# *Plag1* Cas9-KO Strategy

Designer: Xueting Zhang
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集萃药康 GemPharmatech
GemPharmatech Co.,Ltd

# Project Overview

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|---|---|
| **Project Name** | ***Plag1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plag1* gene. The schematic diagram is as follows:

# Technical routes

➢ The *Plag1* gene has 4transcripts. According to the structure of *Plag1* gene, exon5-exon6 of *Plag1-201* (ENSMUST00000003369.9) transcript is recommended as the knockout region.The region contains all the coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Plag1* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

# Notice

- According to the existing MGI data,Homozygous null mice display reduced male fertility, small seminal vesicles and ventral prostate, reduced litter size (females only), reduced embryonic and postnatal growth, and delayed eyelid opening.
- The *Plag1* gene is located on the Chr4. 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.
- Transcript *Plag1*-203 may not be affected .
- 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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## Plag1 pleiomorphic adenoma gene 1 [ *Mus musculus* (house mouse) ]

Gene ID: 56711, updated on 11-May-2019

### Summary

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|---|---|
| **Official Symbol** | Plag1 provided by MGI |
| **Official Full Name** | pleiomorphic adenoma gene 1 provided by MGI |
| **Primary source** | MGI:MGI:1891916 |
| **See related** | Ensembl:ENSMUSG00000003282 |
| **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 |
| **Expression** | Broad expression in limb E14.5 (RPKM 2.3), CNS E11.5 (RPKM 1.2) and 15 other tissues See more |
| **Orthologs** | human all |

### Genomic context

**Location:** 4; 4 A1

See Plag1 in Genome Data Viewer

**Exon count:** 8

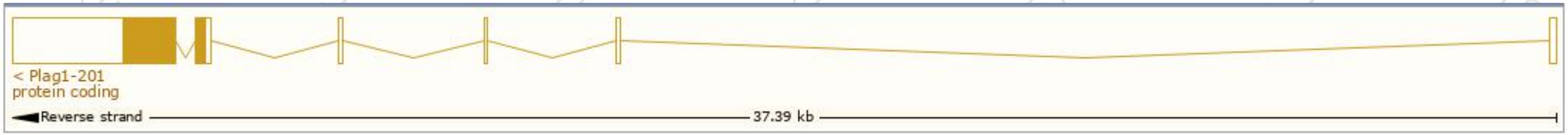
| Annotation release | Status | Assembly | Chr | Location |
|---|---|---|---|---|
| 106 | current | GRCm38.p4 (GCF_000001635.24) | 4 | NC_000070.6 (3898769..3938435, complement) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 4 | NC_000070.5 (3828305..3865552, complement) |

