

Pex3 Cas9-KO Strategy

Designer: Longyun Hu

Reviewer: Rui Xiong

Design Date: 2021-3-2

Project Overview

Project Name

Pex3

Project type

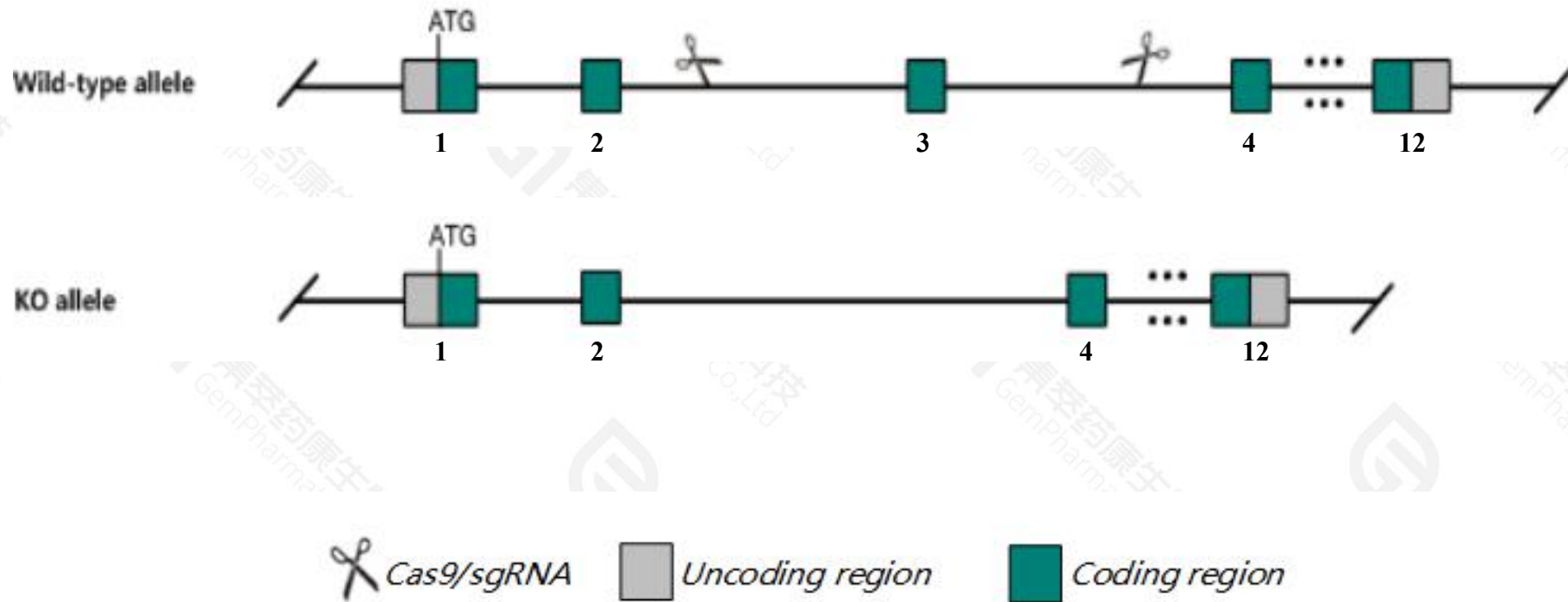
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pex3* gene. The schematic diagram is as follows:



- The *Pex3* gene has 7 transcripts. According to the structure of *Pex3* gene, exon3 of *Pex3-201*(ENSMUST00000019945.14) transcript is recommended as the knockout region. The region contains 82bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pex3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, homozygous mutants exhibit abnormal sebaceous gland, hair follicle bulge, and cornea morphology. An increase in B and T cell numbers and mean platelet volume, and vertebral transformation are also seen.
- The *Pex3* gene is located on the Chr10. 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.

Pex3 peroxisomal biogenesis factor 3 [Mus musculus (house mouse)]

Gene ID: 56535, updated on 13-Mar-2020

Summary



Official Symbol Pex3 provided by [MGI](#)

Official Full Name peroxisomal biogenesis factor 3 provided by [MGI](#)

Primary source [MGI:MGI:1929646](#)

See related [Ensembl:ENSMUSG00000019809](#)

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 1700014F15Rik, 2810027F19Rik, 2900010N04Rik

Expression Ubiquitous expression in testis adult (RPKM 24.6), bladder adult (RPKM 9.4) and 24 other tissues [See more](#)

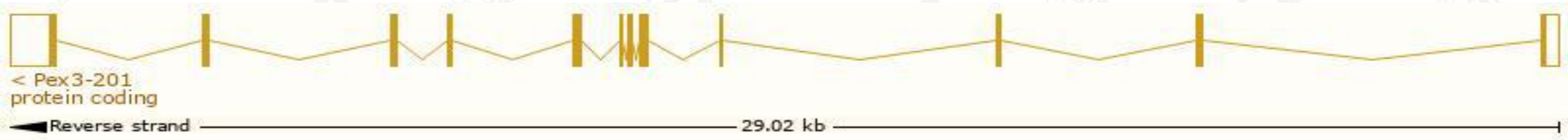
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

