

Pparg Cas9-KO Strategy

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Project Overview

Project Name

Pparg

Project type

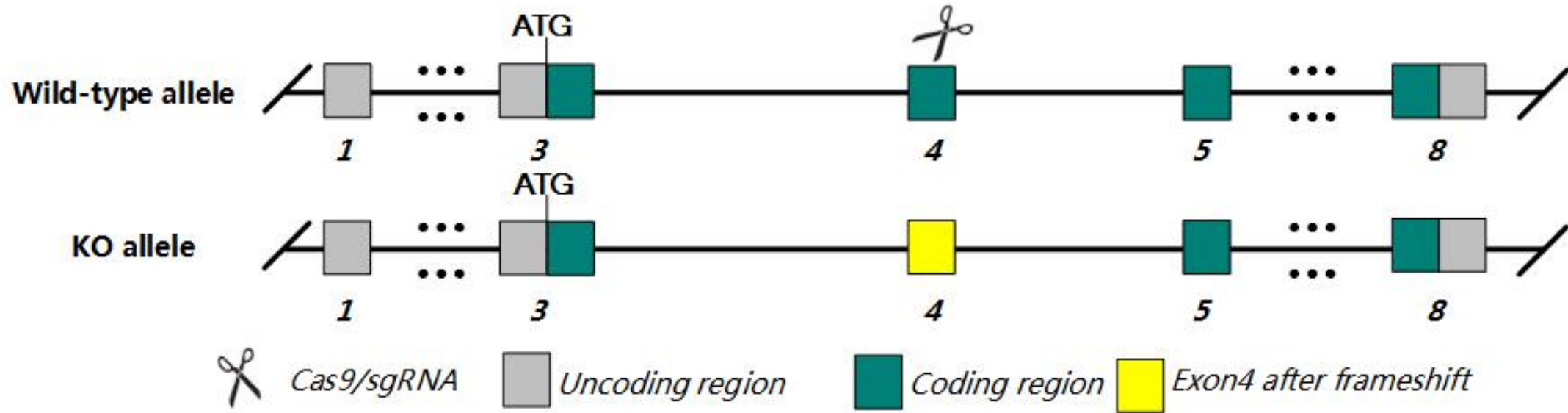
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

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



- The *Pparg* gene has 7 transcripts. According to the structure of *Pparg* gene, partial sequence of exon4 of *Pparg*-202 (ENSMUST00000171644.7) transcript is recommended as the knockout region. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pparg* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit lethality due to placental defects. Heterozygotes show greater B cell proliferation, enhanced leptin secretion, and resistance to diet-induced adipocyte hypertrophy and insulin resistance.
- The *Pparg* gene is located on the Chr6. 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)

Pparg peroxisome proliferator activated receptor gamma [Mus musculus (house mouse)]

Gene ID: 19016, updated on 9-Apr-2019

Summary

Official Symbol Pparg provided by [MGI](#)

Official Full Name peroxisome proliferator activated receptor gamma provided by [MGI](#)

Primary source [MGI:MGI:97747](#)

See related [Ensembl:ENSMUSG00000000440](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Nr1c3, PPAR-gamma, PPAR-gamma2, PPARGgamma, PPARGgamma2

Summary This gene encodes a nuclear receptor protein belonging to the peroxisome proliferator-activated receptor (Ppar) family. The encoded protein is a ligand-activated transcription factor that is involved in the regulation of adipocyte differentiation and glucose homeostasis. The encoded protein forms a heterodimer with retinoid X receptors and binds to DNA motifs termed "peroxisome proliferator response elements" to either activate or inhibit gene expression. Mice lacking the encoded protein die at an embryonic stage due to severe defects in placental vascularization. When the embryos lacking this gene are supplemented with healthy placentas, the mutants survive to term, but succumb to lipodystrophy and multiple hemorrhages. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Apr 2015]

Expression Biased expression in subcutaneous fat pad adult (RPKM 32.5), mammary gland adult (RPKM 26.1) and 13 other tissues [See more](#)

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

Transcript information (Ensembl)

