Cul7 Cas9-KO *Strategy*

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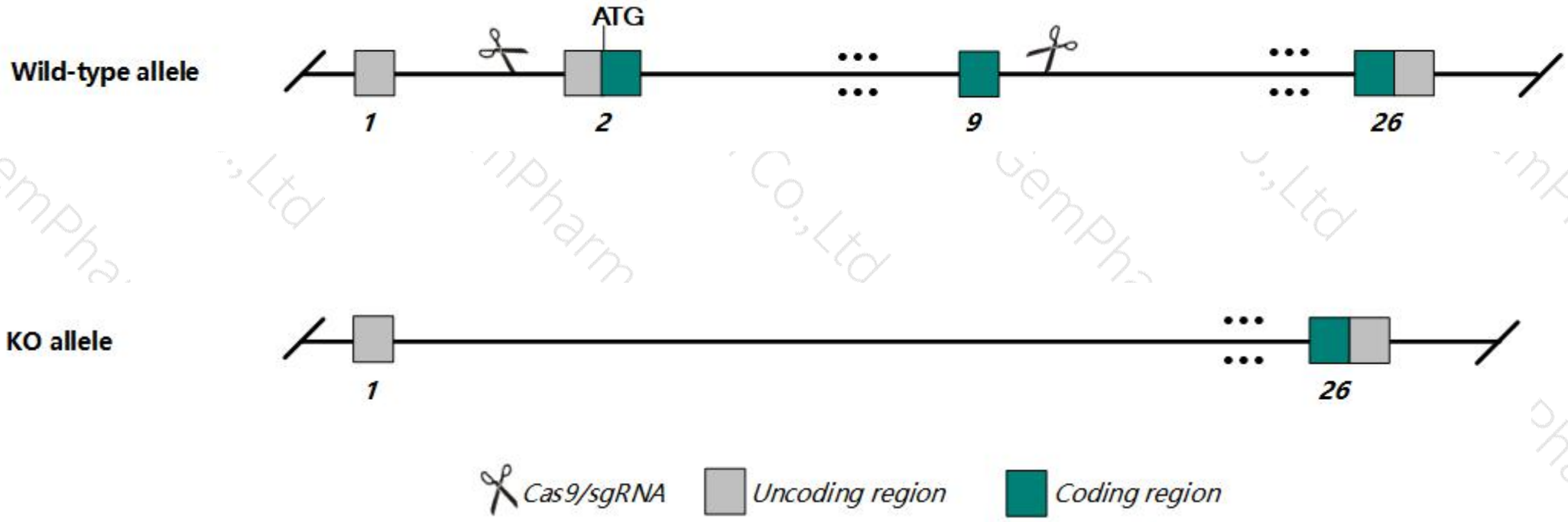
Project Overview

Project Name	***Cul7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cul7* gene. The schematic diagram is as follows:



Technical routes

- The *Cul7* gene has 7 transcripts.According to the structure of *Cul7* gene, exon2-9 of *Cul7*-201 (ENSMUST00000043464.13) 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 *Cul7* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9, gRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

- According to the existing MGI data，during late gestation, homozygous null fetuses display reduced growth associated with abnormal placental development and hemorrhaging due to vascular defects. Mutant mice are born but die shortly after birth, succumbing to respiratory distress.
- The *Cul7* gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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Cul7 cullin 7 [*Mus musculus* (house mouse)]

Gene ID: 66515, updated on 13-Mar-2020

Summary

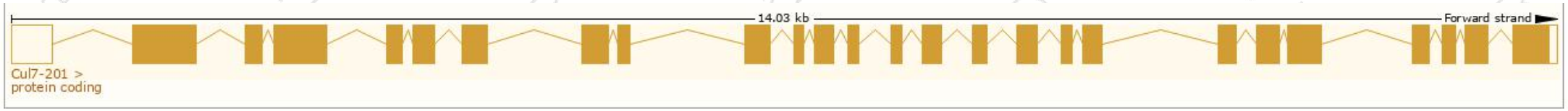
Official Symbol	Cul7 provided by MGI
Official Full Name	cullin 7 provided by MGI
Primary source	MGI:MGI:1913765
See related	Ensembl:ENSMUSG00000038545
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	p185; p193; AA409809; 2510004L20Rik; C230011P08Rik
Expression	Ubiquitous expression in limb E14.5 (RPKM 31.4), placenta adult (RPKM 28.7) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cul7-201	ENSMUST00000043464.13	5530	1689aa	Protein coding	CCDS28833	A9C491 Q8VE73	TSL:1 GENCODE basic APPRIS P1
Cul7-206	ENSMUST00000145567.7	5016	649aa	Nonsense mediated decay	-	E9Q6H4	TSL:1
Cul7-204	ENSMUST00000133393.7	4047	577aa	Nonsense mediated decay	-	F6Q1R4	CDS 5' incomplete TSL:5
Cul7-205	ENSMUST00000144966.1	628	No protein	Processed transcript	-	-	TSL:5
Cul7-203	ENSMUST00000132790.1	3056	No protein	Retained intron	-	-	TSL:1
Cul7-207	ENSMUST00000151002.7	3010	No protein	Retained intron	-	-	TSL:1
Cul7-202	ENSMUST00000125949.1	1321	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Cul7*-201 transcript, the transcription is shown below



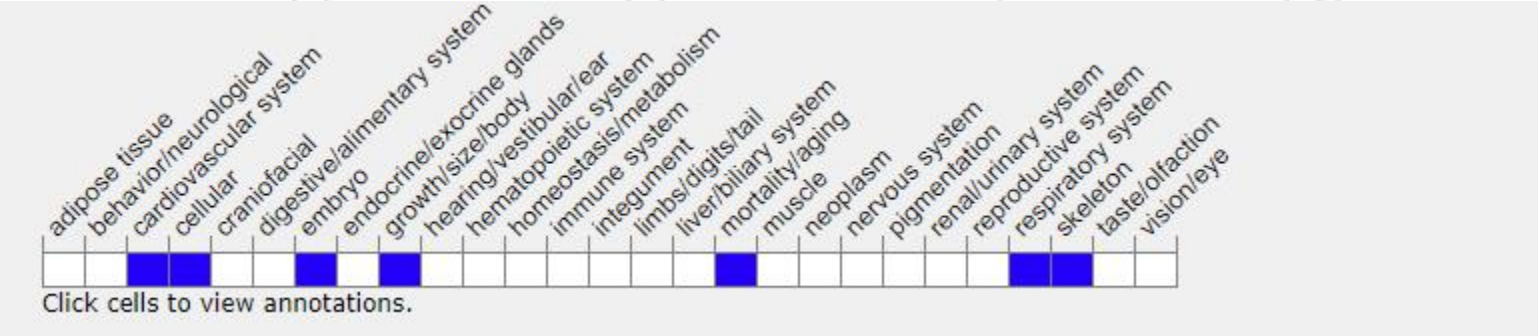
Genomic location distribution

Protein domain

Statistics

Ave. residue weight: 113.850 g/mol
Charge: -8.5
Isoelectric point: 6.2429
Molecular weight: 192,292.17 g/mol
Number of residues: 1,689 aa

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