Chst10 Cas9-KO Strategy

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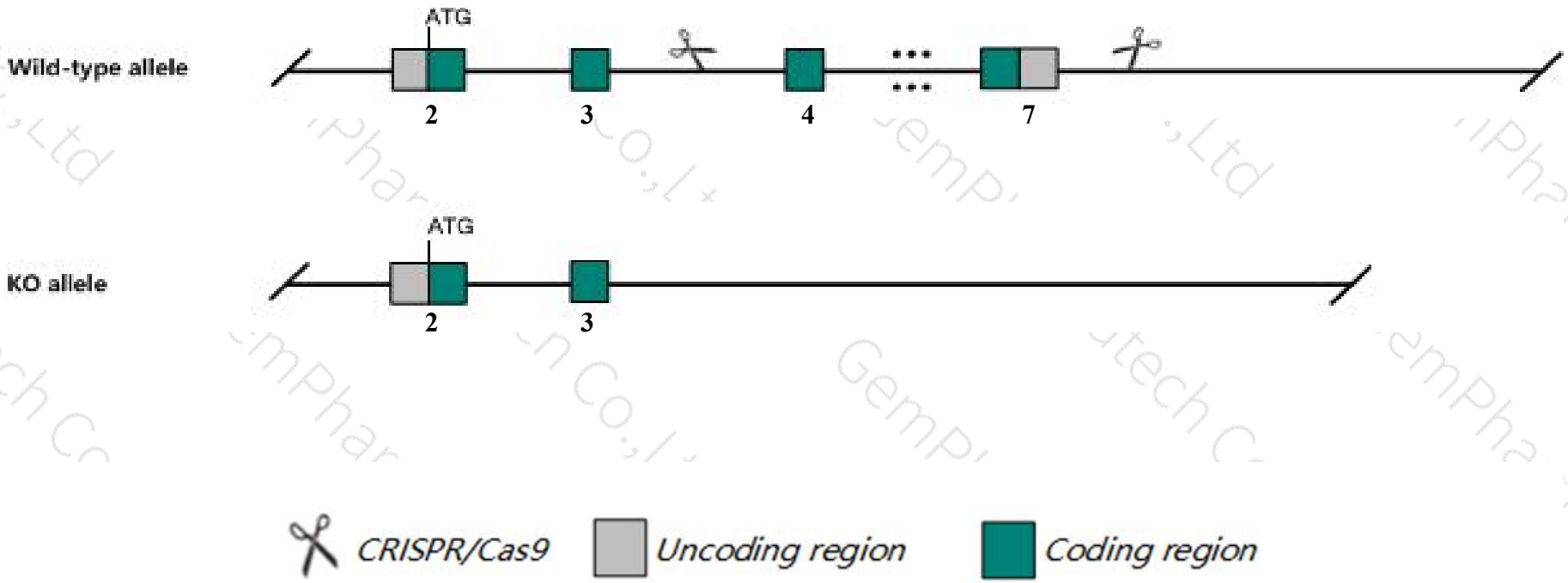
Design Date: 2020-2-17

Project Overview

Project Name	***Chst10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chst10* gene. The schematic diagram is as follows:



Technical routes

➢ The *Chst10* gene has 8 transcripts. According to the structure of *Chst10* gene, exon4-exon7 of *Chst10-201* (ENSMUST00000027249.11) transcript is recommended as the knockout region.The region contains 971bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Chst10* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

➢ According to the existing MGI data,Homozygous mutation of this gene results in altered synaptic transmission and long term potentiation. Mutant animals exhibit impaired spatial learning and long term memory deficits. Mice homozygous for a different knock-out allele exhibit reduced male and female fertility.

