

Pigr Cas9-KO Strategy

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Date: 2019-11-24

Project Overview

Project Name

Pigr

Project type

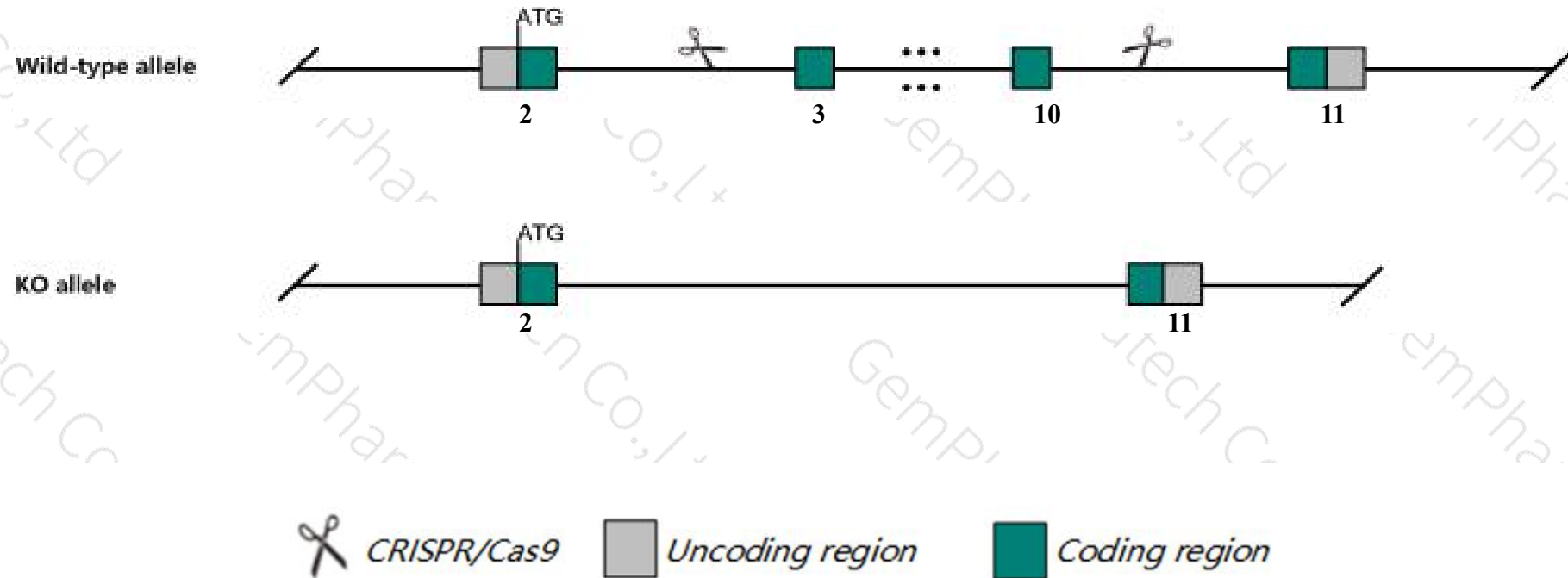
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Pigr* gene has 3 transcripts. According to the structure of *Pigr* gene, exon3-exon10 of *Pigr-201* (ENSMUST00000027675.13) transcript is recommended as the knockout region. The region contains 2177bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pigr* gene. The brief process is as follows: CRISPR/Cas9 system were

- According to the existing MGI data, Nullizygous mice show impaired transepithelial transport of dimeric IgA, increased serum IgA levels and mucosal leakiness. Studies of one null allele show increased susceptibility to mycobacterial infections while another allele causes impaired clearance of the protozoan parasite Giardia.
- The *Pigr* gene is located on the Chr1. 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)

Pigr polymeric immunoglobulin receptor [*Mus musculus* (house mouse)]

