Il11ra1 Cas9-KO Strategy

Designer: QiongZhou

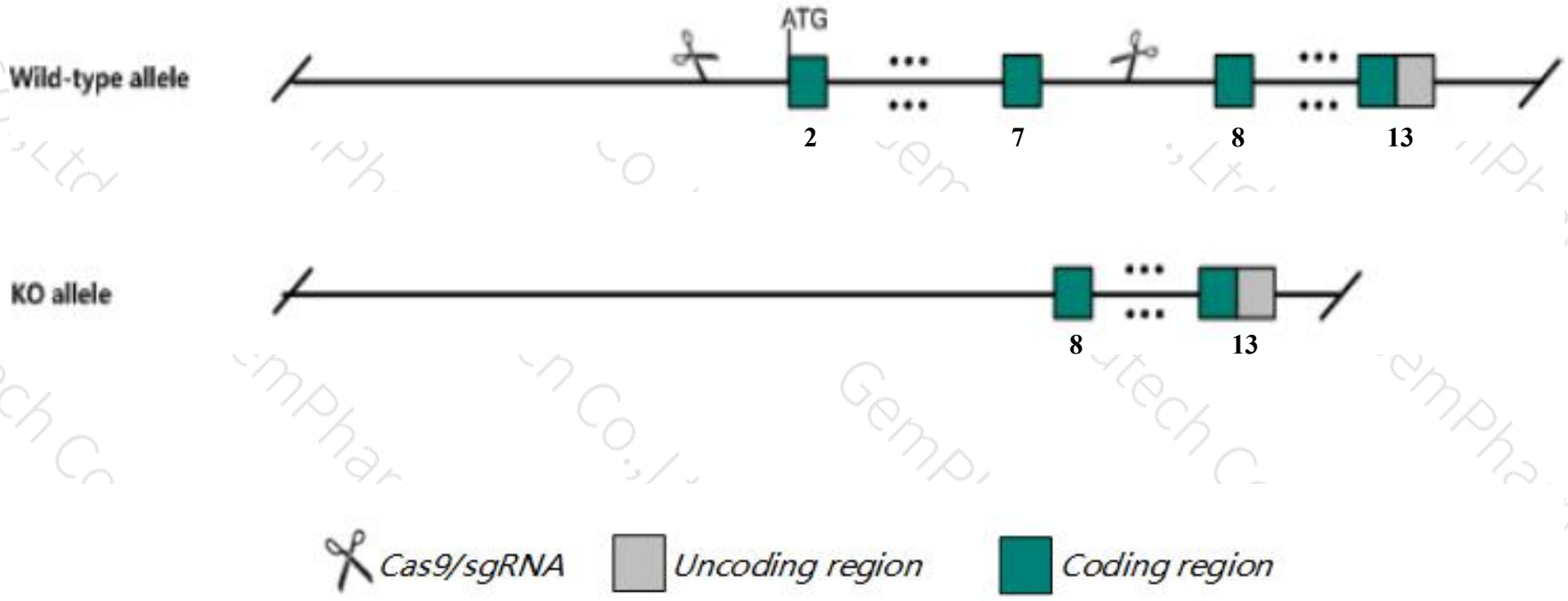
集萃药康 GemPharmatech

Project Overview

Project Name	***Il11ra1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Il1ra1* gene. The schematic diagram is as follows:



Technical routes

- The *Il11ra1* gene has 10 transcripts. According to the structure of *Il11ra1* gene, exon2-exon7 of *Il11ra1-201* (ENSMUST00000098132.10) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Il11ra1* 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.

Notice

- According to the existing MGI data,female homozygotes for targeted null mutations are infertile due to defective decidua formation.

- The sequences of *Il11ra1*、*Il11ra2* and *Gm13305* are highly similar,5 'end sequences are inconsistent, so specific primers should be designed for genetic and mRNA identification.（*Il11ra1*、*Il11ra2* 与*Gm13305* 序列高度相似,但5’端序列不一致，基因鉴定和mRNA鉴定时请注意设计特异性的引物）

- The *Il11ra1* gene is located on the Chr4. 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）

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Il11ra1 interleukin 11 receptor, alpha chain 1 [Mus musculus (house mouse)]

Gene ID: 16157, updated on 13-Mar-2020

Summary

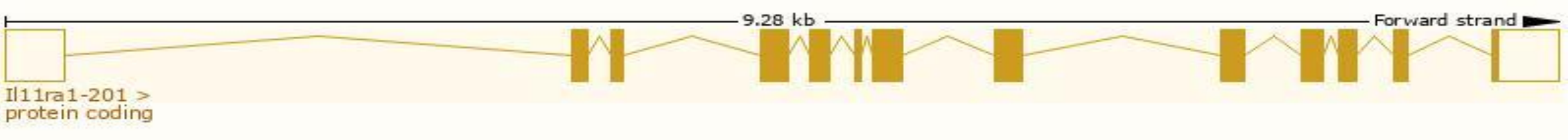
Official Symbol	Il11ra1 provided by MGI
Official Full Name	interleukin 11 receptor, alpha chain 1 provided byMGI
Primary source	MGI:MGI:107426
See related	Ensembl:ENSMUSG00000073889
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI314697, GP130, Il-11ra, Il11ra, Il11ra2, NR1
Expression	Ubiquitous expression in limb E14.5 (RPKM 66.0), ovary adult (RPKM 58.5) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

