Prex1 Cas9-KO Strategy

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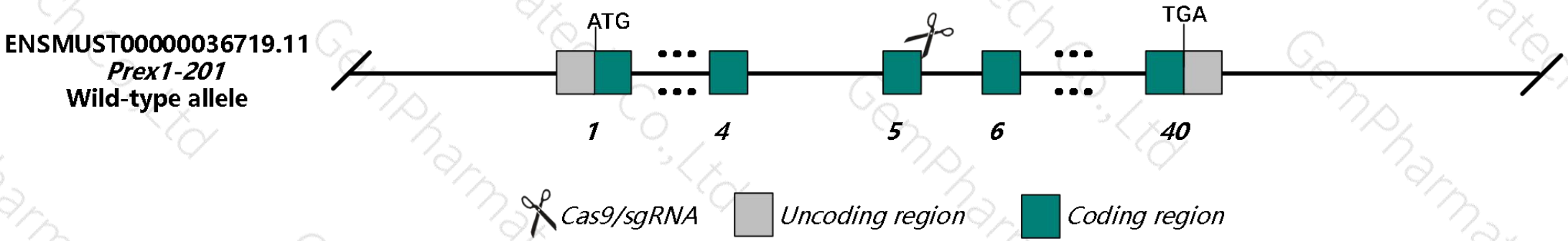
Project Overview

Project Name	***Prex1***
Project type	**Cas9-KO**
Strain background	**C57BL/6N**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prex1* gene. The schematic diagram is as follows:



Technical routes

- In this project we use CRISPR/Cas9 technology to modify *Prex1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6N 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/6N mice.

Notice

- The *Prex1* gene is located on the Chr2. 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）

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Prex1 phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 [*Mus musculus* (house mouse)]

Gene ID: 277360, updated on 12-Aug-2019

Summary

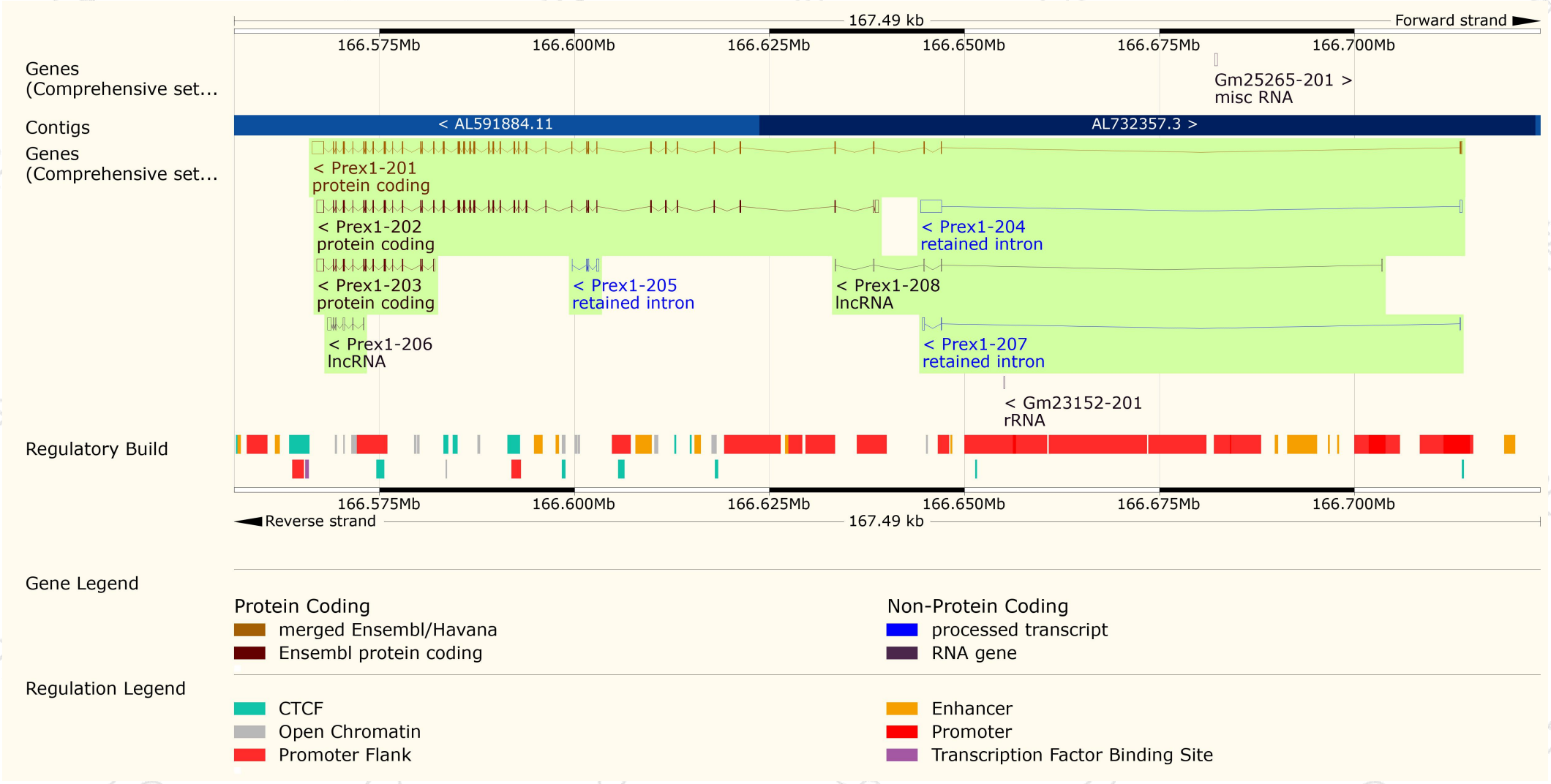
Official Symbol	Prex1 provided by MGI
Official Full Name	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 provided by MGI
Primary source	MGI:MGI:3040696
See related	Ensembl:ENSMUSG00000039621
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Setd6; P-REX1; G630042G04
Expression	Broad expression in thymus adult (RPKM 69.0), spleen adult (RPKM 46.4) and 25 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

