

Uckl1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Uckl1

Project type

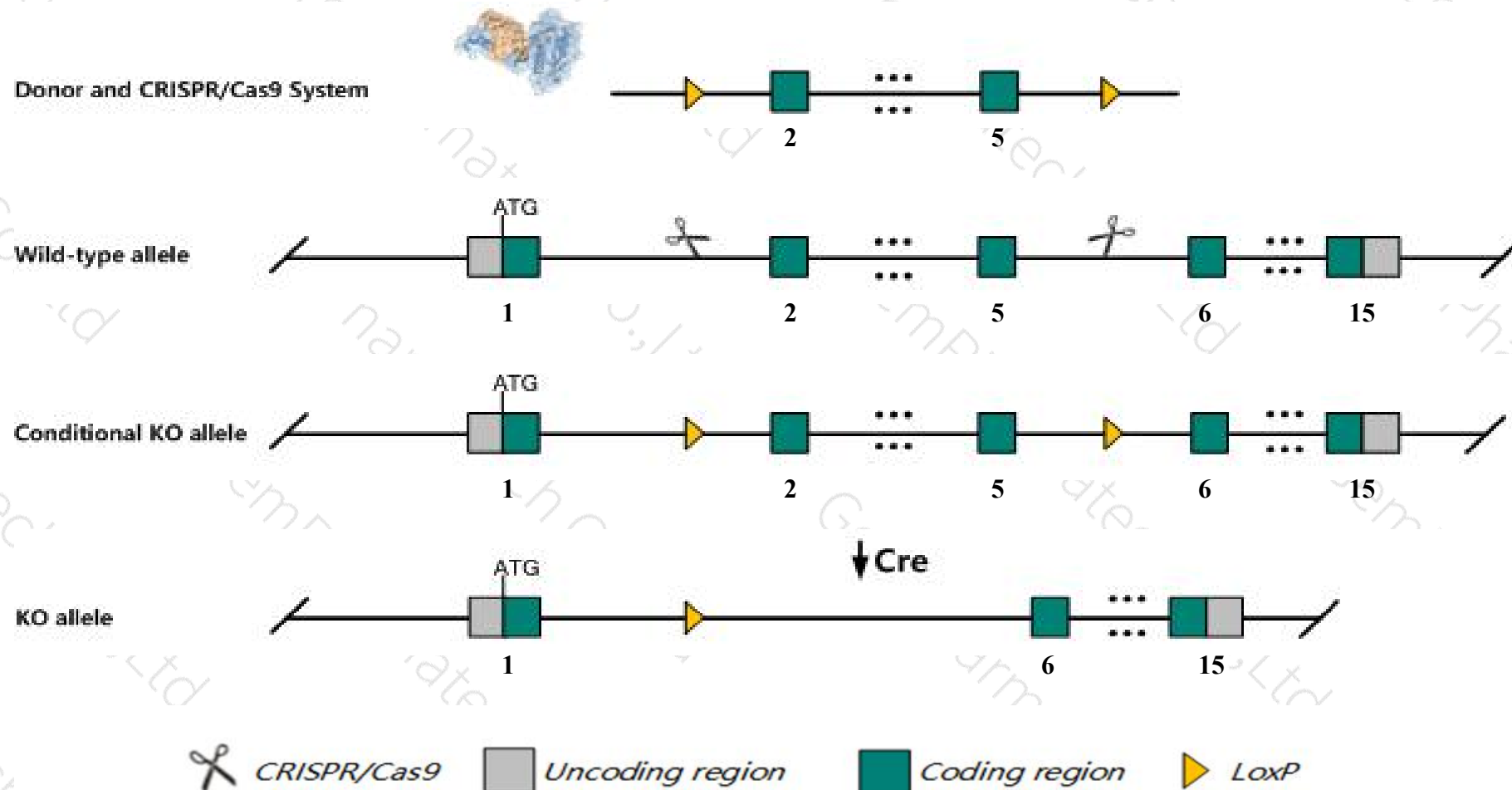
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Uck1l* gene. The schematic diagram is as follows:



Technical routes

- The *Uckl1* gene has 18 transcripts. According to the structure of *Uckl1* gene, exon2-exon5 of *Uckl1*-201 (ENSMUST00000057816.14) transcript is recommended as the knockout region. The region contains 541bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Uckl1* 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.

Notice

- The *Uckl1* gene is located on the Chr2. 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.
- Transcript *Uckl1-206* may not be affected.

