Pex26 Cas9-CKO Strategy

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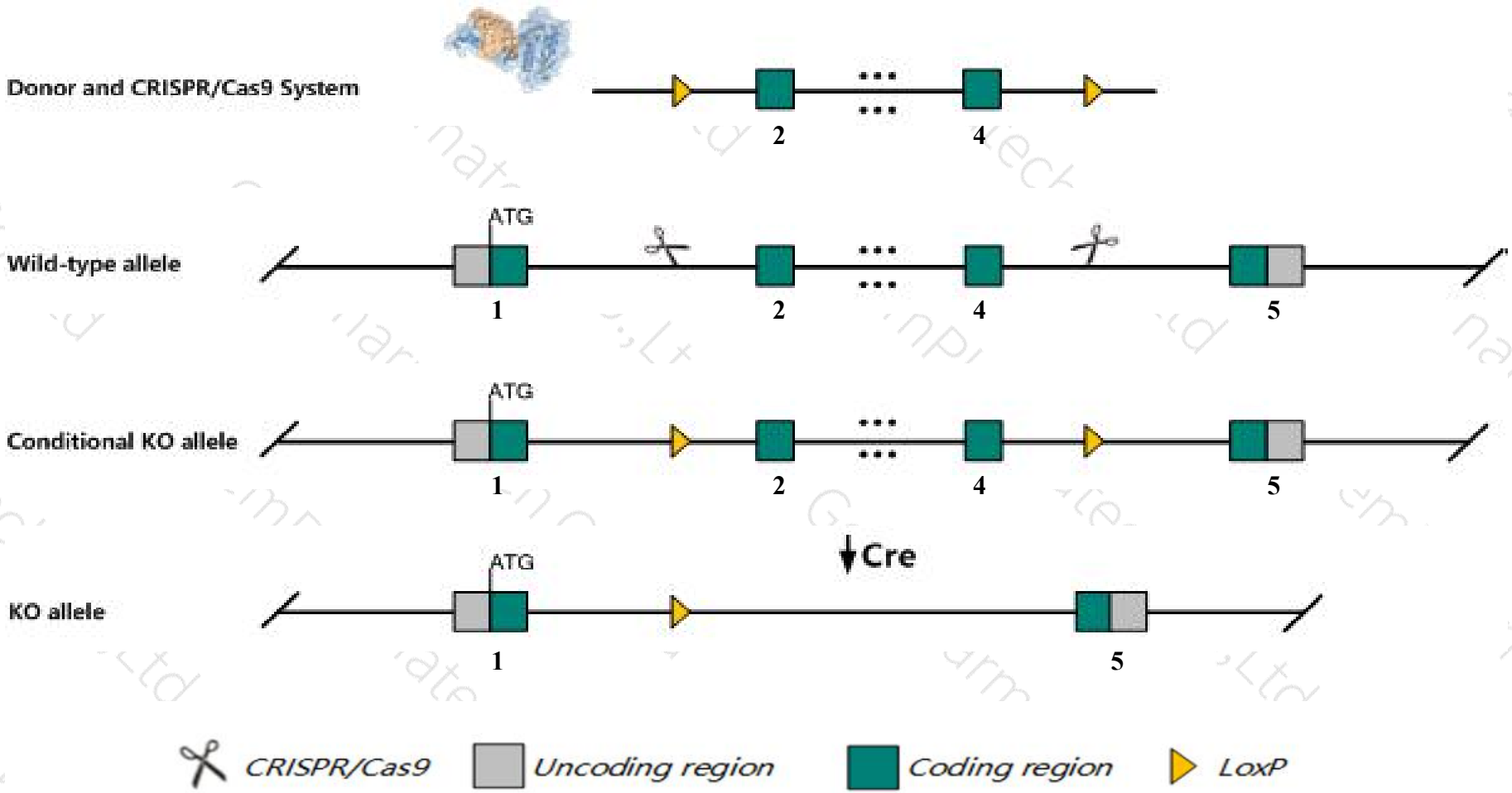
Project Overview

Project Name	***Pex26***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pex26* gene. The schematic diagram is as follows:



Technical routes

- The *Pex26* gene has 6 transcripts. According to the structure of *Pex26* gene, exon2-exon4 of *Pex26-201* (ENSMUST00000088561.9) transcript is recommended as the knockout region.The region contains 596bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Pex26* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- 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.

