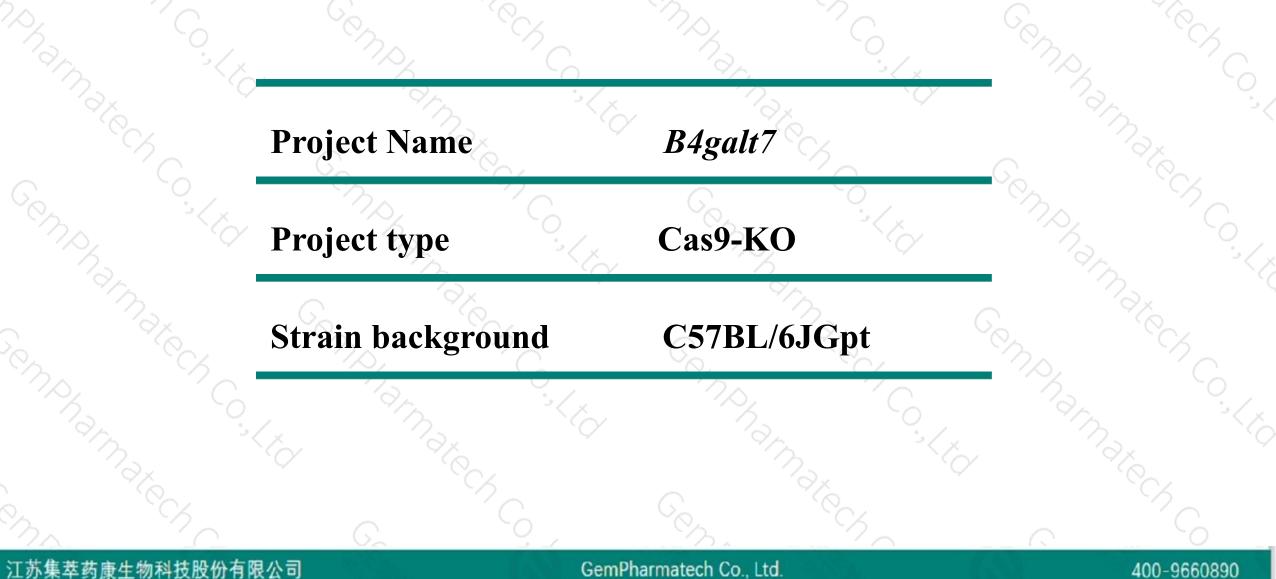


B4galt7 Cas9-KO Strategy

Designer: Yanhua Shen Reviewer: Xueting Zhang Design Date: 2020-2-15

Project Overview



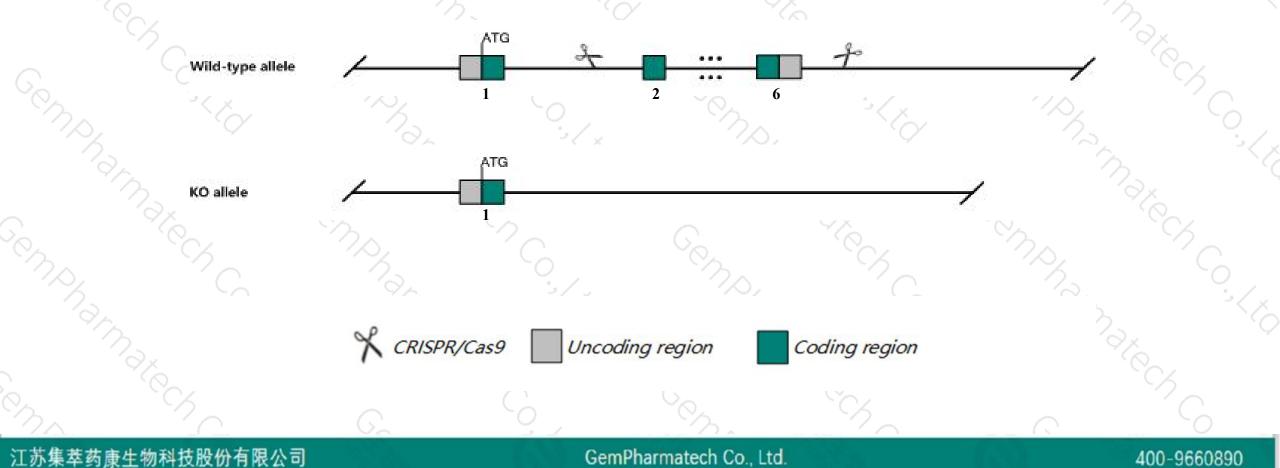


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Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *B4galt7* gene. The schematic diagram is as follows:





The B4galt7 gene has 4 transcripts. According to the structure of B4galt7 gene, exon2-exon6 of B4galt7-201 (ENSMUST00000064701.7) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify B4galt7 gene. The brief process is as follows: CRISPR/Cas9 system



>*Gm15911*-201 gene may be destroyed.

Notice

≻The effect of transcript 203 is unknown.

➤The B4galt7 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.

