

Pex1 Cas9-CKO Strategy

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Project Overview

Project Name

Pex1

Project type

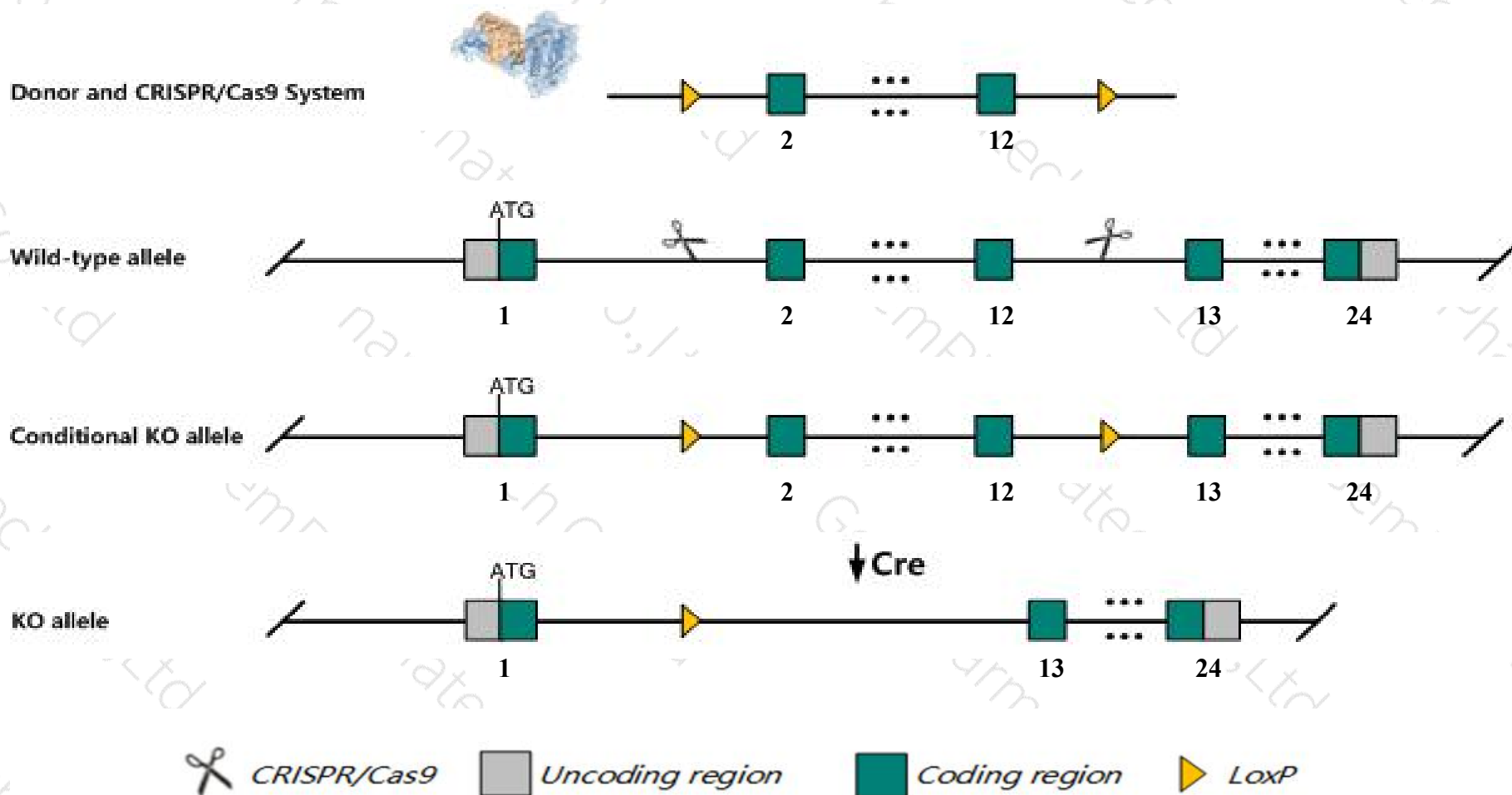
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pex1* gene. The schematic diagram is as follows:



- The *Pex1* gene has 14 transcripts. According to the structure of *Pex1* gene, exon2-exon12 of *Pex1*-202 (ENSMUST00000121291.7) transcript is recommended as the knockout region. The region contains 1945bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pex1* 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.

