Extl3 Cas9-CKO Strategy

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Design Date: 2023-02-22

Overview

Target Gene Name
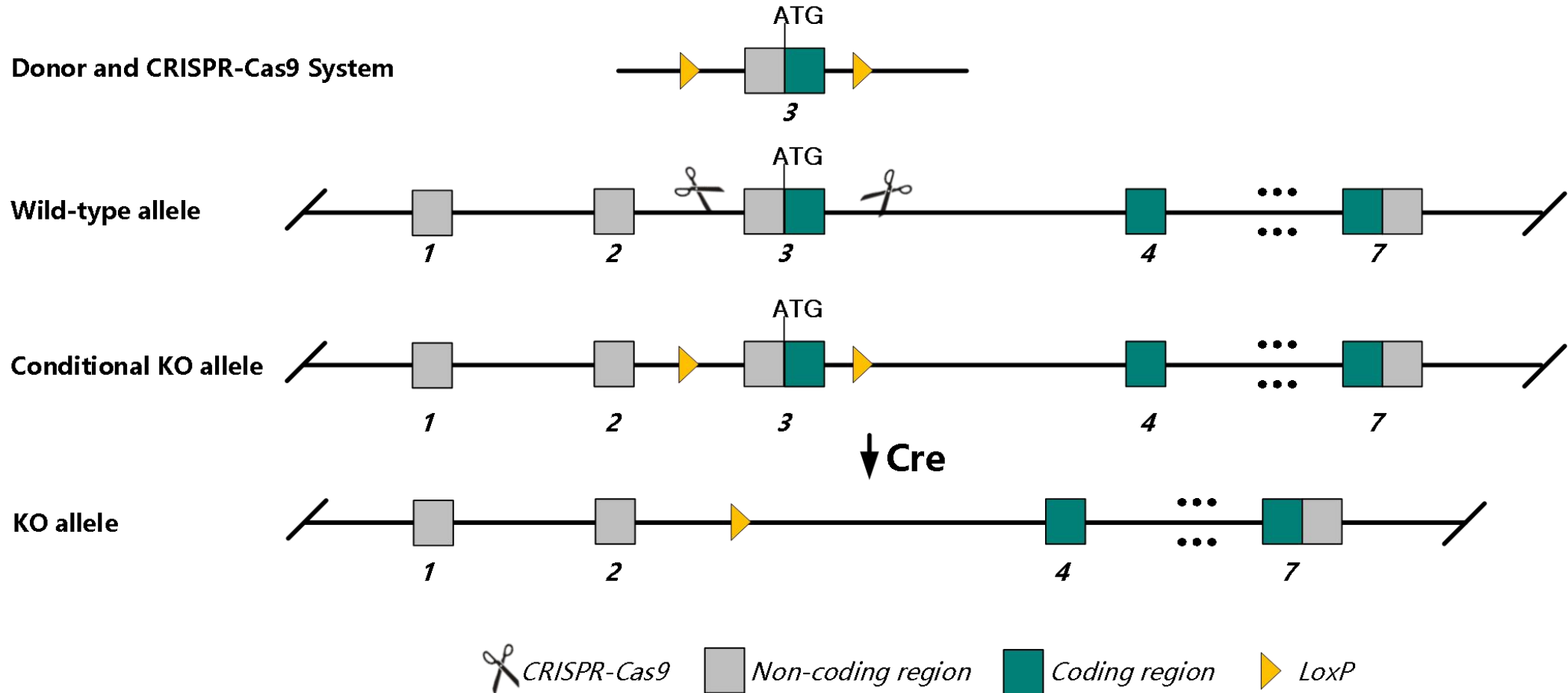
- Extl3

Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

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Strain Strategy

Schematic representation of CRISPR-Cas9 engineering used to edit the *Extl3* gene.

Technical Information

- The *Extl3* gene has 3 transcripts. According to the structure of *Extl3* gene, exon3 of *Extl3*-203 (ENSMUST00000225633.2) transcript is recommended as the knockout region. The region contains ATG and most of coding sequences. Knocking out the region will result in disruption of protein function.

- In this project we use CRISPR-Cas9 technology to modify *Extl3* 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

Extl3 exostosin-like glycosyltransferase 3 [*Mus musculus* (house mouse)]