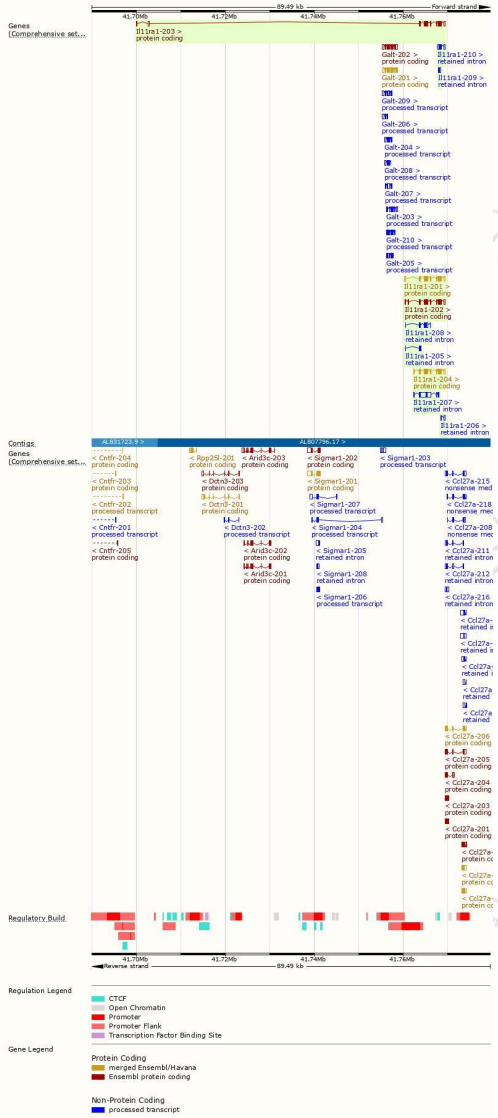
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Il11ra1-201	ENSMUST00000098132.10	2009	432aa	Protein coding	CCDS18071	Q64385	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Il11ra1-203	ENSMUST00000108041.7	1953	432aa	Protein coding	CCDS18071	Q64385	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Il11ra1-202	ENSMUST00000108040.7	1837	432aa	Protein coding	CCDS18071	Q64385	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Il11ra1-204	ENSMUST00000108042.2	1768	432aa	Protein coding	CCDS18071	Q64385	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Il11ra1-207	ENSMUST00000145445.1	2605	No protein	Retained intron	-	-	TSL:2
Il11ra1-210	ENSMUST00000155538.7	848	No protein	Retained intron	-	-	TSL:2
Il11ra1-208	ENSMUST00000146608.7	756	No protein	Retained intron	-	-	TSL:5
Il11ra1-206	ENSMUST00000142059.1	523	No protein	Retained intron	-	-	TSL:2
Il11ra1-209	ENSMUST00000152748.1	438	No protein	Retained intron	-	-	TSL:5
Il11ra1-205	ENSMUST00000140894.7	325	No protein	Retained intron	-	-	TSL:3

