# *Eloc* Cas9-KO Strategy

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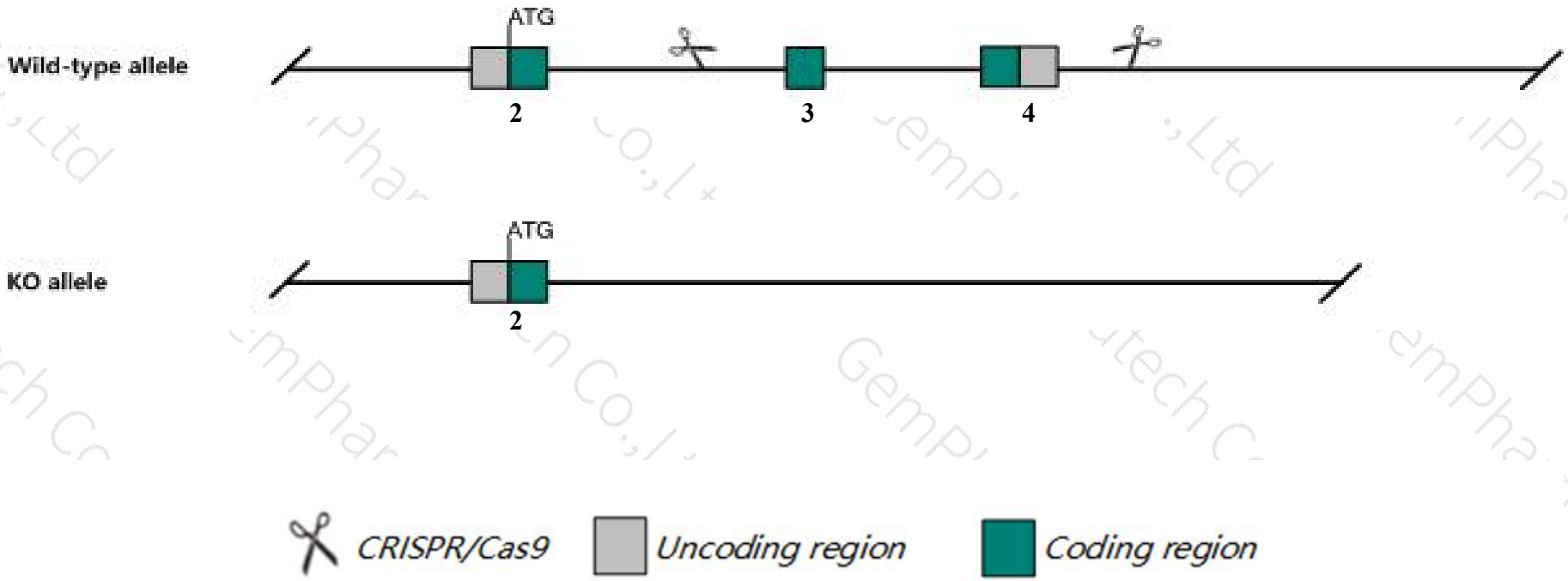
# Project Overview

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

# Knockout strategy

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



# Technical routes

➢ The *Eloc* gene has 11 transcripts. According to the structure of *Eloc* gene, exon3-exon4 of *Eloc-208* (ENSMUST00000188641.6) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Eloc* gene. The brief process is as follows: CRISPR/Cas9 system w

# Notice

➢Transcript *Eloc*-204&209&210&211 may not be affected.

➢ The *Eloc* gene is located on the Chr1. 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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## Eloc elongin C [ *Mus musculus* (house mouse) ]

Gene ID: 67923, updated on 5-Feb-2020

### Summary

| | |
|---|---|
| **Official Symbol** | Eloc provided by MGI |
| **Official Full Name** | elongin C provided by MGI |
| **Primary source** | MGI:MGI:1915173 |
| **See related** | Ensembl:ENSMUSG00000079658 |
| **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** | Tceb1; AA407206; AI987979; AW049146; 2610043E24Rik; 2610301I15Rik |
| **Expression** | Broad expression in CNS E18 (RPKM 25.1), frontal lobe adult (RPKM 20.4) and 21 other tissues See more |
| **Orthologs** | human all |

