

# ***Ell2 Cas9-KO Strategy***

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**Reviewer:**

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# Project Overview

**Project Name**

***Ell2***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ell2* gene. The schematic diagram is as follows:



- The *Ell2* gene has 9 transcripts. According to the structure of *Ell2* gene, exon3-exon4 of *Ell2-201* (ENSMUST00000001583.7) transcript is recommended as the knockout region. The region contains 286bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ell2* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Ell2* gene is located on the Chr13. 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)

## ElI2 elongation factor RNA polymerase II 2 [Mus musculus (house mouse)]

Gene ID: 192657, updated on 31-Jan-2019

### Summary



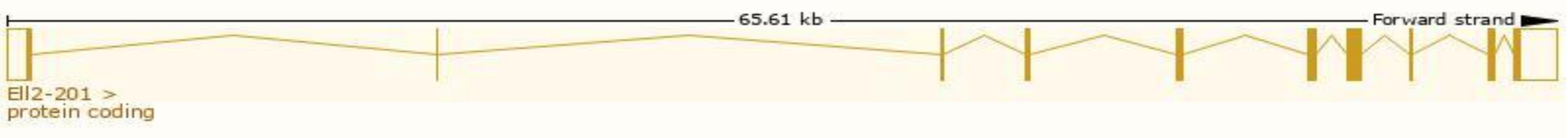
<b>Official Symbol</b>	ElI2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	elongation factor RNA polymerase II 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2183438</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000001542</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Expression</b>	Broad expression in liver E14 (RPKM 25.8), liver E14.5 (RPKM 21.9) and 24 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