Gene ID: 54616, updated on 5-Jan-2023

Download Datasets

Summary

Official Symbol	Extl3 provided by MGI
Official Full Name	exostosin-like glycosyltransferase 3 provided by MGI
Primary source	MGI:MGI:1860765
See related	Ensembl:ENSMUSG00000021978 AllianceGenome:MGI:1860765
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	Ext1l; mKIAA0519; 2900009G18Rik
Summary	Predicted to enable glycosyltransferase activity. Predicted to be involved in heparan sulfate proteoglycan biosynthetic process and positive regulation of cell growth. Predicted to be located in endoplasmic reticulum and membrane. Predicted to be active in Golgi apparatus. Is expressed in several structures, including alimentary system; central nervous system; heart; metanephros; and sensory organ. Orthologous to human EXTL3 (exostosin like glycosyltransferase 3). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 31.2), mammary gland adult (RPKM 19.2) and 27 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 14; 14 D1
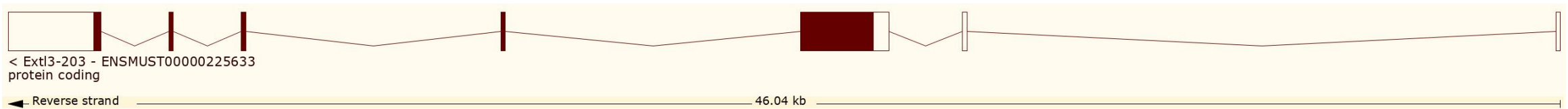
Exon count: 8

See Extl3 in Genome Data Viewer

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

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Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000225633.2	Extl3-203	6013	919aa	Protein coding	CCDS27211	Q6P1H4	Ensembl Canonical GENCODE basic APPRIS P1
ENSMUST00000022550.8	Extl3-201	5977	919aa	Protein coding	CCDS27211	Q6P1H4	GENCODE basic APPRIS P1 TSL:5
ENSMUST00000223989.2	Extl3-202	582	No protein	Protein coding CDS not defined		-	-

The strategy is based on the design of *Extl3*-203 transcript, the transcription is shown below:
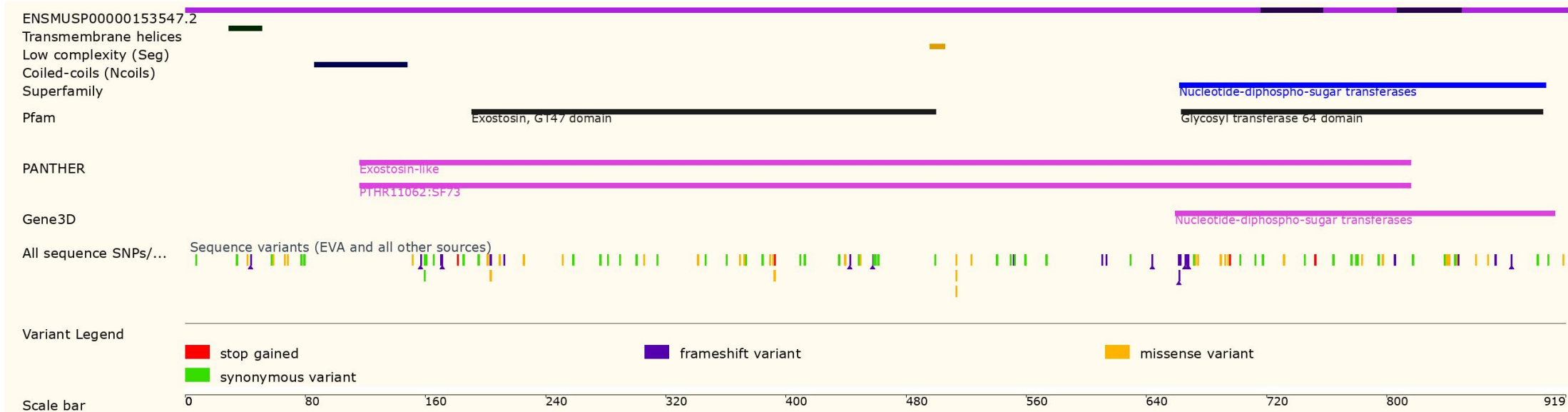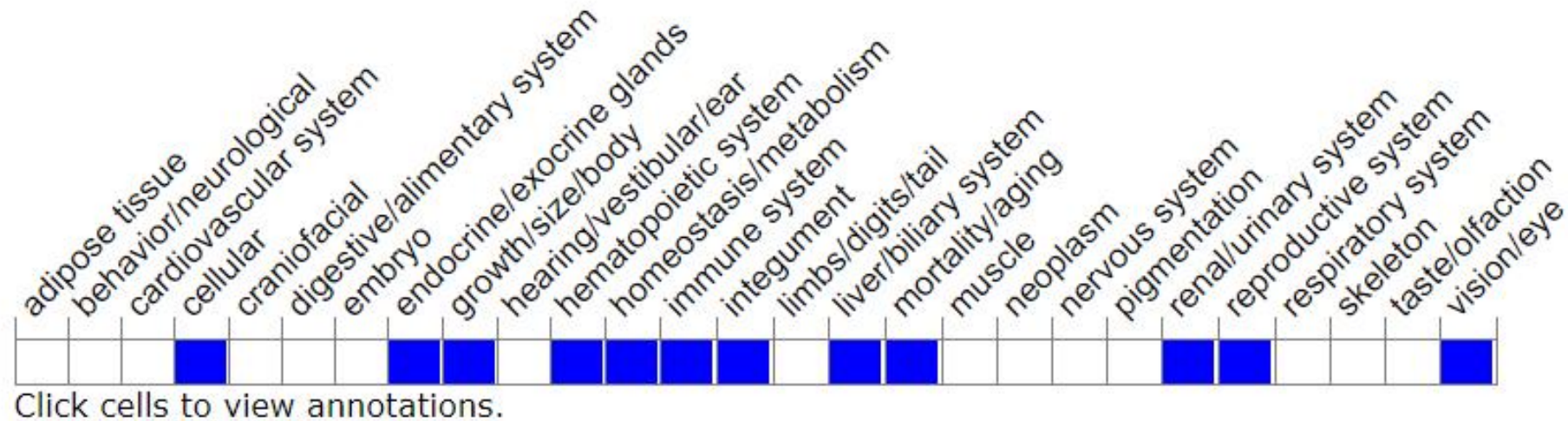