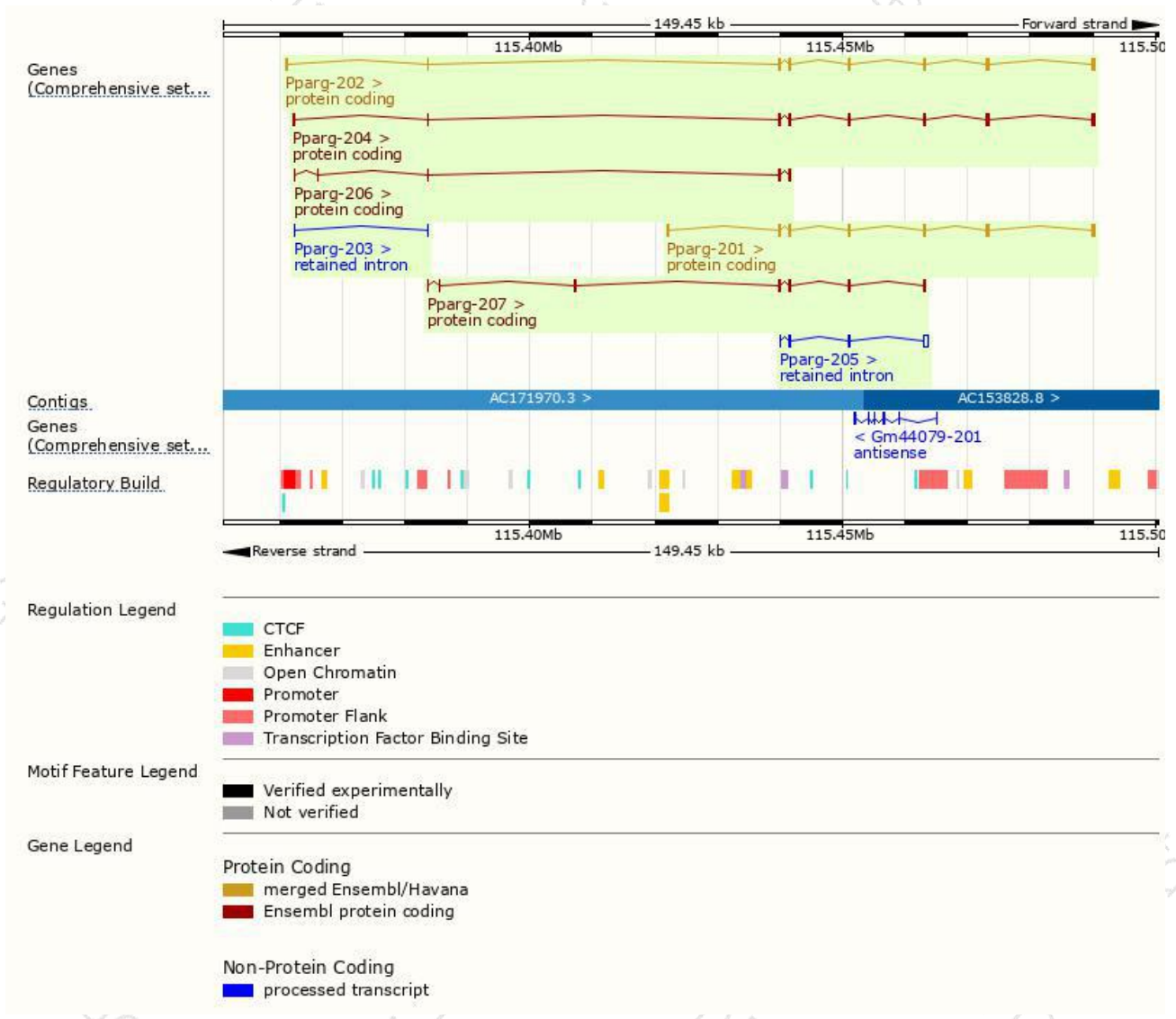
The gene has 7 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|-----------------------|-----------------|---------------------------|----------------------------|----------------------------------|
| Pparg-202 | ENSMUST00000171644.7 | 2125 | 475aa | Protein coding | CCDS51876 | M1VPI1 | TSL:1 GENCODE basic APPRIS ALT 1 |
| Pparg-204 | ENSMUST00000203732.2 | 1826 | 475aa | Protein coding | CCDS51876 | M1VPI1 | TSL:1 GENCODE basic APPRIS ALT 1 |
| Pparg-201 | ENSMUST00000000450.4 | 1767 | 505aa | Protein coding | CCDS20439 | Q6GU14 | TSL:1 GENCODE basic APPRIS P3 |
| Pparg-207 | ENSMUST00000205213.2 | 835 | 222aa | Protein coding | - | A0A0N4SV67 | CDS 3' incomplete TSL:3 |
| Pparg-206 | ENSMUST00000204305.2 | 497 | 96aa | Protein coding | - | A0A0N4SVF8 | CDS 3' incomplete TSL:3 |
| Pparg-205 | ENSMUST00000203896.1 | 915 | No protein | Retained intron | - | - | TSL:2 |
| Pparg-203 | ENSMUST00000203308.1 | 213 | No protein | Retained intron | - | - | TSL:5 |

