Pik3cg Cas9-KO Strategy

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Project Overview

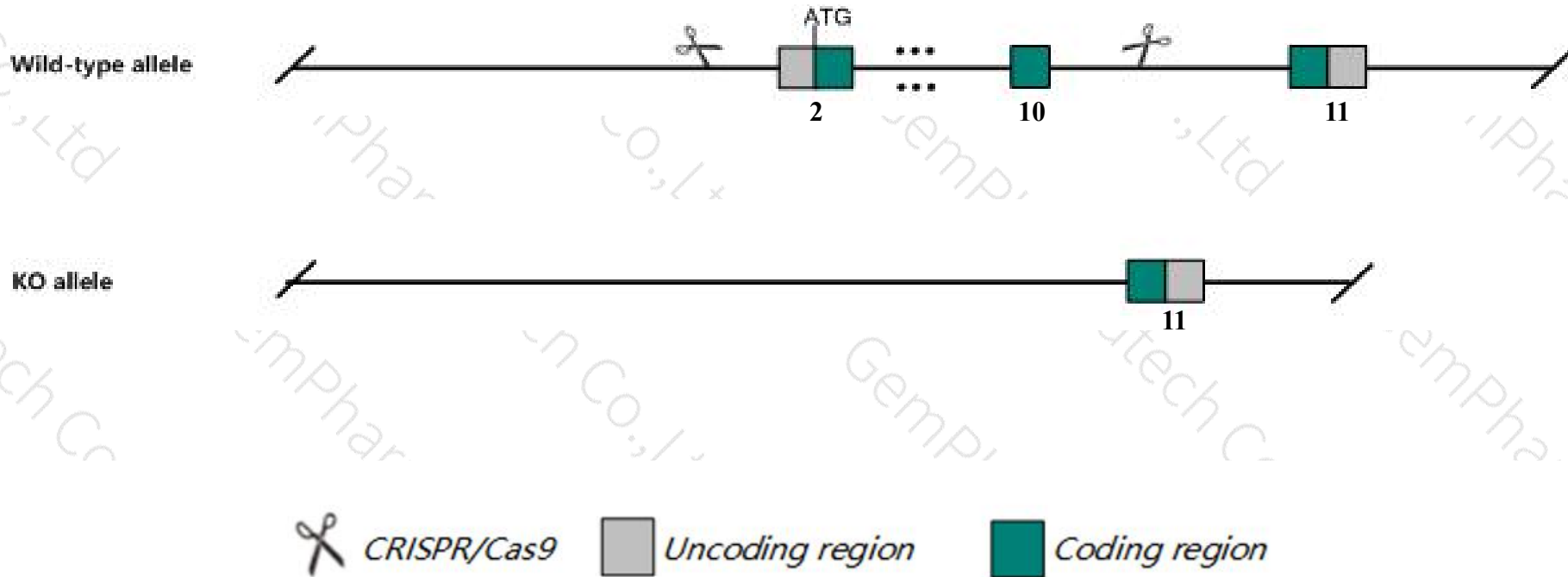|	
Project Name	*Pik3cg*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pik3cg* gene. The schematic diagram is as follows:

Technical routes

➢ The *Pik3cg* gene has 7 transcripts. According to the structure of *Pik3cg* gene, exon2-exon10 of *Pik3cg-201* (ENSMUST00000053215.13) 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 *Pik3cg* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ Transcript *Pik3cg*-206 may not be affected.

➢ According to the existing MGI data,Mice homozygous for disruptions in this gene display defects in thymocyte development, T cell activation, and neutrophil migration.

