

Cul2 Cas9-KO Strategy

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Project Overview

Project Name

Cul2

Project type

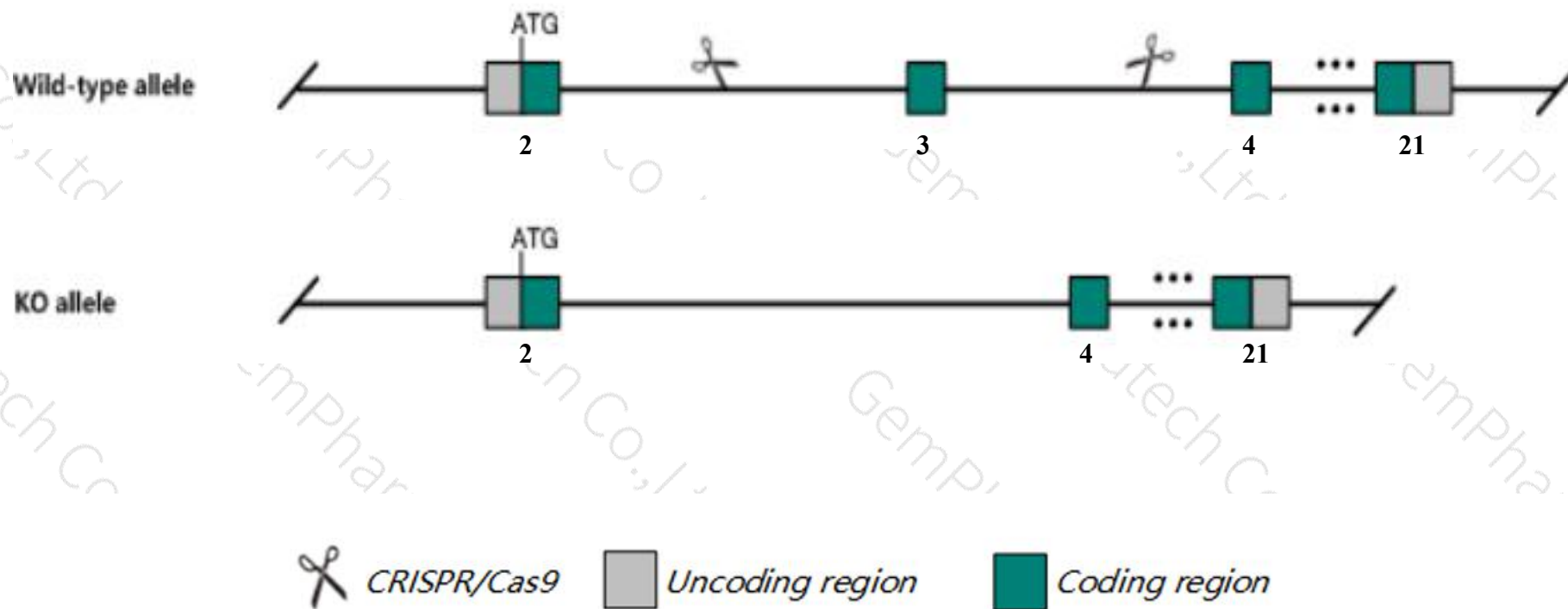
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cul2* gene. The schematic diagram is as follows:



- The *Cul2* gene has 7 transcripts. According to the structure of *Cul2* gene, exon3 of *Cul2-205* (ENSMUST00000162301.7) transcript is recommended as the knockout region. The region contains 103bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cul2* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Cul2* gene is located on the Chr18. 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)

Cul2 cullin 2 [Mus musculus (house mouse)]

Gene ID: 71745, updated on 31-Jan-2019

Summary



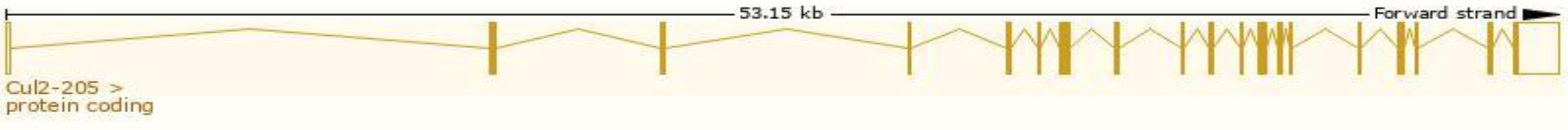
Official Symbol	Cul2 provided by MGI
Official Full Name	cullin 2 provided by MGI
Primary source	MGI:MGI:1918995
See related	Ensembl:ENSMUSG00000024231
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1300003D18Rik, 4932411N15Rik, AI327301, mKIAA4106
Expression	Ubiquitous expression in placenta adult (RPKM 8.3), CNS E18 (RPKM 7.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

