

# *Eed* Cas9-KO Strategy

**Designer:**

**Huan Fan**

**Reviewer:**

**Huan Wang**

**Design Date:**

**2019-11-29**

# Project Overview

**Project Name**

*Eed*

**Project type**

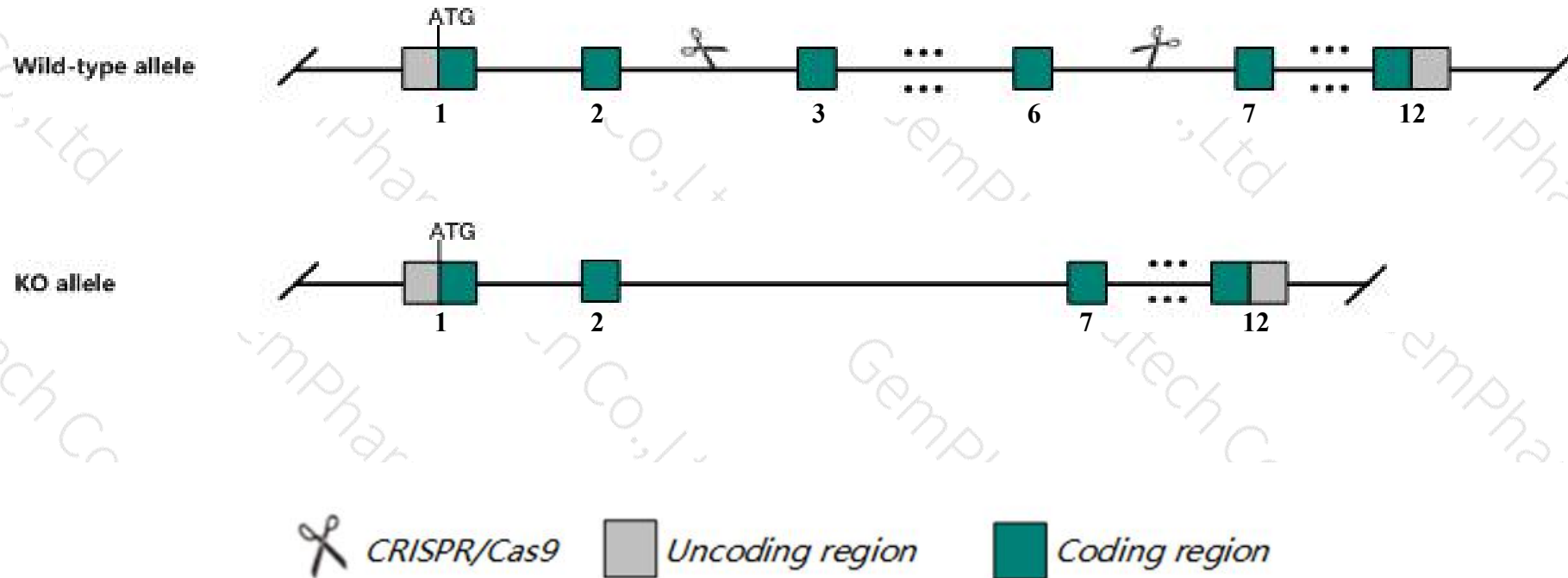
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Eed* gene has 12 transcripts. According to the structure of *Eed* gene, exon3-exon6 of *Eed-201* (ENSMUST00000107234.2) transcript is recommended as the knockout region. The region contains 367bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eed* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous mutant mice are dwarfed and their coat color is dilute.
- Transcript *Eed-205* may not be affected.
- The *Eed* gene is located on the Chr7. 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)

## Eed embryonic ectoderm development [Mus musculus (house mouse)]

Gene ID: 13626, updated on 30-Mar-2019

### Summary



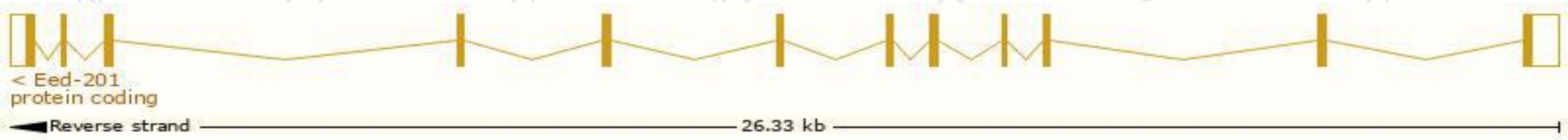
<b>Official Symbol</b>	Eed provided by <a href="#">MGI</a>
<b>Official Full Name</b>	embryonic ectoderm development provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:95286</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030619</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>Also known as</b>	I(7)5Rn, I7Rn5, lusk
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 15.5), liver E14 (RPKM 11.6) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