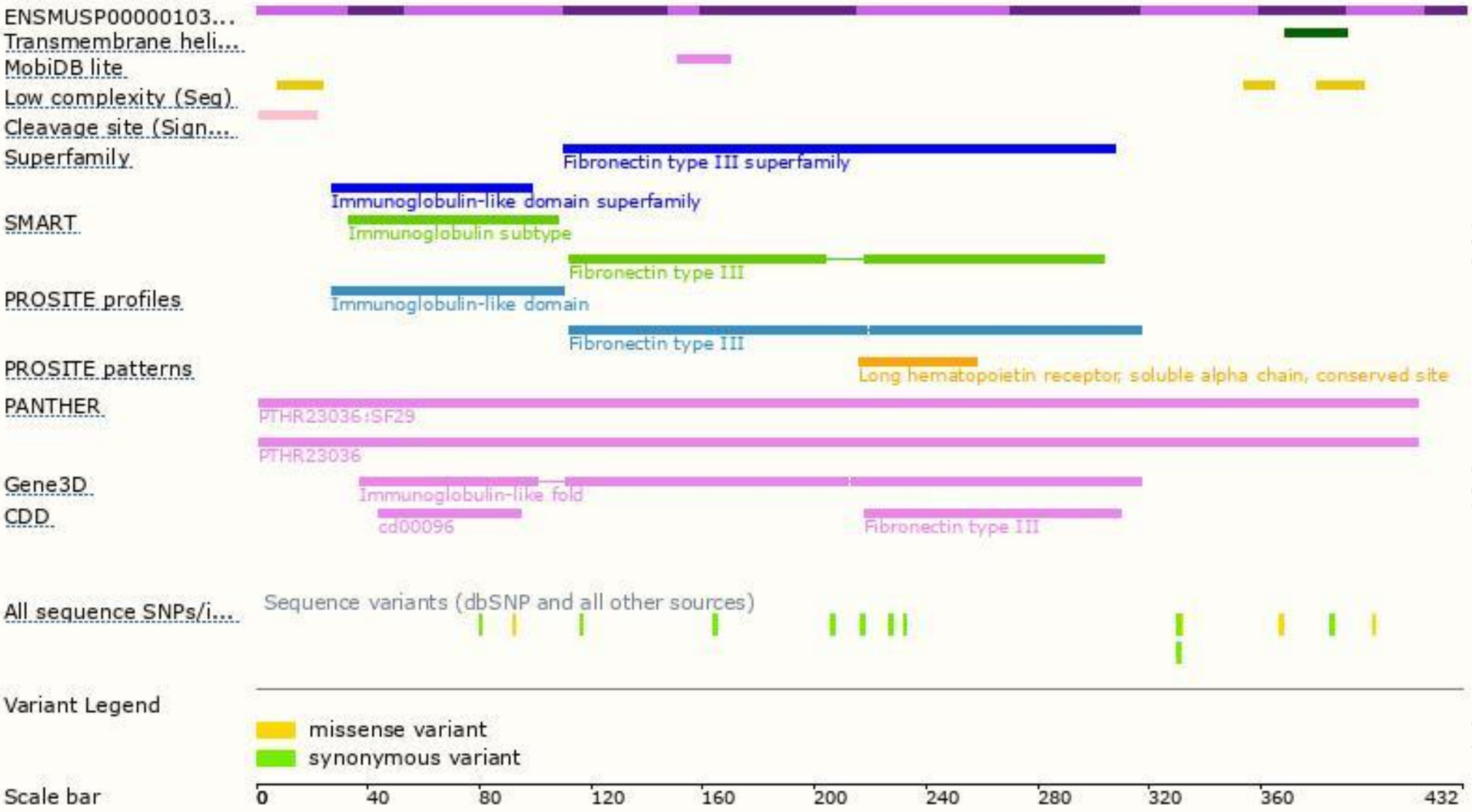
The strategy is based on the design of *Il11ra1-201* transcript,the transcription is shown below:



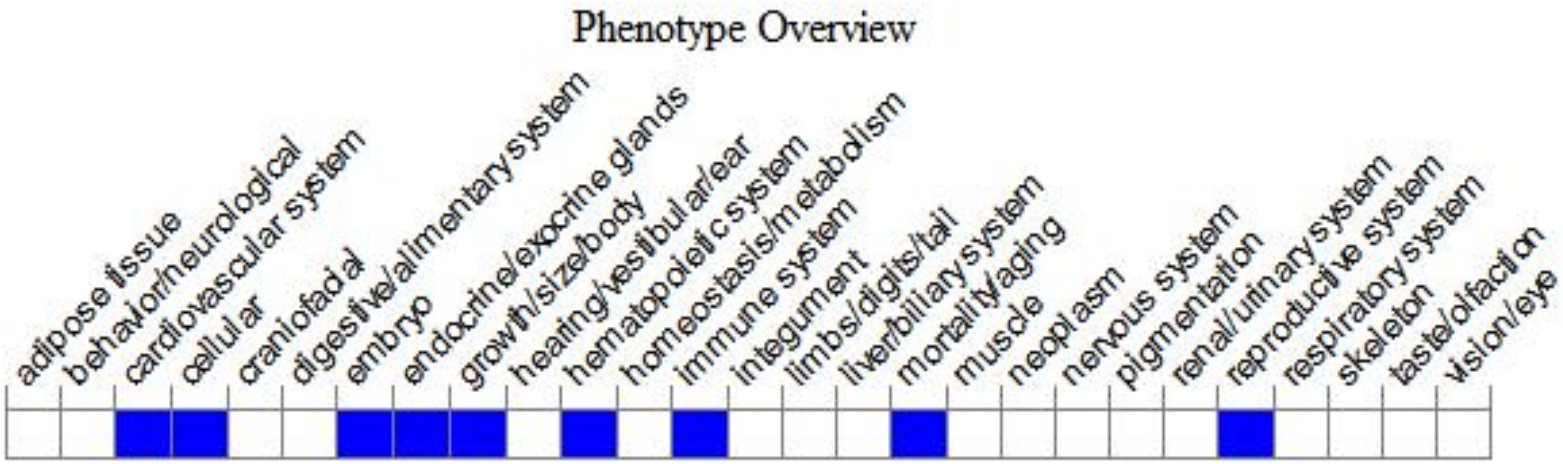
Genomic location distribution



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,female homozygotes for targeted null mutations are infertile due to defective decidua formation.

集萃药康
GemPharmatech

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

Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd