

# *Pus1* Cas9-KO Strategy

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**Reviewer:**

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**Design Date:**

**2020-3-30**

# Project Overview

**Project Name**

*Pus1*

**Project type**

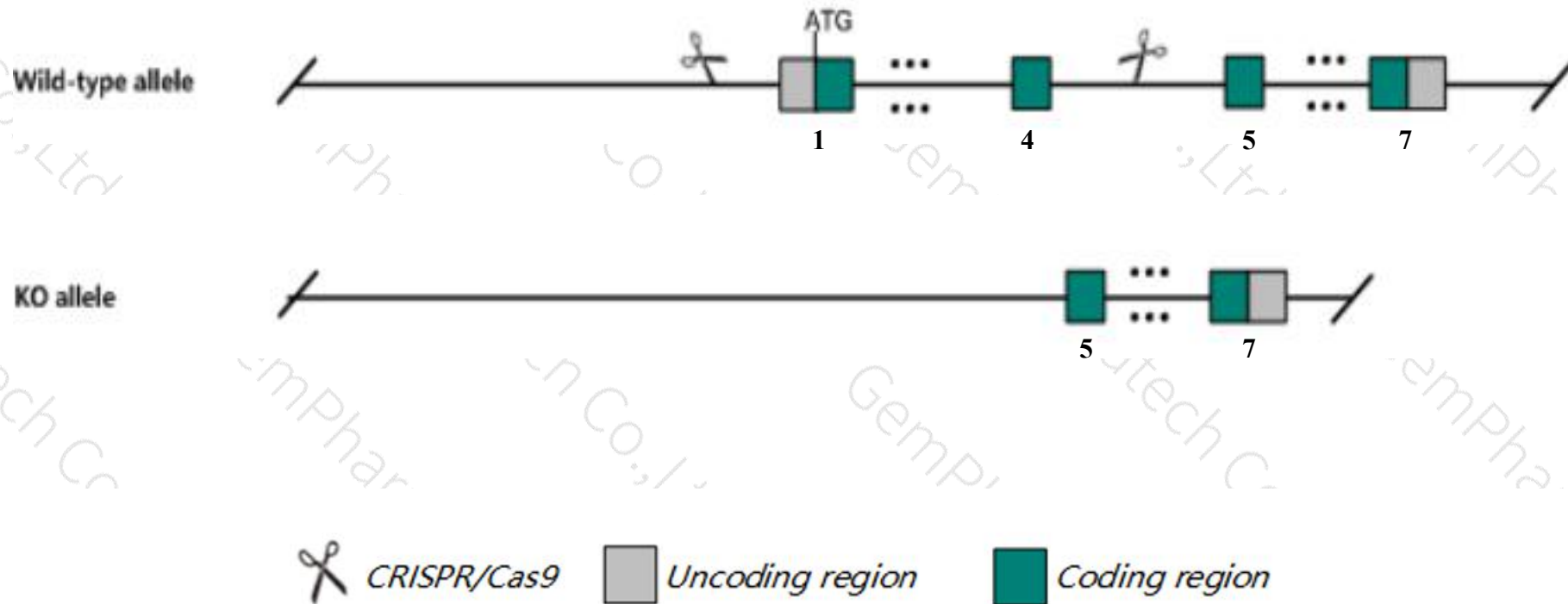
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pus1* gene. The schematic diagram is as follows:



- The *Pus1* gene has 7 transcripts. According to the structure of *Pus1* gene, exon1-exon4 of *Pus1*-203 (ENSMUST00000086643.11) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pus1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit slow postnatal weight gain, impaired exercise endurance, and alterations in muscle metabolism related to mitochondrial content and oxidative capacity.
- The KO region contains functional region of the *Gm15559* gene. Knockout the region may affect the function of *Gm15559* gene.
- The *Pus1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Pus1 pseudouridine synthase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 56361, updated on 13-Mar-2020