- According to the existing MGI data, Mice homozygous for a knock-in allele display premature death, postnatal growth retardation, fatty livers, a bile acid defect associated with intestinal lipid malabsorption and cholestasis, and a retinopathy associated with retinal cone cell degeneration and abnormal cone and rod electrophysiology.
- The floxed region is near to the N-terminal of *Rbm48* gene, this strategy may influence the regulatory function of the N-terminal of *Rbm48* gene.
- Transcript *Pex1*-2029&210&211&212&214 may not be affected.
- The *Pex1* gene is located on the Chr5. 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)

Pex1 peroxisomal biogenesis factor 1 [*Mus musculus* (house mouse)]

Gene ID: 71382, updated on 25-Feb-2020

Summary

- Official Symbol

Pex1 provided by [MGI](#)
- Official Full Name

peroxisomal biogenesis factor 1 provided by [MGI](#)
- Primary source

[MGI:MGI:1918632](#)
- See related

[Ensembl:ENSMUSG00000005907](#)
- 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

ZWS1; 5430414H02Rik; E330005K07Rik
- Expression

Ubiquitous expression in placenta adult (RPKM 4.3), CNS E14 (RPKM 3.6) and 28 other tissues [See more](#)
- Orthologs

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

Genomic context

Location: 5; 5 A1

See Pex1 in [Genome Data Viewer](#)

Exon count: 25

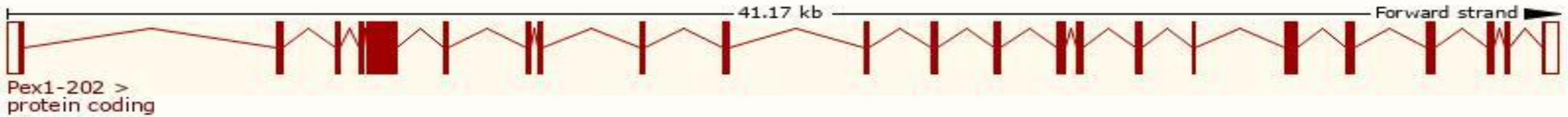
| Annotation release | Status | Assembly | Chr | Location |
|---------------------|-------------------|--|-----|--------------------------------|
| 108 | current | GRCm38.p6 (GCF_000001635.26) | 5 | NC_000071.6 (3596066..3637230) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 5 | NC_000071.5 (3596066..3637101) |

Transcript information (Ensembl)

