

Pigq Cas9-CKO Strategy

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Design Date: 2021-3-23

Project Overview

Project Name

Pigq

Project type

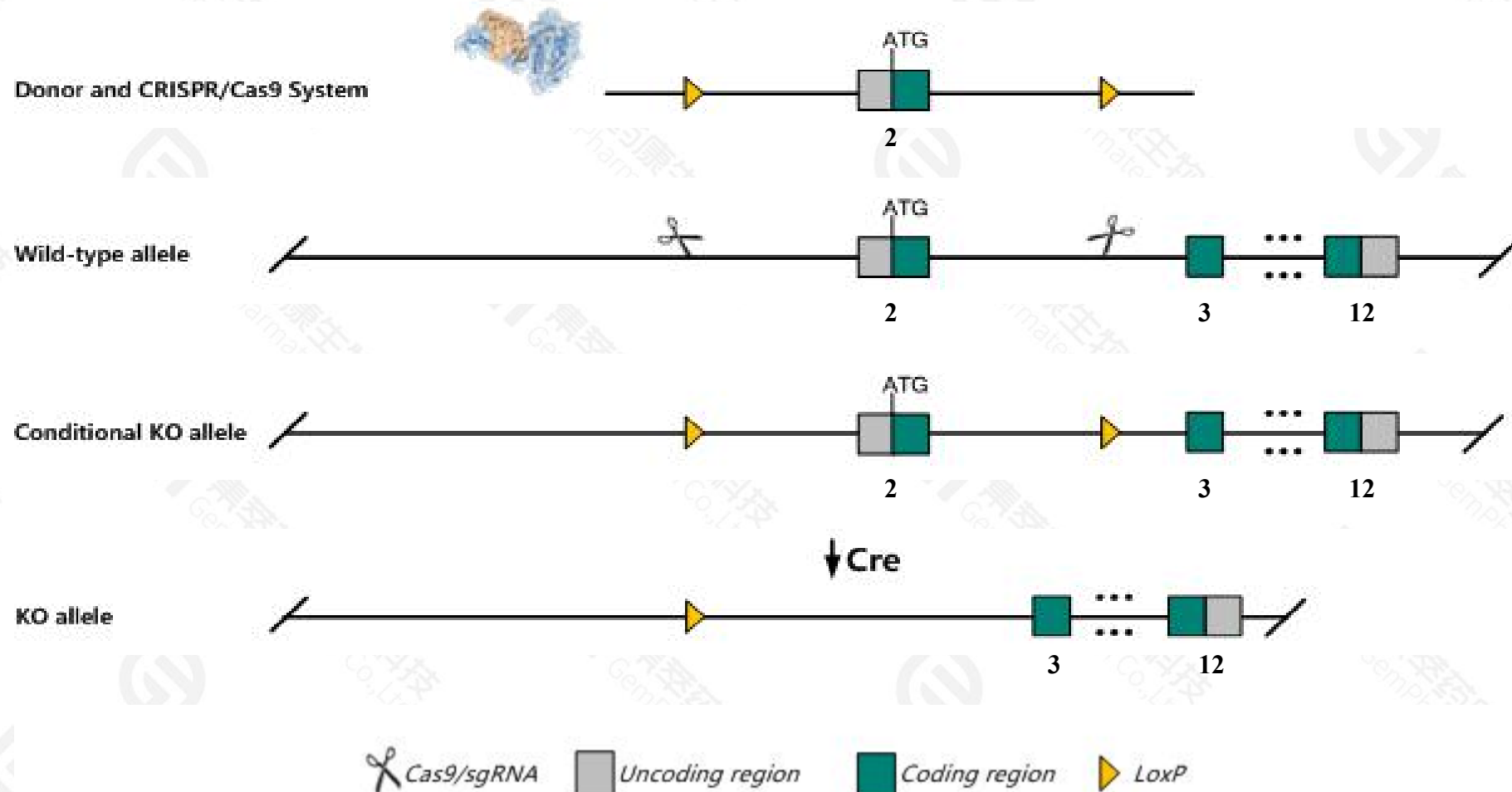
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Pigq* gene has 22 transcripts. According to the structure of *Pigq* gene, exon2 of *Pigq*-202(ENSMUST00000097368.10) 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 *Pigq* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA 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 was 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.