< Extl3-203 - ENSMUST00000225633
protein coding

◀ Reverse strand   46.04 kb

Source: https://www.ensembl.org

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Genomic Information

Source: : https://www.ensembl.org
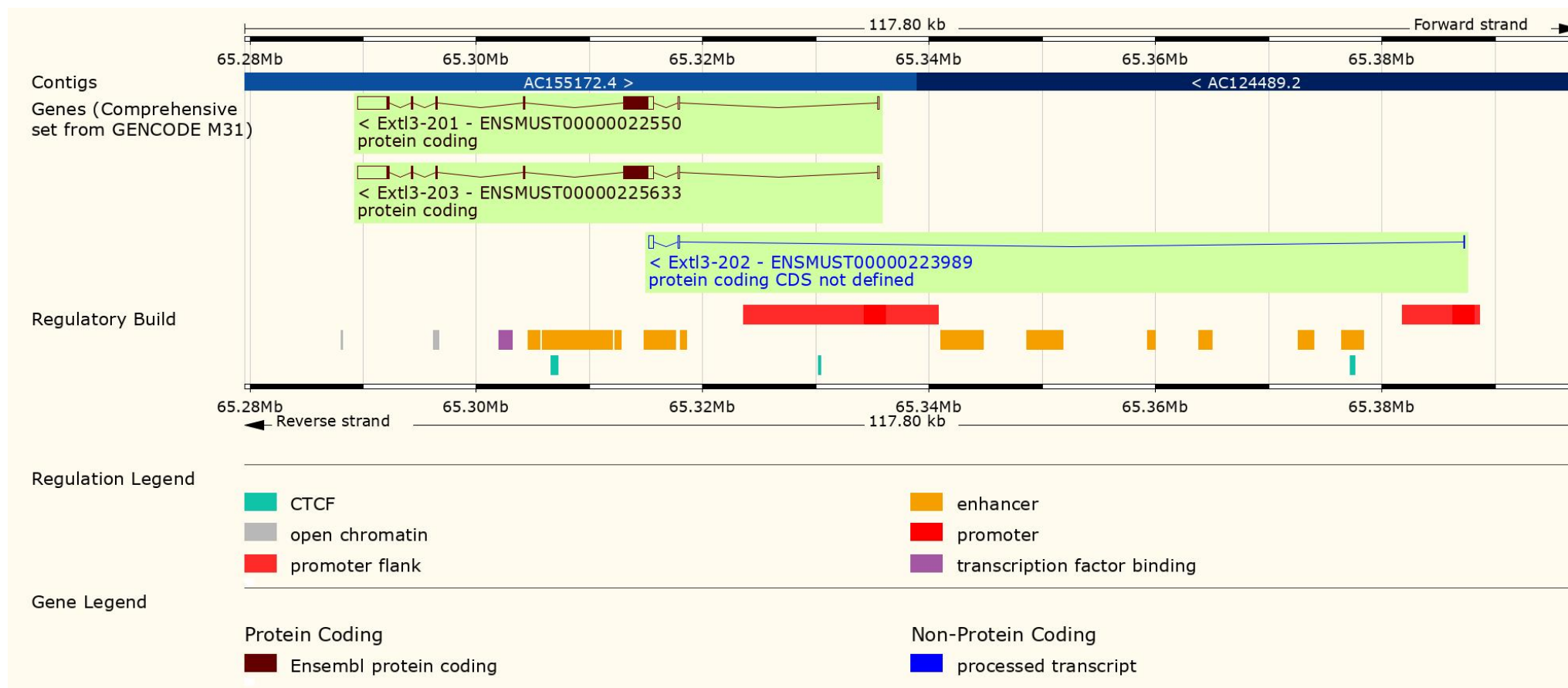
Protein Information

Mouse Phenotype Information (MGI)

- Mice homozygous for a null mutation display embryonic lethality during organogenesis and lack heparan sulfate derived disaccharides.

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

Important Information

- *Extl3* is located on Chr14. 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.