Gene ID: 18703, updated on 12-Aug-2019

Summary

- Official Symbol** Pigr provided by [MGI](#)
- Official Full Name** polymeric immunoglobulin receptor provided by [MGI](#)
- Primary source** [MGI:MGI:103080](#)
- See related** [Ensembl:ENSMUSG00000026417](#)
- 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
- Expression** Biased expression in large intestine adult (RPKM 482.2), colon adult (RPKM 389.4) and 3 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 1 E4; 1 56.89 cM

See Pigr in [Genome Data Viewer](#)

Exon count: 11

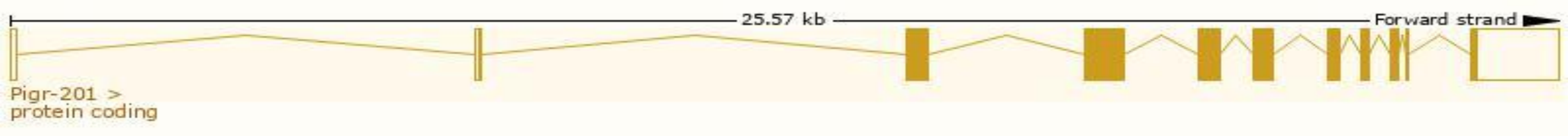
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (130826684..130852249)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (132723261..132748826)

Transcript information (Ensembl)

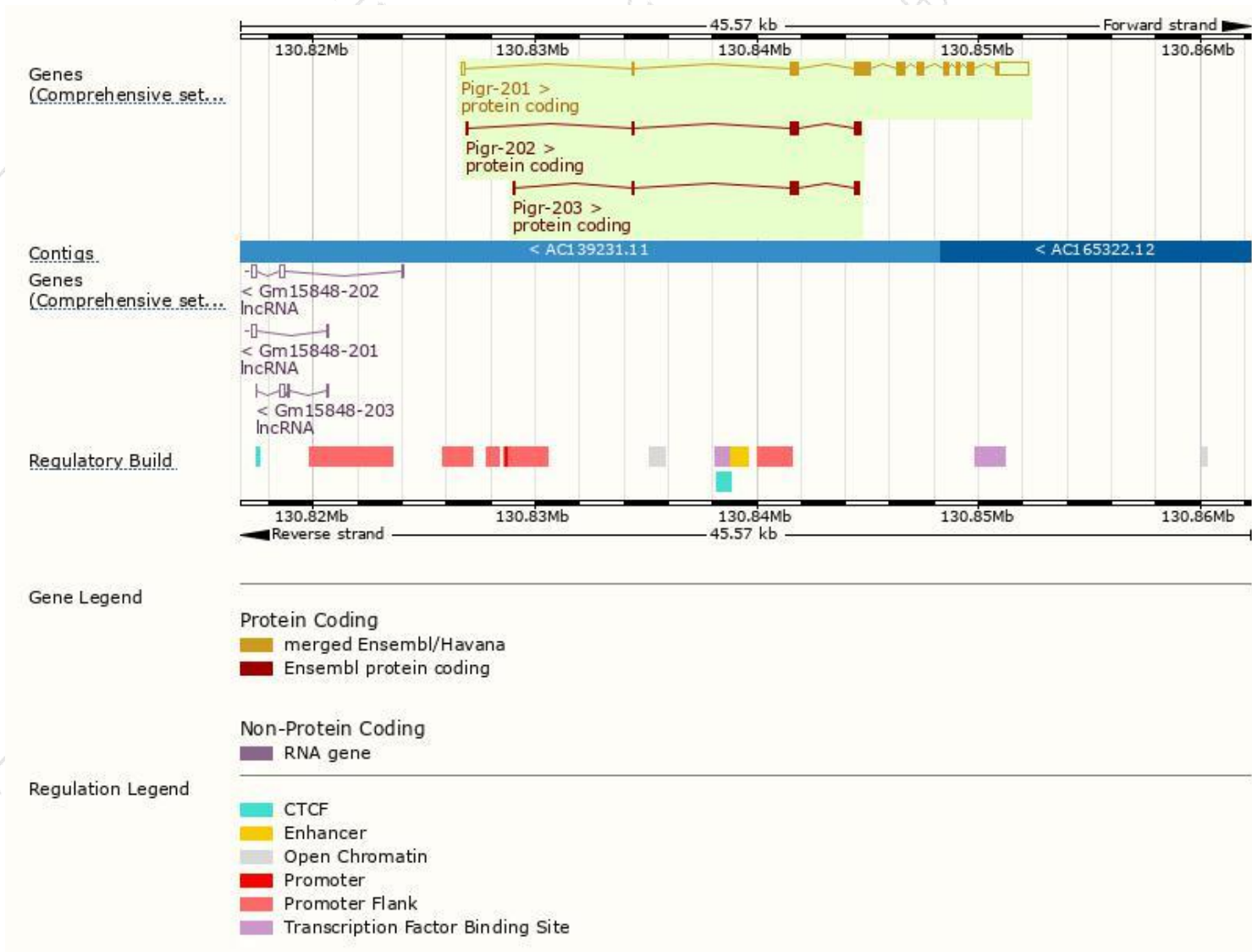
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pigr-201	ENSMUST00000027675.13	3849	771aa	Protein coding	CCDS15260	O70570	TSL:1 GENCODE basic APPRIS P1
Pigr-202	ENSMUST00000133792.7	784	211aa	Protein coding	-	D3Z2D3	CDS 3' incomplete TSL:3
Pigr-203	ENSMUST00000137782.1	740	200aa	Protein coding	-	D3YVM4	CDS 3' incomplete TSL:3