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Gene information (NCBI)

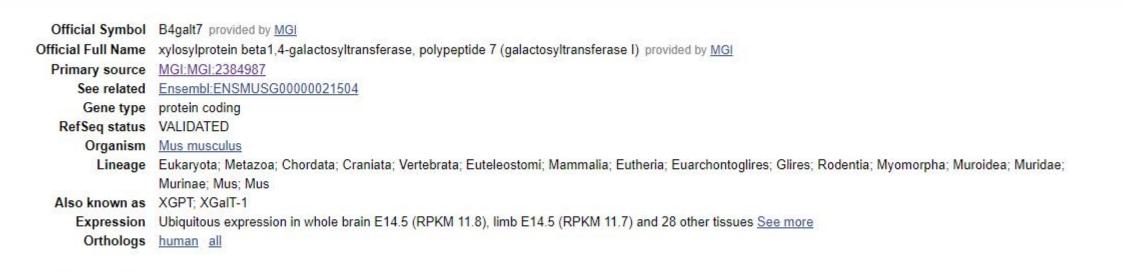


B4galt7 xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) [Mus musculus (house mouse)]

Gene ID: 218271, updated on 12-Aug-2019

Summary

2



Genomic context

Location: 13; 13 B1 Exon count: 6 See B4galt7 in Genome Data Viewer

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Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
B4galt7-202	ENSMUST00000100764.9	2195	<u>292aa</u>	Protein coding	CCDS79190	Q8R087	TSL:1 GENCODE basic
B4galt7-201	ENSMUST0000064701.7	2130	<u>327aa</u>	Protein coding	CCDS26550	Q3TAW1 Q8R087	TSL:1 GENCODE basic APPRIS P1
B4galt7-203	ENSMUST00000133176.7	806	<u>220aa</u>	Protein coding	2	D3Z065	CDS 3' incomplete TSL:3
B4galt7-204	ENSMUST00000142654.7	1213	No protein	Retained intron	2	20	TSL:1

The strategy is based on the design of *B4galt7-201* transcript, The transcription is shown below

BA	4galt7-201 > rotein coding			10.38 kb		Forward strand
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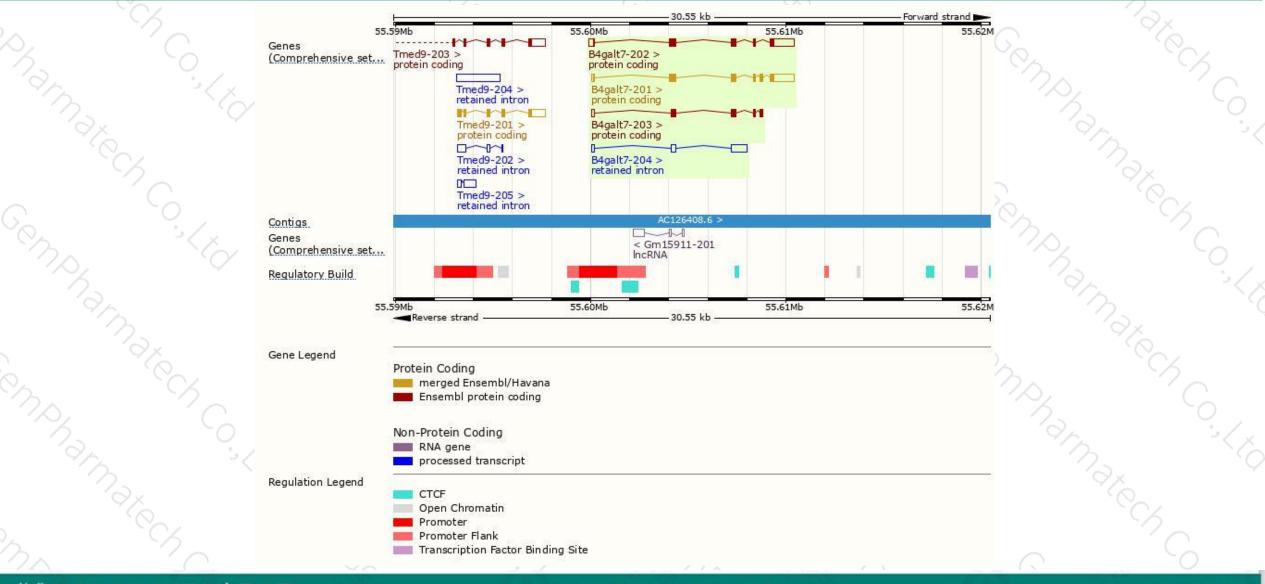
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Genomic location distribution



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Protein domain



membrane.helia Bi lite omplexity.(Sea) family. tetER. Beta-1,4-galactosyltransferase, N-terminal Beta-1,4-galactosyltransferase, C-terminal Beta-1,4-galactosyltransferase, C-terminal Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-galactosyltransferase Beta-1,4-gal	ISMUSP0000068	6	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	<u> </u>	<u> </u>		- 4 <u>7</u> -
Beta-1,4-galactosyltransferase Galactosyltransferase, N-terminal Beta-1,4-galactosyltransferase, N-terminal Beta-1,4-galactosyltransferase PTHR193001SF30 3D. Nucleotide-diphospho-sugar transferases cd000399 auence, SNPs/i Sequence variants (dbSNP and all other sources) auence, SNPs/i Sequence variants (dbSNP and all other sources) auence diphospho augar transferases cd000399	ansmembrane heli obiDB lite w complexity (Seg) perfamily	Nucleotide-diphosi	ho-sugar transferases				
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