# Transcript information（Ensembl）

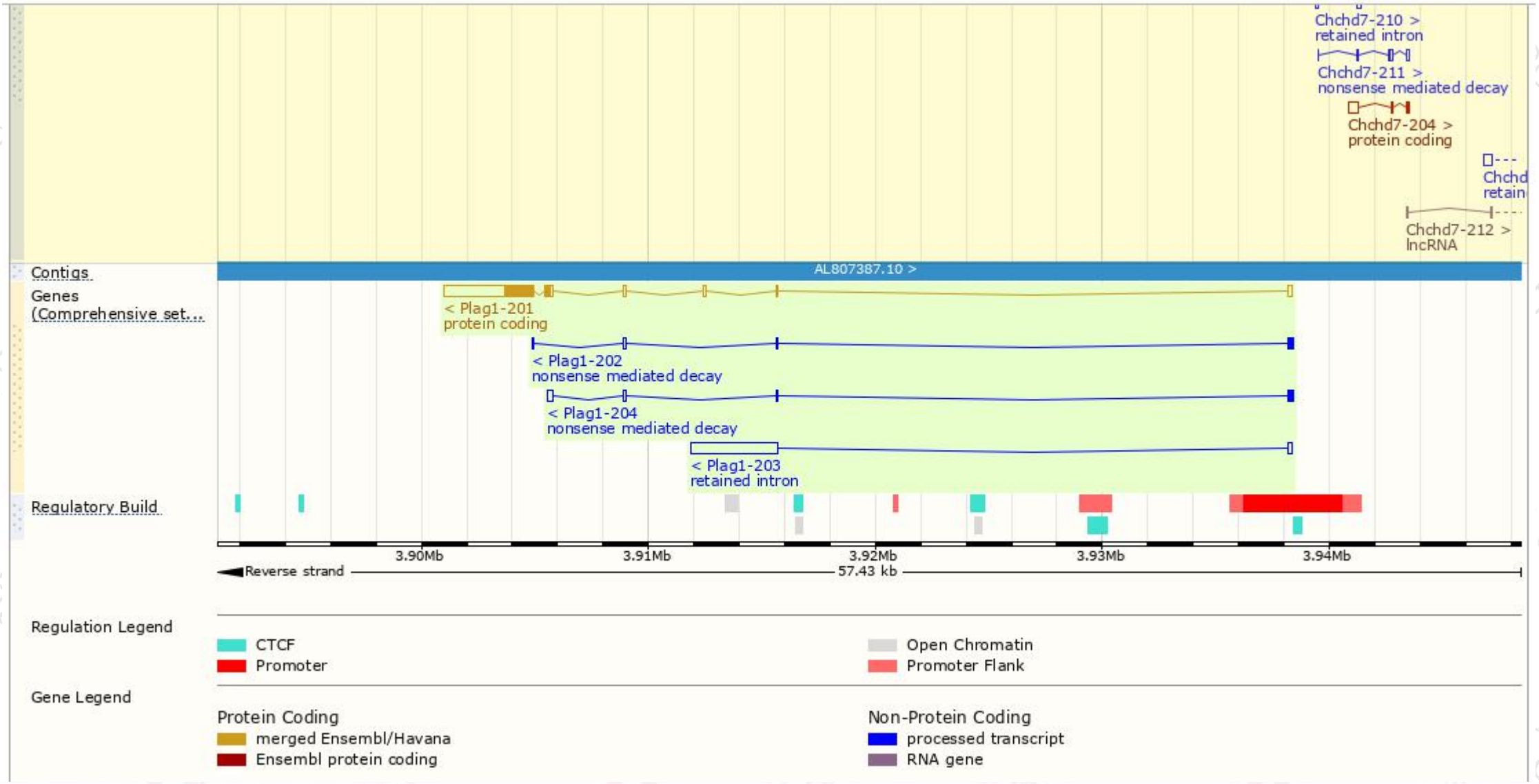
The gene has 4 transcripts,all transcripts are shown below:

| Name | Transcript ID ▲ | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Plag1-201 | ENSMUST00000003369.9 | 4774 | 499aa | Protein coding | CCDS17941 | Q9QYE0 | TSL:1 GENCODE basic APPRIS P1 |
| Plag1-202 | ENSMUST00000137439.7 | 452 | 43aa | Nonsense mediated decay | - | D6RES7 | TSL:2 |
| Plag1-203 | ENSMUST00000147035.1 | 4049 | No protein | Retained intron | - | - | TSL:1 |
| Plag1-204 | ENSMUST00000151543.1 | 669 | 43aa | Nonsense mediated decay | - | D6RES7 | TSL:3 |

