

# *Pex13* Cas9-KO Strategy

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**Reviewer**

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# Project Overview

**Project Name**

*Pex13*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pex13* gene. The schematic diagram is as follows:



- The *Pex13* gene has 4 transcripts. According to the structure of *Pex13* gene, exon2 of *Pex13-201* (ENSMUST00000020523.3) transcript is recommended as the knockout region. The region contains 695bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pex13* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, targeted disruption of this gene results in intrauterine growth retardation, hypotonia, aphagia, abnormal lamination of the cerebral cortex associated with a neuronal migration defect, liver steatosis, delayed differentiation of renal glomeruli, impaired peroxisome metabolism, and neonatal death.
- The *Pex13* gene is located on the Chr11. 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)

## Pex13 peroxisomal biogenesis factor 13 [ *Mus musculus* (house mouse) ]

Gene ID: 72129, updated on 12-Aug-2019

### Summary

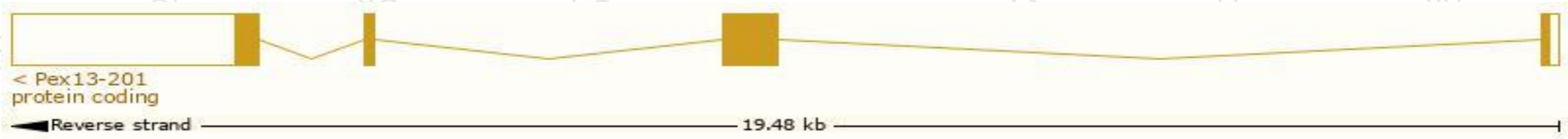
Official Symbol	Pex13 provided by <a href="#">MGI</a>
Official Full Name	peroxisomal biogenesis factor 13 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1919379</a>
See related	<a href="#">Ensembl:ENSMUSG000000020283</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610008O20Rik
Expression	Ubiquitous expression in testis adult (RPKM 13.1), adrenal adult (RPKM 11.3) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

