

Xylt1 Cas9-KO Strategy

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Design Date: 2020-3-25

Project Overview

Project Name

Xylt1

Project type

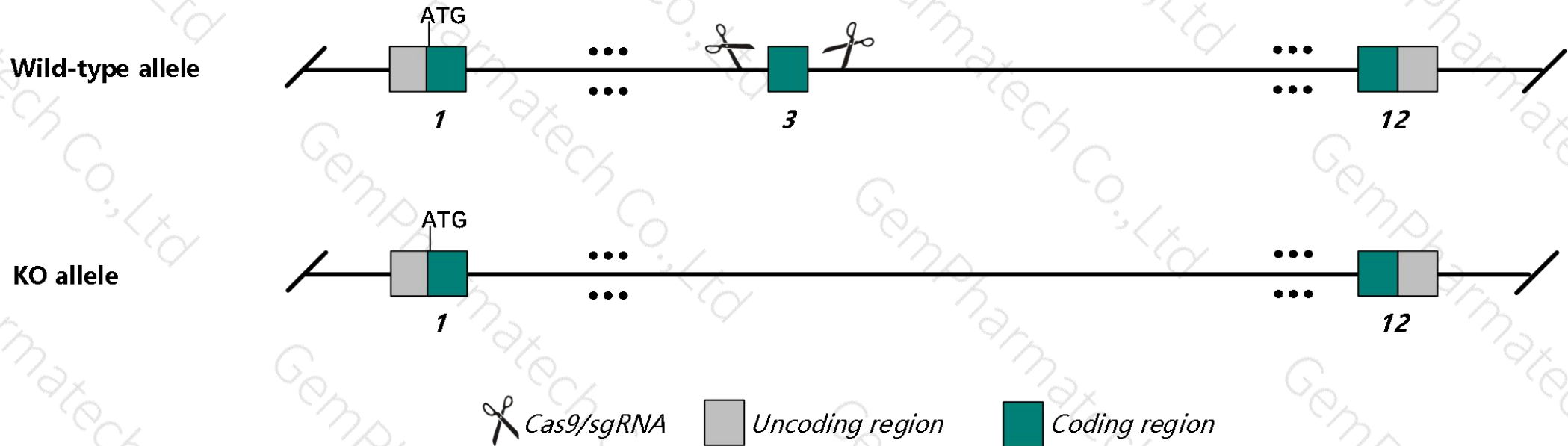
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Xylt1* gene. The schematic diagram is as follows:



- The *Xylt1* gene has 3 transcripts. According to the structure of *Xylt1* gene, exon3 of *Xylt1-201* (ENSMUST00000032892.6) transcript is recommended as the knockout region. The region contains 514bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Xylt1* gene. The brief process is as follows: CRISPR/Cas9 system we

- According to the existing MGI data, Mice homozygous for an ENU-induced allele exhibit partial preweaning lethality, impaired chondrocyte maturation and decreased skeletal length.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Xylt1* gene is located on the Chr7. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Xylt1 xylosyltransferase 1 [*Mus musculus* (house mouse)]

Gene ID: 233781, updated on 13-Mar-2020

Summary

Official Symbol	Xylt1 provided by MGI
Official Full Name	xylosyltransferase 1 provided by MGI
Primary source	MGI:MGI:2451073
See related	Ensembl:ENSMUSG00000030657
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	8030490L12
Expression	Ubiquitous expression in spleen adult (RPKM 4.7), limb E14.5 (RPKM 4.2) and 27 other tissues See more
Orthologs	human all

Genomic context

Location: 7; 7 F1

Exon count: 12

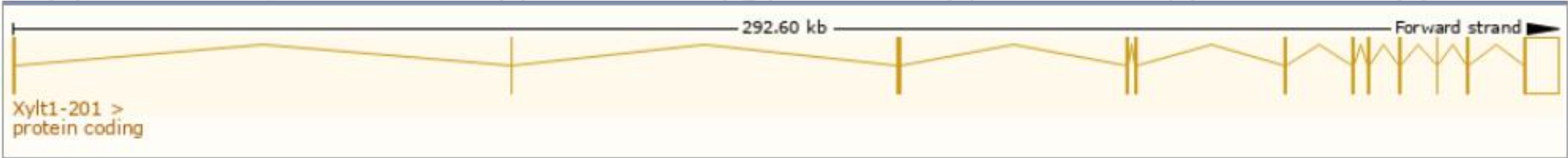
See Xylt1 in [Genome Data Viewer](#)