### Genomic context

**Location:** 1; 1 A3

See Eloc in Genome Data Viewer

**Exon count:** 9

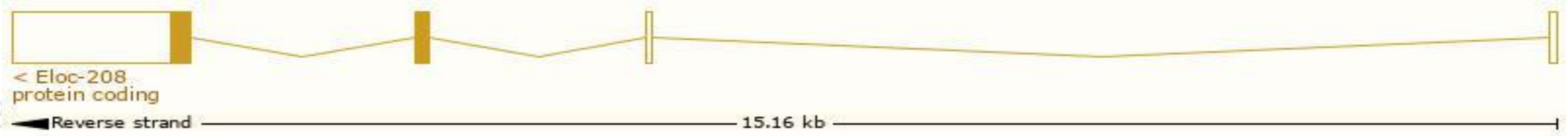
| Annotation release | Status | Assembly | Chr | Location |
|---|---|---|---|---|
| 108 | current | GRCm38.p6 (GCF_000001635.26) | 1 | NC_000067.6 (16641725..16657428, complement) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 1 | NC_000067.5 (16632846..16646946, complement) |

# Transcript information（Ensembl）

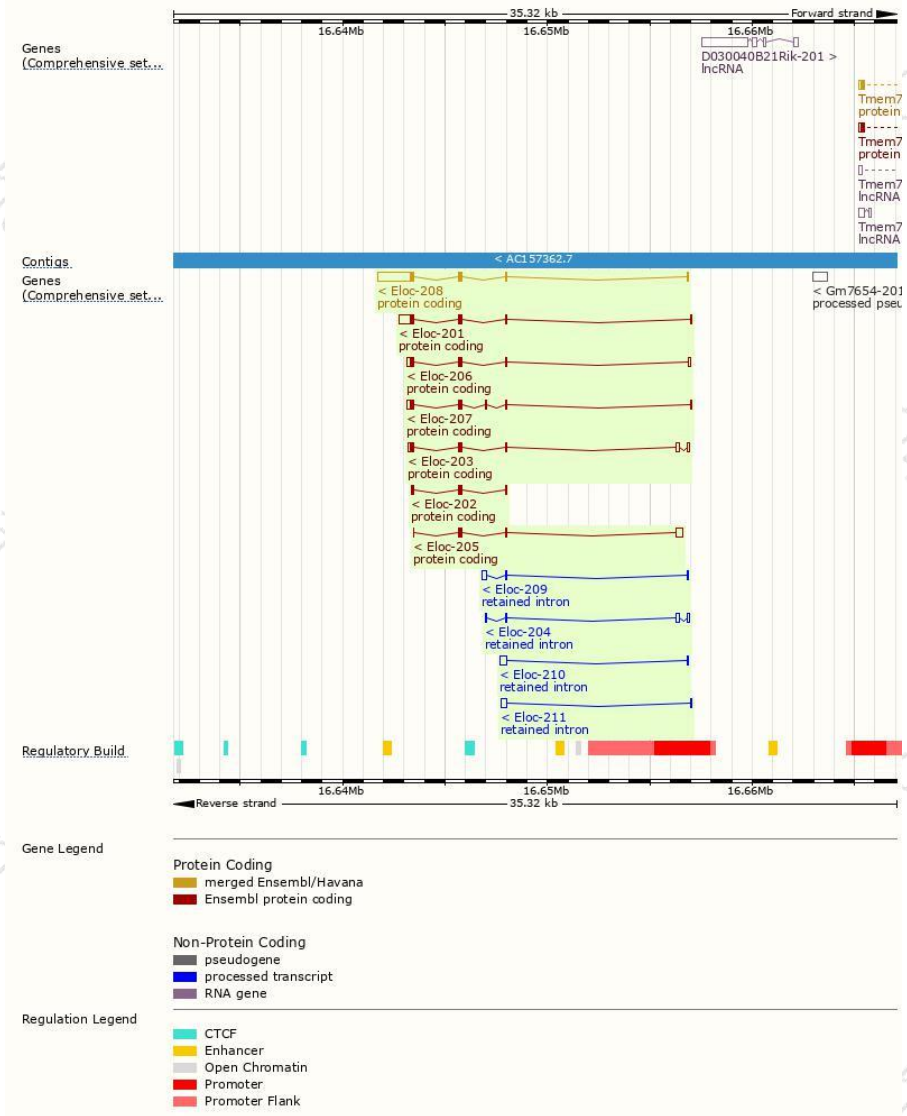
The gene has 11 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Eloc-208 | ENSMUST00000188641.6 | 2014 | 112aa | Protein coding | CCDS35517 | P83940 | TSL:1 GENCODE basic APPRIS P1 |
| Eloc-201 | ENSMUST00000115352.9 | 960 | 112aa | Protein coding | CCDS35517 | P83940 | TSL:1 GENCODE basic APPRIS P1 |
| Eloc-203 | ENSMUST00000185771.6 | 742 | 112aa | Protein coding | CCDS35517 | P83940 | TSL:5 GENCODE basic APPRIS P1 |
| Eloc-206 | ENSMUST00000186948.6 | 641 | 112aa | Protein coding | CCDS35517 | P83940 | TSL:2 GENCODE basic APPRIS P1 |
| Eloc-207 | ENSMUST00000187910.6 | 620 | 134aa | Protein coding | CCDS78549 | A0A087WNT1 | TSL:2 GENCODE basic |
| Eloc-205 | ENSMUST00000186701.1 | 534 | 51aa | Protein coding | - | A0A087WPE4 | CDS 3' incomplete TSL:5 |
| Eloc-202 | ENSMUST00000185393.6 | 366 | 95aa | Protein coding | - | A0A087WQE6 | CDS 3' incomplete TSL:2 |
| Eloc-204 | ENSMUST00000186541.1 | 410 | No protein | Retained intron | - | - | TSL:3 |
| Eloc-210 | ENSMUST00000190986.1 | 384 | No protein | Retained intron | - | - | TSL:2 |
| Eloc-209 | ENSMUST00000188987.6 | 350 | No protein | Retained intron | - | - | TSL:3 |
| Eloc-211 | ENSMUST00000191535.1 | 323 | No protein | Retained intron | - | - | TSL:3 |