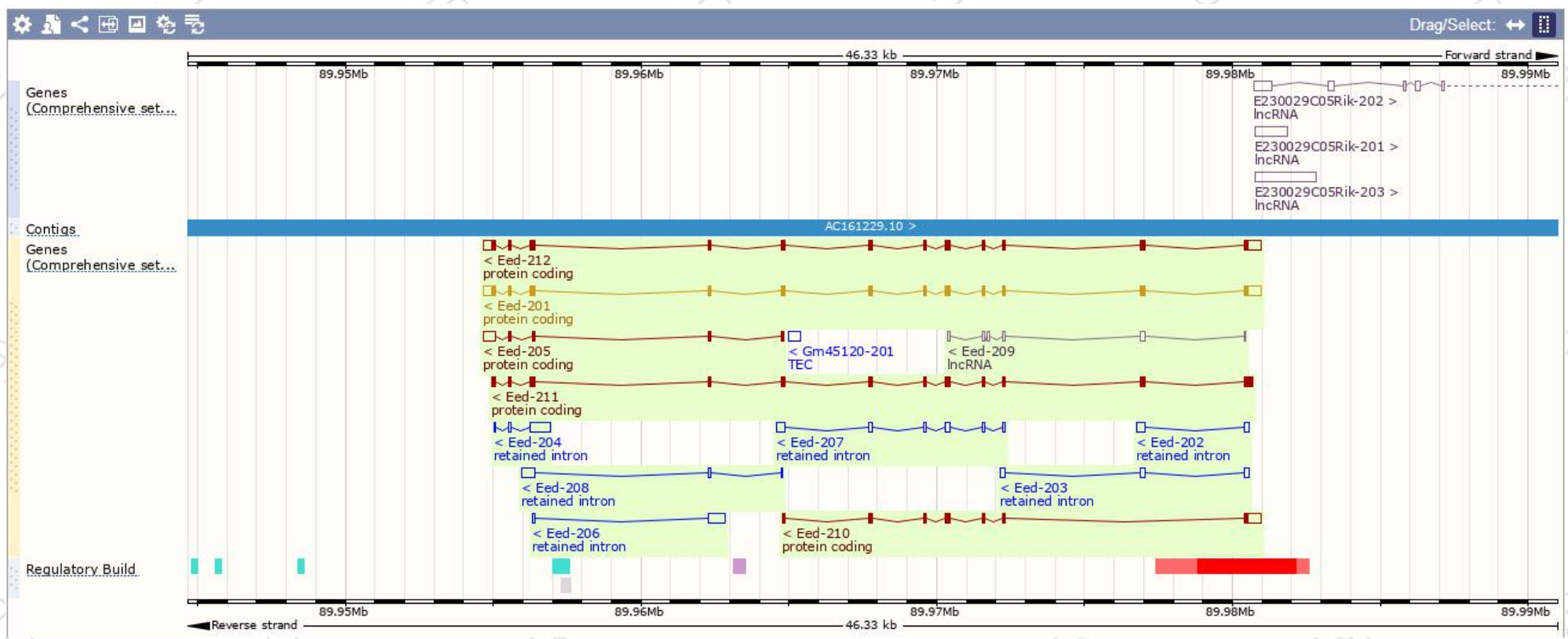
The gene has 12 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Eed-201	<a href="#">ENSMUST00000107234.2</a>	2067	<a href="#">441aa</a>	Protein coding	<a href="#">CCDS40016</a>	<a href="#">Q921E6</a>	TSL:1	GENCODE basic APPRIS P1
Eed-212	<a href="#">ENSMUST00000238981.1</a>	2060	<a href="#">441aa</a>	Protein coding	<a href="#">CCDS40016</a>	-	GENCODE basic	APPRIS P1
Eed-211	<a href="#">ENSMUST00000238792.1</a>	1503	<a href="#">500aa</a>	Protein coding	-	-	GENCODE basic	
Eed-210	<a href="#">ENSMUST00000208977.1</a>	1111	<a href="#">220aa</a>	Protein coding	-	<a href="#">A0A140LIG5</a>	CDS 3' incomplete	TSL:3
Eed-205	<a href="#">ENSMUST00000207980.1</a>	767	<a href="#">118aa</a>	Protein coding	-	<a href="#">A0A140LIN6</a>	CDS 5' incomplete	TSL:3
Eed-204	<a href="#">ENSMUST00000207609.1</a>	774	No protein	Retained intron	-	-	TSL:2	
Eed-207	<a href="#">ENSMUST00000208196.1</a>	703	No protein	Retained intron	-	-	TSL:3	
Eed-206	<a href="#">ENSMUST00000207996.1</a>	639	No protein	Retained intron	-	-	TSL:2	
Eed-208	<a href="#">ENSMUST00000208245.1</a>	609	No protein	Retained intron	-	-	TSL:3	
Eed-203	<a href="#">ENSMUST00000207568.1</a>	491	No protein	Retained intron	-	-	TSL:2	
Eed-202	<a href="#">ENSMUST00000157001.1</a>	454	No protein	Retained intron	-	-	TSL:2	
Eed-209	<a href="#">ENSMUST00000208643.1</a>	528	No protein	lncRNA	-	-	TSL:5	