Gene information (NCBI)

Uckl1 uridine-cytidine kinase 1-like 1 [Mus musculus (house mouse)]

Gene ID: 68556, updated on 2-Apr-2019

Summary



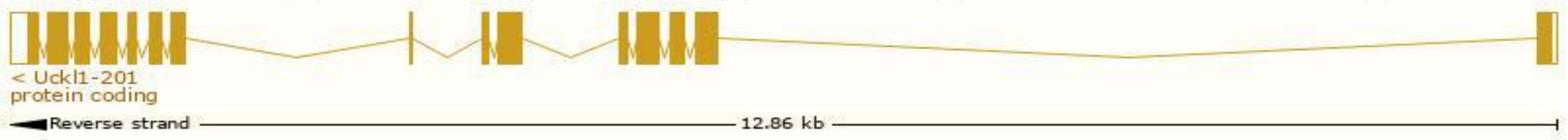
| | |
|---------------------------|---|
| Official Symbol | Uckl1 provided by MGI |
| Official Full Name | uridine-cytidine kinase 1-like 1 provided by MGI |
| Primary source | MGI:MGI:1915806 |
| See related | Ensembl:ENSMUSG00000089917 |
| Gene type | protein coding |
| RefSeq status | PROVISIONAL |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 1110007H10Rik, Urkl1 |
| Expression | Ubiquitous expression in colon adult (RPKM 15.0), thymus adult (RPKM 14.7) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

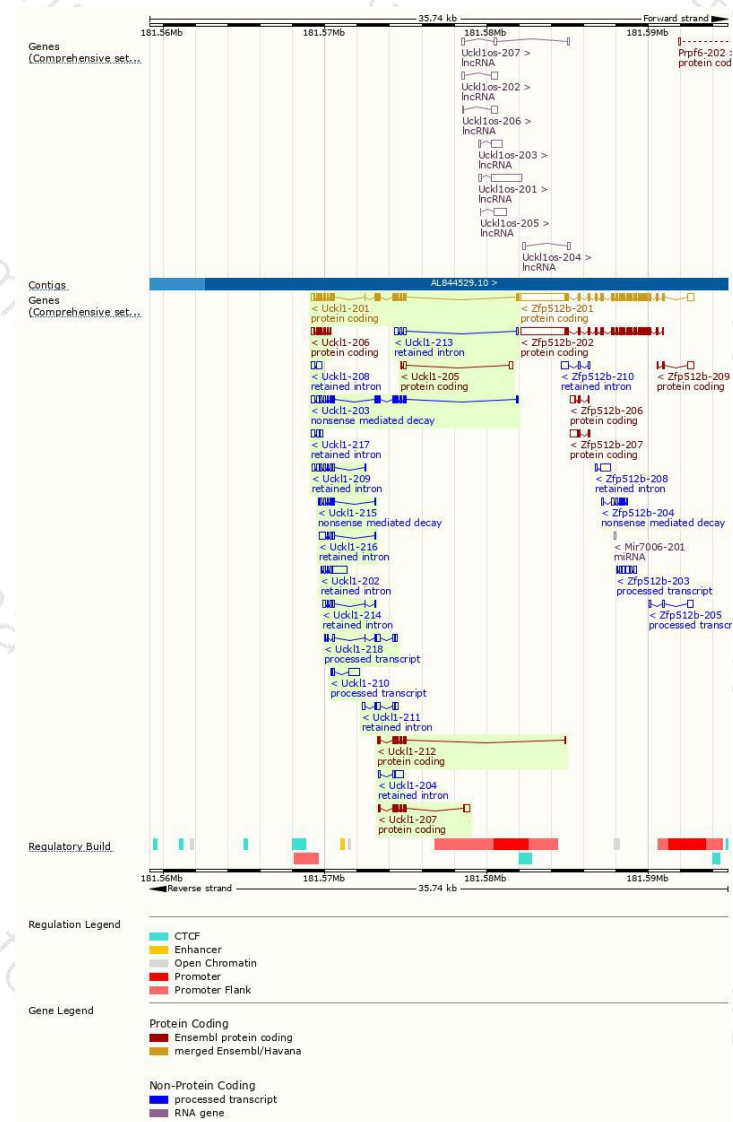
The gene has 18 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|---|
| Uckl1-201 | ENSMUST0000057816.14 | 1849 | 548aa | Protein coding | CCDS17216 | Q91YL3 | TSL:1 GENCODE basic APPRIS P1 |
| Uckl1-207 | ENSMUST00000136875.1 | 1043 | 235aa | Protein coding | - | B7ZCR1 | CDS 3' incomplete TSL:5 |
| Uckl1-212 | ENSMUST00000144856.7 | 760 | 253aa | Protein coding | - | F6V4H6 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3 |
| Uckl1-206 | ENSMUST00000134340.7 | 757 | 198aa | Protein coding | - | F7CAK3 | CDS 5' incomplete TSL:5 |
| Uckl1-205 | ENSMUST00000131949.1 | 507 | 16aa | Protein coding | - | B7ZCR0 | CDS 3' incomplete TSL:3 |
| Uckl1-203 | ENSMUST00000129469.7 | 1782 | 339aa | Nonsense mediated decay | - | D6RJ84 | TSL:5 |
| Uckl1-215 | ENSMUST00000154613.7 | 537 | 55aa | Nonsense mediated decay | - | F6W7K4 | CDS 5' incomplete TSL:3 |
| Uckl1-202 | ENSMUST00000124315.7 | 1196 | No protein | Retained intron | - | - | TSL:2 |
| Uckl1-209 | ENSMUST00000138408.7 | 877 | No protein | Retained intron | - | - | TSL:3 |
| Uckl1-216 | ENSMUST00000155182.7 | 689 | No protein | Retained intron | - | - | TSL:3 |
| Uckl1-213 | ENSMUST00000146823.7 | 676 | No protein | Retained intron | - | - | TSL:1 |
| Uckl1-204 | ENSMUST00000130893.1 | 645 | No protein | Retained intron | - | - | TSL:3 |
| Uckl1-211 | ENSMUST00000142491.7 | 618 | No protein | Retained intron | - | - | TSL:3 |
| Uckl1-208 | ENSMUST00000136997.1 | 569 | No protein | Retained intron | - | - | TSL:2 |
| Uckl1-217 | ENSMUST00000156308.7 | 569 | No protein | Retained intron | - | - | TSL:2 |
| Uckl1-214 | ENSMUST00000149332.7 | 518 | No protein | Retained intron | - | - | TSL:3 |
| Uckl1-210 | ENSMUST00000142296.1 | 797 | No protein | lncRNA | - | - | TSL:5 |
| Uckl1-218 | ENSMUST00000156998.7 | 637 | No protein | lncRNA | - | - | TSL:5 |