➢ The *Pik3cg* gene is located on the Chr12. 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）

Pik3cg phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma [Mus musculus (house mouse)]

Gene ID: 30955, updated on 5-Mar-2019

▲ Summary

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Official Symbol	Pik3cg provided by MGI
Official Full Name	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma provided by MGI
Primary source	MGI:MGI:1353576
See related	Ensembl:ENSMUSG00000020573
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	5830428L06Rik, PI3Kgamma, p110gamma, p120-PI3K
Expression	Biased expression in thymus adult (RPKM 8.2), spleen adult (RPKM 4.8) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pik3cg-201	ENSMUST00000053215.13	5871	1102aa	Protein coding	CCDS25870	Q9JHG7	TSL:1 GENCODE basic APPRIS P1
Pik3cg-207	ENSMUST00000220366.1	4660	1102aa	Protein coding	CCDS25870	Q9JHG7	TSL:1 GENCODE basic APPRIS P1
Pik3cg-202	ENSMUST00000085469.5	4584	1102aa	Protein coding	CCDS25870	Q9JHG7	TSL:1 GENCODE basic APPRIS P1
Pik3cg-205	ENSMUST00000217915.1	3340	1024aa	Protein coding	-	A0A1W2P8F6	TSL:1 GENCODE basic
Pik3cg-204	ENSMUST00000156904.7	4805	1102aa	Nonsense mediated decay	-	Q9JHG7	TSL:1
Pik3cg-206	ENSMUST00000218848.1	2803	No protein	Retained intron	-	-	TSL:NA
Pik3cg-203	ENSMUST00000126814.1	350	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Pik3cg-201* transcript,The transcription is shown below