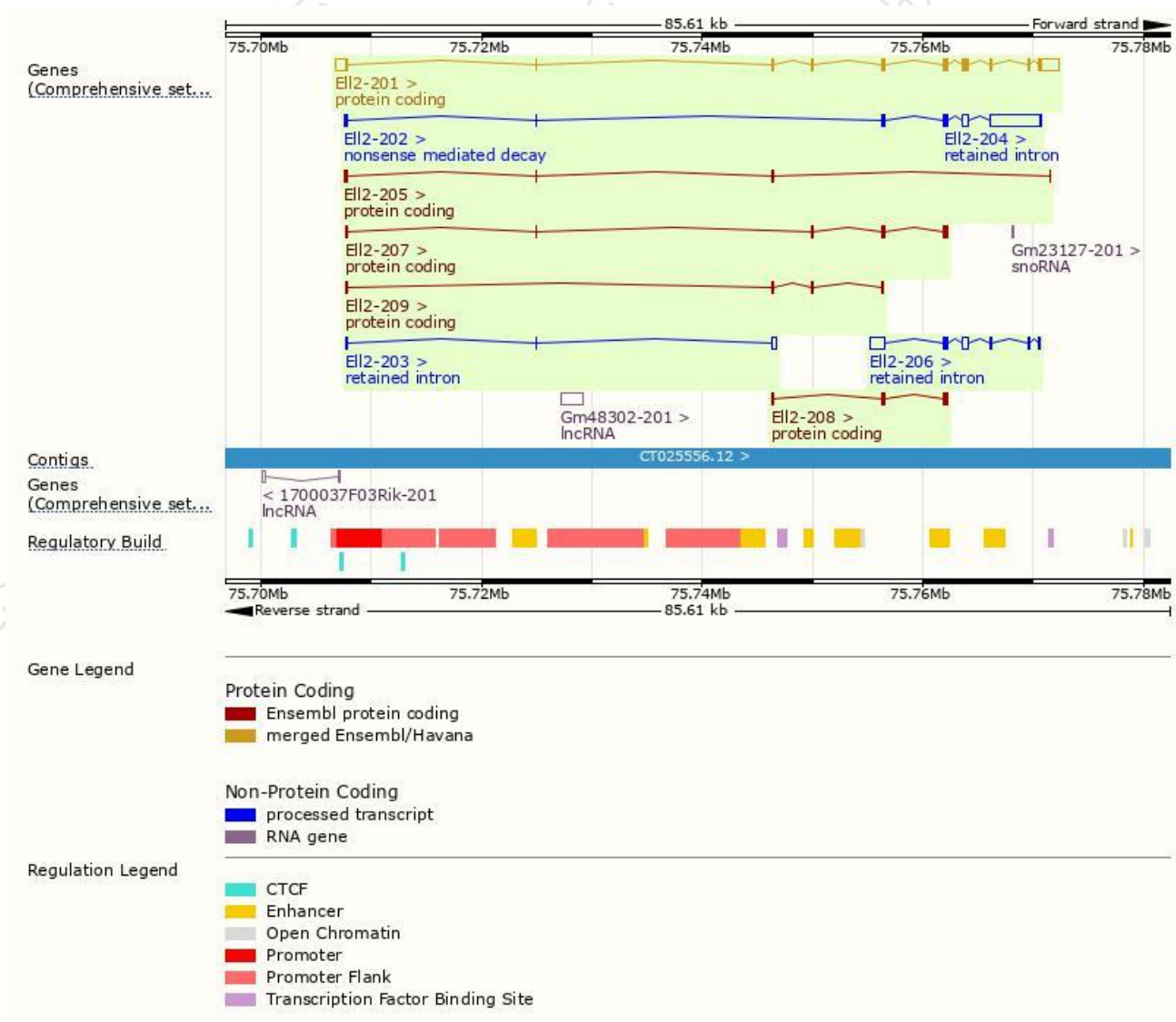
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ell2-201	<a href="#">ENSMUST00000001583.7</a>	4382	<a href="#">639aa</a>	Protein coding	<a href="#">CCDS36734</a>	<a href="#">Q3UKU1</a>	TSL:1 GENCODE basic APPRIS P1
Ell2-207	<a href="#">ENSMUST00000222853.1</a>	732	<a href="#">172aa</a>	Protein coding	-	<a href="#">A0A1Y7VLE0</a>	CDS 3' incomplete TSL:5
Ell2-209	<a href="#">ENSMUST00000223535.1</a>	543	<a href="#">181aa</a>	Protein coding	-	<a href="#">A0A1Y7VIP4</a>	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
Ell2-208	<a href="#">ENSMUST00000222892.1</a>	508	<a href="#">169aa</a>	Protein coding	-	<a href="#">A0A1Y7VMV7</a>	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
Ell2-205	<a href="#">ENSMUST00000222194.1</a>	434	<a href="#">111aa</a>	Protein coding	-	<a href="#">A0A1Y7VNQ8</a>	TSL:3 GENCODE basic
Ell2-202	<a href="#">ENSMUST00000220572.1</a>	586	<a href="#">90aa</a>	Nonsense mediated decay	-	<a href="#">A0A1Y7VKD2</a>	TSL:5
Ell2-204	<a href="#">ENSMUST00000221979.1</a>	5126	No protein	Retained intron	-	-	TSL:5
Ell2-206	<a href="#">ENSMUST00000222564.1</a>	2351	No protein	Retained intron	-	-	TSL:5
Ell2-203	<a href="#">ENSMUST00000221432.1</a>	511	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Ell2-201* transcript,The transcription is shown below