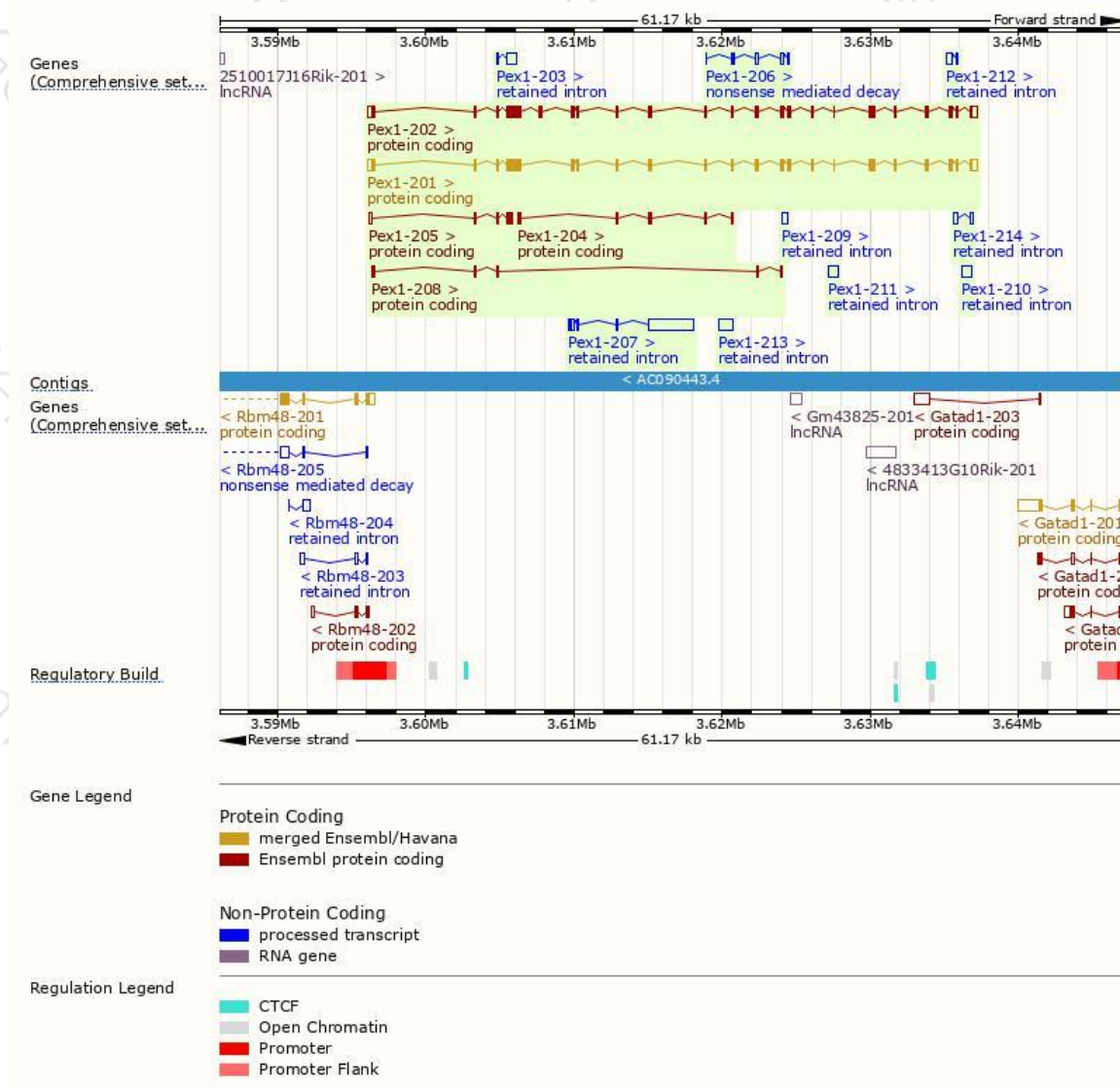
The gene has 14 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|--------------------------------------|------|------------------------|-------------------------|---------------------------|----------------------------|---|
| Pex1-202 | ENSMUST00000121291.7 | 4555 | 1284aa | Protein coding | CCDS80201 | Q5BL07 | TSL:5 GENCODE basic APPRIS ALT2 |
| Pex1-201 | ENSMUST0000006061.12 | 4433 | 1244aa | Protein coding | CCDS19065 | Q5BL07 | TSL:1 GENCODE basic APPRIS P3 |
| Pex1-205 | ENSMUST00000142516.1 | 727 | 69aa | Protein coding | - | D3Z5A7 | CDS 3' incomplete TSL:3 |
| Pex1-204 | ENSMUST00000126545.1 | 639 | 213aa | Protein coding | - | F6RUH9 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3 |
| Pex1-208 | ENSMUST00000195894.1 | 528 | 143aa | Protein coding | - | A0A0G2JE39 | TSL:3 GENCODE basic |
| Pex1-206 | ENSMUST00000143132.1 | 664 | 76aa | Nonsense mediated decay | - | F7CF88 | CDS 5' incomplete TSL:5 |
| Pex1-207 | ENSMUST00000143959.1 | 3491 | No protein | Retained intron | - | - | TSL:1 |
| Pex1-213 | ENSMUST00000199035.1 | 987 | No protein | Retained intron | - | - | TSL:NA |
| Pex1-203 | ENSMUST00000123268.1 | 746 | No protein | Retained intron | - | - | TSL:3 |
| Pex1-210 | ENSMUST00000196432.1 | 668 | No protein | Retained intron | - | - | TSL:NA |
| Pex1-211 | ENSMUST00000196692.1 | 638 | No protein | Retained intron | - | - | TSL:NA |
| Pex1-214 | ENSMUST00000199213.1 | 487 | No protein | Retained intron | - | - | TSL:2 |
| Pex1-212 | ENSMUST00000197167.1 | 474 | No protein | Retained intron | - | - | TSL:2 |
| Pex1-209 | ENSMUST00000196124.1 | 403 | No protein | Retained intron | - | - | TSL:NA |

