

Uqcrfs1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Uqcrfs1

Project type

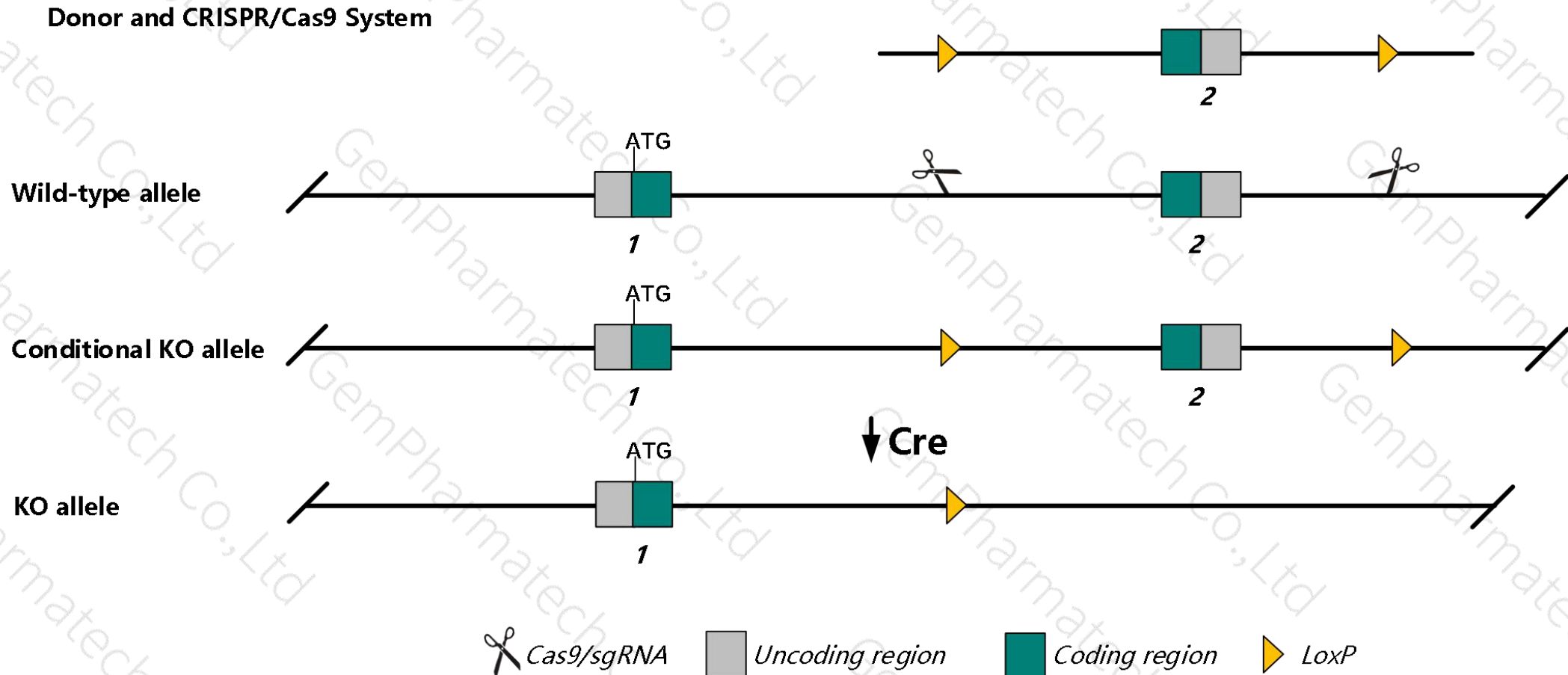
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Uqcrfs1* gene. The schematic diagram is as follows:



- The *Uqcrfs1* gene has 1 transcript. According to the structure of *Uqcrfs1* gene, exon2 of *Uqcrfs1-201* (ENSMUST00000042834.3) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Uqcrfs1* 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, mutant mice harboring a 3' UTR insertion that reduces expression specifically in skin acquire dark patches in the dorsal brown coat at 4-7 months of age. In heterozygotes, the dark patches eventually fill the entire dorsal region; in homozygotes, the dark patches eventually turn grey.
- The N-terminal of *Uqcrfs1* gene will remain some amino acid, it may remain the partial function of *Uqcrfs1* gene.
- The *Uqcrfs1* gene is located on the Chr13. 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)

Uqcrrs1 ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [*Mus musculus* (house mouse)]

