Ube3c Cas9-CKO Strategy

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Overview

Target Gene Name

- Ube3c
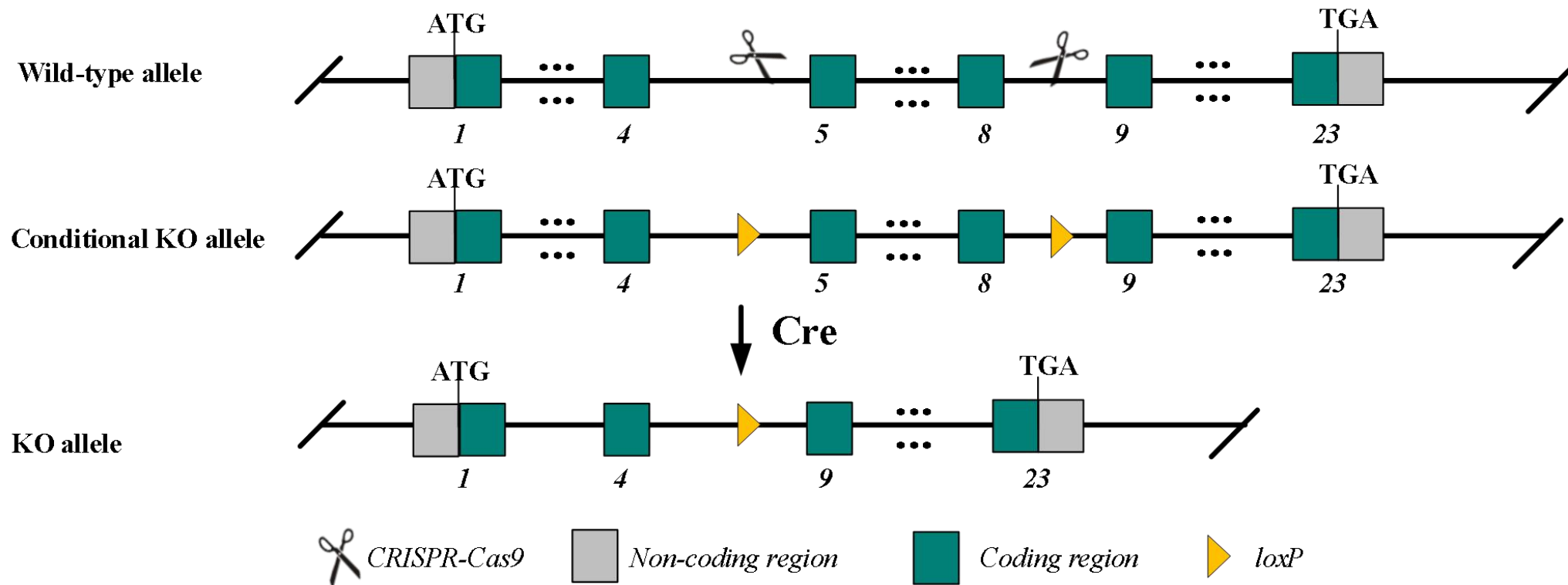
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

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Strain Strategy

Schematic representation of CRISPR-Cas9 engineering used to edit the *Ube3c* gene.

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Technical Information

- The *Ube3c* gene has 5 transcripts. According to the structure of *Ube3c* gene, exon 5-exon 8 of *Ube3c*-201 (ENSMUST00000049453.9) transcript is recommended as the knockout region. The region contains 649 bp coding sequence. Knocking out the region will result in disruption of protein function.

- In this project we use CRISPR-Cas9 technology to modify *Ube3c* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

- 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.

Gene Information

Ube3c   ubiquitin protein ligase E3C [*Mus musculus* (house mouse)]

⬇ Download Datasets

Gene ID: 100763, updated on 7-Sep-2023

🔺 **Summary**

Official Symbol	Ube3c provided by MGI
Official Full Name	ubiquitin protein ligase E3C provided by MGI
Primary source	MGI:MGI:2140998
See related	Ensembl:ENSMUSG00000039000 AllianceGenome:MGI:2140998
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	RAUL; mKIAA0010
Summary	Predicted to enable ubiquitin protein ligase activity. Predicted to be involved in protein polyubiquitination and ubiquitin-dependent protein catabolic process. Predicted to be located in nucleus. Is expressed in several structures, including alimentary system; genitourinary system; integumental system; nervous system; and sensory organ. Orthologous to human UBE3C (ubiquitin protein ligase E3C). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in CNS E18 (RPKM 14.0), testis adult (RPKM 12.7) and 28 other tissues See more
Orthologs	human all
NEW	**Try the new** Gene table **Try the new** Transcript table

