Cul3 Cas9-KO Strategy

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Project Overview

Project Name	*Cul3*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cul3* gene. The schematic diagram is as follows:

Technical routes

➢ The *Cul3* gene has 6 transcripts. According to the structure of *Cul3* gene, exon2-exon6 of *Cul3-201* (ENSMUST00000163119.7) transcript is recommended as the knockout region.The region contains 817bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cul3* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

➢ According to the existing MGI data,Homozygotes for a targeted null mutation accumulate cyclin E, exhibit abnormal cycling in cells of extraembryonic ectoderm and trophectoderm, reduced size, abnormal gastrulation and trophoblast cells, absence of an amnion, and death by embryonic day 7.5.

➢ Transcript *Cul3*-204 may not be affected . And the effect on transcript *Cul3*-203&205&206 is unknown.

➢ The *Cul3* gene is located on the Chr1. 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）

Cul3 cullin 3 [Mus musculus (house mouse)]
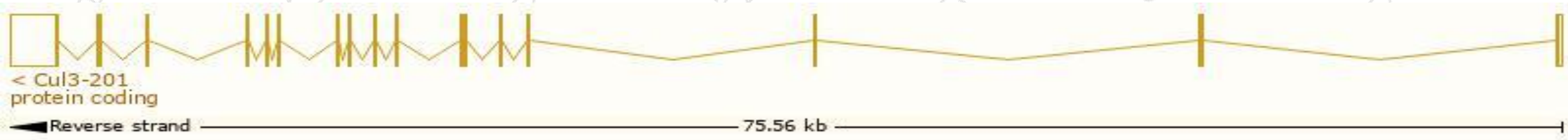
Gene ID: 26554, updated on 12-Mar-2019

▲ Summary

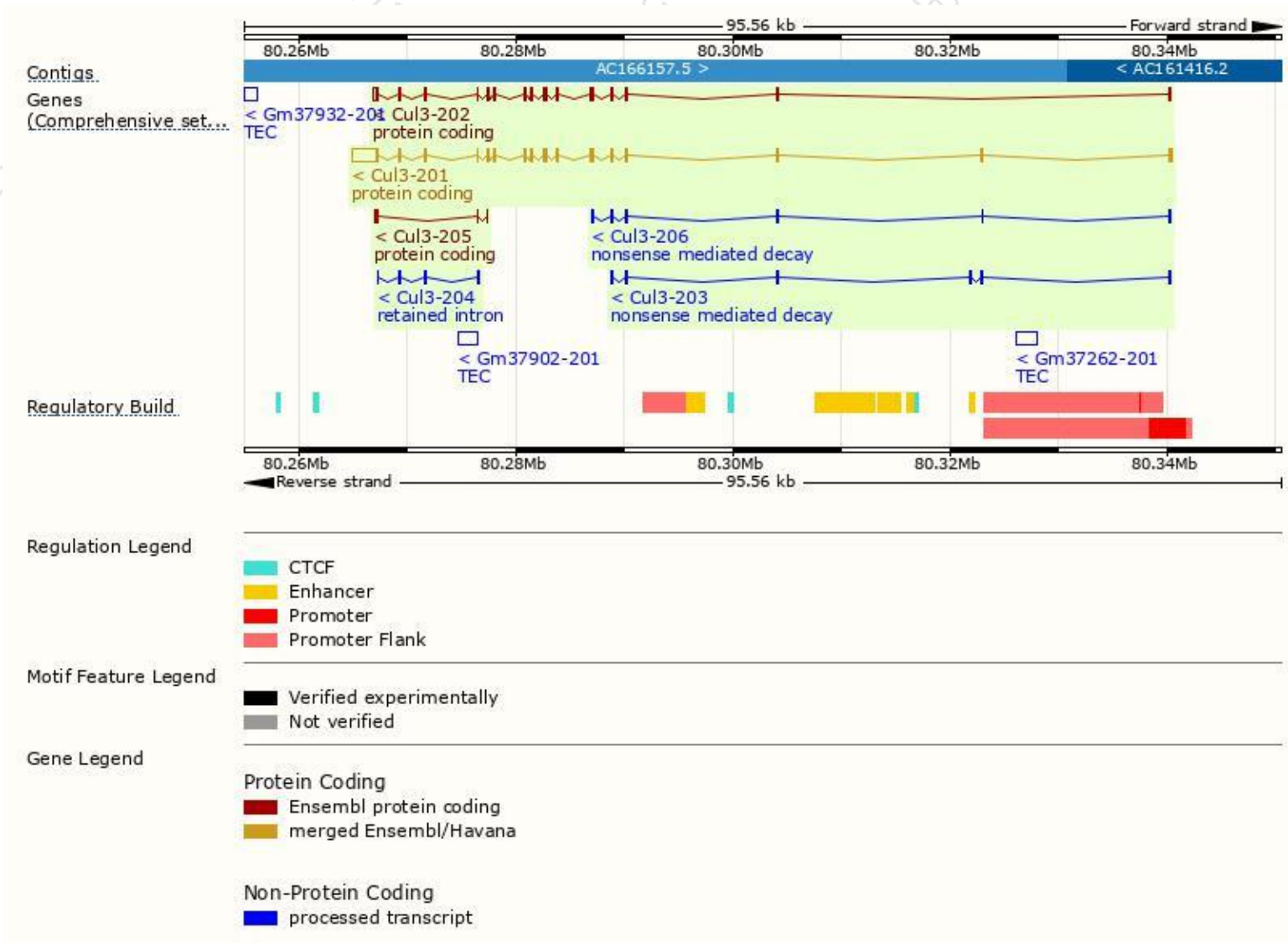|	
Official Symbol	Cul3 provided by MGI
Official Full Name	cullin 3 provided by MGI
Primary source	MGI:MGI:1347360
See related	Ensembl:ENSMUSG00000004364
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	KIAA0617
Expression	Ubiquitous expression in testis adult (RPKM 22.2), CNS E18 (RPKM 16.3) and 25 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cul3-201	ENSMUST00000163119.7	4709	768aa	Protein coding	CCDS15094	Q9JLV5	TSL:1 GENCODE basic APPRIS P1
Cul3-202	ENSMUST00000164108.7	2442	702aa	Protein coding	-	E9Q4T8	TSL:5 GENCODE basic
Cul3-205	ENSMUST00000168372.1	543	111aa	Protein coding	-	F6UY44	CDS 5' incomplete TSL:2
Cul3-203	ENSMUST00000167293.1	681	85aa	Nonsense mediated decay	-	F6ZZK0	CDS 5' incomplete TSL:5
Cul3-206	ENSMUST00000170897.7	600	54aa	Nonsense mediated decay	-	F6R0N8	CDS 5' incomplete TSL:3
Cul3-204	ENSMUST00000167794.1	532	No protein	Retained intron	-	-	TSL:2