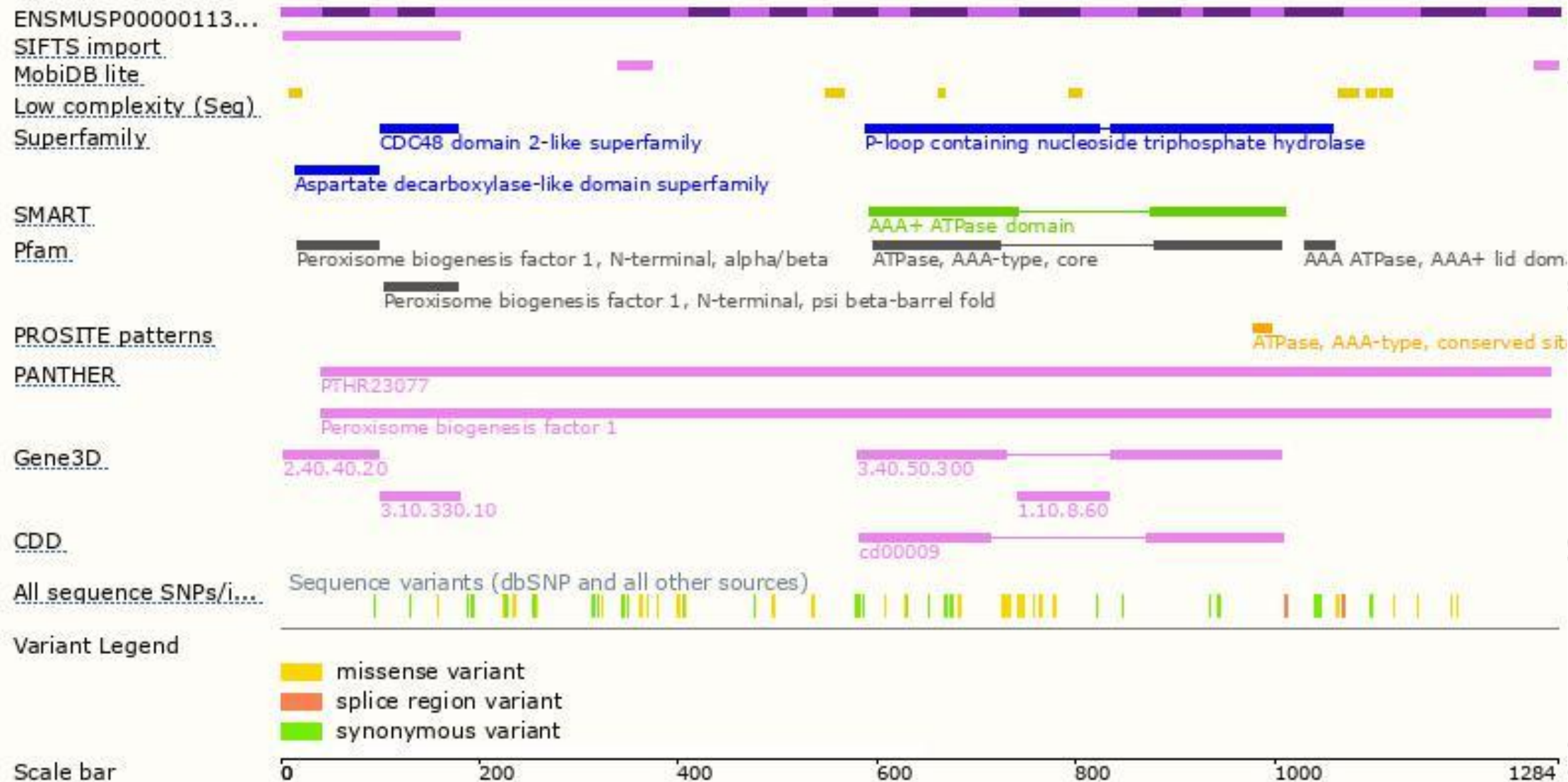
The strategy is based on the design of *Pex1-202* transcript,The transcription is shown below



Genomic location distribution

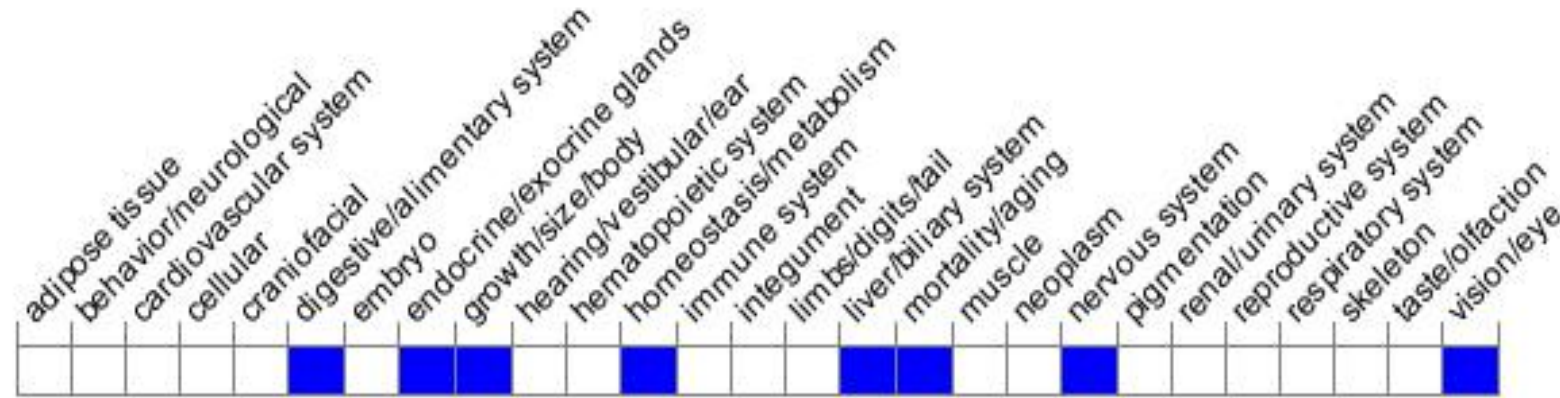


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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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