- Transcript *Pigq-215,216,220* may not be affected.
- The *Pigq* gene is located on the Chr17. 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)

Pigq phosphatidylinositol glycan anchor biosynthesis, class Q [Mus musculus (house mouse)]

Gene ID: 14755, updated on 22-Nov-2020

Summary



Official Symbol Pigq provided by [MGI](#)

Official Full Name phosphatidylinositol glycan anchor biosynthesis, class Q provided by [MGI](#)

Primary source [MGI:MGI:1333114](#)

See related [Ensembl:ENSMUSG00000025728](#)

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 Gp, Gpi, Gpi1, Gpi1h, Gpi1p, Gpih

Expression Ubiquitous expression in liver E14.5 (RPKM 87.8), liver E14 (RPKM 63.2) and 28 other tissues [See more](#)

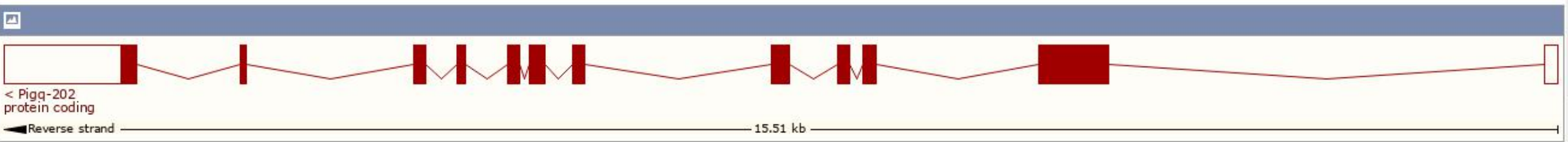
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