< Pik3cg-201
protein coding

Reverse strand

34.49 kb
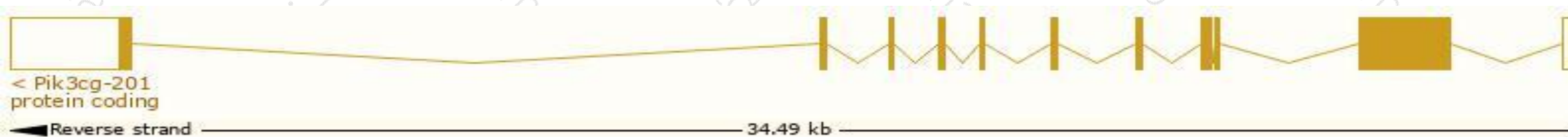
Genomic location distribution

Protein domain
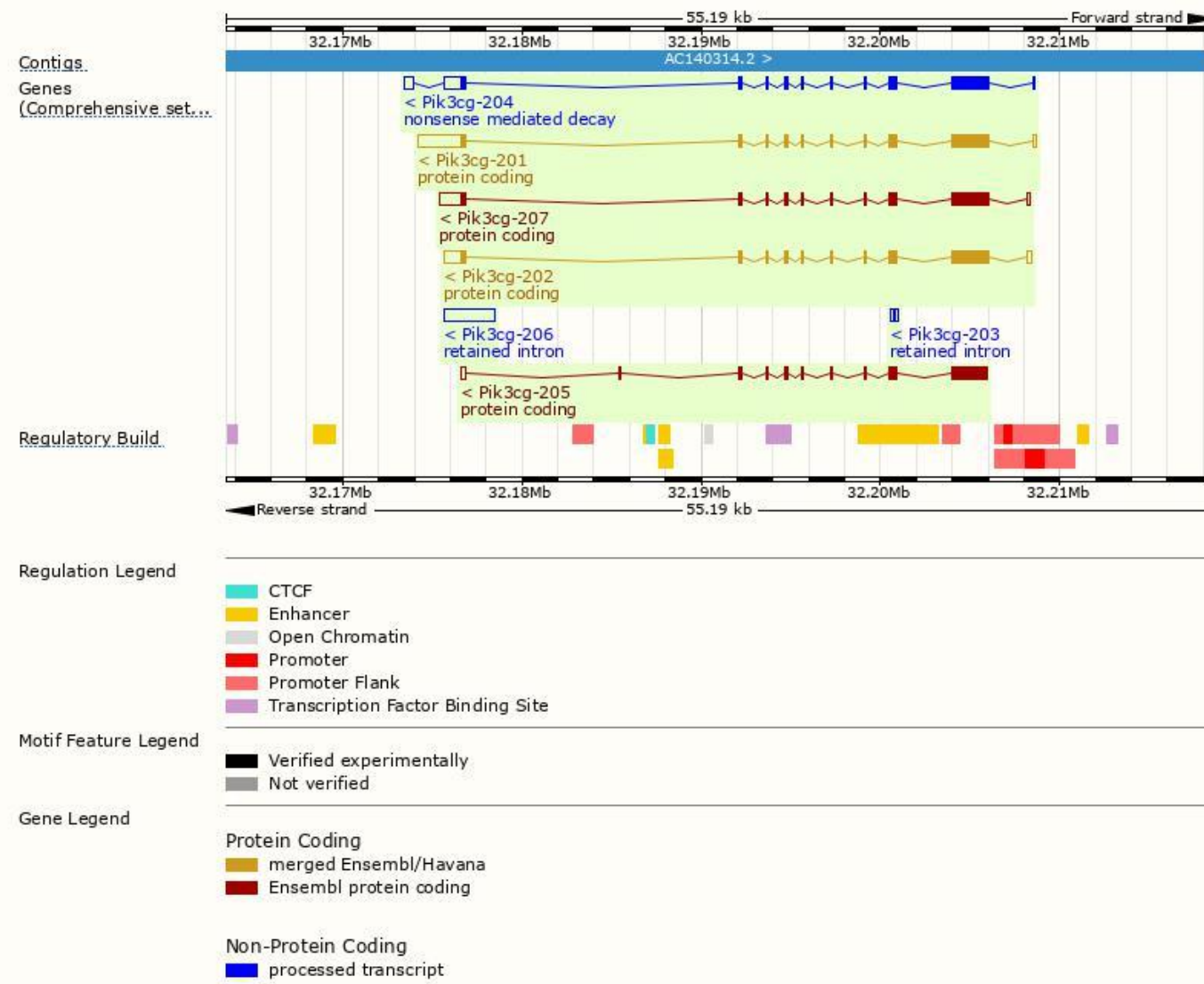
Mouse phenotype description(MGI)
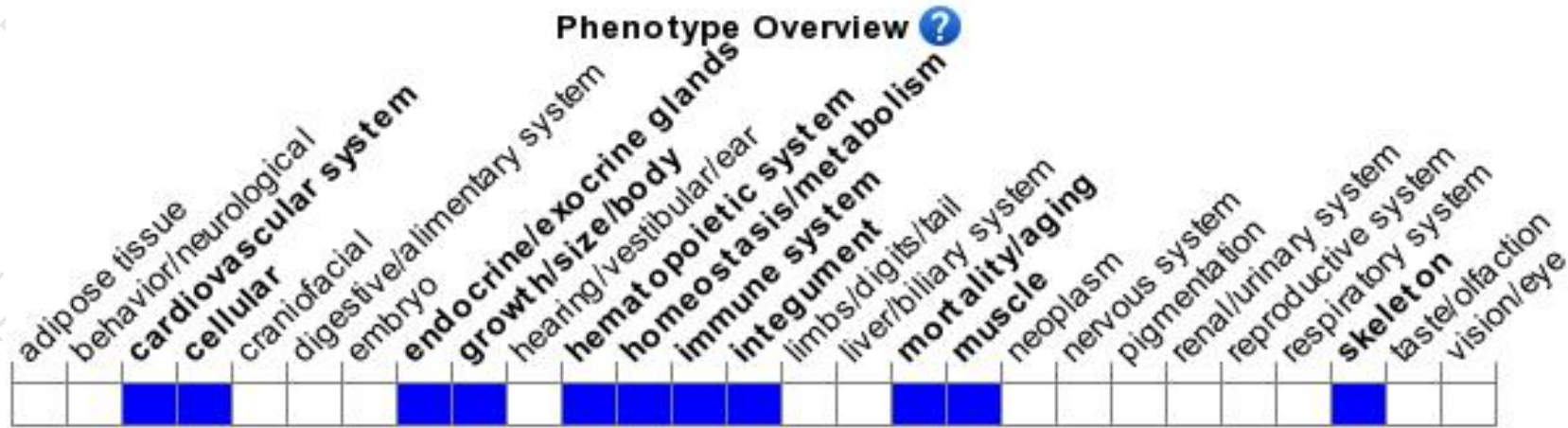
Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data,Mice homozygous for disruptions in this gene display defects in thymocyte development, T cell activation, and neutrophil migration.

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