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



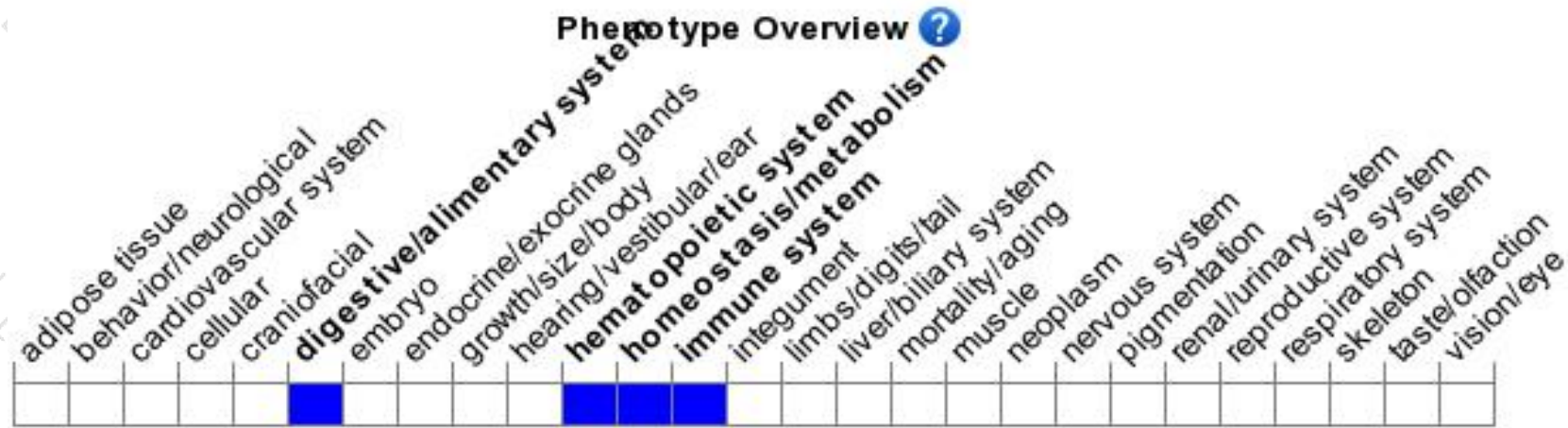
Genomic location distribution



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, Nullizygous mice show impaired transepithelial transport of dimeric IgA, increased serum IgA levels and mucosal leakiness. Studies of one null allele show increased susceptibility to mycobacterial infections while another allele causes impaired clearance of the protozoan parasite Giardia.

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

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