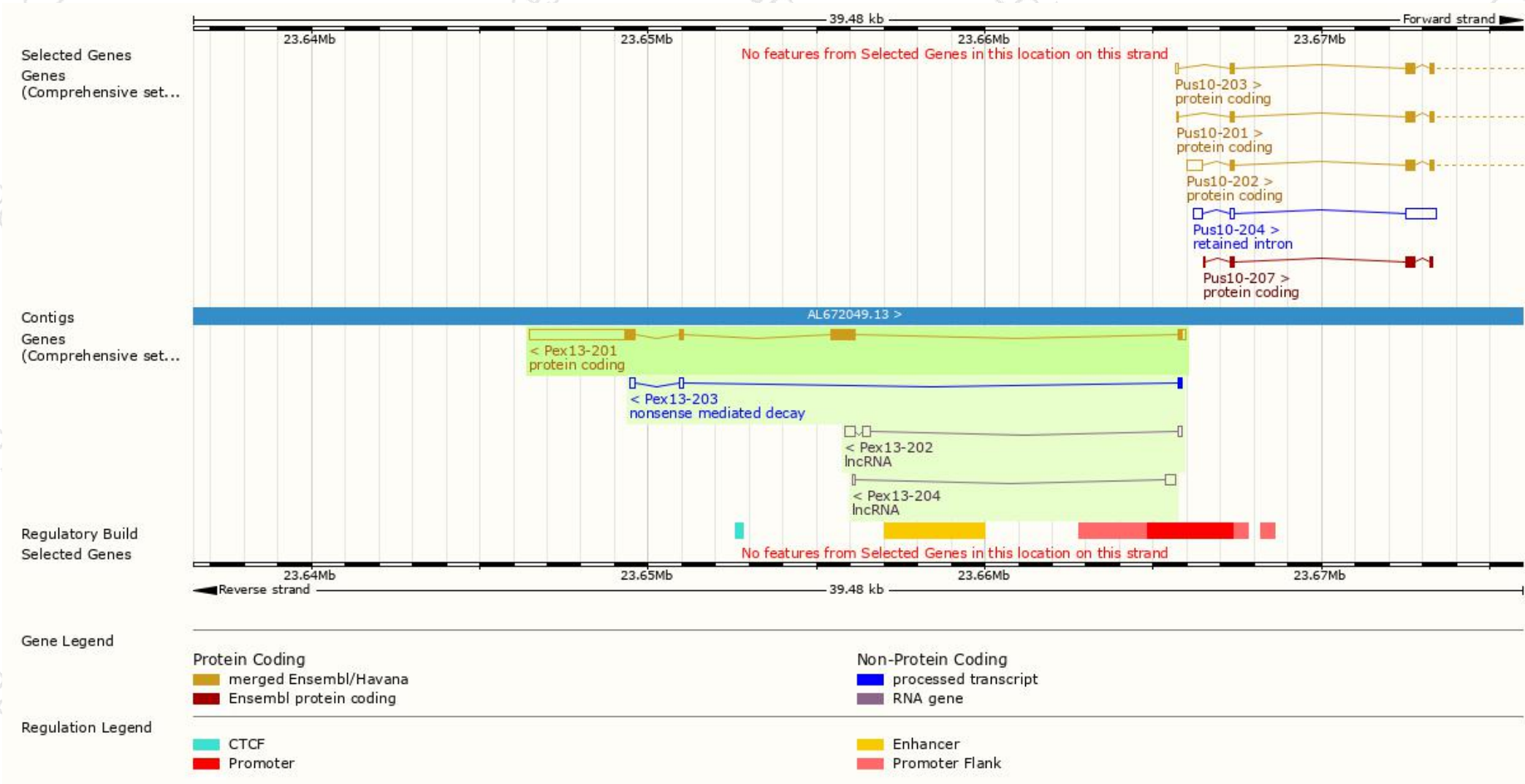
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pex13-201	<a href="#">ENSMUST00000020523.3</a>	4146	<a href="#">405aa</a>	Protein coding	<a href="#">CCDS24478</a>	<a href="#">Q9D0K1</a>	TSL:1 GENCODE basic APPRIS P1
Pex13-203	<a href="#">ENSMUST00000130811.1</a>	367	<a href="#">40aa</a>	Nonsense mediated decay	-	<a href="#">D6RH41</a>	TSL:3
Pex13-202	<a href="#">ENSMUST00000124839.1</a>	592	No protein	Processed transcript	-	-	TSL:3
Pex13-204	<a href="#">ENSMUST00000146533.1</a>	345	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Pex13-201* transcript,The transcription is shown below

