Pex16 Cas9-CKO Strategy

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Design Date: 2024-03-08

Overview

Target Gene Name

- Pex16

Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy
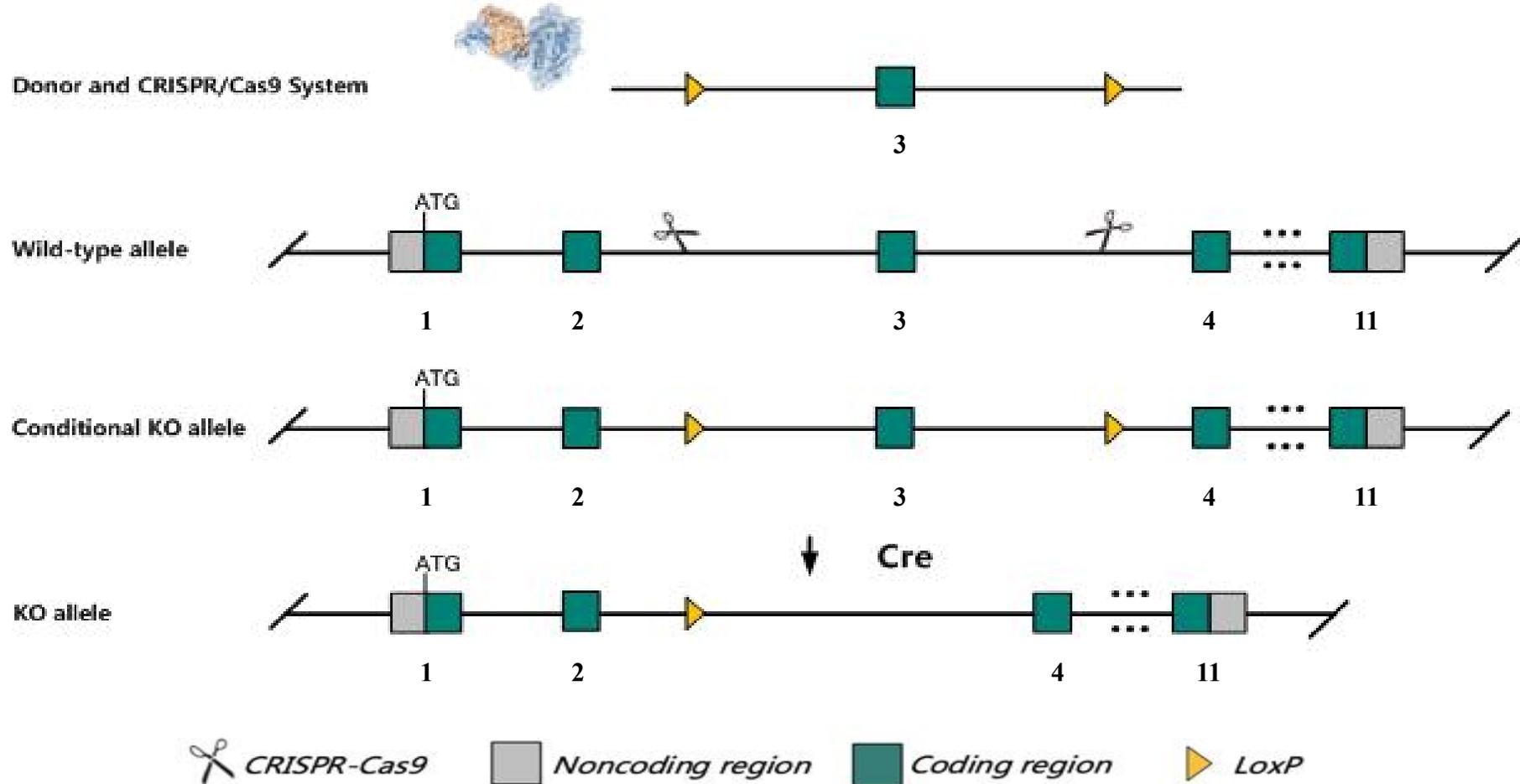
Schematic representation of CRISPR-Cas9 engineering used to edit the *Pex16* gene.