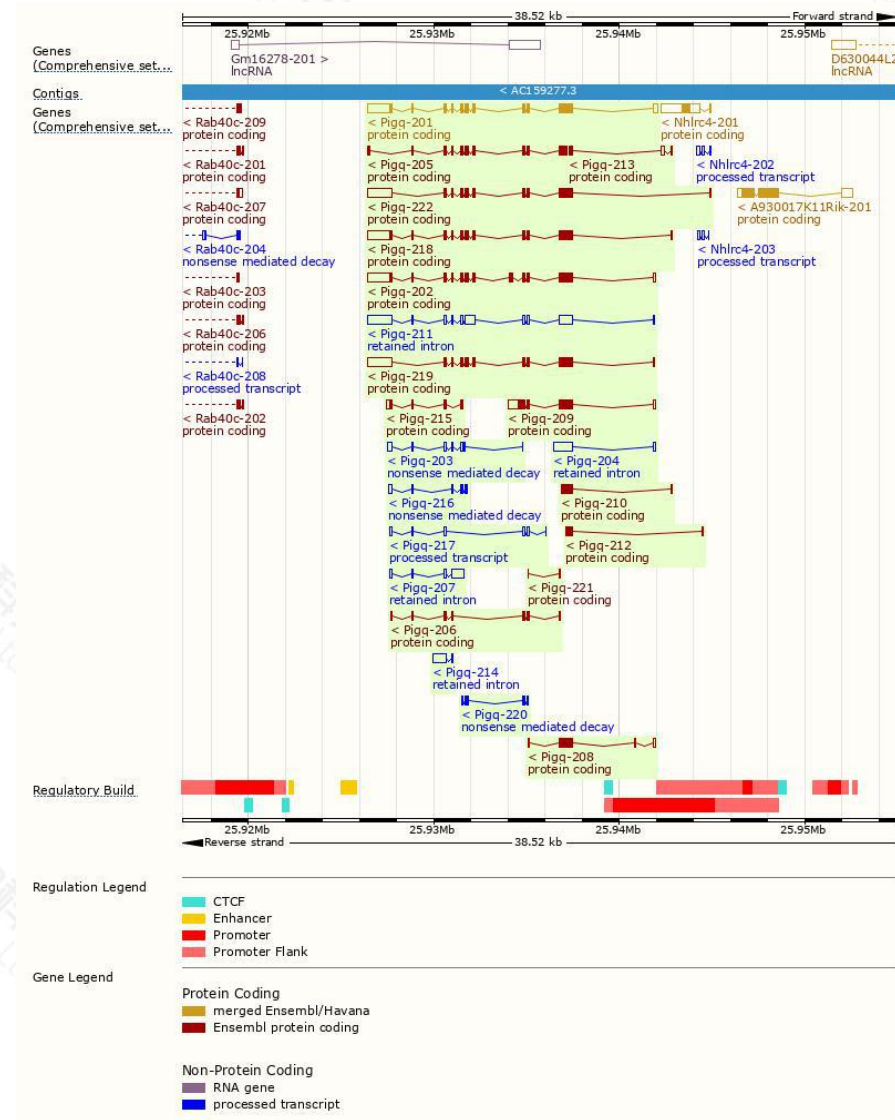
The gene has 22 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pigq-202	ENSMUST00000097368.10	3233	641aa	Protein coding	CCDS70774		TSL:1 , GENCODE basic ,
Pigq-201	ENSMUST00000026823.16	3173	581aa	Protein coding	CCDS28538		TSL:1 , GENCODE basic , APPRIS P2 ,
Pigq-218	ENSMUST00000208043.2	2987	581aa	Protein coding	CCDS28538		TSL:5 , GENCODE basic , APPRIS P2 ,
Pigq-222	ENSMUST00000237570.2	2931	516aa	Protein coding	-		GENCODE basic , APPRIS ALT2 ,
Pigq-219	ENSMUST00000208071.2	2926	516aa	Protein coding	-		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Pigq-209	ENSMUST00000140304.2	1835	378aa	Protein coding	-		TSL:1 , GENCODE basic ,
Pigq-205	ENSMUST00000133650.9	1398	452aa	Protein coding	-		CDS 5' incomplete , TSL:5 ,
Pigq-208	ENSMUST00000139226.2	946	248aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Pigq-206	ENSMUST00000135253.3	681	227aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:5 ,
Pigq-210	ENSMUST00000145745.3	679	200aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Pigq-215	ENSMUST00000207073.2	586	139aa	Protein coding	-		CDS 5' incomplete , TSL:5 ,
Pigq-212	ENSMUST00000148307.2	375	106aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Pigq-213	ENSMUST00000148382.2	368	63aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Pigq-221	ENSMUST00000208499.2	107	35aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:1 ,
Pigq-203	ENSMUST00000123929.9	779	45aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:3 ,
Pigq-216	ENSMUST00000207496.2	586	102aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Pigq-220	ENSMUST00000208242.2	389	86aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:1 ,
Pigq-217	ENSMUST00000207777.2	621	No protein	Processed transcript	-		TSL:3 ,
Pigq-211	ENSMUST00000148045.8	3278	No protein	Retained intron	-		TSL:1 ,
Pigq-204	ENSMUST00000124032.2	1103	No protein	Retained intron	-		TSL:1 ,
Pigq-207	ENSMUST00000139078.3	1014	No protein	Retained intron	-		TSL:2 ,
Pigq-214	ENSMUST00000156924.2	763	No protein	Retained intron	-		TSL:2 ,