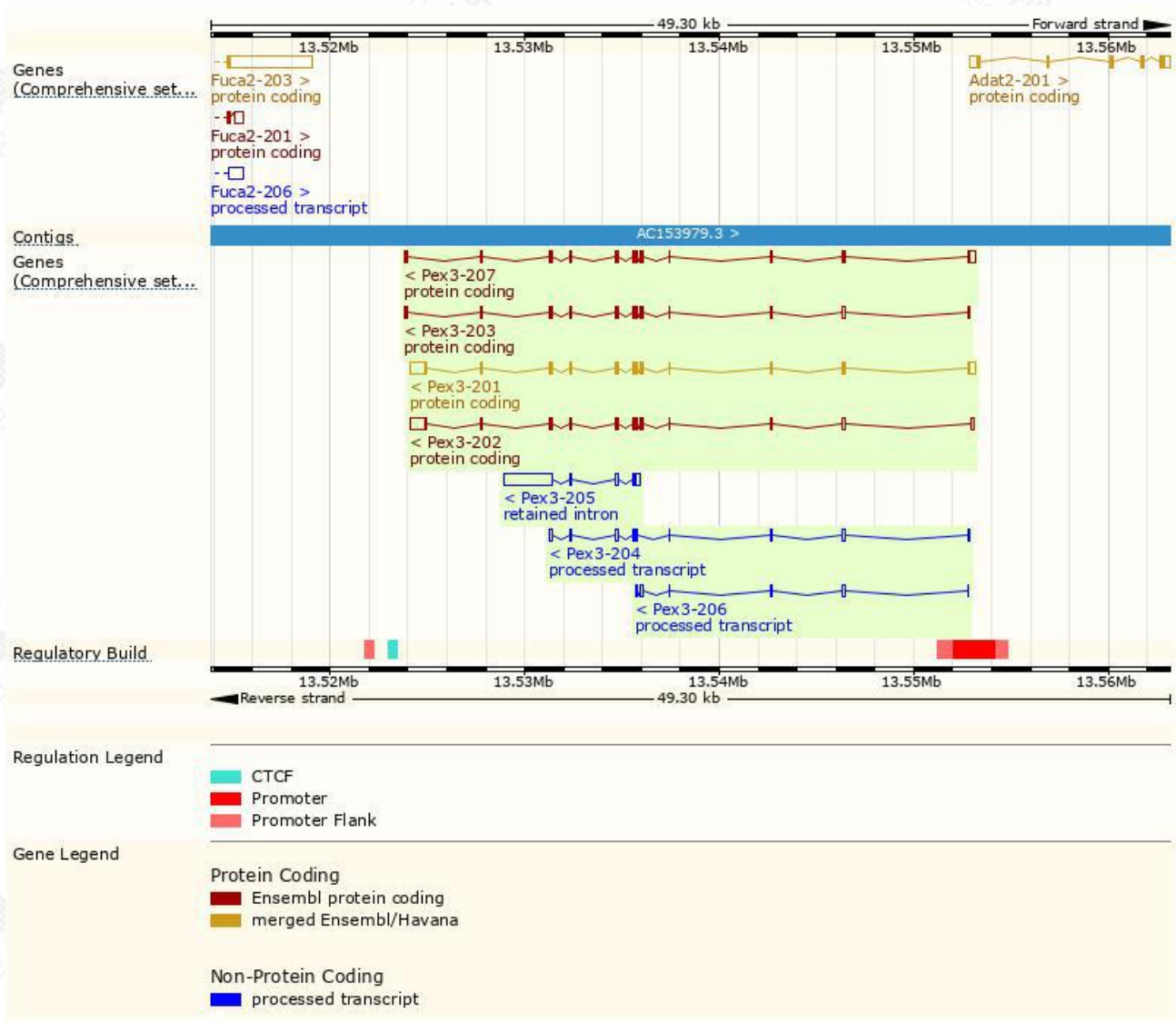
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pex3-201	ENSMUST00000019945.14	2129	372aa	Protein coding	CCDS23702	Q3UIG2 Q9QXY9	TSL:1 GENCODE basic APPRIS P1
Pex3-202	ENSMUST00000105539.1	1961	306aa	Protein coding	CCDS83681	D3Z6X4	TSL:1 GENCODE basic
Pex3-207	ENSMUST00000170376.7	1381	359aa	Protein coding	CCDS48503	E9QA46	TSL:1 GENCODE basic
Pex3-203	ENSMUST00000105541.7	1072	293aa	Protein coding	-	D3Z6X3	TSL:1 GENCODE basic
Pex3-204	ENSMUST00000125207.7	771	No protein	Processed transcript	-	-	TSL:3
Pex3-206	ENSMUST00000145337.1	480	No protein	Processed transcript	-	-	TSL:5
Pex3-205	ENSMUST00000133332.7	2959	No protein	Retained intron	-	-	TSL:1

