

***Cul9* Cas9-CKO Strategy**

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Project Overview

Project Name

Cul9

Project type

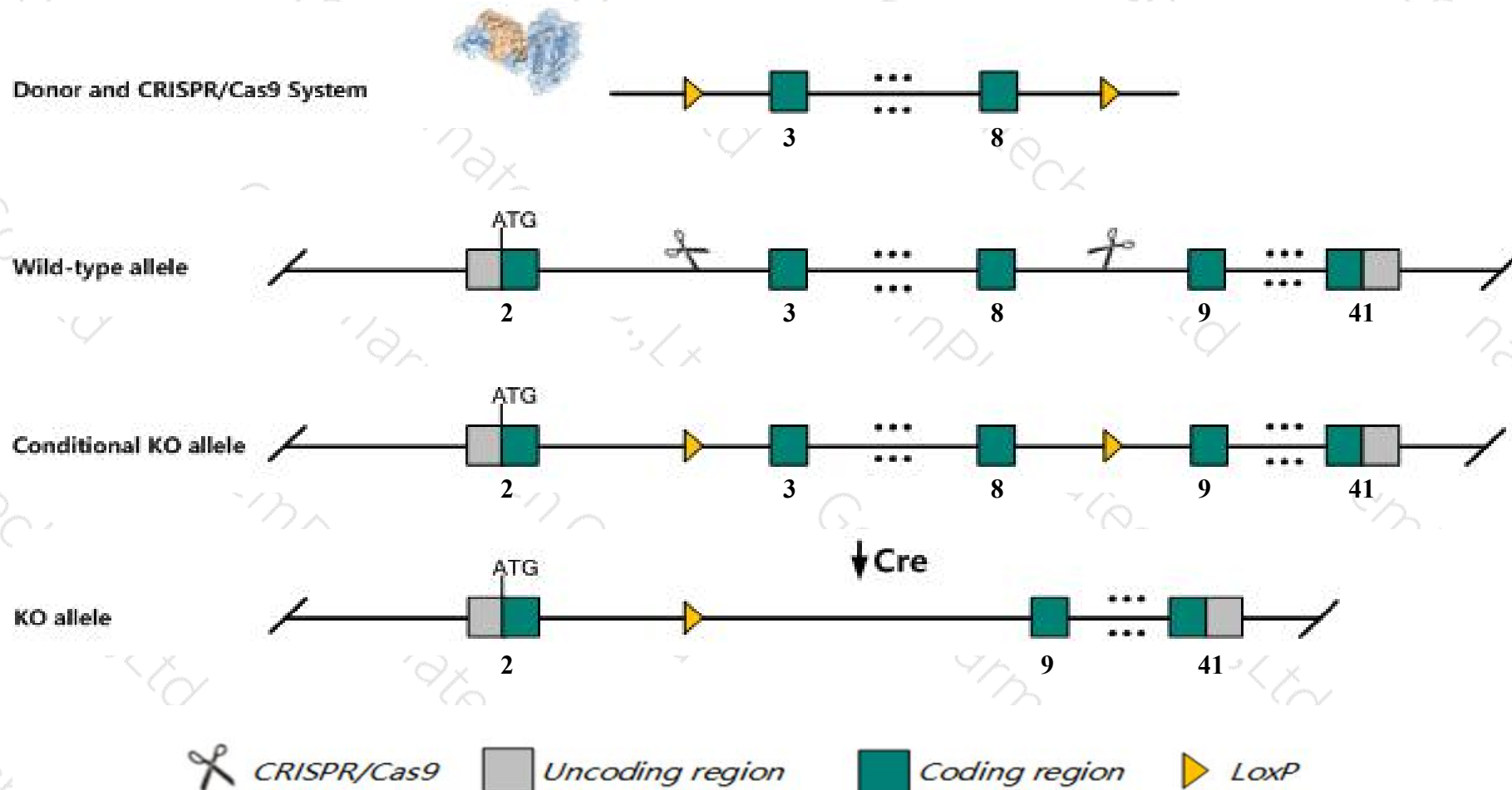
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cul9* gene. The schematic diagram is as follows:



Technical routes

- The *Cul9* gene has 11 transcripts. According to the structure of *Cul9* gene, exon3-exon8 of *Cul9-204* (ENSMUST00000182485.7) transcript is recommended as the knockout region. The region contains 1591bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cul9* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased body weight, increased incidence of tumors, and decreased cellular sensitivity to radiation-induced apoptosis.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The transcripts 205, 206, 207, 208, 209, 211 are unaffected.
- The flox region coincides with Gm26904-201 and the effect on this gene is unknown.
- The *Cul9* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Cul9 cullin 9 [*Mus musculus* (house mouse)]

Gene ID: 78309, updated on 13-Aug-2019

Summary

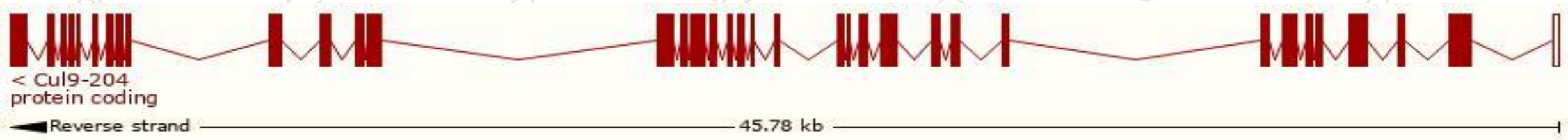
Official Symbol	Cul9 provided by MGI
Official Full Name	cullin 9 provided by MGI
Primary source	MGI:MGI:1925559
See related	Ensembl: ENSMUSG00000040327
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Parc; Cul-9; mKIAA0708; 1810035I07Rik
Expression	Ubiquitous expression in ovary adult (RPKM 12.3), adrenal adult (RPKM 12.3) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

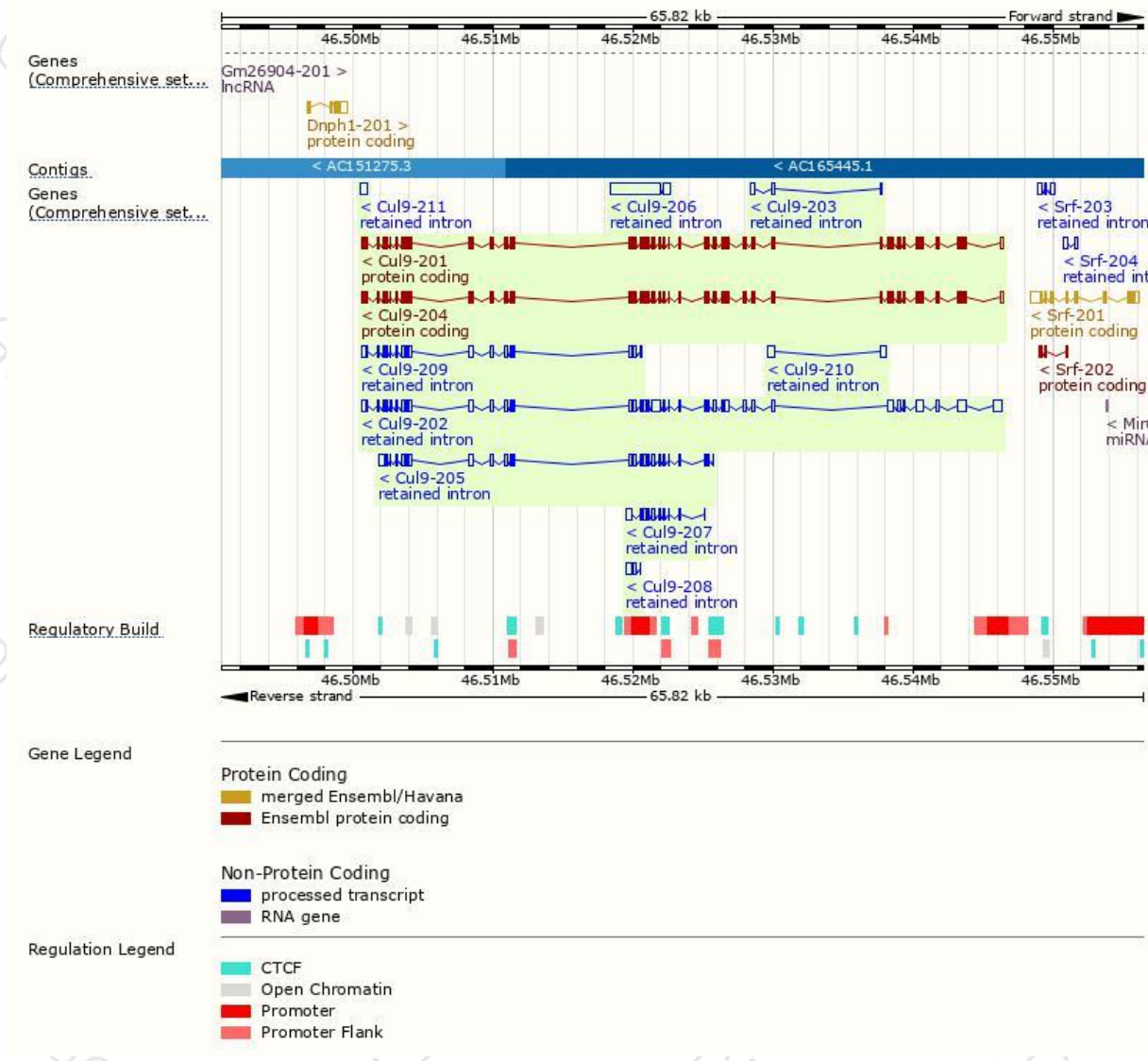
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cul9-204	ENSMUST00000182485.7	7848	2530aa	Protein coding	CCDS37636	S4R1Y1	TSL:5 GENCODE basic APPRIS P2
Cul9-201	ENSMUST00000066026.7	7818	2520aa	Protein coding	-	E9QP09	TSL:5 GENCODE basic APPRIS ALT 2
Cul9-202	ENSMUST00000182315.7	8451	No protein	Retained intron	-	-	TSL:2
Cul9-205	ENSMUST00000182530.7	4151	No protein	Retained intron	-	-	TSL:5
Cul9-206	ENSMUST00000182668.1	4109	No protein	Retained intron	-	-	TSL:2
Cul9-209	ENSMUST00000183078.7	3070	No protein	Retained intron	-	-	TSL:1
Cul9-207	ENSMUST00000182799.1	1673	No protein	Retained intron	-	-	TSL:1
Cul9-210	ENSMUST00000183163.1	1017	No protein	Retained intron	-	-	TSL:3
Cul9-208	ENSMUST00000183016.7	791	No protein	Retained intron	-	-	TSL:2
Cul9-203	ENSMUST00000182451.1	700	No protein	Retained intron	-	-	TSL:2
Cul9-211	ENSMUST00000183312.1	500	No protein	Retained intron	-	-	TSL:NA