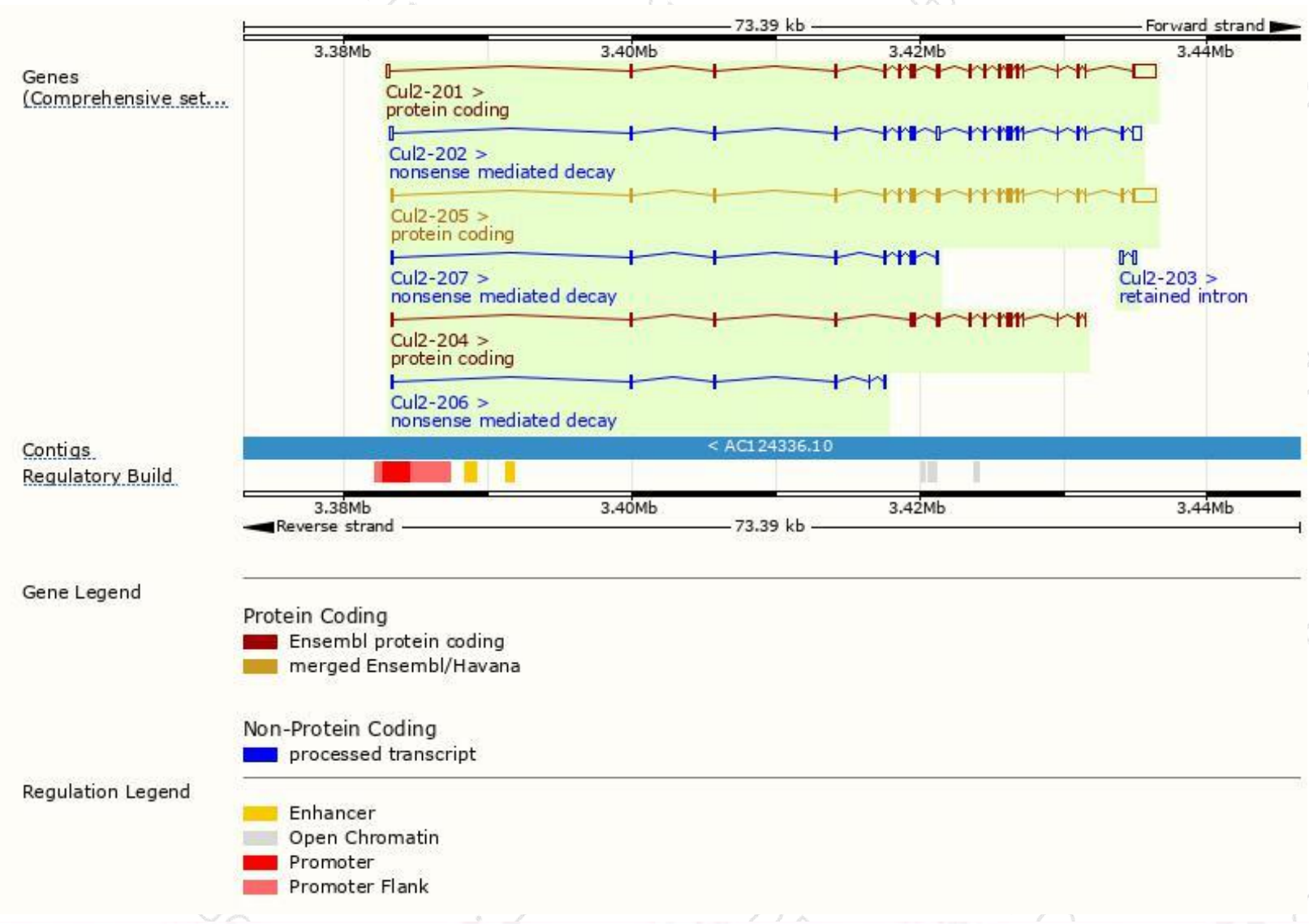
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cul2-205	ENSMUST00000162301.7	3828	745aa	Protein coding	CCDS29032	Q9D4H8	TSL:1 GENCODE basic APPRIS P1
Cul2-201	ENSMUST00000025073.11	3727	706aa	Protein coding	-	Q9D4H8	TSL:1 GENCODE basic
Cul2-204	ENSMUST00000161317.1	1909	582aa	Protein coding	-	E0CYT5	CDS 3' incomplete TSL:5
Cul2-202	ENSMUST00000080089.10	2799	90aa	Nonsense mediated decay	-	H7BX52	TSL:1
Cul2-207	ENSMUST00000234843.1	993	49aa	Nonsense mediated decay	-	-	
Cul2-206	ENSMUST00000234414.1	618	111aa	Nonsense mediated decay	-	-	
Cul2-203	ENSMUST00000159443.1	397	No protein	Retained intron	-	-	TSL:2