Gene ID: 66694, updated on 10-Oct-2019

Summary

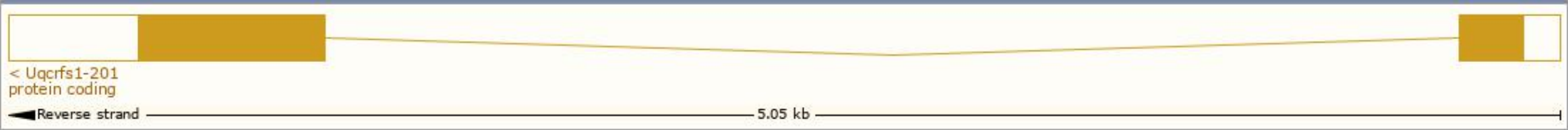
Official Symbol	Uqcrrs1 provided by MGI
Official Full Name	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 provided by MGI
Primary source	MGI:MGI:1913944
See related	Ensembl:ENSMUSG00000038462
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI875505; 4430402G14Rik
Expression	Ubiquitous expression in adrenal adult (RPKM 429.8), duodenum adult (RPKM 371.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

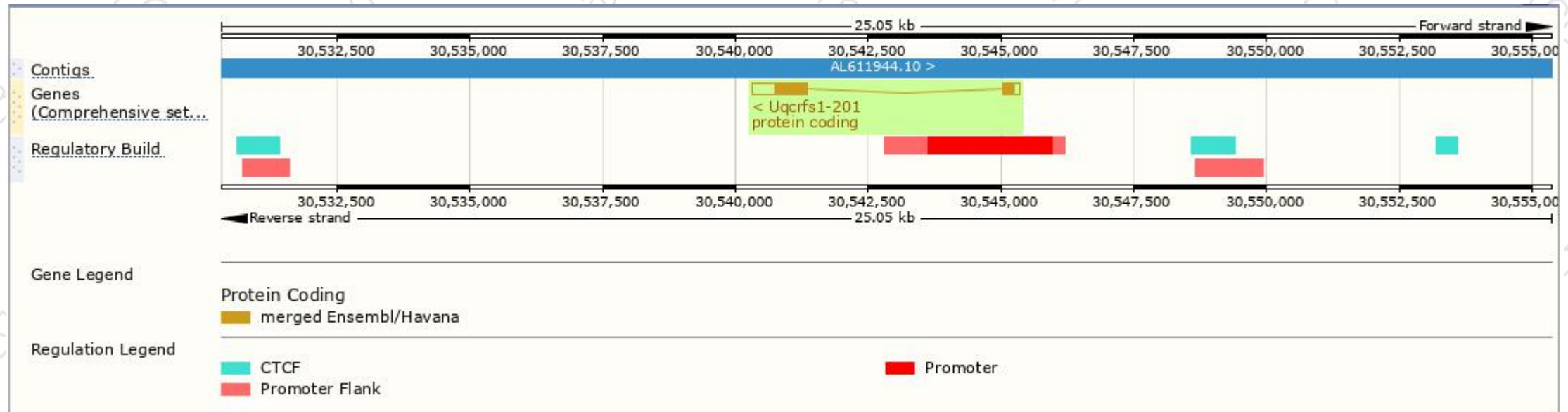
The gene has 1 transcript,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Uqcrfs1-201	ENSMUST00000042834.3	1363	274aa	Protein coding	CCDS26416	Q9CR68	TSL:1 Gencode basic APPRIS P1