➢ The *Chst10* gene is located on the Chr1. 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）

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Chst10 carbohydrate sulfotransferase 10 [Mus musculus (house mouse)]

Gene ID: 98388, updated on 9-Apr-2019

Summary

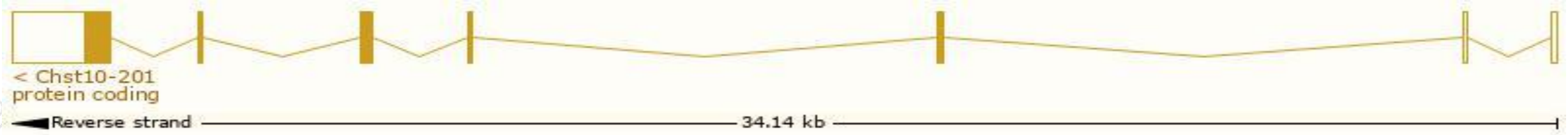
Official Symbol	Chst10 provided by MGI
Official Full Name	carbohydrate sulfotransferase 10 provided by MGI
Primary source	MGI:MGI:2138283
See related	Ensembl:ENSMUSG00000026080
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI507003, AU041319, Hnk-1st, ST
Expression	Biased expression in cerebellum adult (RPKM 8.7), CNS E18 (RPKM 7.3) and 14 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

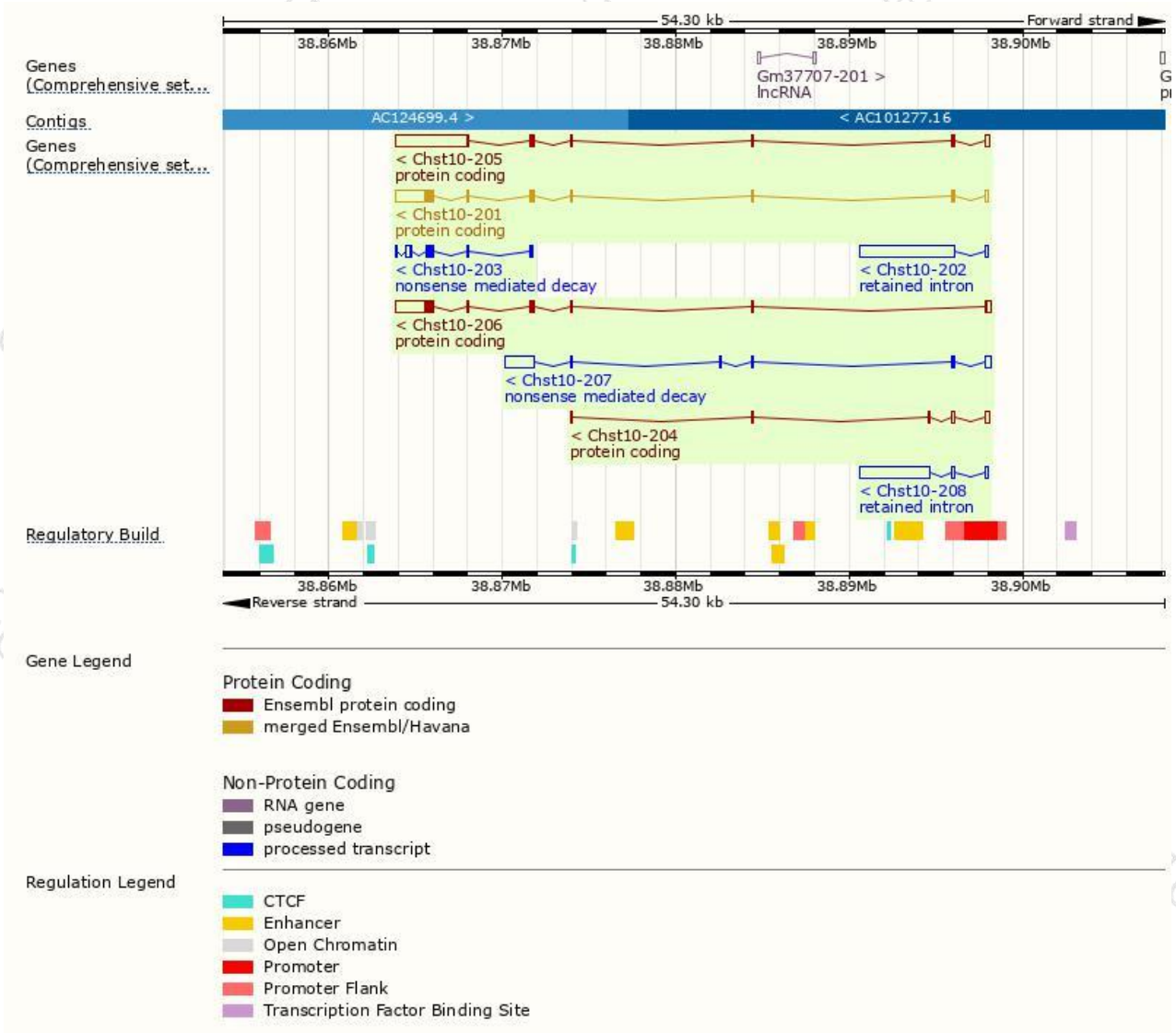
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chst10-201	ENSMUST00000027249.11	2975	374aa	Protein coding	CCDS14901	A2RSS2	TSL:1 GENCODE basic APPRIS P2
Chst10-205	ENSMUST00000193441.5	4999	196aa	Protein coding	-	A0A0A6YXK3	TSL:1 GENCODE basic
Chst10-206	ENSMUST00000194361.5	2996	370aa	Protein coding	-	A0A0A6YVW5	TSL:1 GENCODE basic APPRIS ALT2
Chst10-204	ENSMUST00000193435.5	697	64aa	Protein coding	-	A0A0A6YWM2	CDS 3' incomplete TSL:3
Chst10-207	ENSMUST00000194657.1	2431	77aa	Nonsense mediated decay	-	A0A0A6YWB7	TSL:1
Chst10-203	ENSMUST00000192948.5	1086	242aa	Nonsense mediated decay	-	A0A0A6YWA7	CDS 5' incomplete TSL:5
Chst10-202	ENSMUST00000192175.1	5522	No protein	Retained intron	-	-	TSL:1
Chst10-208	ENSMUST00000195731.1	4280	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Chst10-201* transcript,The transcription is shown below

