

Cul1 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Cul1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cull1* gene. The schematic diagram is as follows:



- The *Cull* gene has 9 transcripts. According to the structure of *Cull* gene, exon2 of *Cull*-201 (ENSMUST00000031697.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cull* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygotes for targeted null mutations accumulate cyclin E1 and exhibit arrested development and lethality around embryonic day 6.5.
- The *Cull* gene is located on the Chr6. 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)

Cul1 cullin 1 [Mus musculus (house mouse)]

Gene ID: 26965, updated on 19-Feb-2019

Summary



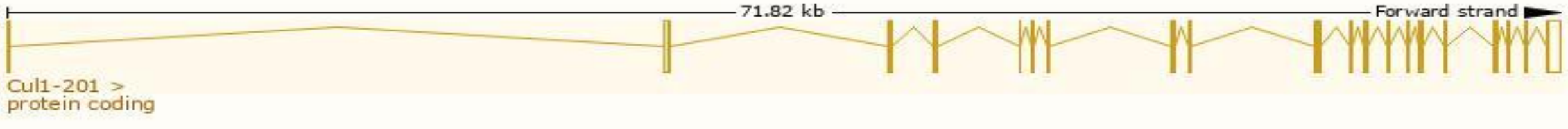
Official Symbol	Cul1 provided by MGI
Official Full Name	cullin 1 provided by MGI
Primary source	MGI:MGI:1349658
See related	Ensembl:ENSMUSG00000029686
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cul-1
Expression	Ubiquitous expression in CNS E11.5 (RPKM 25.9), bladder adult (RPKM 24.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

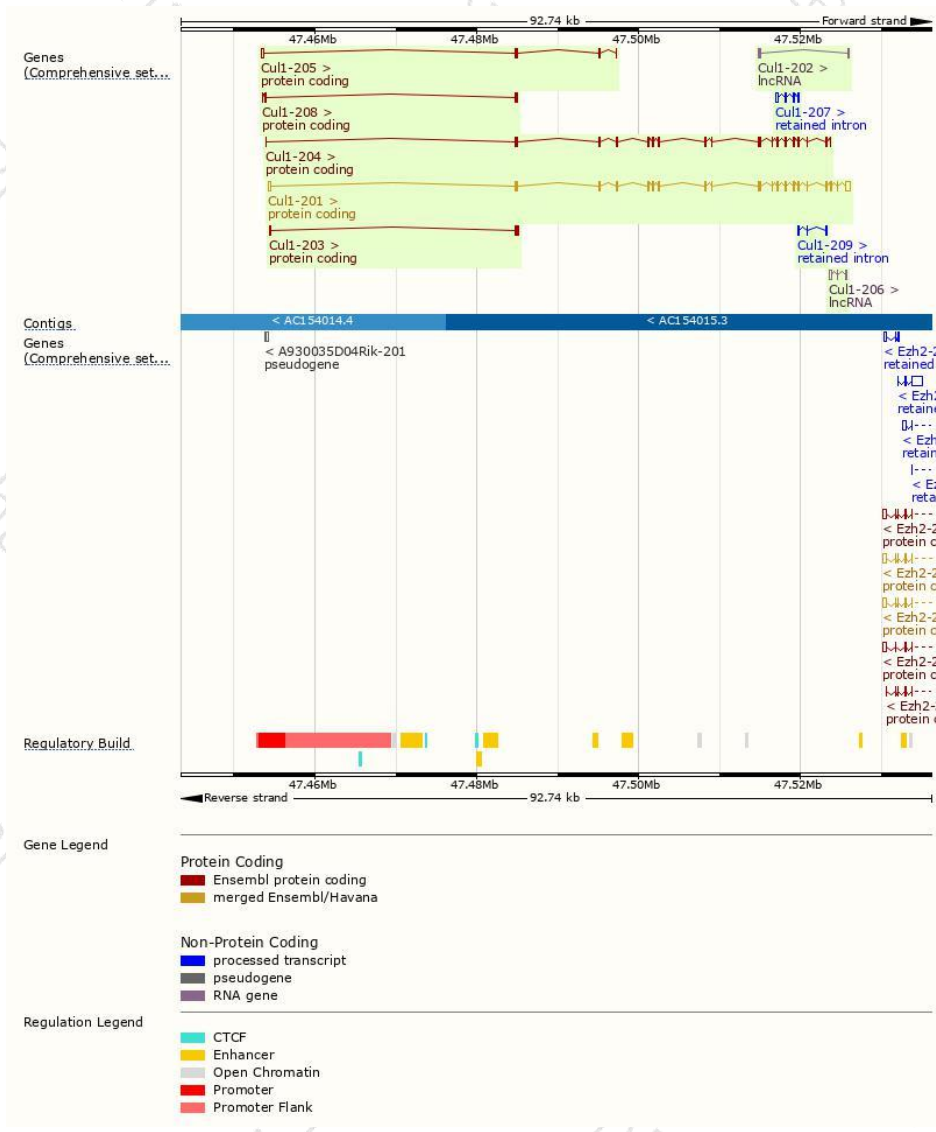
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cul1-201	ENSMUST00000031697.8	3161	776aa	Protein coding	CCDS20095	Q9WTX6	TSL:1 GENCODE basic APPRIS P1
Cul1-204	ENSMUST00000146200.7	2385	699aa	Protein coding	-	Q3TPM3	CDS 3' incomplete TSL:1
Cul1-205	ENSMUST00000146828.7	723	110aa	Protein coding	-	D3Z2H3	CDS 3' incomplete TSL:2
Cul1-203	ENSMUST00000143941.2	530	51aa	Protein coding	-	A0A0N4SUW1	TSL:1 GENCODE basic
Cul1-208	ENSMUST00000152547.5	501	20aa	Protein coding	-	D3YUS8	CDS 3' incomplete TSL:2
Cul1-207	ENSMUST00000151934.1	569	No protein	Retained intron	-	-	TSL:5
Cul1-209	ENSMUST00000154201.1	381	No protein	Retained intron	-	-	TSL:3
Cul1-206	ENSMUST00000149531.1	581	No protein	lncRNA	-	-	TSL:2
Cul1-202	ENSMUST00000126877.1	368	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Cul1-201* transcript,The transcription is shown below