### Summary

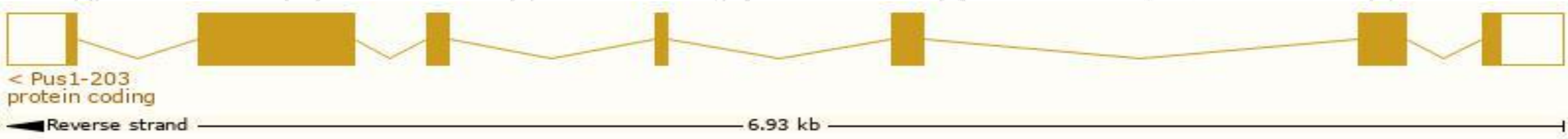
Official Symbol	Pus1 provided by MGI
Official Full Name	pseudouridine synthase 1 provided by MGI
Primary source	MGI:MGI:1929237
See related	Ensembl:ENSMUSG00000029507
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MPUS1; mPus1p; A730013B20Rik
Expression	Ubiquitous expression in large intestine adult (RPKM 13.1), liver E14 (RPKM 13.0) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

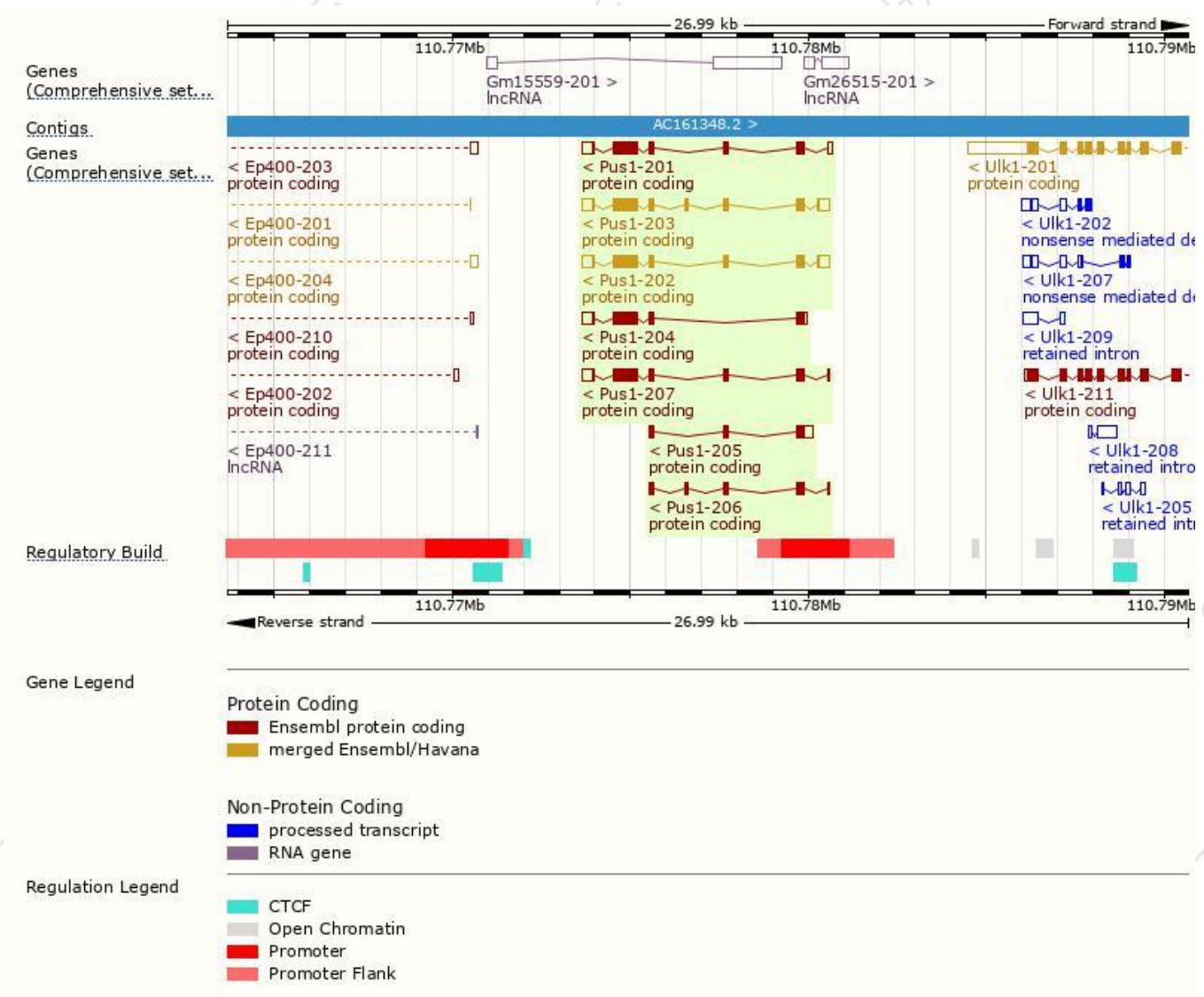
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pus1-203	<a href="#">ENSMUST00000086643.11</a>	1868	<a href="#">441aa</a>	Protein coding	<a href="#">CCDS19530</a>	<a href="#">H7BX59</a>	TSL:1 GENCODE basic APPRIS P4
Pus1-202	<a href="#">ENSMUST00000031483.14</a>	1814	<a href="#">423aa</a>	Protein coding	<a href="#">CCDS19531</a>	<a href="#">Q9WU56</a>	TSL:1 GENCODE basic APPRIS ALT2
Pus1-201	<a href="#">ENSMUST00000031481.12</a>	1563	<a href="#">393aa</a>	Protein coding	<a href="#">CCDS39212</a>	<a href="#">Q9WU56</a>	TSL:1 GENCODE basic APPRIS ALT2
Pus1-207	<a href="#">ENSMUST00000170468.7</a>	1510	<a href="#">393aa</a>	Protein coding	<a href="#">CCDS39212</a>	<a href="#">Q9WU56</a>	TSL:5 GENCODE basic APPRIS ALT2
Pus1-204	<a href="#">ENSMUST00000112426.7</a>	1389	<a href="#">347aa</a>	Protein coding	<a href="#">CCDS84929</a>	<a href="#">Q9WU56</a>	TSL:1 GENCODE basic
Pus1-205	<a href="#">ENSMUST00000136483.7</a>	701	<a href="#">147aa</a>	Protein coding	-	<a href="#">D3YWU8</a>	CDS 3' incomplete TSL:3
Pus1-206	<a href="#">ENSMUST00000149208.1</a>	527	<a href="#">162aa</a>	Protein coding	-	<a href="#">D3Z092</a>	CDS 3' incomplete TSL:3

