Pigr Cas9-CKO Strategy

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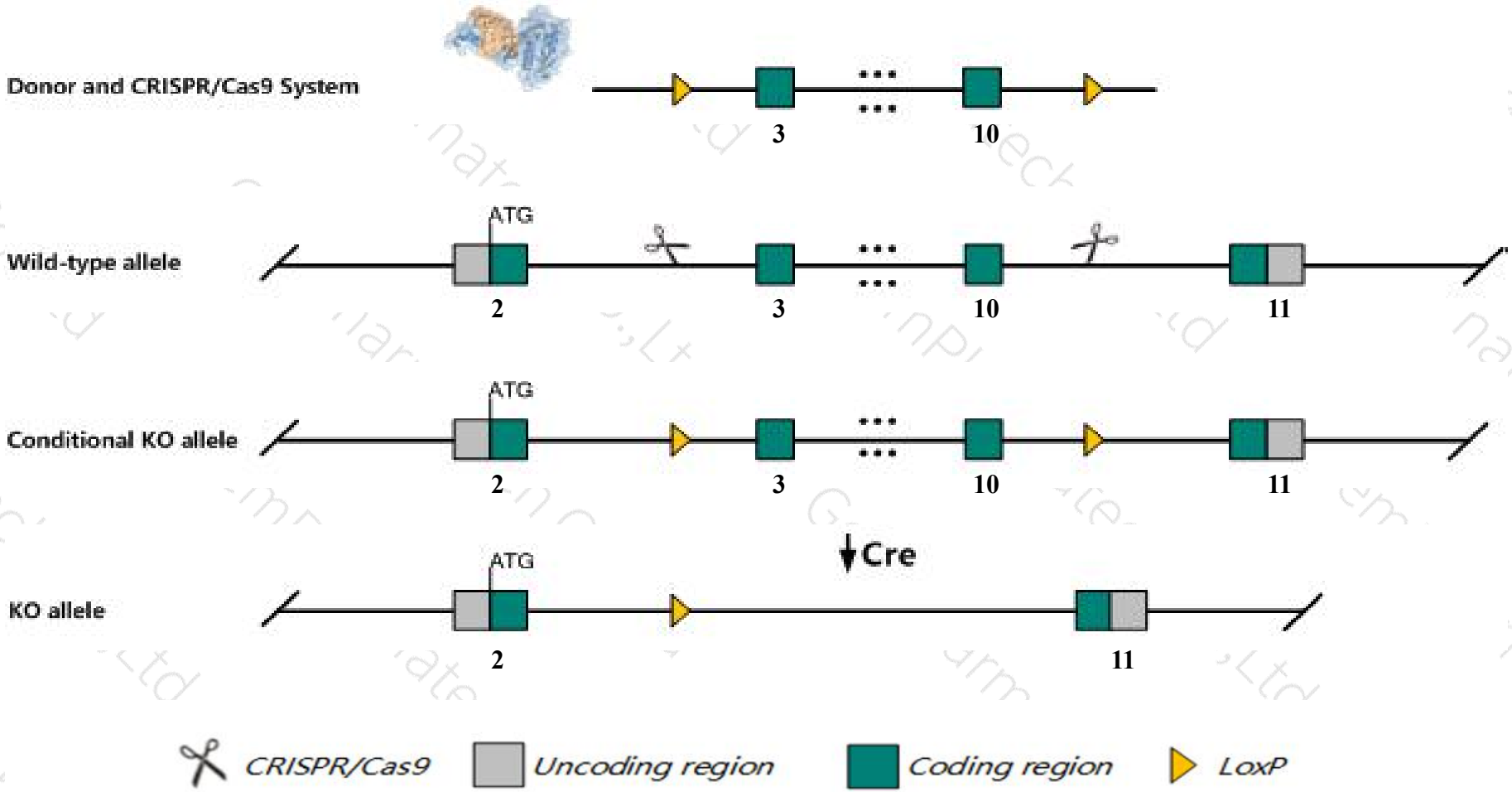
Project Overview

Project Name	***Pigr***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- 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 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.

Notice

➢ 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 clearanceof 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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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)