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

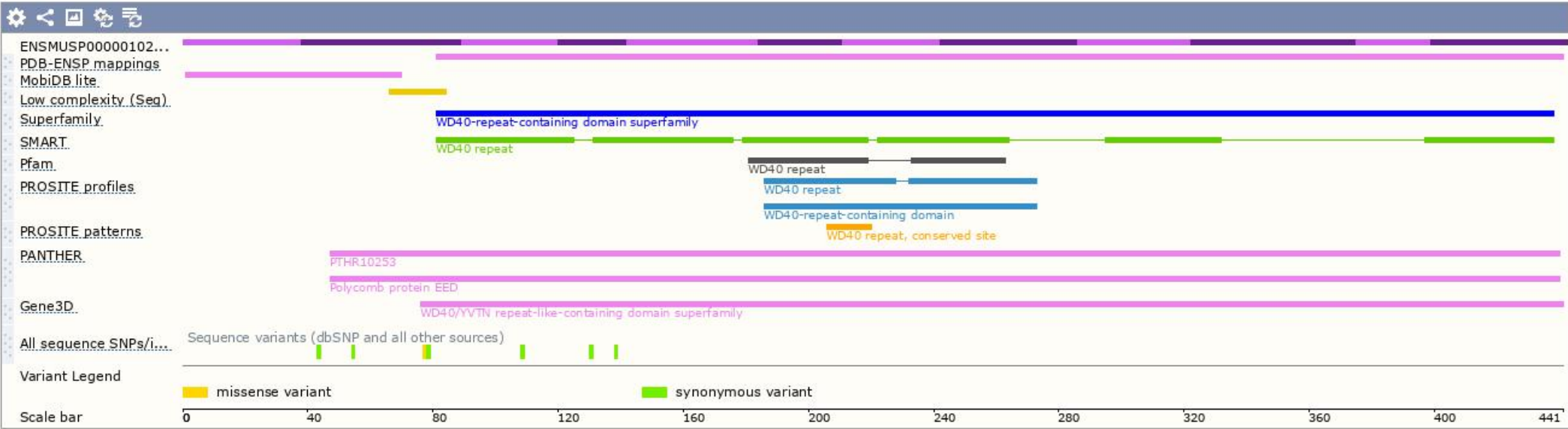


# Genomic location distribution

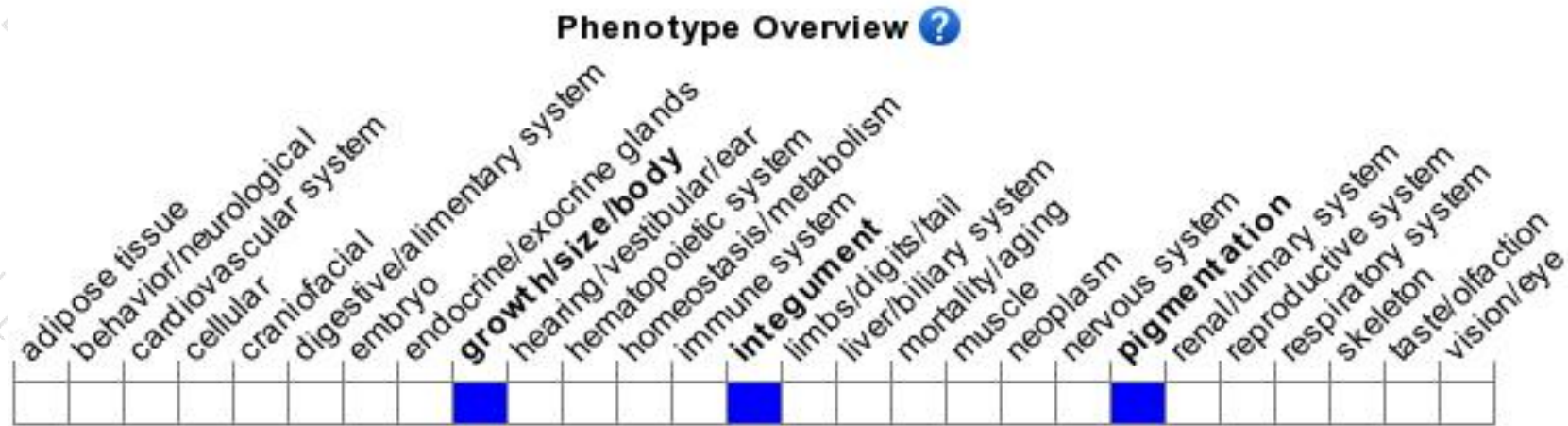




# Protein domain



# Mouse phenotype description(MGI )



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

According to the existing MGI data, Homozygous mutant mice are dwarfed and their coat color is dilute.

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

Tel: 400-9660890