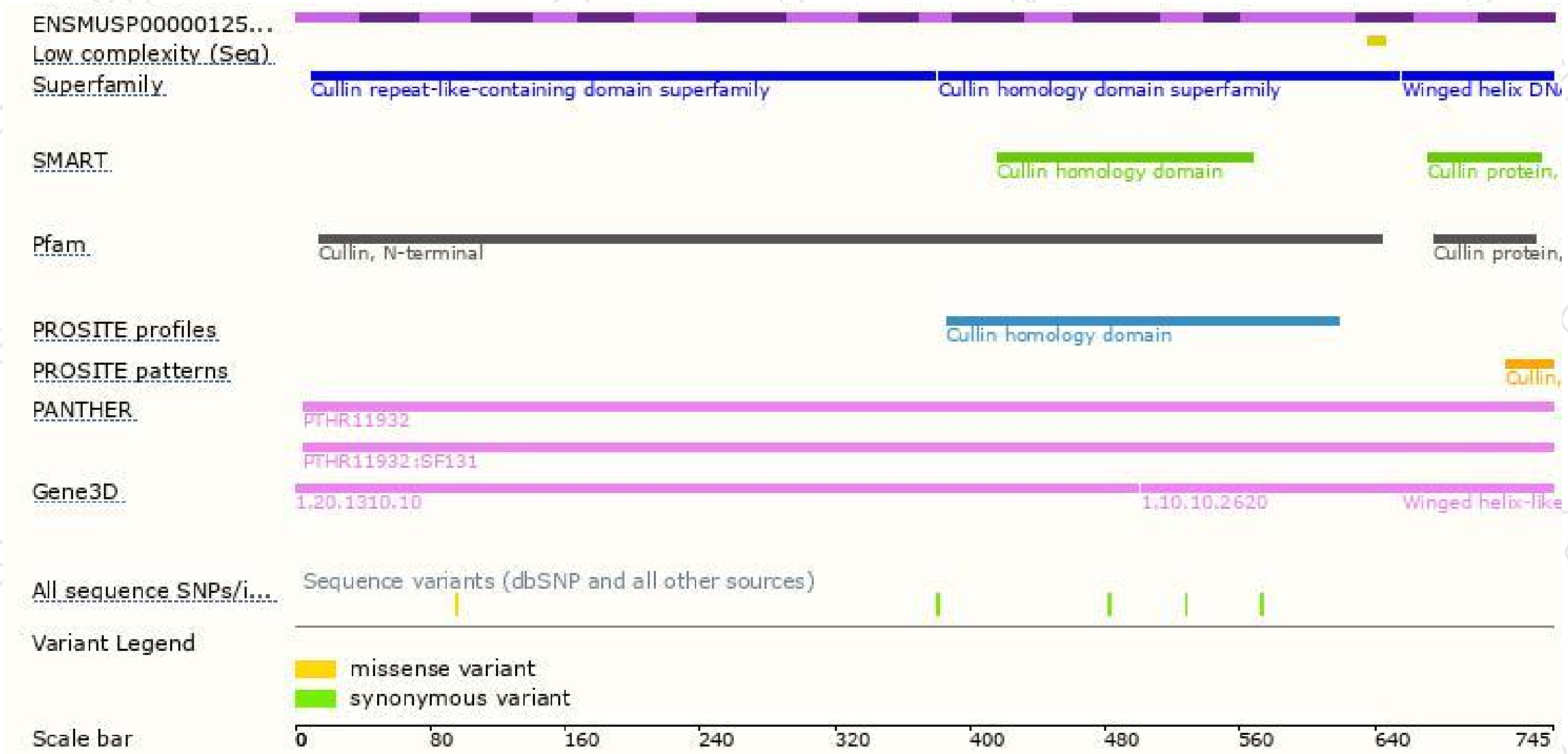
The strategy is based on the design of *Cul2-205* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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