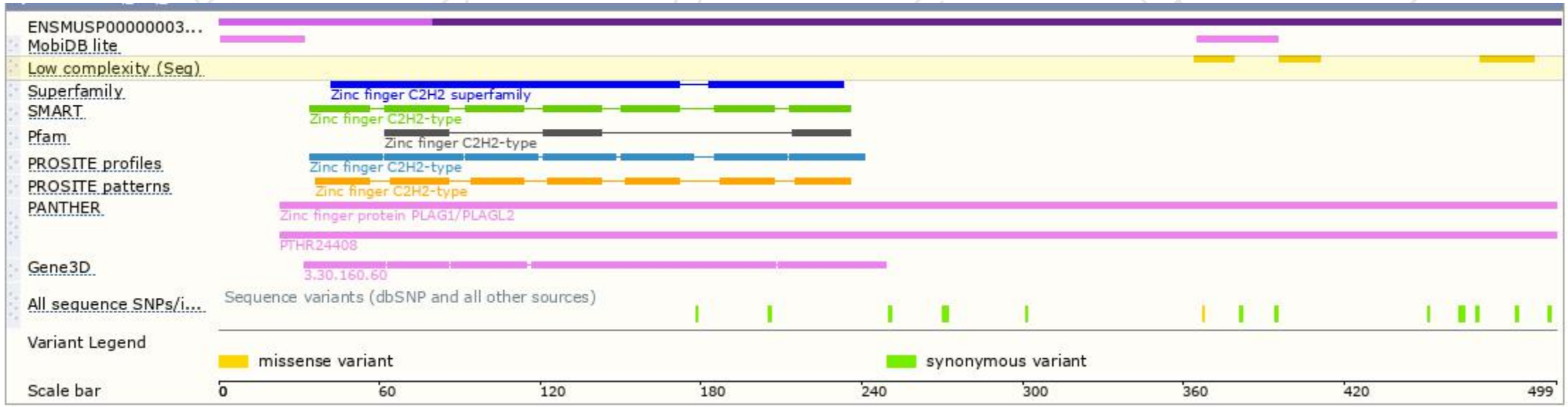
The strategy is based on the design of *Plag1-201* transcript,The transcription is shown below



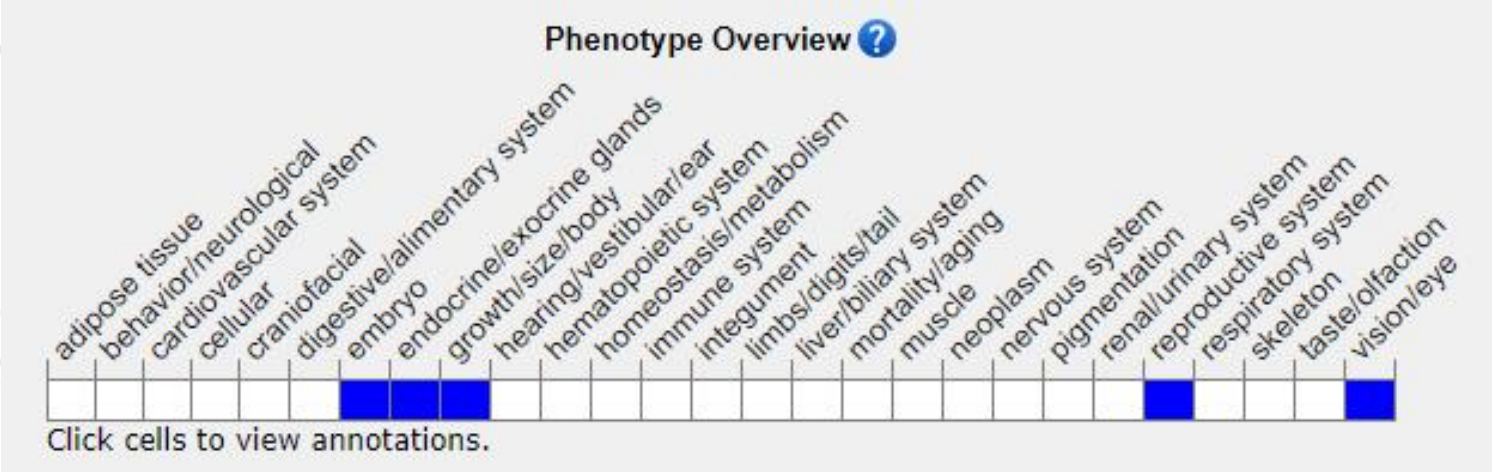
# Genomic location distribution



# 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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集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd

GemPharmatech Co.,Ltd