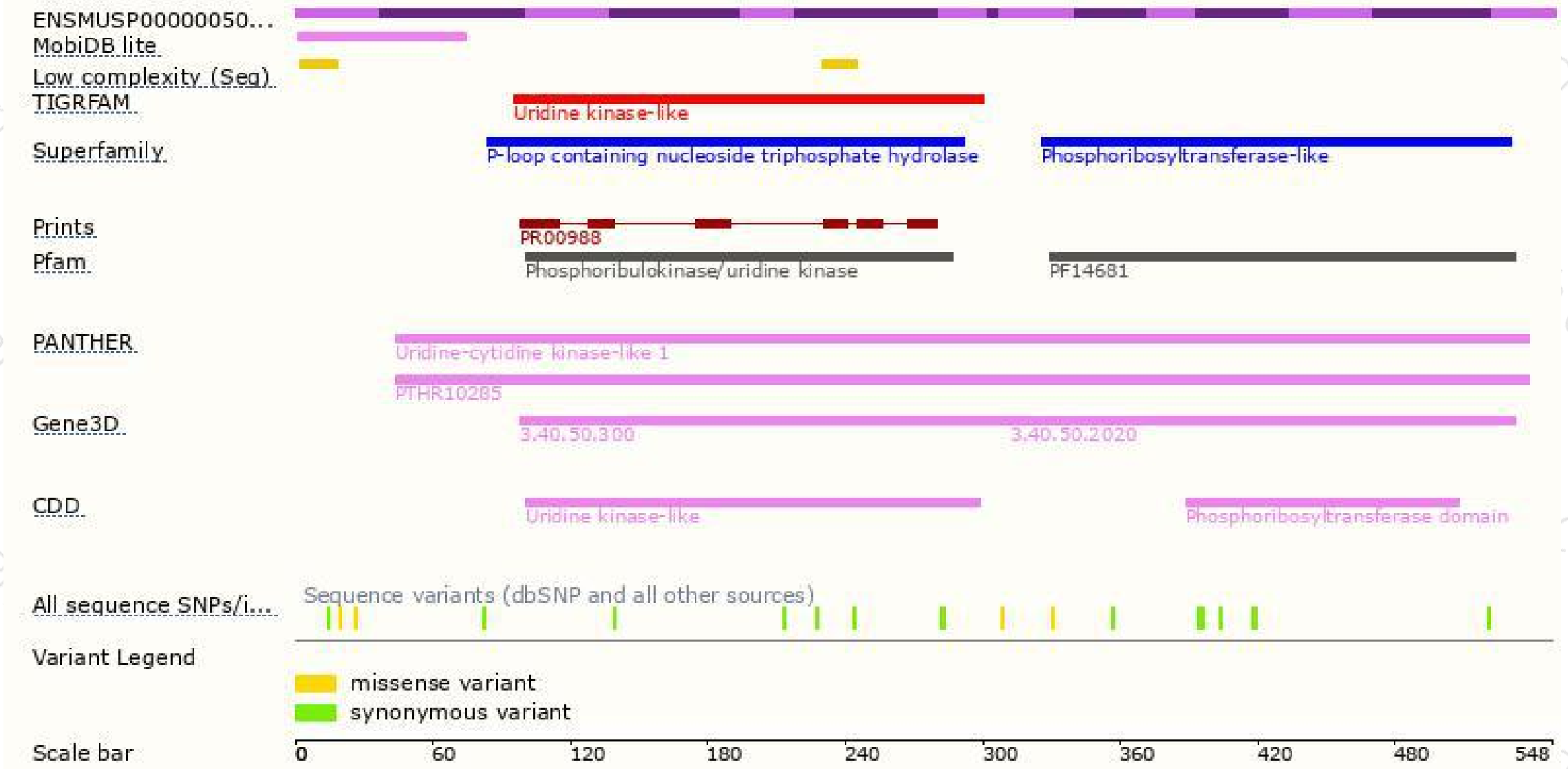
The strategy is based on the design of *Uckl1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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