Transcript information (Ensembl)

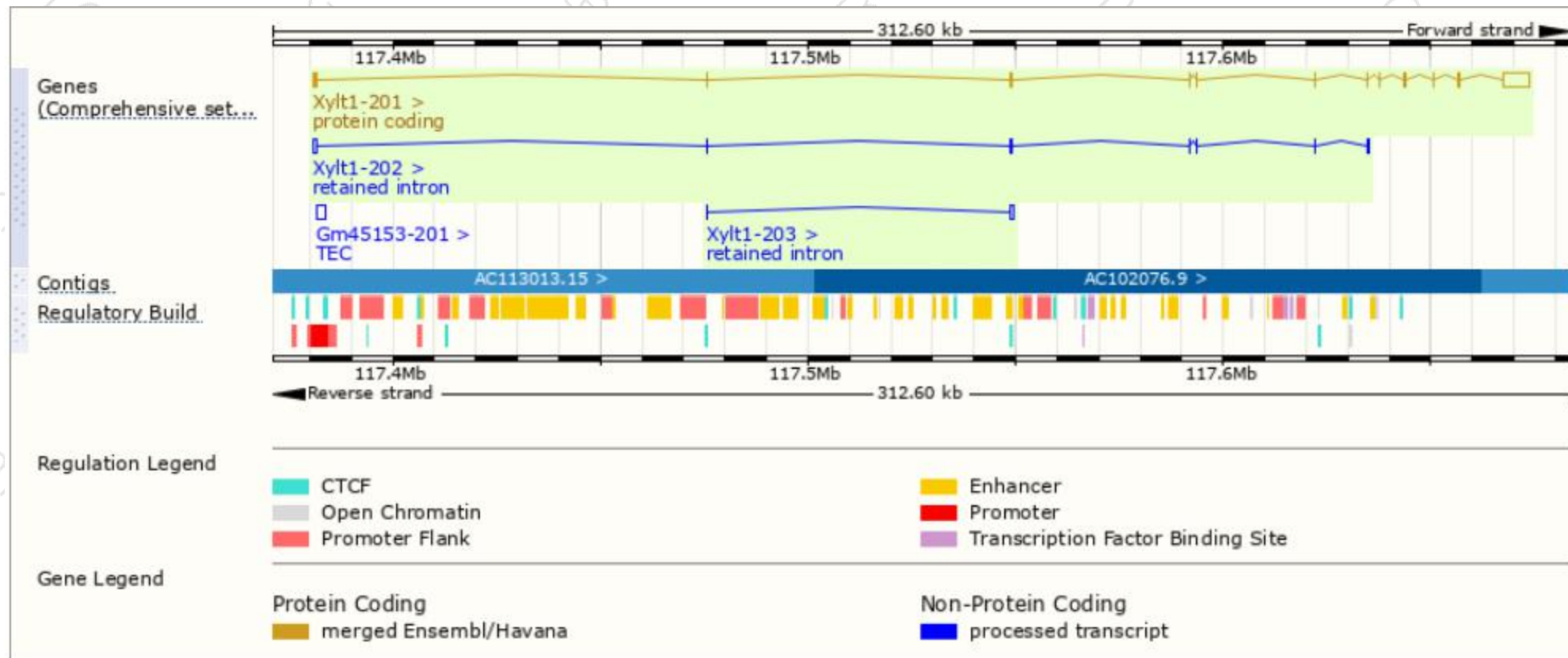
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Xylt1-201	ENSMUST00000032892.6	9020	953aa	Protein coding	CCDS40101	F8VPK6	TSL:1 GENCODE basic APPRIS P1
Xylt1-202	ENSMUST00000160035.7	2138	No protein	Retained intron	-	-	TSL:1
Xylt1-203	ENSMUST00000161889.1	815	No protein	Retained intron	-	-	TSL:1

