B3galnt2 Cas9-KO Strategy

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Project Overview

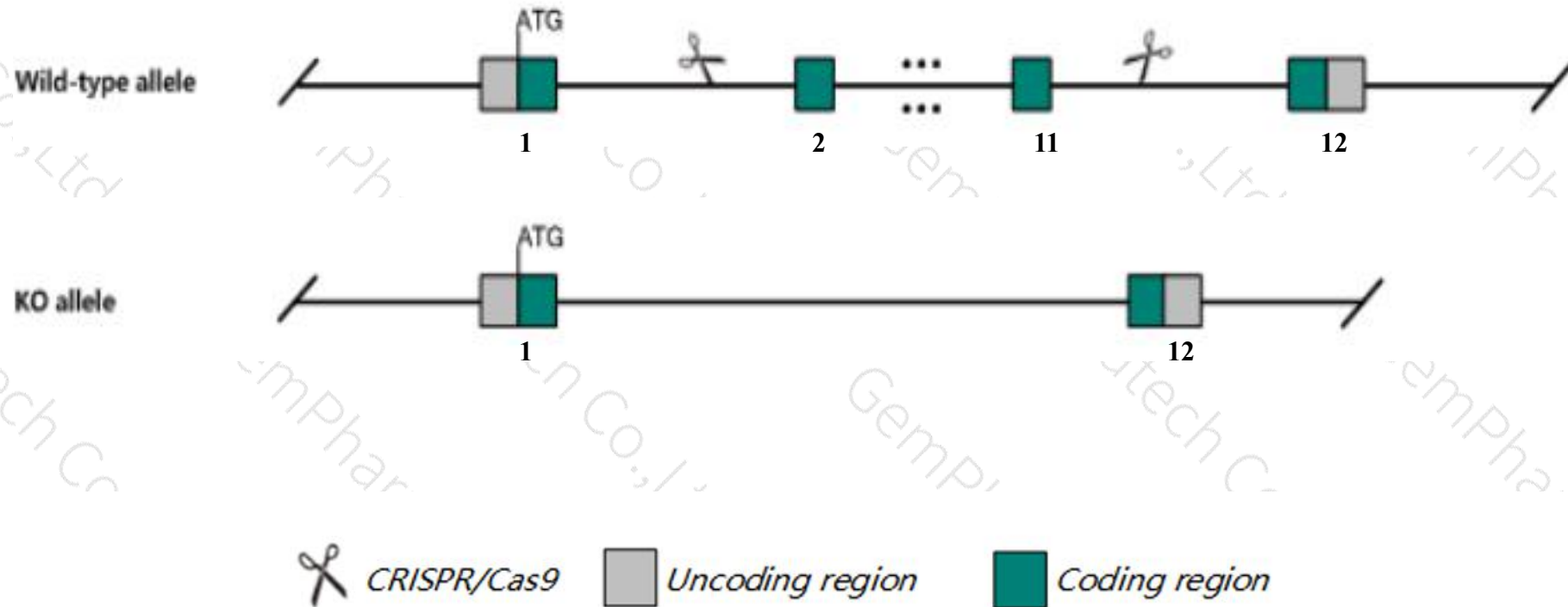|	
Project Name	*B3galnt2*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *B3galnt2* gene. The schematic diagram is as follows:

Technical routes

➢ The *B3galnt2* gene has 12 transcripts. According to the structure of *B3galnt2* gene, exon2-exon11 of *B3galnt2-201* (ENSMUST00000099747.4) transcript is recommended as the knockout region.The region contains 1259bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *B3galnt2* gene. The brief process is as follows: CRISPR/Cas9 syst

Notice

➢ The effect of transcripts 202,205,209 is unknown.

➢ *Gm18856* gene may be destroyed.

➢ The *B3galnt2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

B3galnt2 UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2 [Mus musculus (house mouse)]