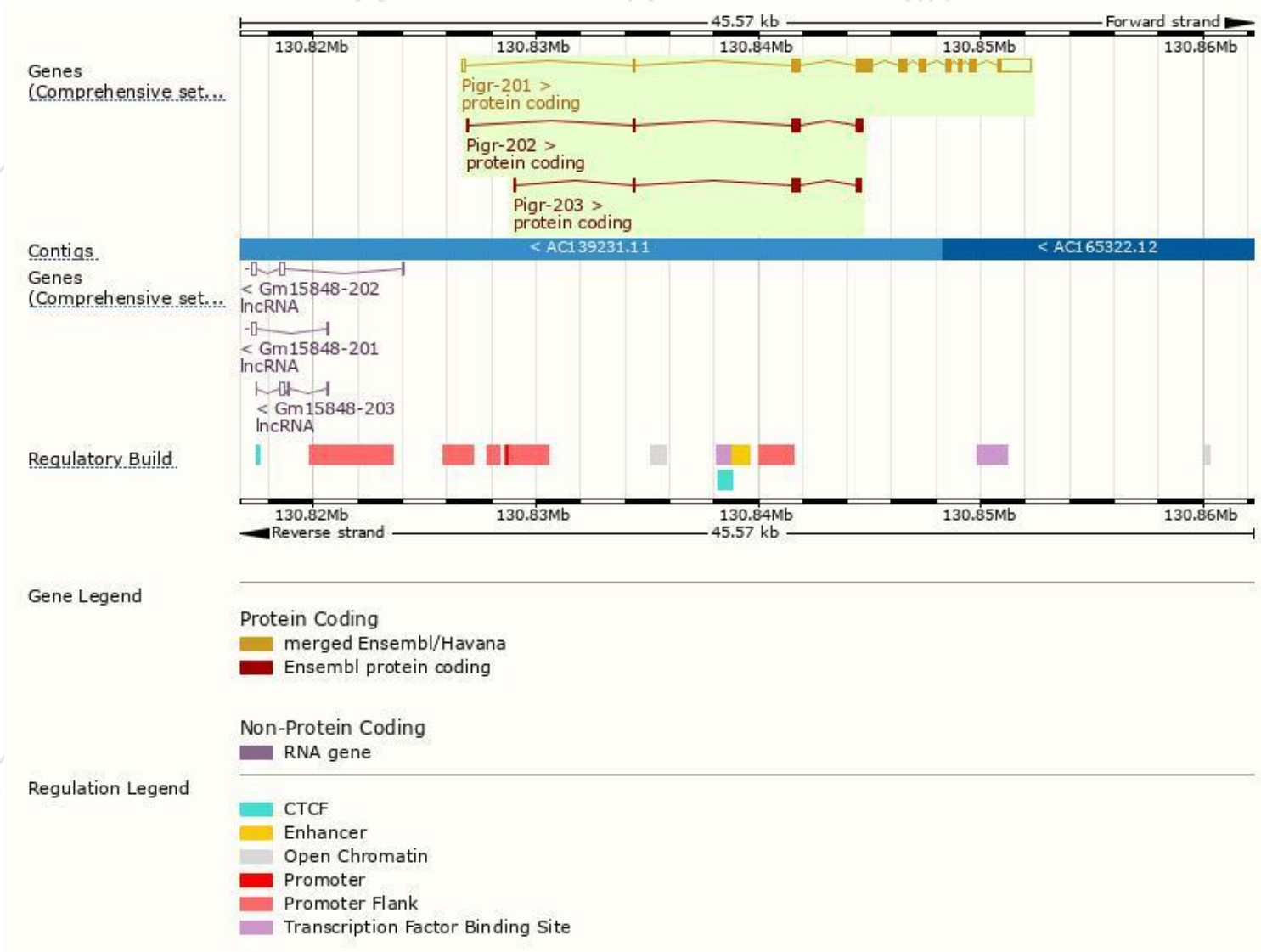
Transcript information（Ensembl）

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

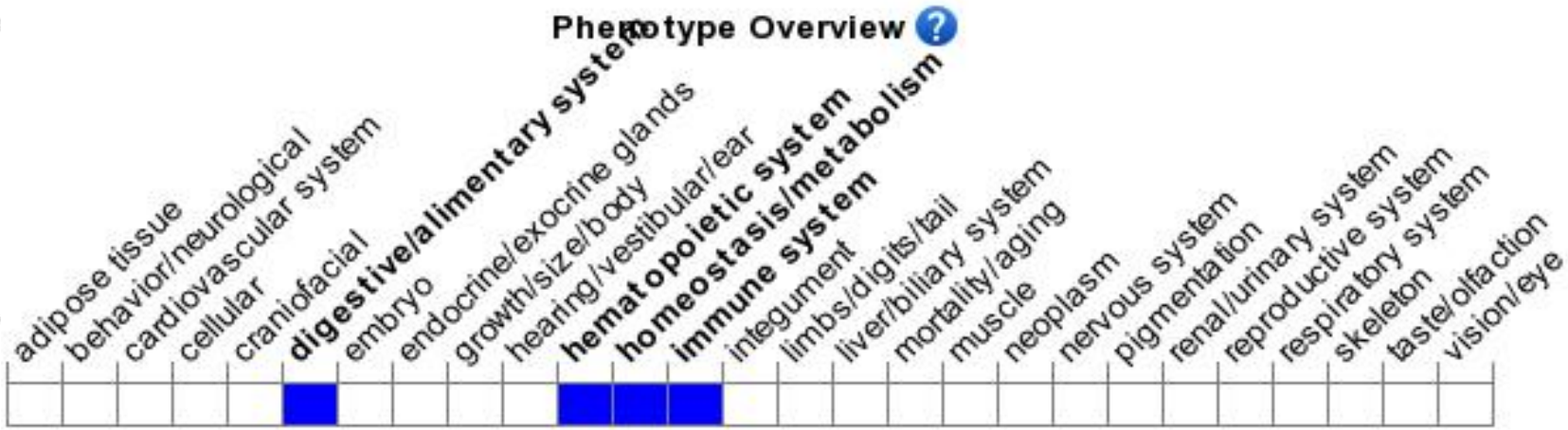
The strategy is based on the design of *Pigr-201* transcript,The transcription is shown below

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/).

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

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