Source: https://www.ncbi.nlm.nih.gov/

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Transcript Information

The gene has 5 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein ▼	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000049453.9	Ube3c-201	5048	1083aa	Protein coding	CCDS39042 ☒	Q80U95 ☒	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000199032.2	Ube3c-204	3171	644aa	Protein coding		A0A0G2JDR9 ☒	GENCODE basic TSL:1
ENSMUST00000197953.2	Ube3c-203	670	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000197193.2	Ube3c-202	3490	No protein	Retained intron		-	TSL:1
ENSMUST00000199598.2	Ube3c-205	1572	No protein	Retained intron		-	TSL:NA

The strategy is based on the design of *Ube3c*-201 transcript, the transcription is shown below:
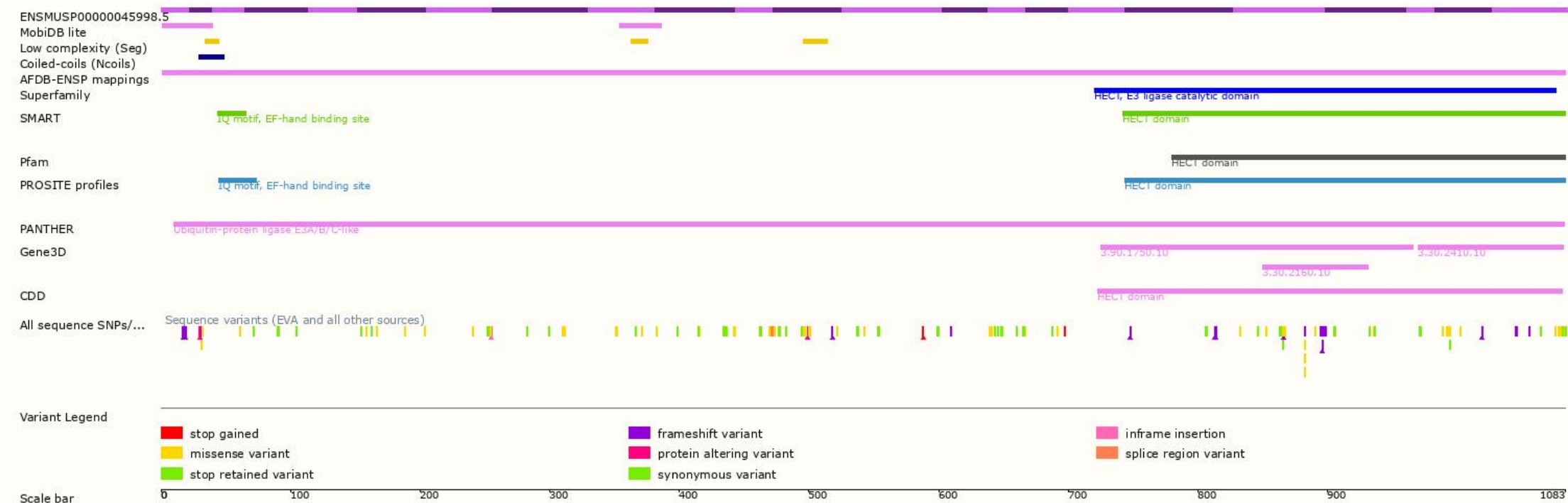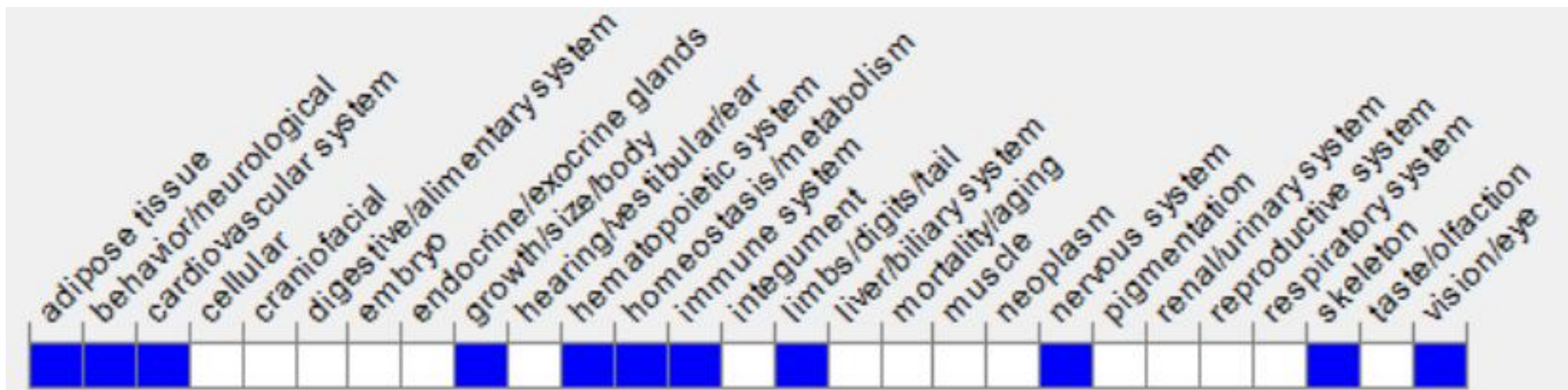