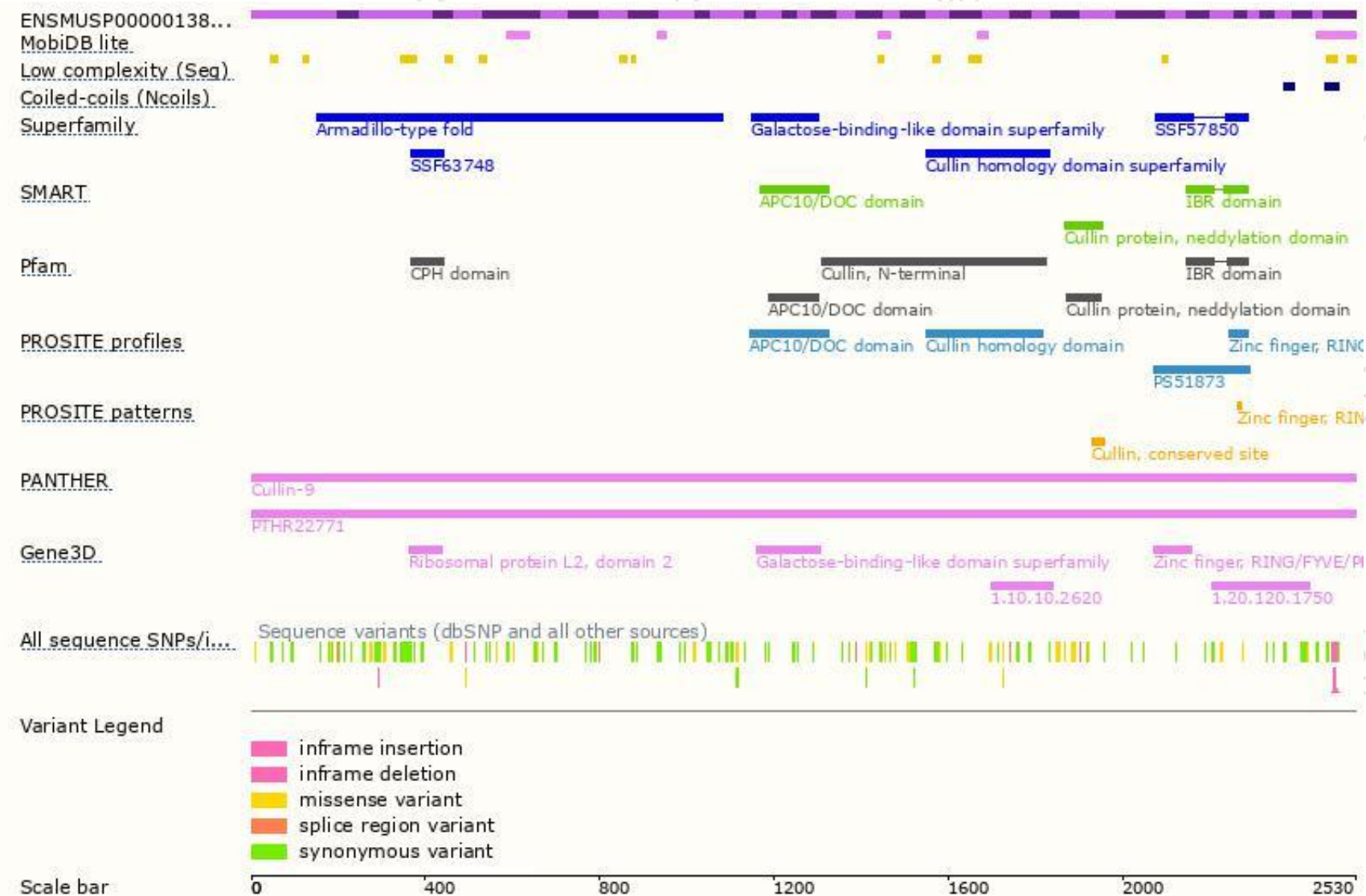
The strategy is based on the design of *Cul9-204* transcript,The transcription is shown below