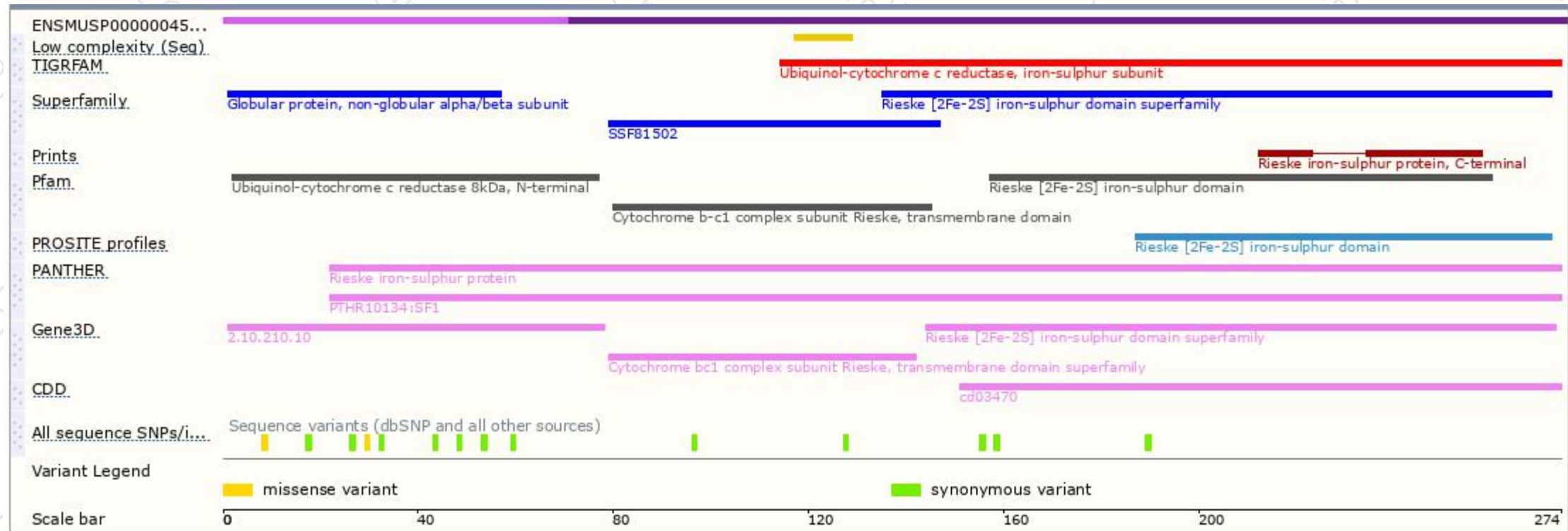
The strategy is based on the design of *Uqcrfs1-201* transcript,The transcription is shown below



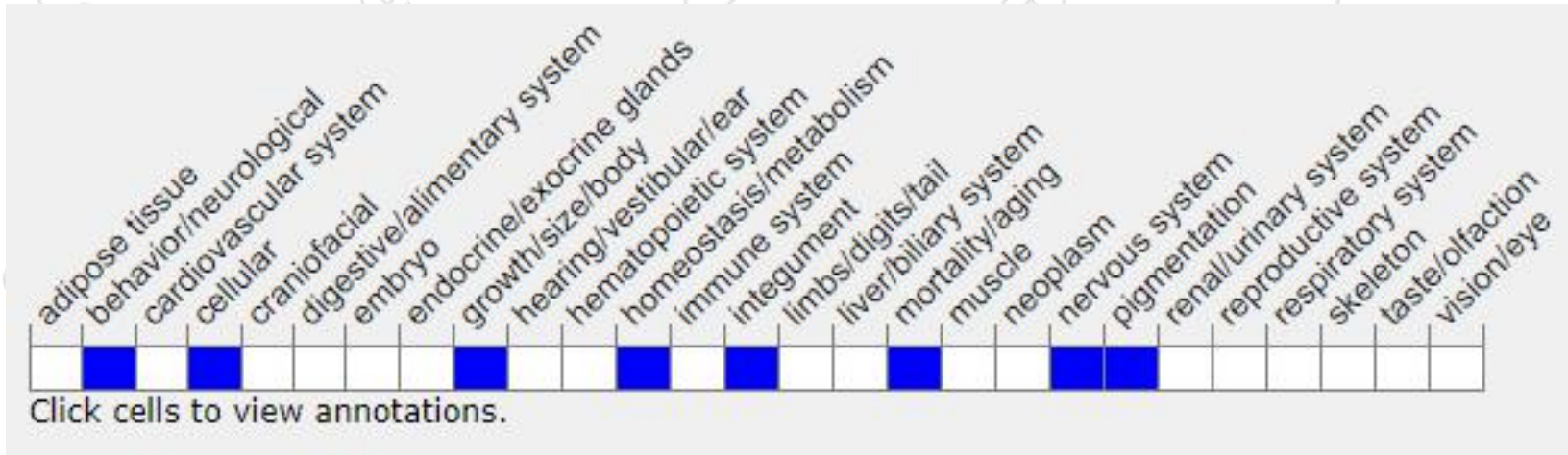
Genomic location distribution



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, mutant mice harboring a 3' UTR insertion that reduces expression specifically in skin acquire dark patches in the dorsal brown coat at 4-7 months of age. In heterozygotes, the dark patches eventually fill the entire dorsal region; in homozygotes, the dark patches eventually turn grey.

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

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