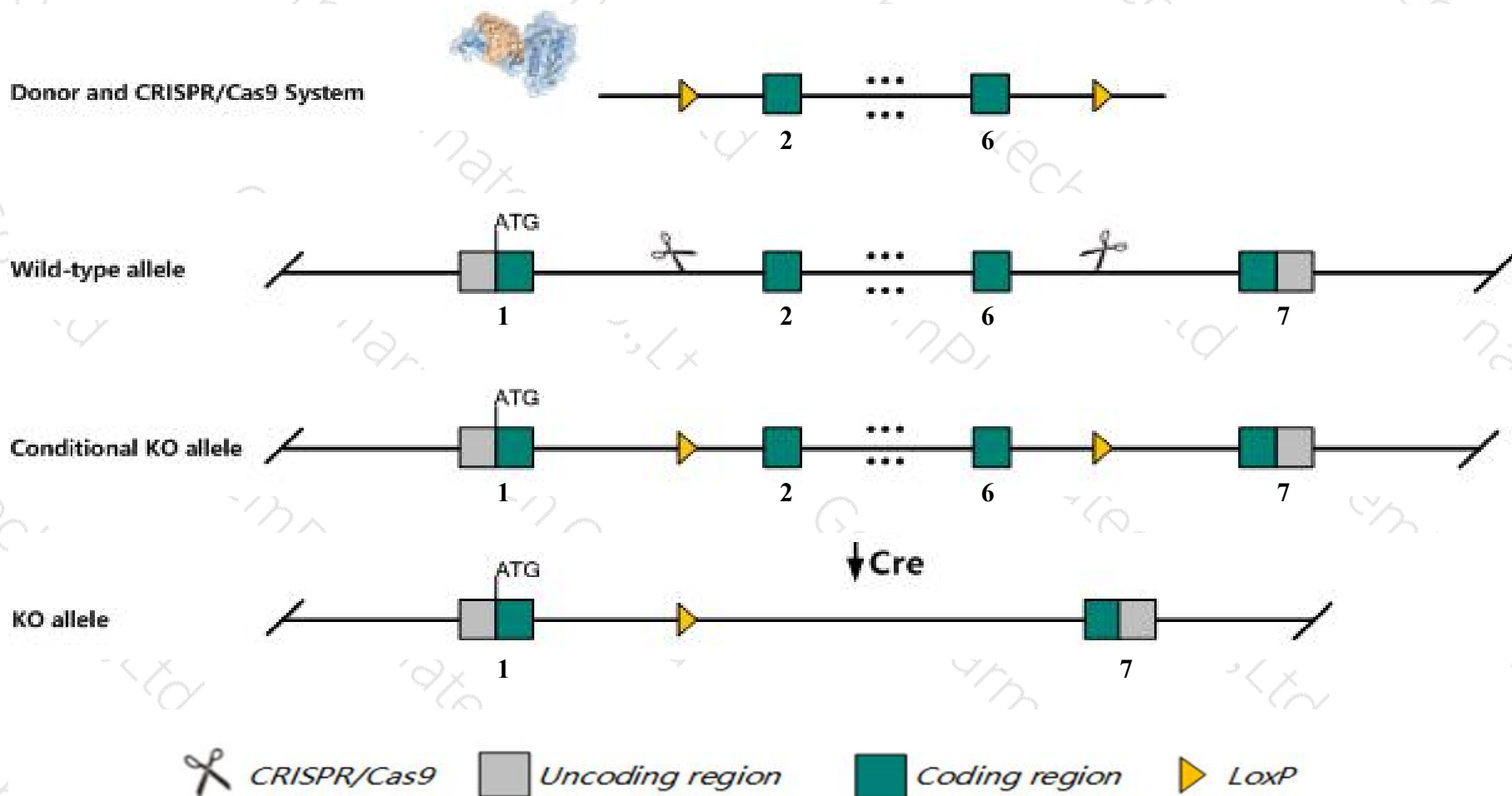
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Il12a* gene. The schematic diagram is as follows:



# Technical routes

- The *Il12a* gene has 6 transcripts. According to the structure of *Il12a* gene, exon2-exon6 of *Il12a*-202 (ENSMUST00000107816.3) transcript is recommended as the knockout region. The region contains 476bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Il12a* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

- According to the existing MGI data, Null homozygotes have decreased NK cell responses, altered effector T cell differentiation, and increased susceptibility to parasitic infections.
- The *Il12a* gene is located on the Chr3. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Il12a interleukin 12a [Mus musculus (house mouse)]