The strategy is based on the design of *Pus1-203* transcript,The transcription is shown below

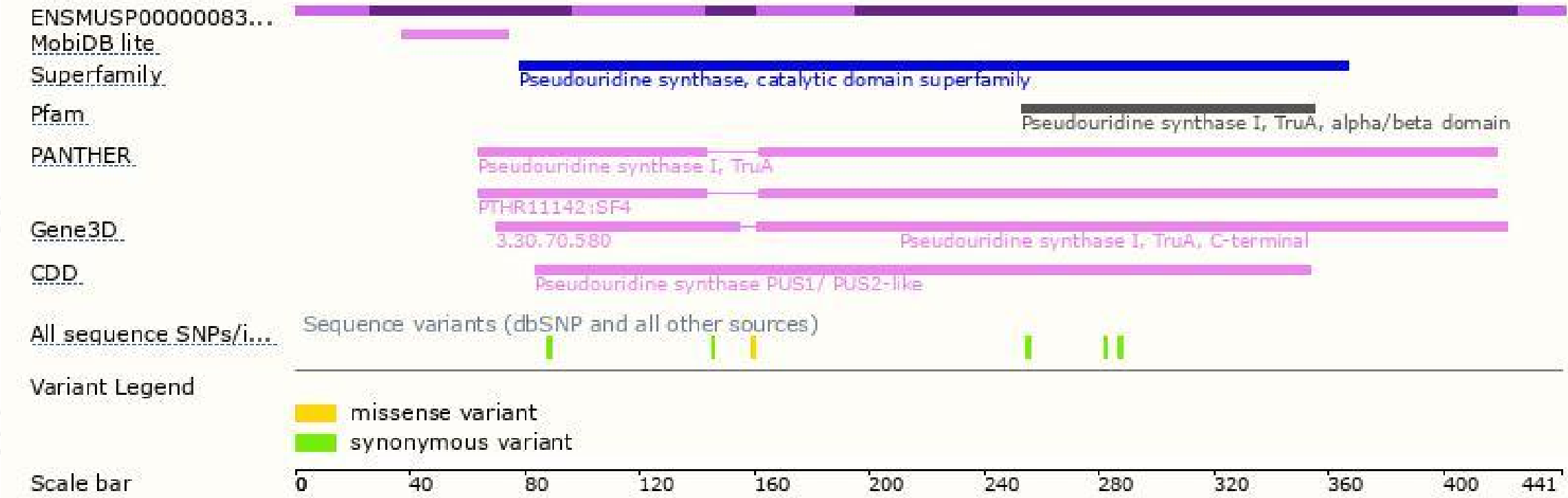


# Genomic location distribution

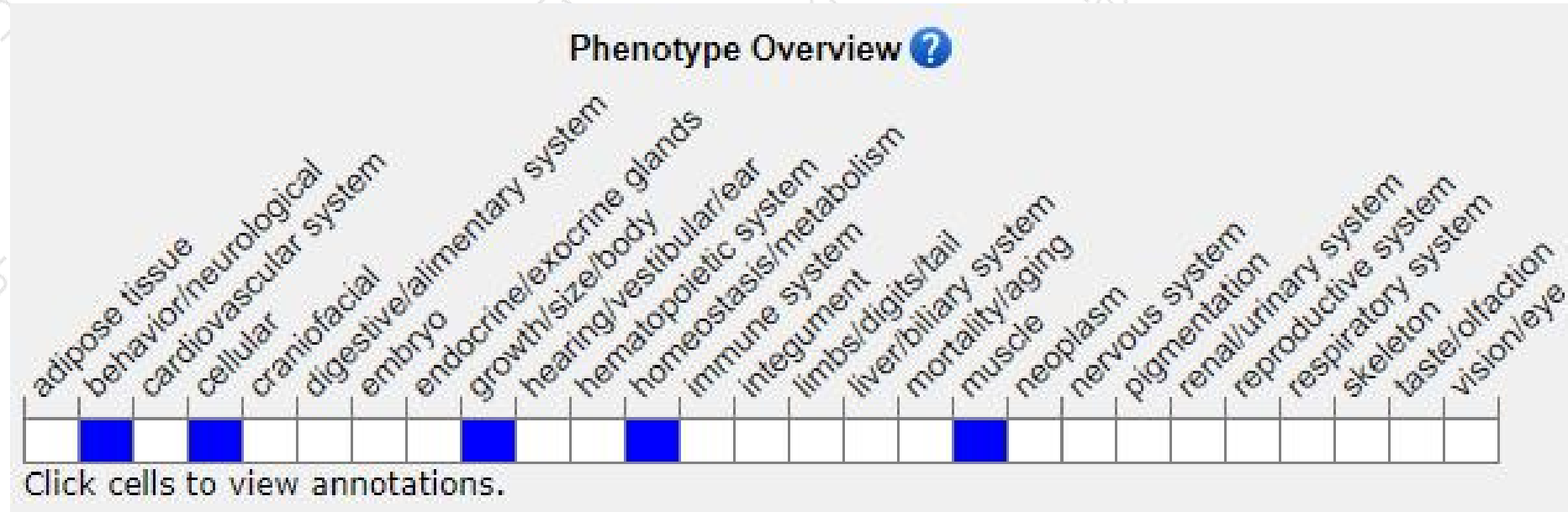




# Protein domain



# 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, Mice homozygous for a knock-out allele exhibit slow postnatal weight gain, impaired exercise endurance, and alterations in muscle metabolism related to mitochondrial content and oxidative capacity.

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

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