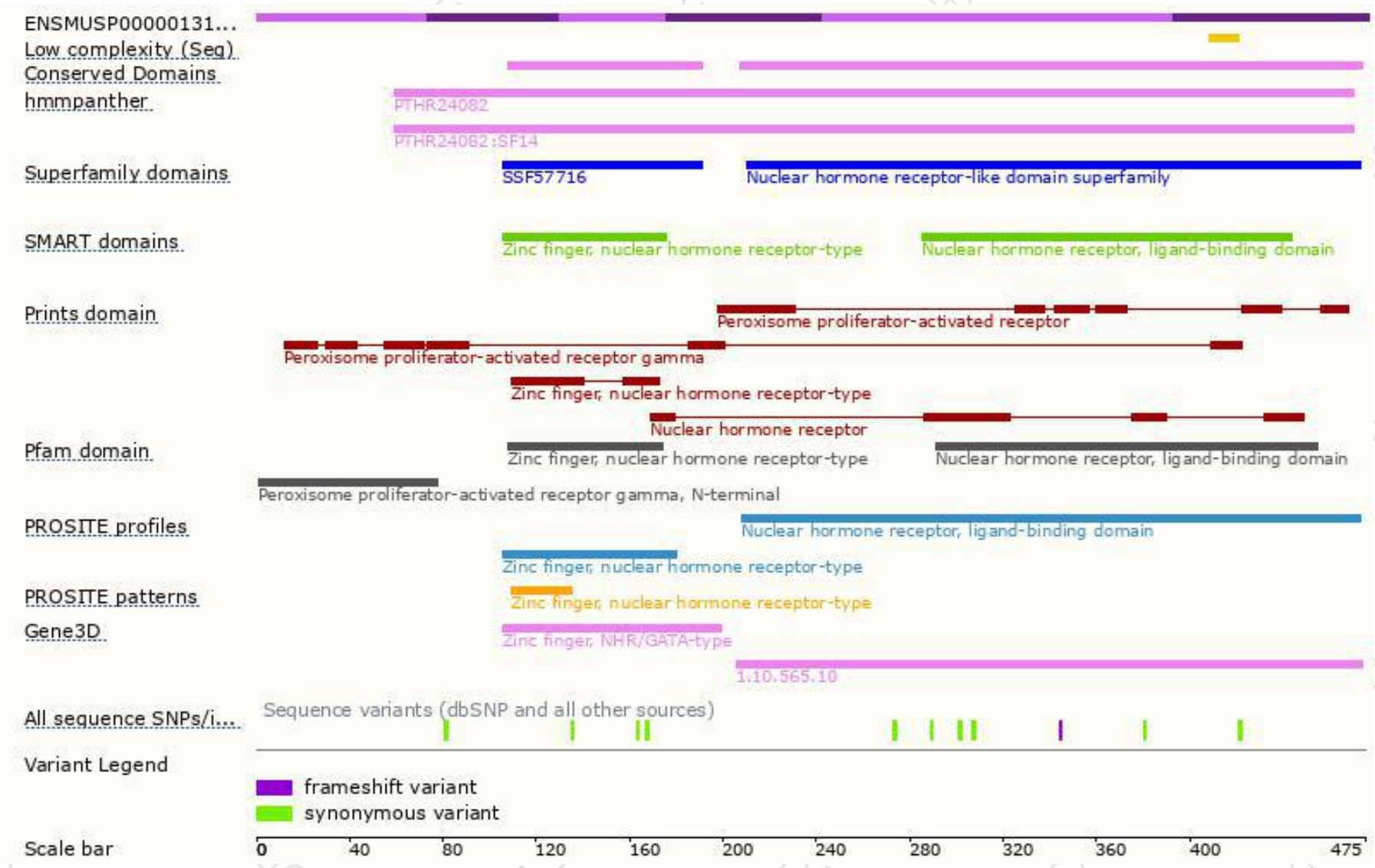
The strategy is based on the design of *Pparg-202* transcript,The transcription is shown below