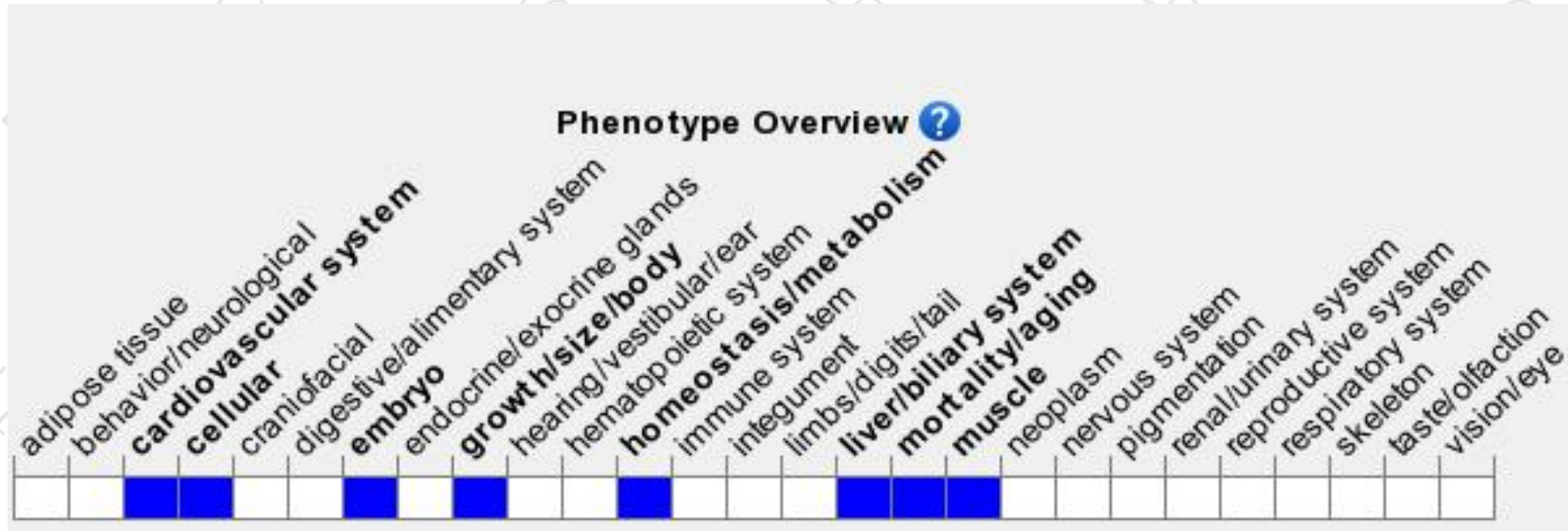The strategy is based on the design of *Cul3-201* transcript,The transcription is shown below

< Cul3-201
protein coding

◄ Reverse strand

75.56 kb

Genomic location distribution

Protein domain

ENSMUSP00000130...	
MobiDB lite	
Low complexity (Seg)	
hmmpanther	PTHR11932
	PTHR11932:SF126
Superfamily domains	Cullin homology domain superfamily — Winged helix DN
	Cullin repeat-like-containing domain superfamily
SMART domains	Cullin homology domain — Cullin protein,
Pfam domain	Cullin, N-terminal — Cullin protein
PROSITE profiles	Cullin homology domain
PROSITE patterns	Cullin,
Gene3D	1.20.1310.10 — 1.10.10.2620 — Winged helix-like

All sequence SNPs/i... — Sequence variants (dbSNP and all other sources)

Variant Legend

- missense variant
- synonymous variant

Scale bar: 0 80 160 240 320 400 480 560 640 768

Mouse phenotype description(MGI)

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

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