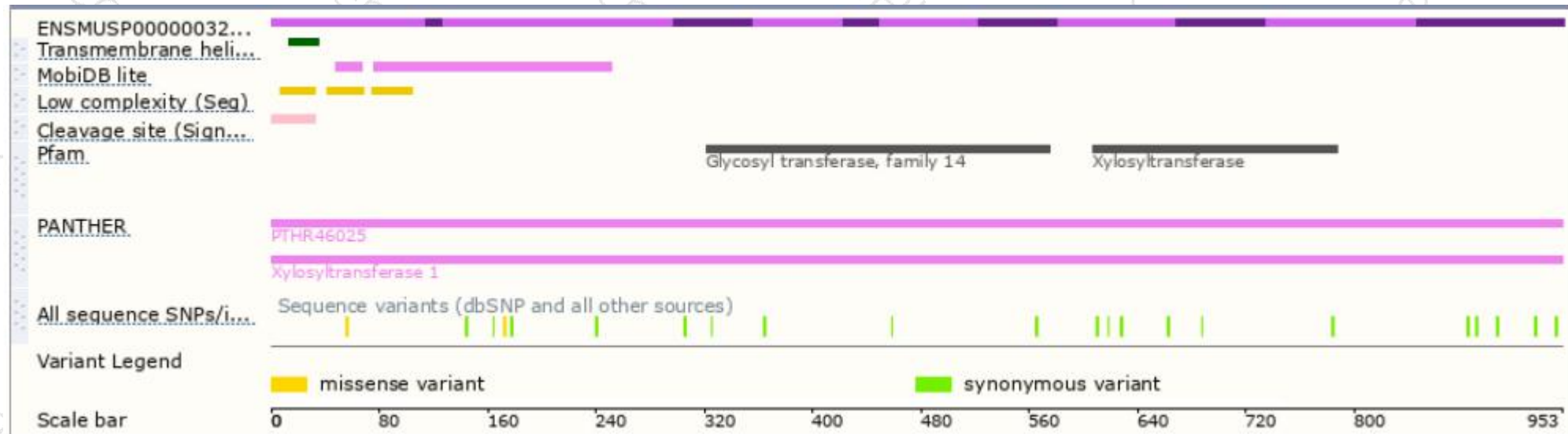
The strategy is based on the design of *Xylt1-201* transcript,The transcription is shown below



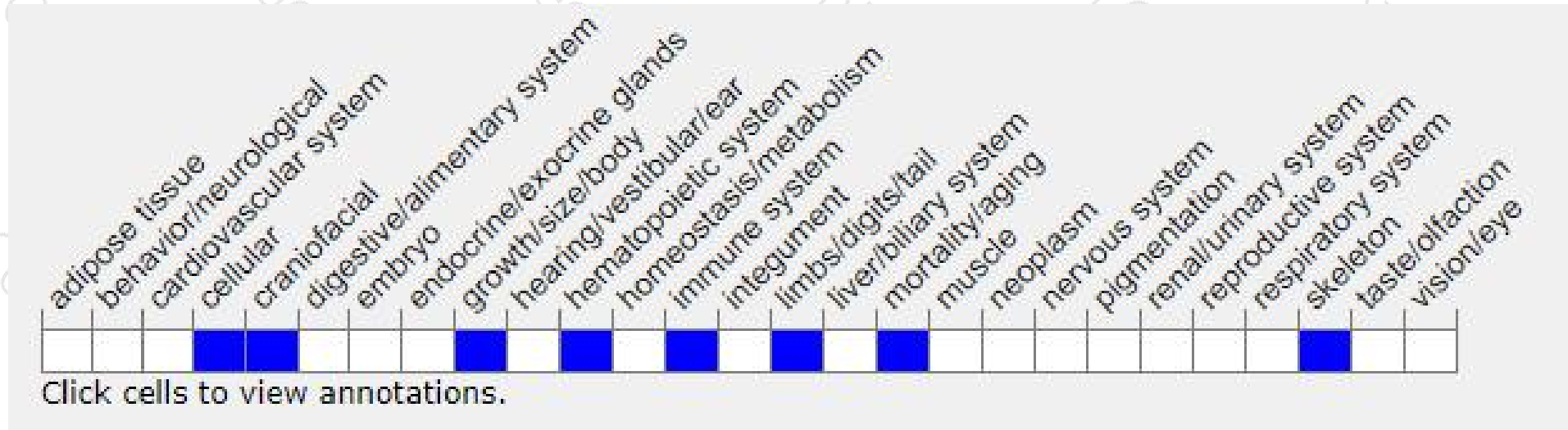
Genomic location distribution



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, Mice homozygous for an ENU-induced allele exhibit partial preweaning lethality, impaired chondrocyte maturation and decreased skeletal length.

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

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