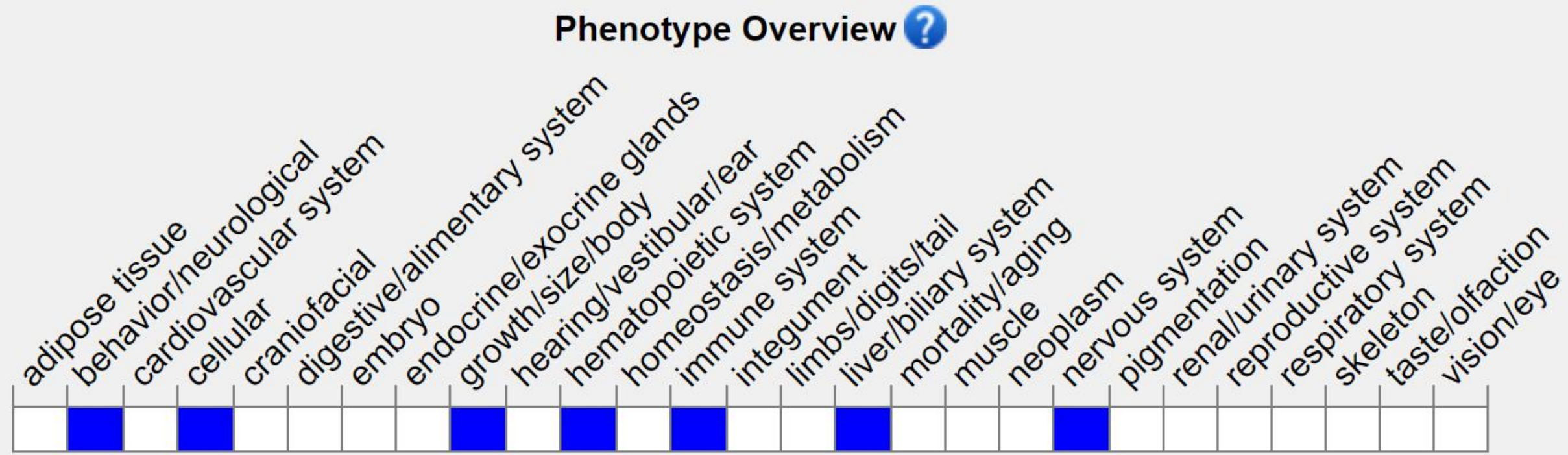
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Prex1-201	ENSMUST00000036719.11	6533	1650aa	ENSMUSP00000037180.5	Protein coding	CCDS38334	Q69ZK0	TSL:1 GENCODE basic APPRIS P1
Prex1-202	ENSMUST00000099080.8	5818	1480aa	ENSMUSP00000096679.2	Protein coding	-	I7HPV9	TSL:1 GENCODE basic
Prex1-203	ENSMUST00000109246.1	2386	462aa	ENSMUSP00000104869.1	Protein coding	-	Q69ZK0	TSL:1 GENCODE basic
Prex1-204	ENSMUST00000127553.1	2941	No protein	-	Retained intron	-	-	TSL:1
Prex1-207	ENSMUST00000140624.1	437	No protein	-	Retained intron	-	-	TSL:2
Prex1-205	ENSMUST00000136564.1	430	No protein	-	Retained intron	-	-	TSL:5
Prex1-206	ENSMUST00000136974.1	929	No protein	-	lncRNA	-	-	TSL:3
Prex1-208	ENSMUST00000152238.7	467	No protein	-	lncRNA	-	-	TSL:3

Genomic location distribution



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(http://www.informatics.jax.org/).

Mice homozygous for a null allele have impaired neutrophil migration and autism-like social behavior with defective AMPA-mediated LTD. Mice with other alleles exhibit reduced weight, smaller livers and increased peripheral neutrophil numbers.

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

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