Notice

➢ The *Pex26* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Pex26 peroxisomal biogenesis factor 26 [Mus musculus (house mouse)]

Gene ID: 74043, updated on 31-Jan-2019

Summary

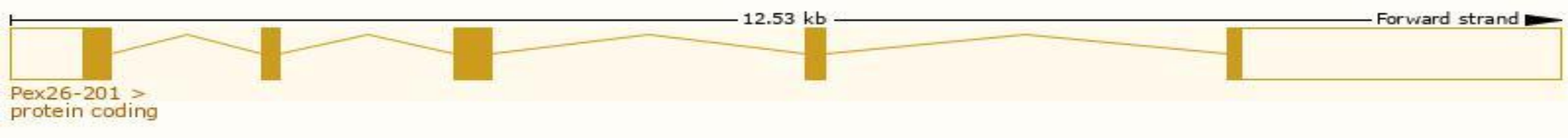
Official Symbol	Pex26 provided by MGI
Official Full Name	peroxisomal biogenesis factor 26 provided by MGI
Primary source	MGI:MGI:1921293
See related	Ensembl:ENSMUSG00000067825
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4632428M11Rik
Summary	This gene is a member of the peroxin-26 family. The encoded protein is probably required for protein import into peroxisomes. It may anchor Pex1 and Pex6 to peroxisome membranes. Defects in a similar gene in human are the cause of peroxisome biogenesis disorder complementation group 8 (PBD-CG8). PBD refers to a group of four disorders: Zellweger syndrome (ZWS), neonatal adrenoleukodystrophy (NALD), infantile Refsum disease (IRD), and classical rhizomelic chondrodysplasia punctata (RCDP). Alternatively spliced transcript variants have been identified for this gene. [provided by RefSeq, Feb 2015]
Expression	Ubiquitous expression in ovary adult (RPKM 8.2), kidney adult (RPKM 7.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

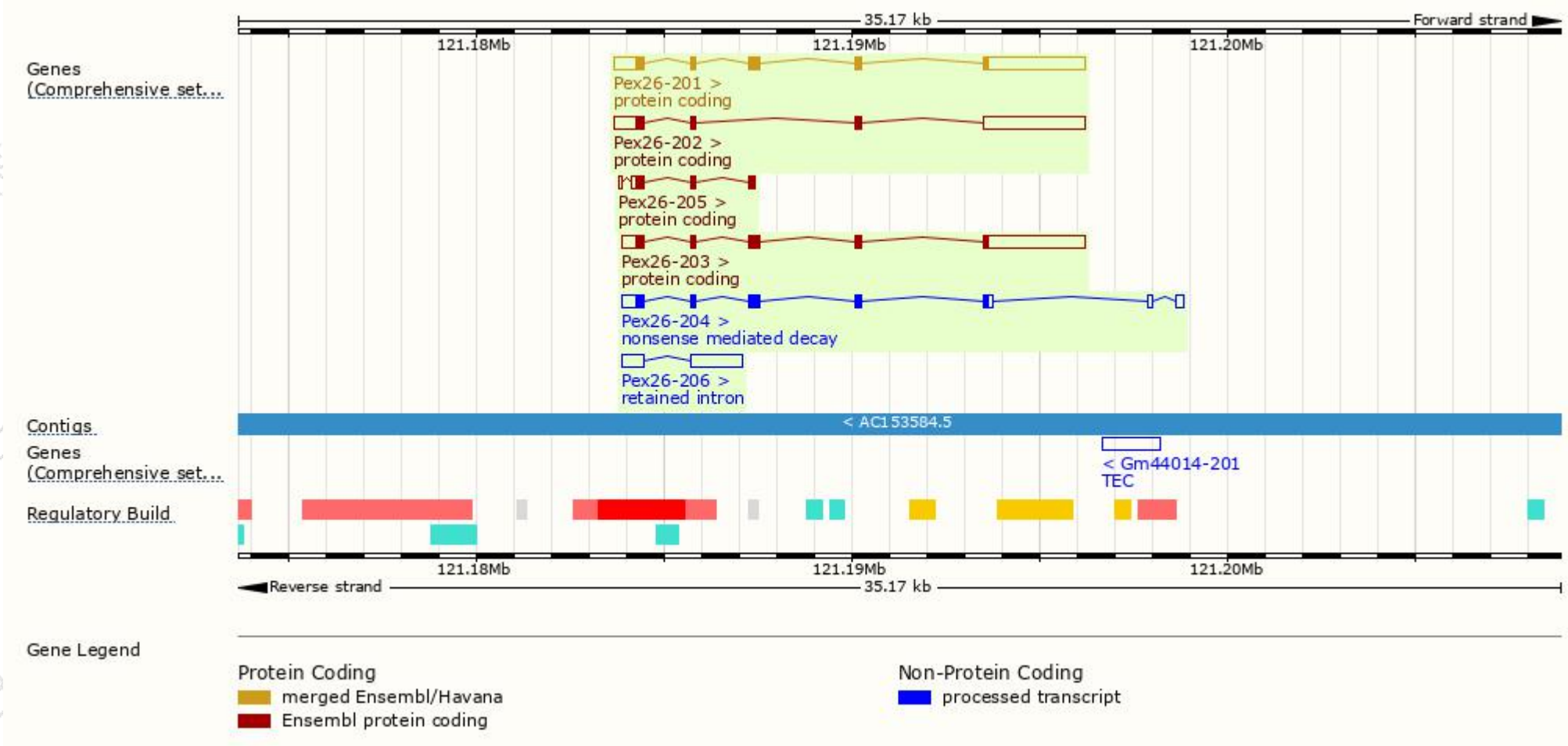
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pex26-201	ENSMUST00000088561.9	4093	305aa	Protein coding	CCDS20488	Q8BGI5	TSL:1 GENCODE basic APPRIS P3
Pex26-203	ENSMUST00000120066.7	3861	304aa	Protein coding	CCDS80603	Q8BGI5	TSL:1 GENCODE basic APPRIS ALT2
Pex26-202	ENSMUST00000118234.7	3778	166aa	Protein coding	CCDS80604	D3Z3F5	TSL:1 GENCODE basic
Pex26-205	ENSMUST00000137432.7	745	180aa	Protein coding	-	D3Z323	CDS 3' incomplete TSL:3
Pex26-204	ENSMUST00000125633.1	1760	305aa	Nonsense mediated decay	-	Q8BGI5	TSL:1
Pex26-206	ENSMUST00000139393.1	1957	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Pex26-201* transcript,The transcription is shown below