Gene ID: 16159, updated on 23-Feb-2019

### Summary



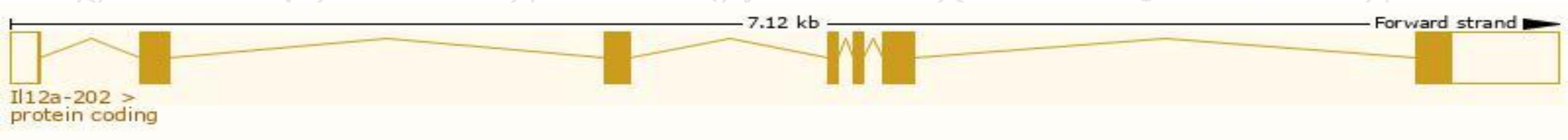
<b>Official Symbol</b>	Il12a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	interleukin 12a provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:96539</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000027776</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	IL-12p35, IL-12a, IL12a, p35
<b>Expression</b>	Biased expression in spleen adult (RPKM 2.9), lung adult (RPKM 1.2) and 8 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

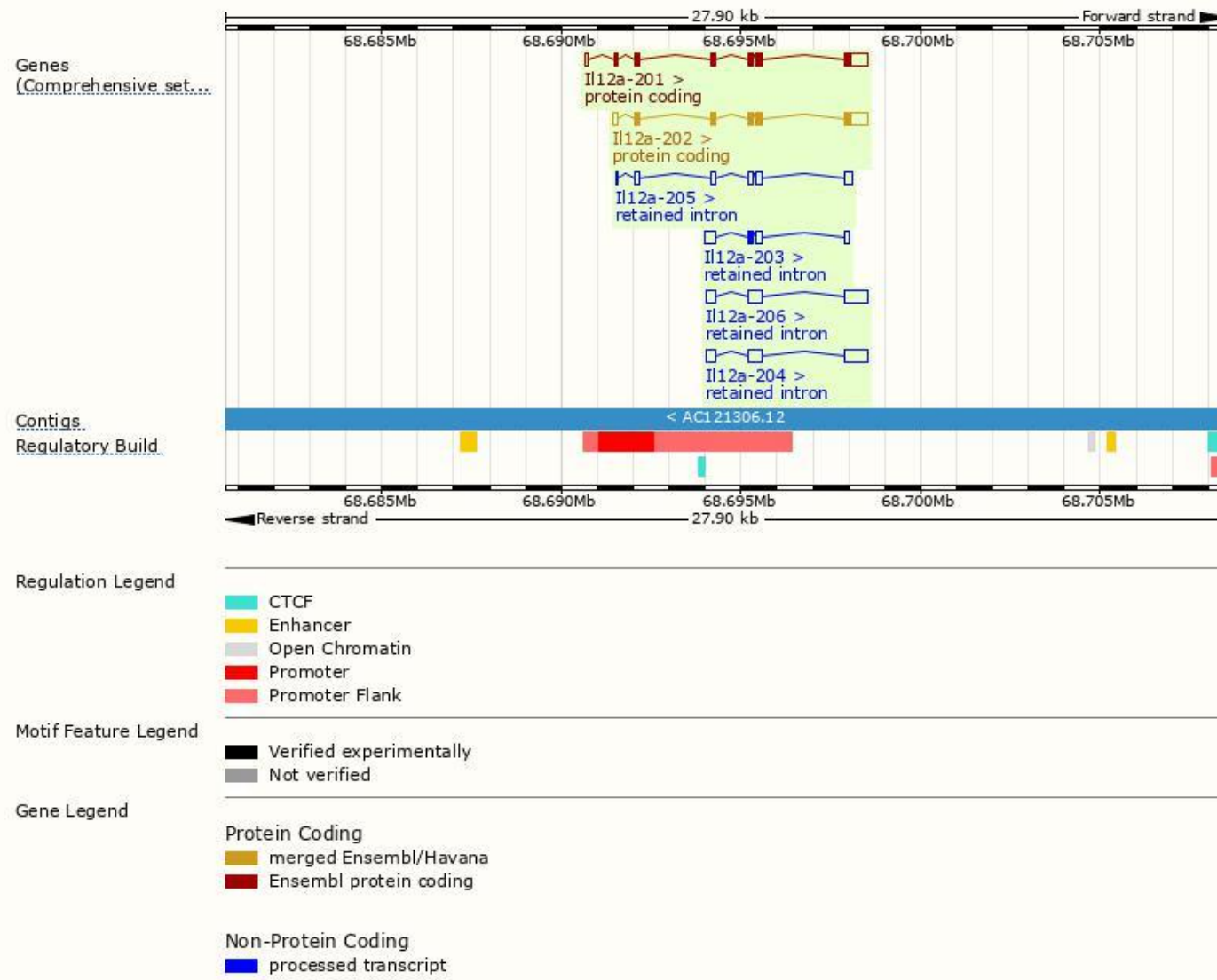
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Il12a-202	<a href="#">ENSMUST00000107816.3</a>	1268	<a href="#">215aa</a>	Protein coding	<a href="#">CCDS17400</a>	<a href="#">P43431 Q549G3</a>	TSL:1 GENCODE basic APPRIS P2
Il12a-201	<a href="#">ENSMUST00000029345.11</a>	1303	<a href="#">236aa</a>	Protein coding	-	<a href="#">F8WI71</a>	TSL:5 GENCODE basic APPRIS ALT2
Il12a-206	<a href="#">ENSMUST00000195517.2</a>	1298	No protein	Retained intron	-	-	TSL:2
Il12a-204	<a href="#">ENSMUST00000192812.4</a>	1296	No protein	Retained intron	-	-	TSL:2
Il12a-205	<a href="#">ENSMUST00000195408.5</a>	786	No protein	Retained intron	-	-	TSL:2
Il12a-203	<a href="#">ENSMUST00000191910.1</a>	639	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Il12a-202* transcript,The transcription is shown below