Ube3c-201 - ENSMUST00000049453 >
protein coding

Source: https://www.ensembl.org

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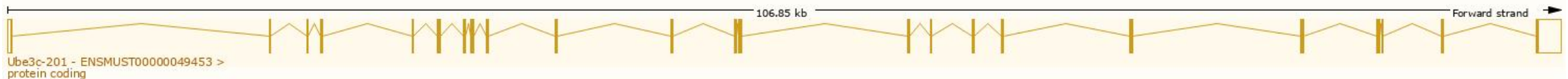
Genomic Information

Protein Information

Source: : https://www.ensembl.org
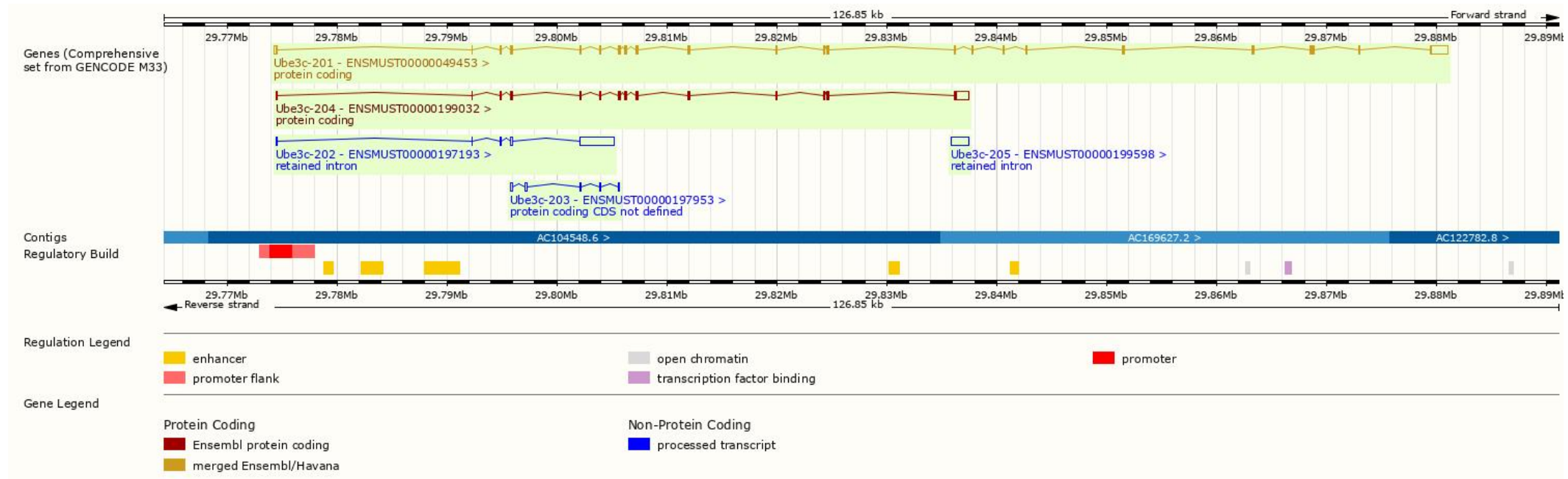
Mouse Phenotype Information (MGI)

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Source: https://www.informatics.jax.org

Important Information

- After cross cre, 114 amino acids remained at the N-terminus of this strategy, with unknown effects.

- *Ube3c* is located on Chr5. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.