Technical Information

- The *Pex16* gene has 4 transcripts. According to the structure of *Pex16* gene, exon3 of *Pex16*-201 (ENSMUST00000028650.9) transcript is recommended as the knockout region. The region contains 77bp coding sequence. Knocking out the region will result in disruption of protein function.

- In this project we use CRISPR-Cas9 technology to modify *Pex16* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

- 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.

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Gene Information

Pex16   peroxisomal biogenesis factor 16 [*Mus musculus* (house mouse)]

⬇ **Download Datasets**

Gene ID: 18633, updated on 5-Mar-2024

🔼 **Summary**

Official Symbol	Pex16 provided by MGI
Official Full Name	peroxisomal biogenesis factor 16 provided by MGI
Primary source	MGI:MGI:1338829
See related	Ensembl:ENSMUSG00000027222 AllianceGenome:MGI:1338829
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
Summary	Predicted to enable protein C-terminus binding activity. Predicted to be involved in peroxisome organization and protein to membrane docking. Predicted to act upstream of or within protein import into peroxisome matrix. Located in peroxisomal membrane. Human ortholog(s) of this gene implicated in peroxisomal biogenesis disorder and peroxisome biogenesis disorder 8A. Orthologous to human PEX16 (peroxisomal biogenesis factor 16). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 68.1), subcutaneous fat pad adult (RPKM 52.9) and 28 other tissues See more
Orthologs	human all
NEW	**Try the new** Gene table **Try the new** Transcript table

Source: https://www.ncbi.nlm.nih.gov/

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Transcript Information

The gene has 4 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000155891.8	Pex16-204	1167	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000154669.8	Pex16-203	852	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000148386.2	Pex16-202	425	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000028650.9	Pex16-201	1392	336aa	Protein coding	CCDS16444	Q91XC9	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1

The strategy is based on the design of *Pex16*-201 transcript, the transcription is shown below:


Source: https://www.ensembl.org

Genomic Information

Source: : https://www.ensembl.org

Protein Information

Source: : https://www.ensembl.org

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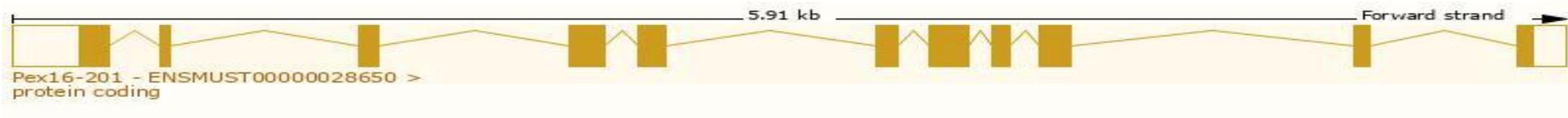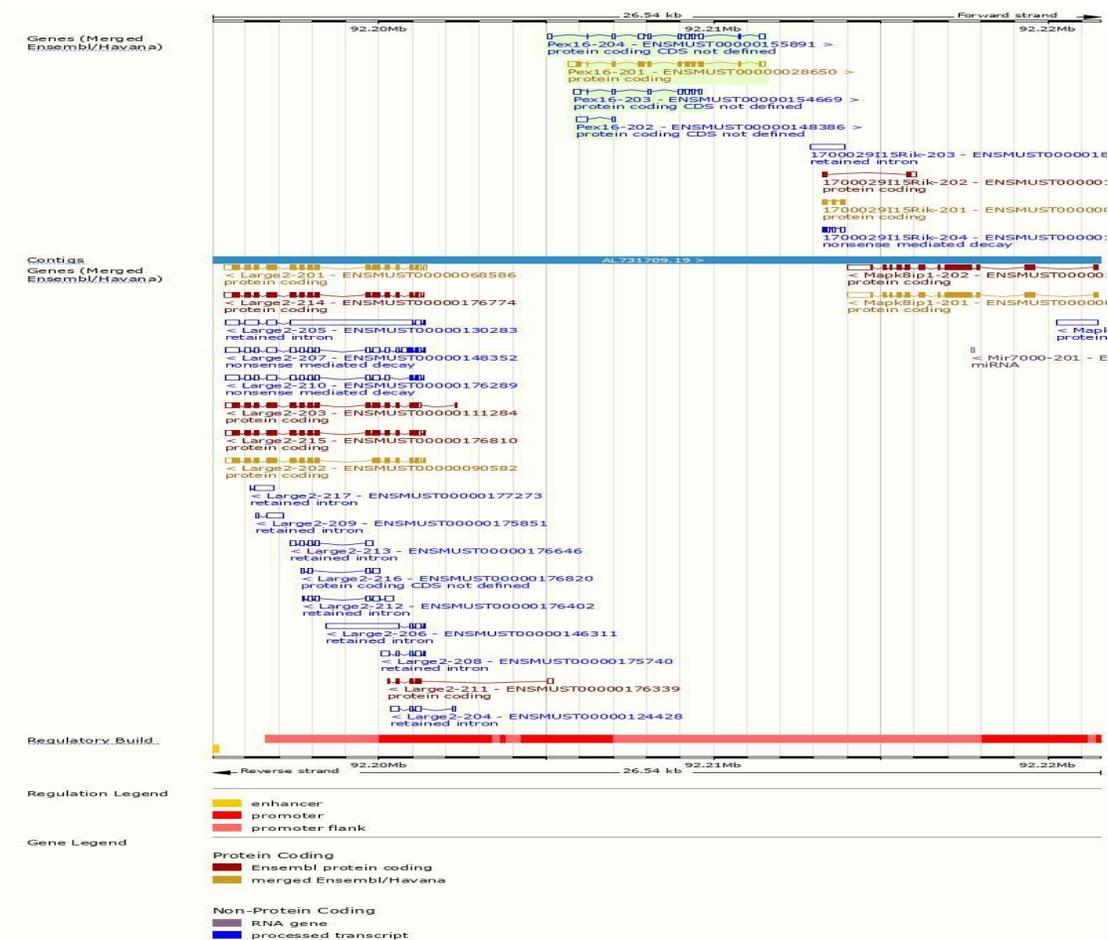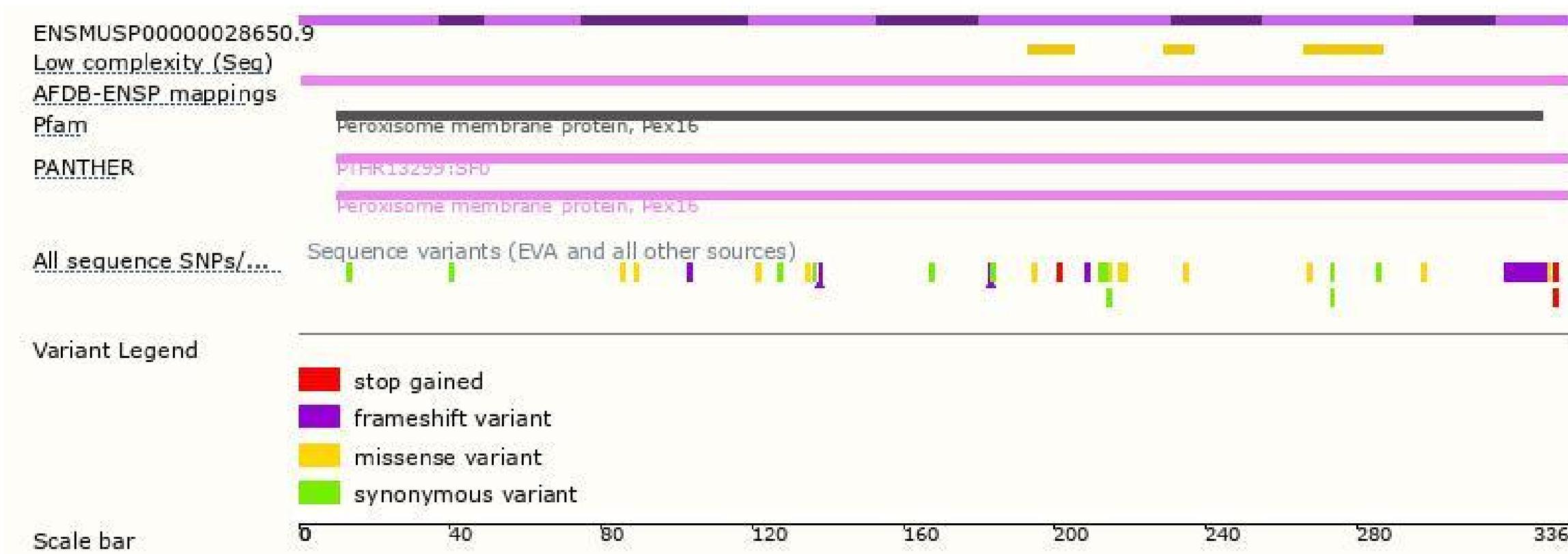
Mouse Phenotype Information (MGI)
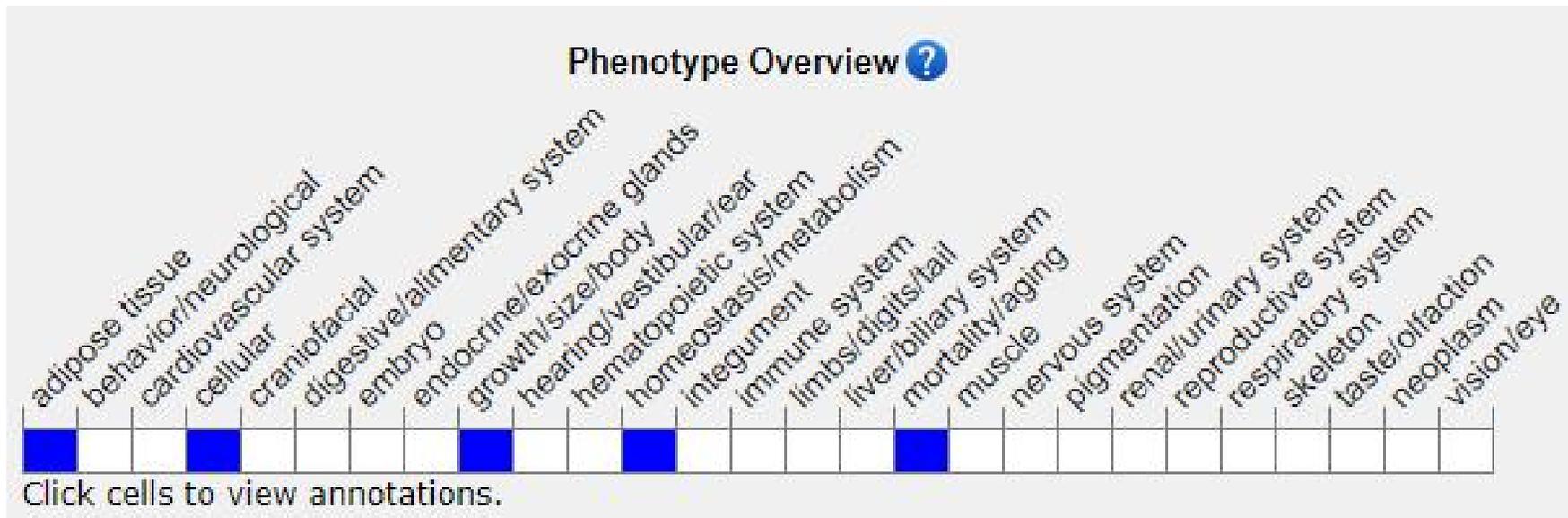
- Mice homozygous for a conditional allele activated in adipose tissue exhibit impaired cold tolerance, decreased energy expenditure, and increased diet-induced obesity.

Source: https://www.informatics.jax.org

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Important Information

- Mice homozygous for a conditional allele activated in adipose tissue exhibit impaired cold tolerance, decreased energy expenditure, and increased diet-induced obesity.

- The flox region is about 1.7 kb away from the N-terminus of the *Large2* gene,this strategy may influence the regulatory function of the N-terminal of *Large2* gene.

- *Pex16* is located on Chr2. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

References

https://www.mousephenotype.org/data/genes/MGI:1338829

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