

# ***Yeats2 Cas9-KO Strategy***

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# Project Overview

**Project Name**

***Yeats2***

**Project type**

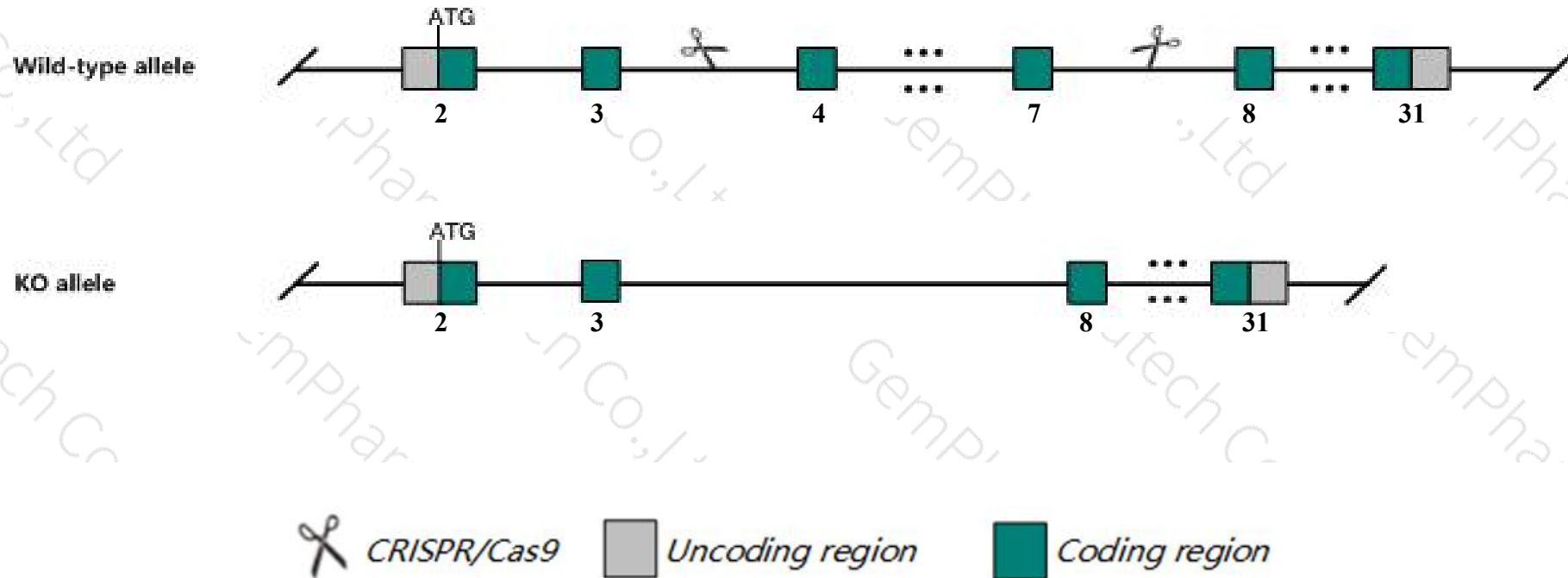
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Yeats2* gene. The schematic diagram is as follows:



- The *Yeats2* gene has 14 transcripts. According to the structure of *Yeats2* gene, exon4-exon7 of *Yeats2-202* (ENSMUST00000115560.3) transcript is recommended as the knockout region. The region contains 617bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Yeats2* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Yeats2* -203,205,206,207,210,213,214 may not be affected.
- The *Yeats2* gene is located on the Chr16. 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)

## Yeats2 YEATS domain containing 2 [Mus musculus (house mouse)]

Gene ID: 208146, updated on 31-Jan-2019

### Summary



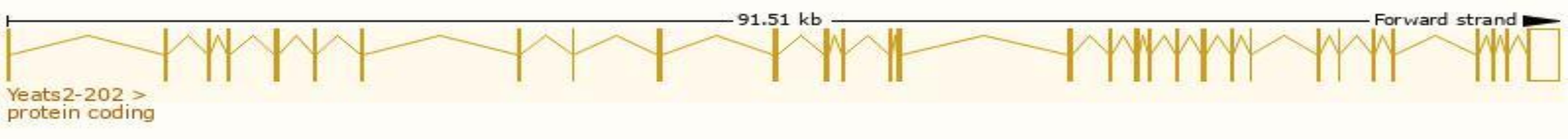
<b>Official Symbol</b>	Yeats2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	YEATS domain containing 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2447762</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000041215</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	BC042768, mKIAA1197
<b>Expression</b>	Broad expression in CNS E11.5 (RPKM 38.3), CNS E14 (RPKM 32.8) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

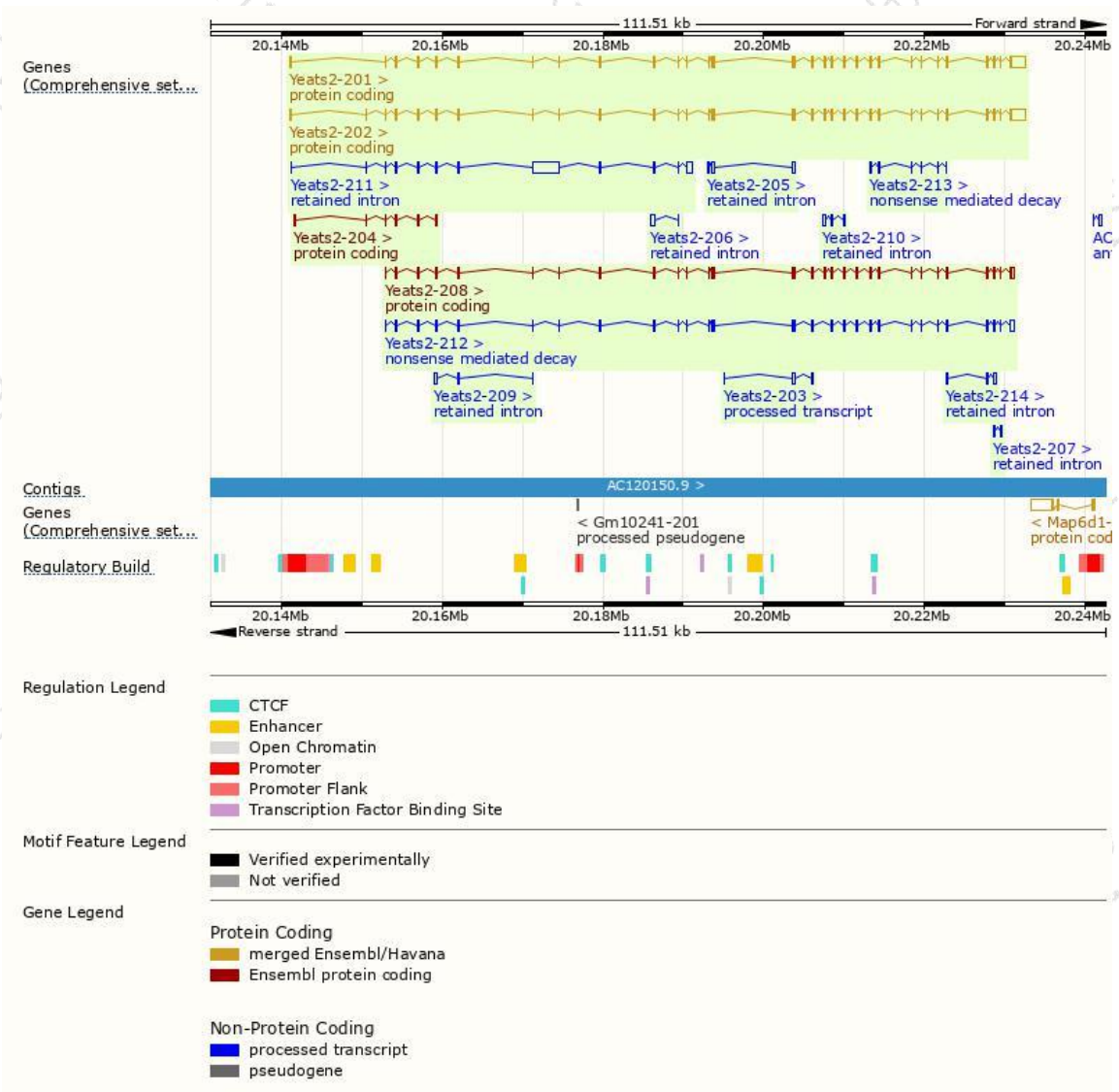
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Yeats2-202	<a href="#">ENSMUST00000115560.3</a>	6112	<a href="#">1407aa</a>	Protein coding	<a href="#">CCDS49790</a>	<a href="#">Q3TUF7</a>	TSL:5 GENCODE basic APPRIS ALT2
Yeats2-201	<a href="#">ENSMUST00000090052.10</a>	5997	<a href="#">1354aa</a>	Protein coding	<a href="#">CCDS28043</a>	<a href="#">Q3TUF7</a>	TSL:1 GENCODE basic APPRIS P3
Yeats2-208	<a href="#">ENSMUST00000232019.1</a>	4559	<a href="#">1369aa</a>	Protein coding	-	<a href="#">A0A338P697</a>	CDS 5' incomplete
Yeats2-204	<a href="#">ENSMUST00000231705.1</a>	772	<a href="#">218aa</a>	Protein coding	-	<a href="#">A0A338P6P2</a>	CDS 3' incomplete
Yeats2-212	<a href="#">ENSMUST00000232338.1</a>	4405	<a href="#">844aa</a>	Nonsense mediated decay	-	<a href="#">A0A338P689</a>	
Yeats2-213	<a href="#">ENSMUST00000232613.1</a>	563	<a href="#">142aa</a>	Nonsense mediated decay	-	<a href="#">A0A338P7J1</a>	CDS 5' incomplete
Yeats2-203	<a href="#">ENSMUST00000231671.1</a>	455	No protein	Processed transcript	-	-	
Yeats2-211	<a href="#">ENSMUST00000232172.1</a>	5671	No protein	Retained intron	-	-	
Yeats2-210	<a href="#">ENSMUST00000232094.1</a>	728	No protein	Retained intron	-	-	
Yeats2-205	<a href="#">ENSMUST00000231795.1</a>	719	No protein	Retained intron	-	-	
Yeats2-214	<a href="#">ENSMUST00000232671.1</a>	714	No protein	Retained intron	-	-	
Yeats2-206	<a href="#">ENSMUST00000231861.1</a>	665	No protein	Retained intron	-	-	
Yeats2-209	<a href="#">ENSMUST00000232054.1</a>	471	No protein	Retained intron	-	-	
Yeats2-207	<a href="#">ENSMUST00000231997.1</a>	406	No protein	Retained intron	-	-	

The strategy is based on the design of *Yeats2-202* transcript,The transcription is shown below

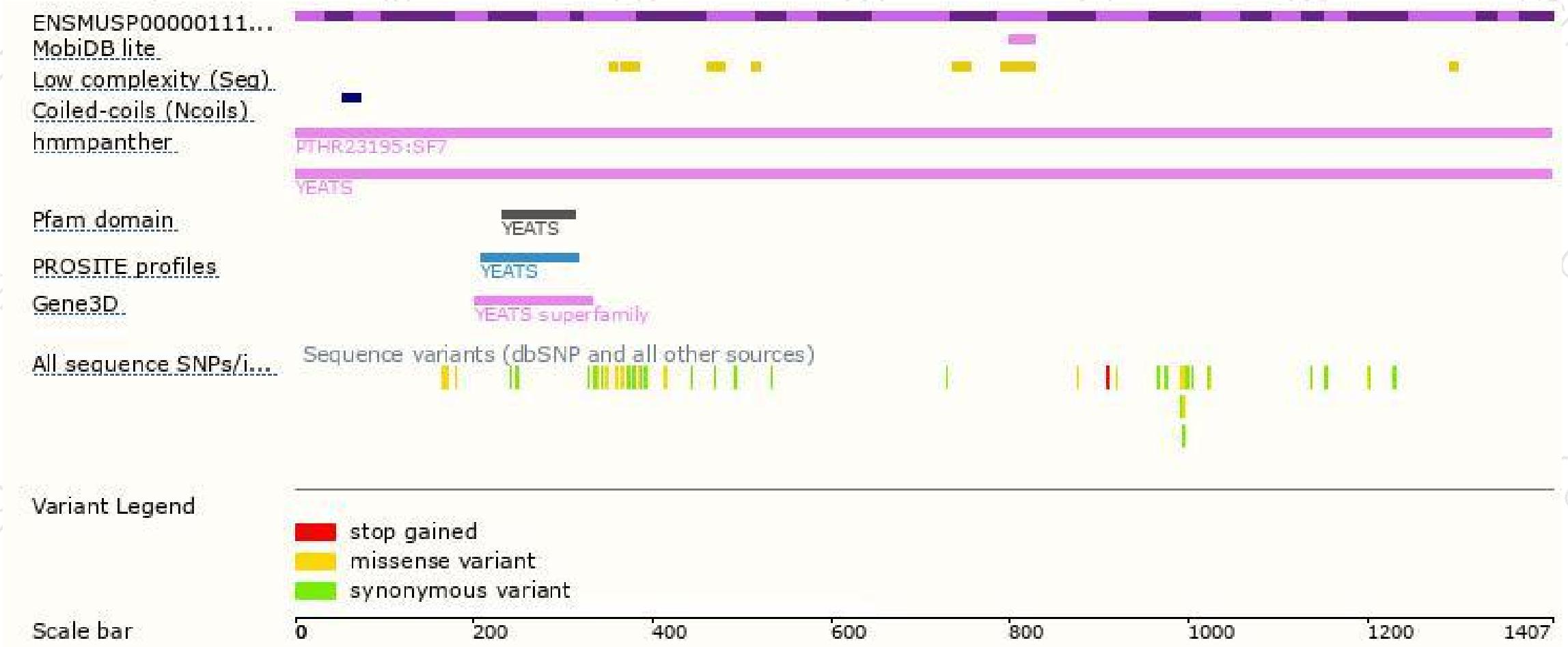


# Genomic location distribution





# Protein domain



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

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