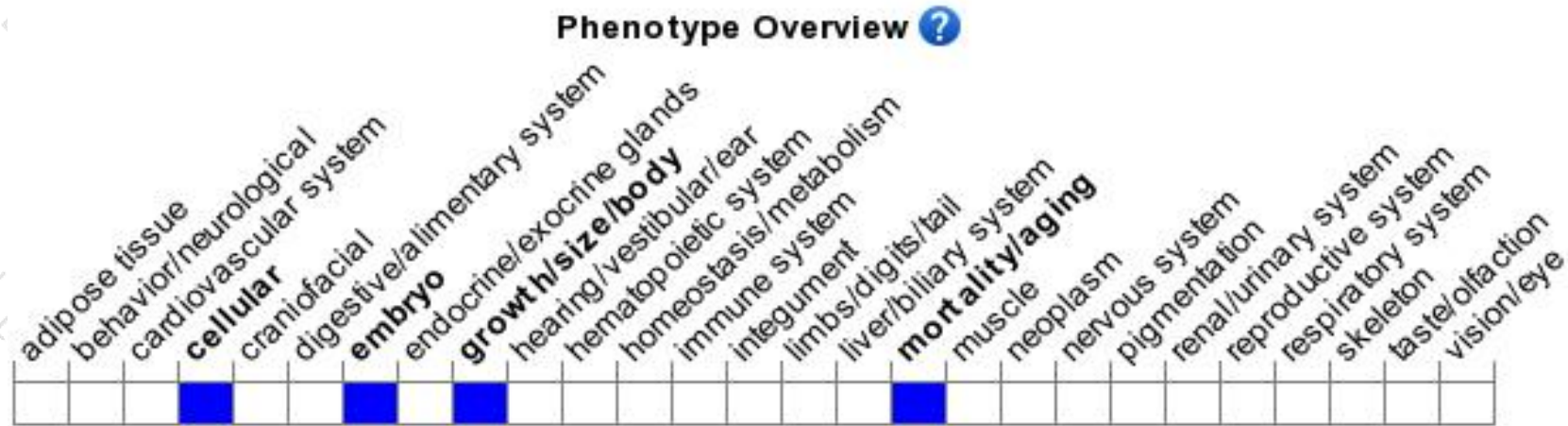
Genomic location distribution



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, Homozygotes for targeted null mutations accumulate cyclin E1 and exhibit arrested development and lethality around embryonic day 6.5.

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

Tel: 400-9660890