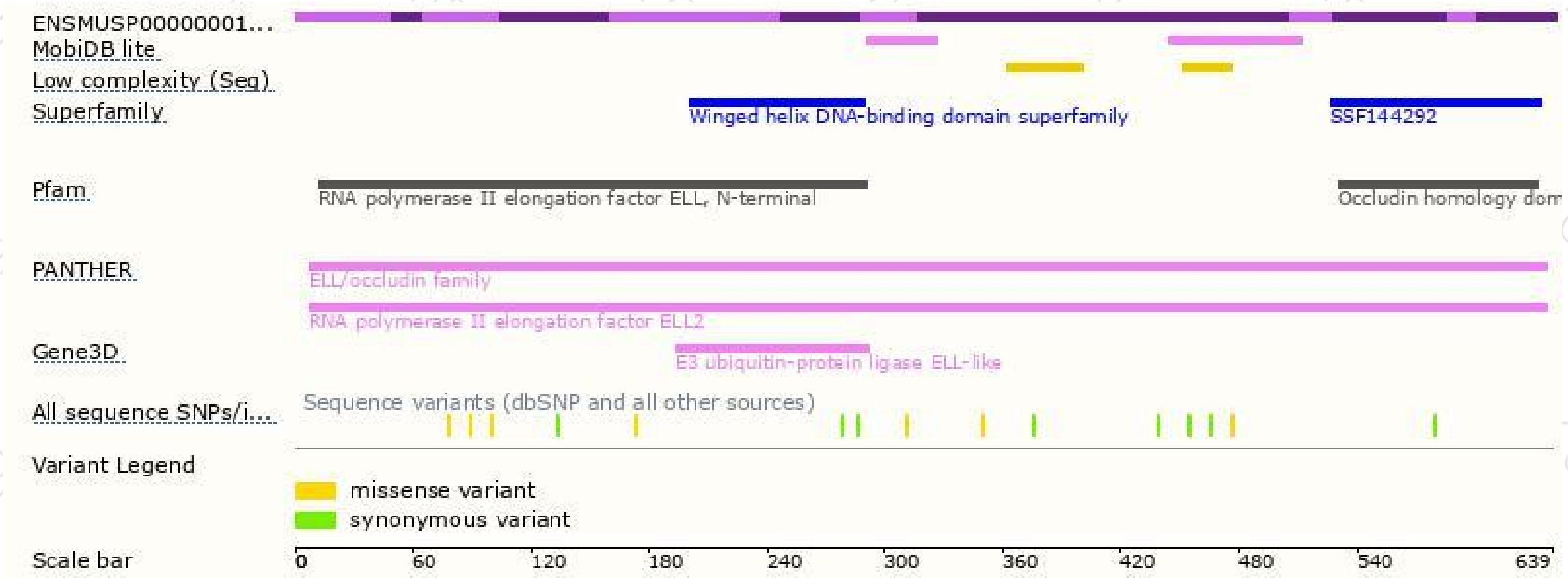


# Genomic location distribution

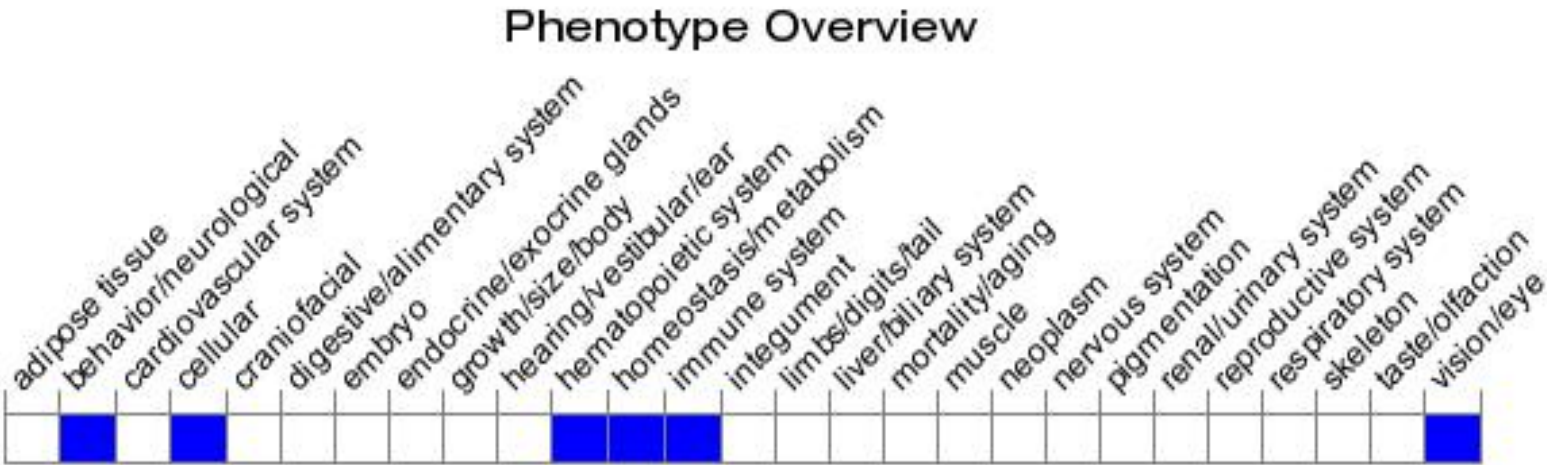




# Protein domain



# Mouse phenotype description(MGI )



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

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

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