Gene ID: 97884, updated on 13-Mar-2020

▲ Summary

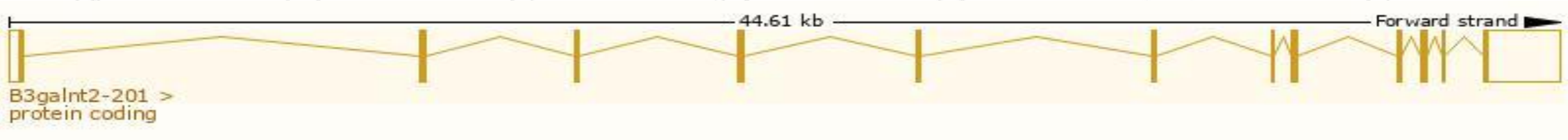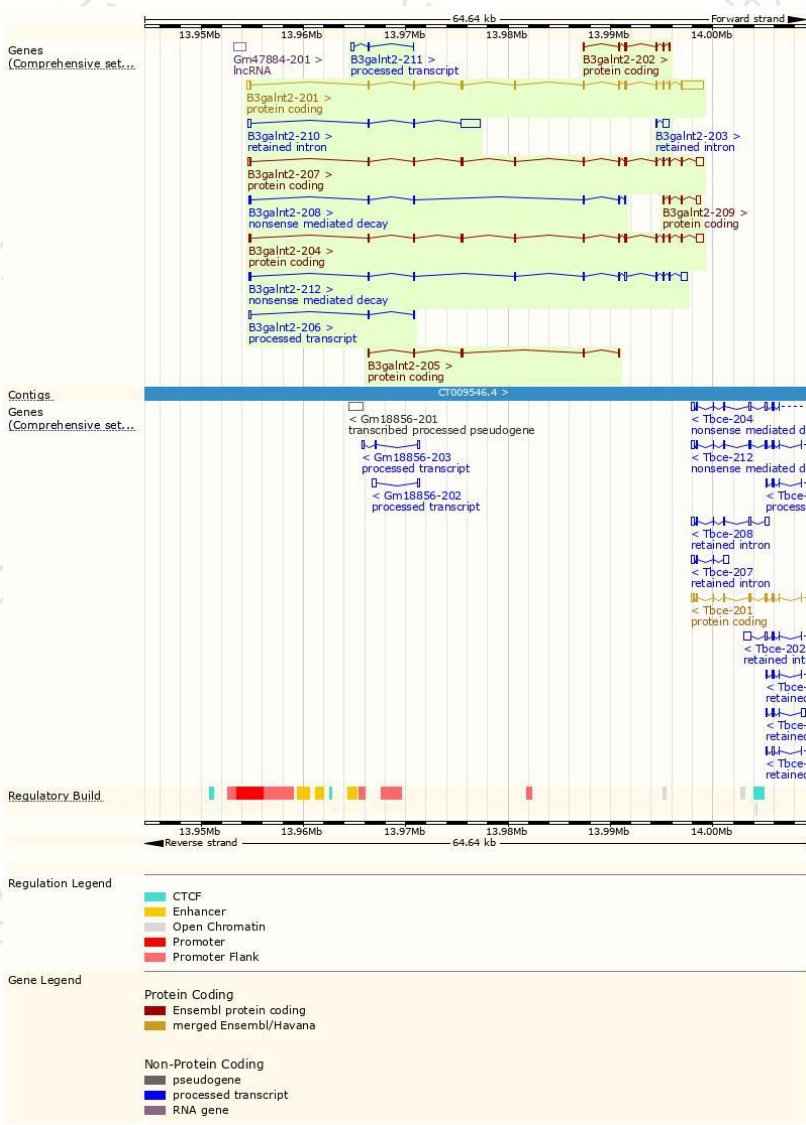|	
Official Symbol	B3galnt2 provided by MGI
Official Full Name	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2 provided byMGI
Primary source	MGI:MGI:2145517
See related	Ensembl:ENSMUSG00000039242
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A930105D20Rik, C80633, D230016N13Rik
Expression	Ubiquitous expression in bladder adult (RPKM 13.6), CNS E11.5 (RPKM 13.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
B3galnt2-201	ENSMUST00000099747.4	3892	504aa	Protein coding	CCDS26246	Q8BG28	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
B3galnt2-207	ENSMUST00000221974.1	2439	504aa	Protein coding	CCDS26246	Q8BG28	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
B3galnt2-204	ENSMUST00000221300.1	2397	504aa	Protein coding	CCDS26246	Q8BG28	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
B3galnt2-202	ENSMUST00000220681.1	767	251aa	Protein coding	-	A0A1Y7VLK8	CDS 5' incomplete TSL:3
B3galnt2-209	ENSMUST00000222420.1	693	124aa	Protein coding	-	A0A1Y7VK56	CDS 5' incomplete TSL:3