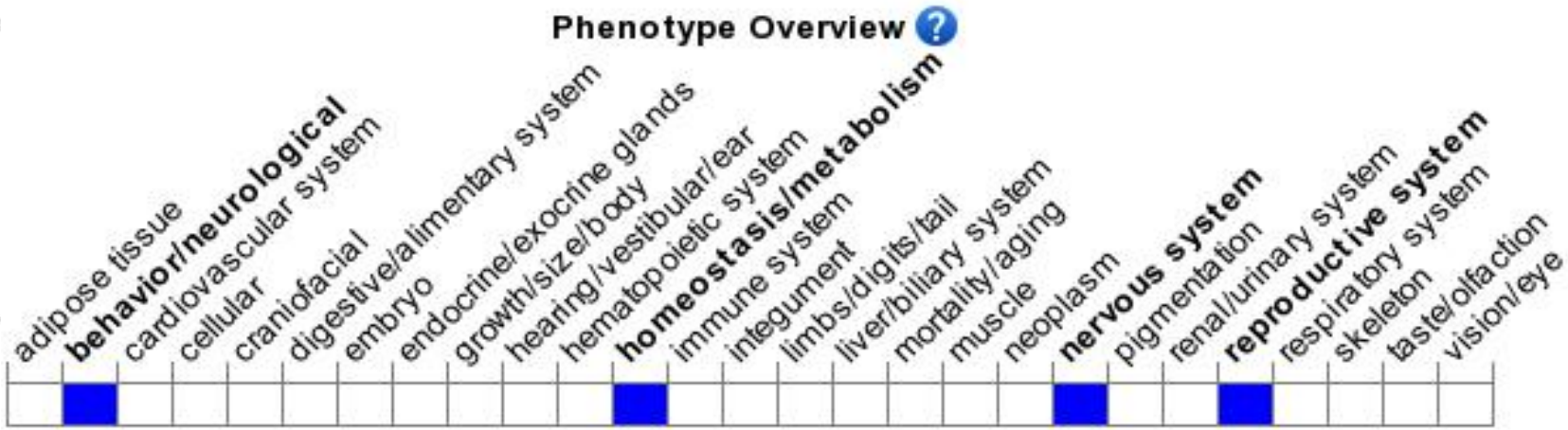


Genomic location distribution



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/).

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

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