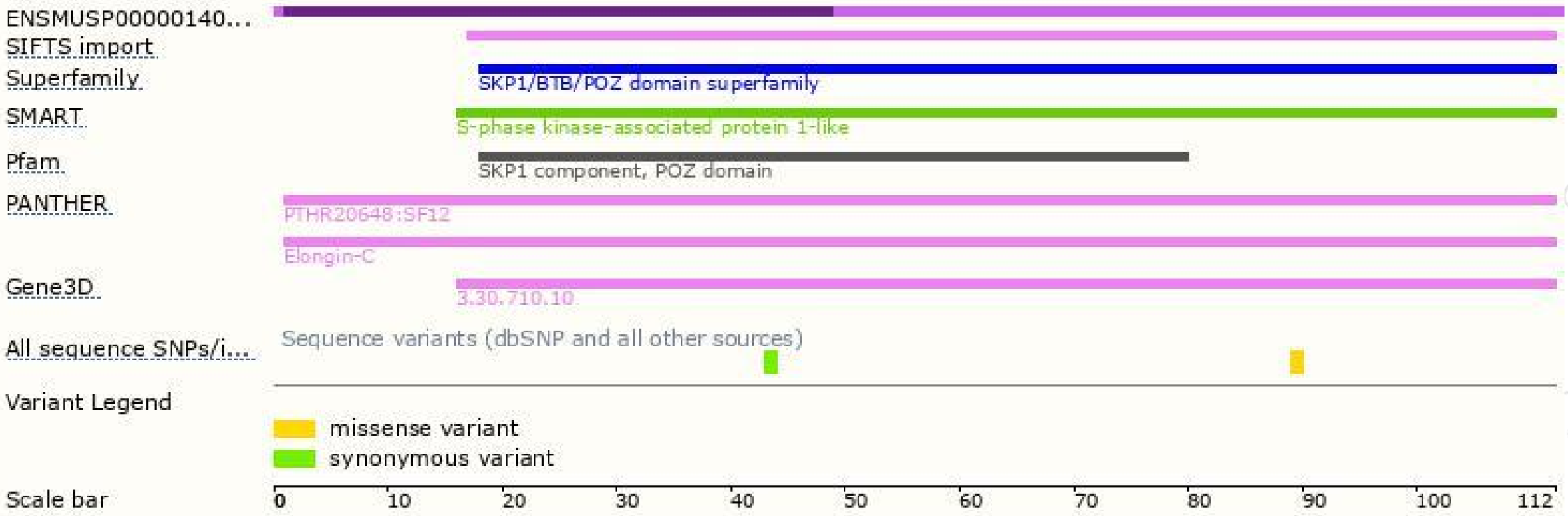
The strategy is based on the design of *Eloc-208* transcript,The transcription is shown below



# Genomic location distribution



# Protein domain



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

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