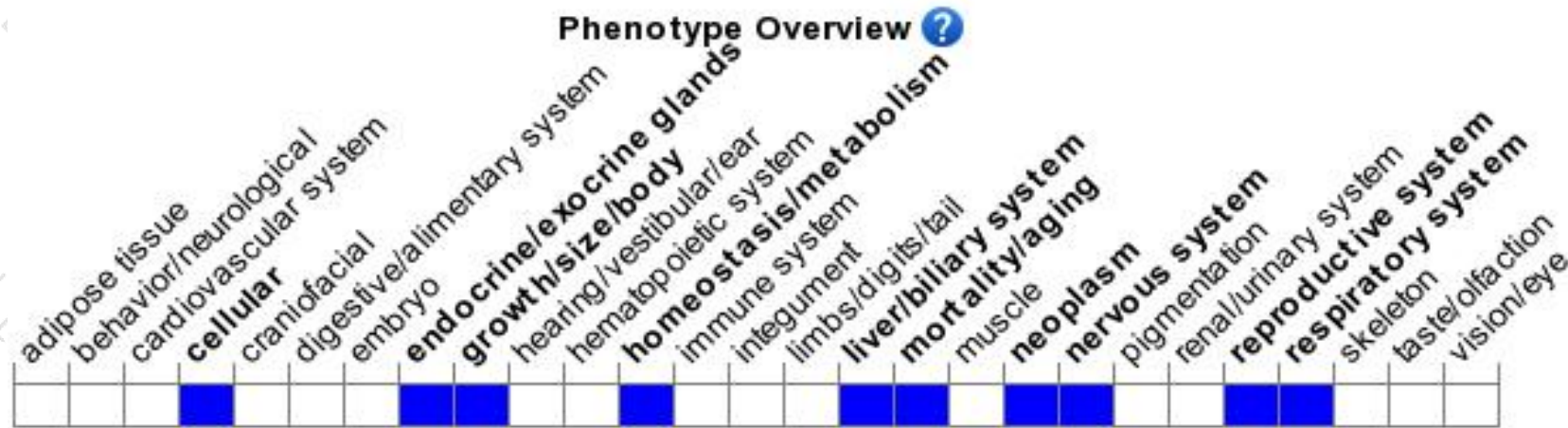
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit decreased body weight, increased incidence of tumors, and decreased cellular sensitivity to radiation-induced apoptosis.

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

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