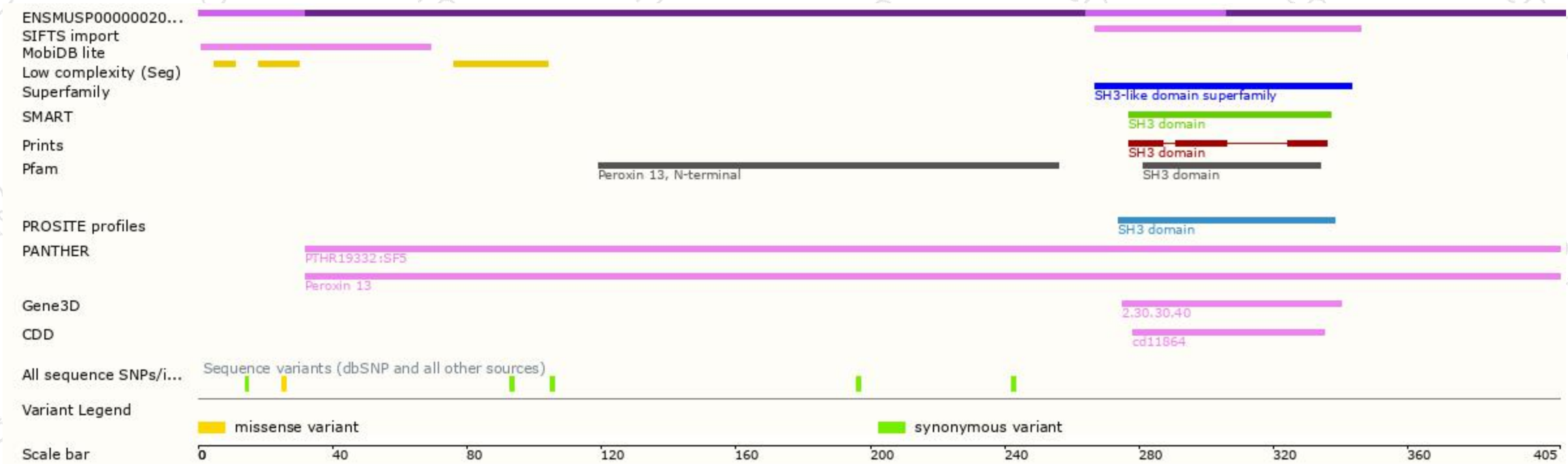


# Genomic location distribution

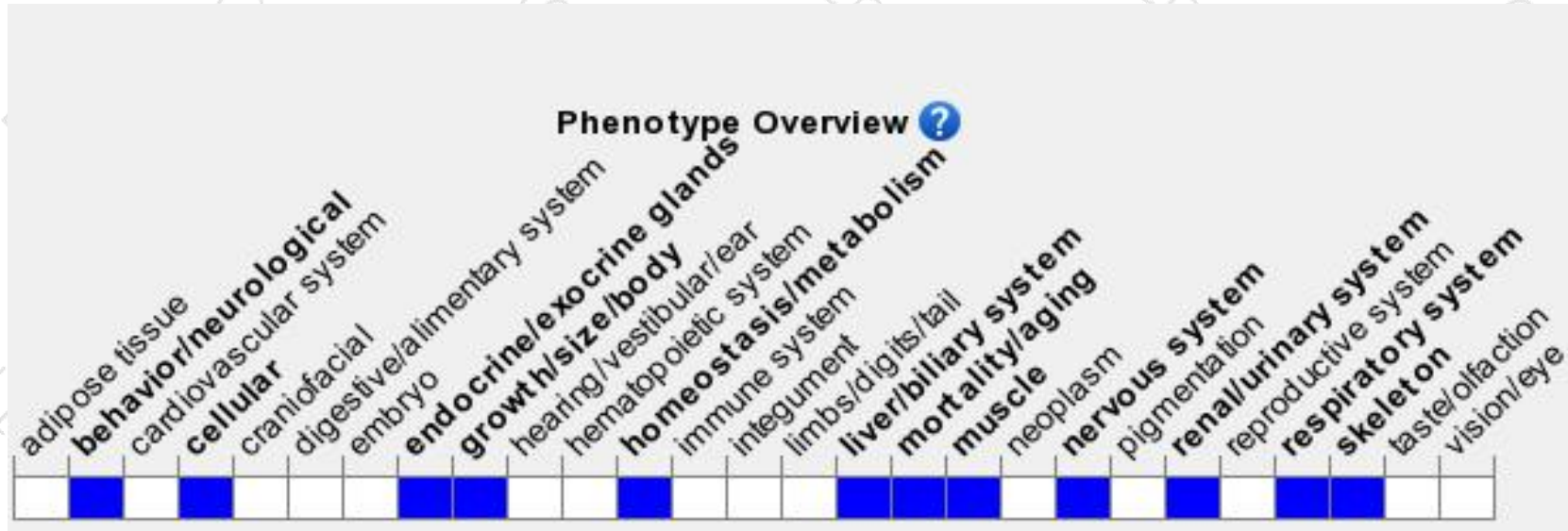




# Protein domain



# 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, Targeted disruption of this gene results in intrauterine growth retardation, hypotonia, aphagia, abnormal lamination of the cerebral cortex associated with a neuronal migration defect, liver steatosis, delayed differentiation of renal glomeruli, impaired peroxisome metabolism, and neonatal death.

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

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