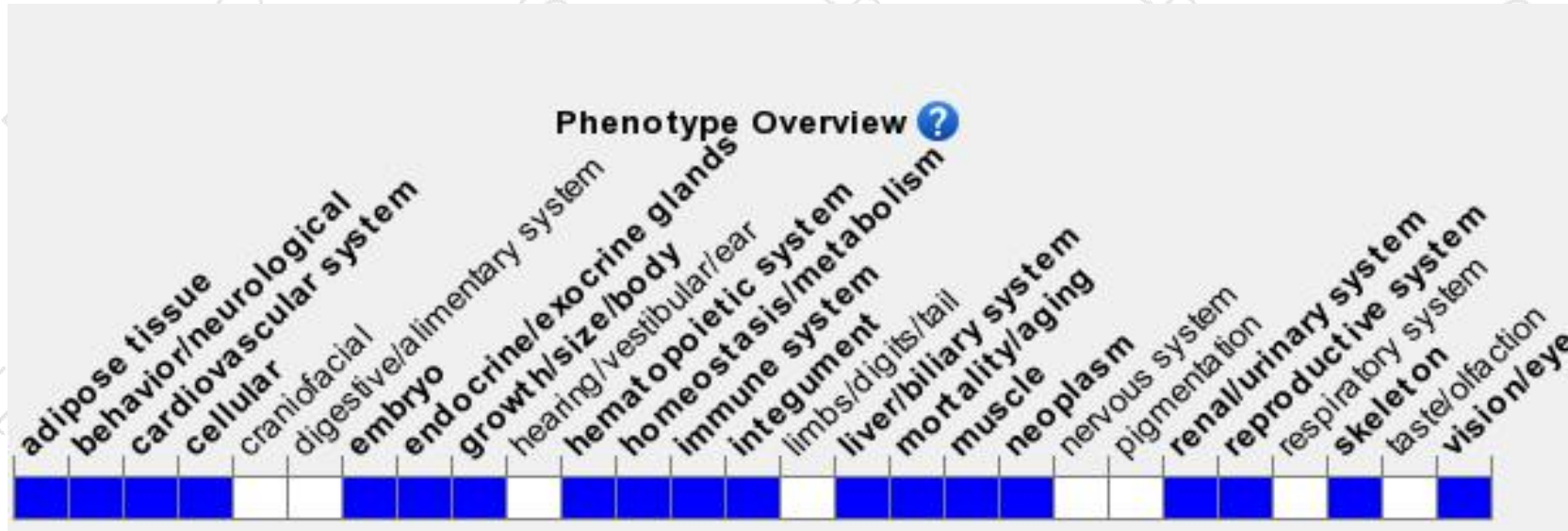
Genomic location distribution



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/>).

According to the existing MGI data, Homozygotes for targeted null mutations exhibit lethality due to placental defects. Heterozygotes show greater B cell proliferation, enhanced leptin secretion, and resistance to diet-induced adipocyte hypertrophy and insulin resistance.

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

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