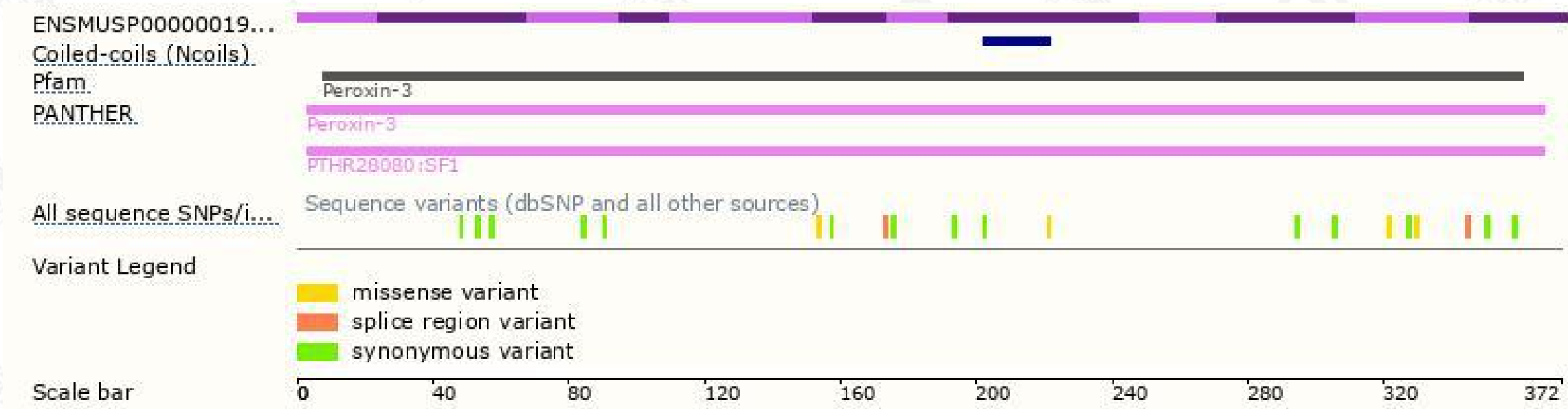
The strategy is based on the design of *Pex3-201* transcript,the transcription is shown below:



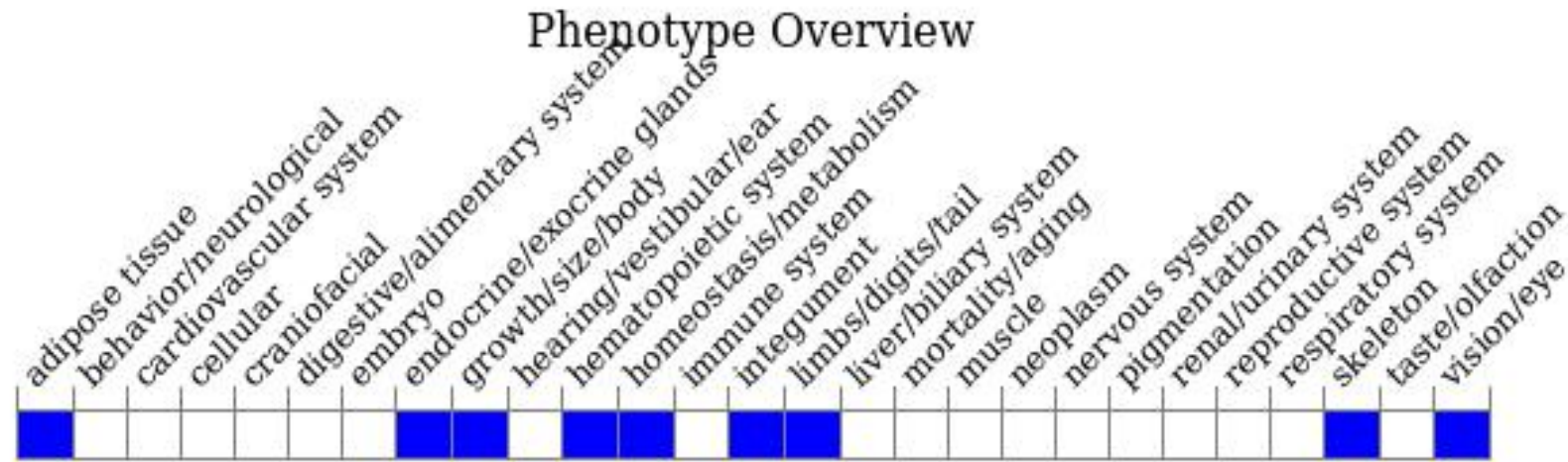
Genomic location distribution



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/>).

According to the existing MGI data, homozygous mutants exhibit abnormal sebaceous gland, hair follicle bulge, and cornea morphology. An increase in B and T cell numbers and mean platelet volume, and vertebral transformation are also seen.

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

Tel: 025-5864 1534