# Genomic location distribution





# Protein domain

ENSMUSP00000103...

Low complexity (Seg)

Cleavage site (Sign...

hmmpanther

Interleukin-12 alpha

Superfamily domains

Four-helical cytokine-like, core

Pfam domain

Interleukin-12 alpha

Gene3D

1.20.1250.10

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

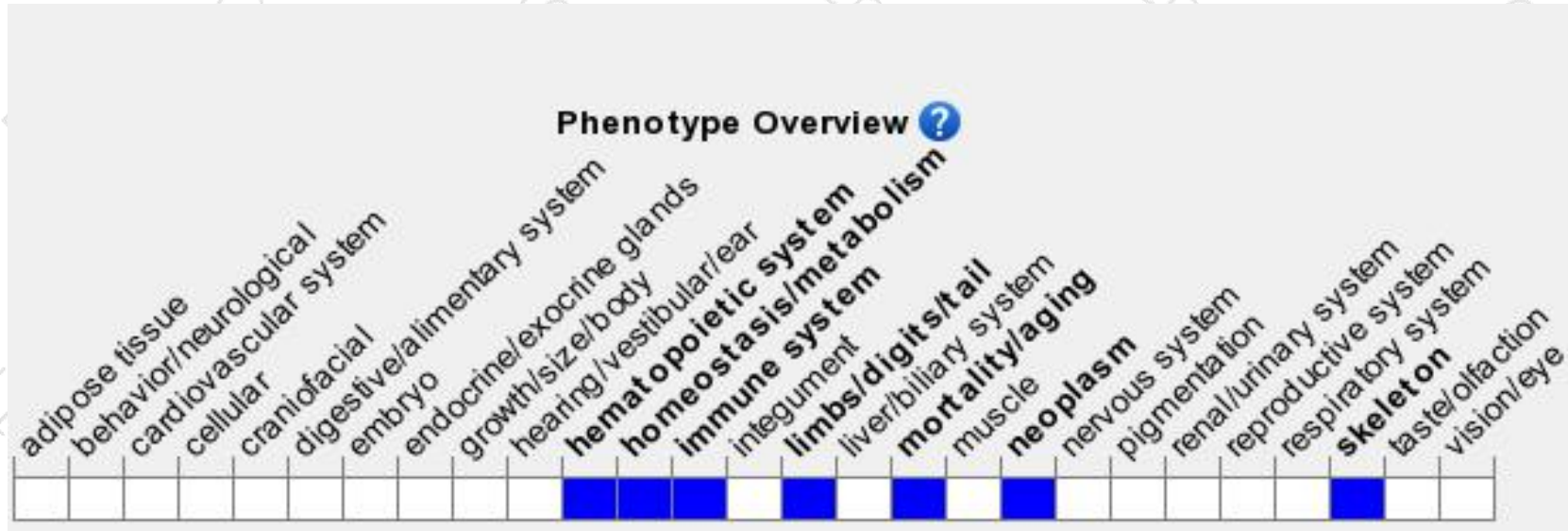
Variant Legend

missense variant  
synonymous variant

Scale bar

0 20 40 60 80 100 120 140 160 180 215

# 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 homozygotes have decreased NK cell responses, altered effector T cell differentiation, and increased susceptibility to parasitic infections.

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

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