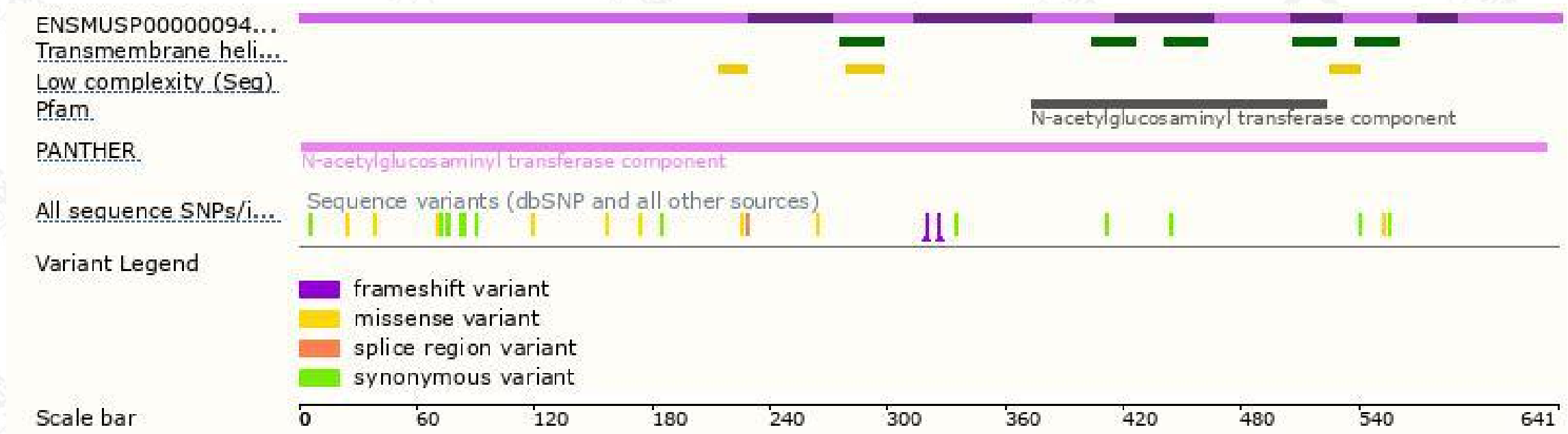
The strategy is based on the design of *Pigq-202* transcript,the transcription is shown below:



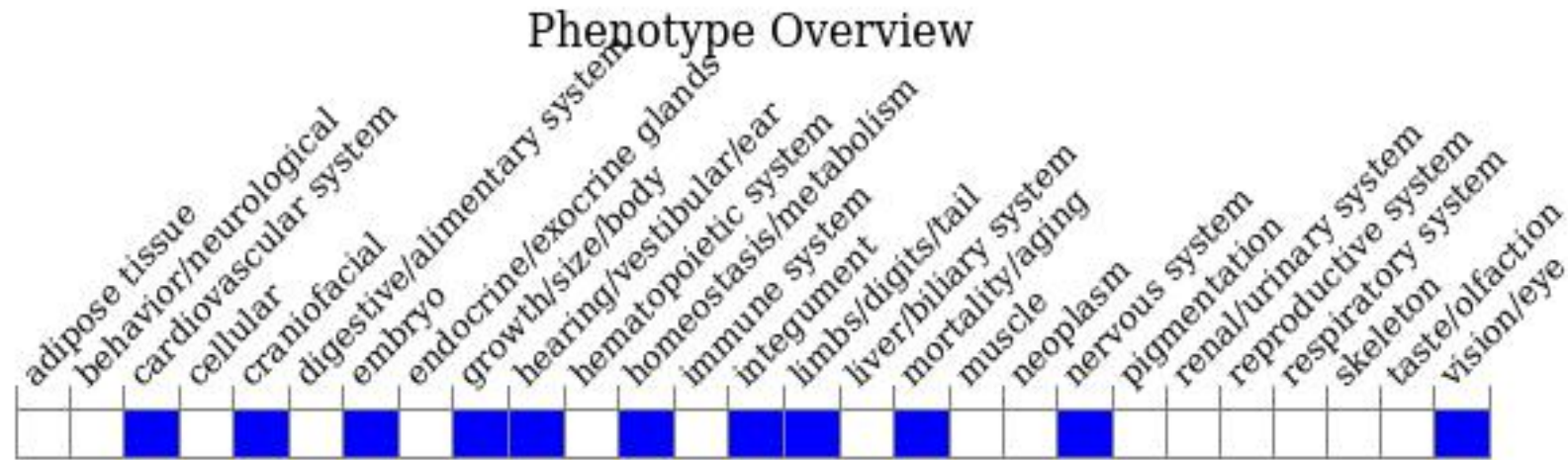
Genomic location distribution



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/>).

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

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