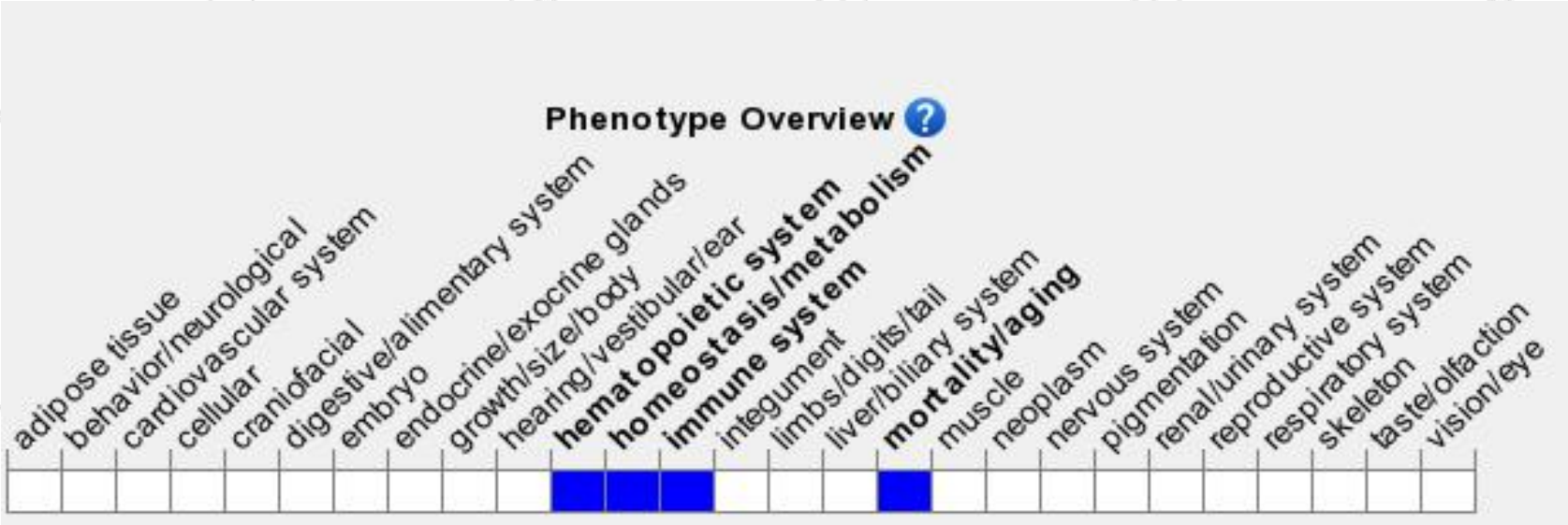


Genomic location distribution



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/).

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

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