B3galnt2-205	ENSMUST00000221333.1	602	201aa	Protein coding	-	A0A1Y7VLV9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
B3galnt2-212	ENSMUST00000223483.1	1876	143aa	Nonsense mediated decay	-	A0A1Y7VJJ6	TSL:1
B3galnt2-208	ENSMUST00000222110.1	795	123aa	Nonsense mediated decay	-	A0A1Y7VLZ2	TSL:5
B3galnt2-206	ENSMUST00000221764.1	435	No protein	Processed transcript	-	-	TSL:3
B3galnt2-211	ENSMUST00000223389.1	434	No protein	Processed transcript	-	-	TSL:5
B3galnt2-210	ENSMUST00000223307.1	2400	No protein	Retained intron	-	-	TSL:1
B3galnt2-203	ENSMUST00000220932.1	751	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *B3galnt2-201* transcript,The transcription is shown below
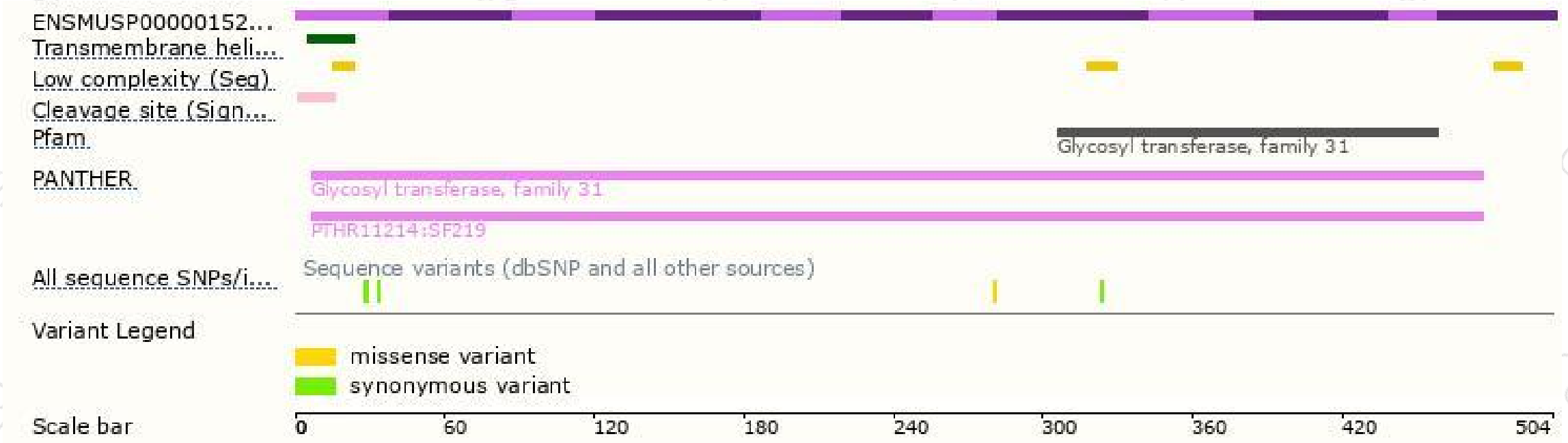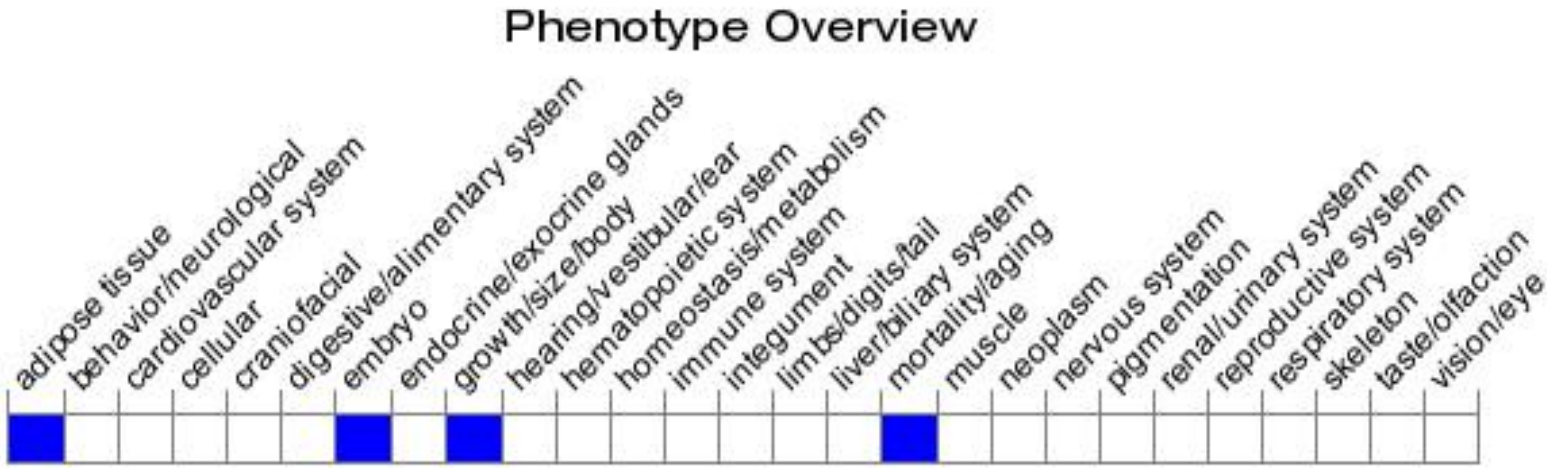
Genomic location distribution

Protein domain

ENSMUSP00000152...	
Transmembrane heli...	
Low complexity (Seg)	
Cleavage site (Sign...	
Pfam	Glycosyl transferase, family 31
PANTHER	Glycosyl transferase, family 31
	PTHR11214:SF219
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

■ missense variant
■ synonymous variant

Scale bar: 0 60 120 180 240 300 360 420 504

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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