

Chst4 Cas9-KO Strategy

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Project Overview

Project Name

Chst4

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chst4* gene. The schematic diagram is as follows:



- The *Chst4* gene has 3 transcripts. According to the structure of *Chst4* gene, exon2 of *Chst4-201* (ENSMUST00000109222.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Chst4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene do not accumulate lymphocytes in peripheral lymph nodes to as great an extent as normal. The animals are phenotypically normal otherwise.
- The *Chst4* gene is located on the Chr8. 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)

Chst4 carbohydrate sulfotransferase 4 [*Mus musculus* (house mouse)]

Gene ID: 26887, updated on 19-Oct-2019

Summary

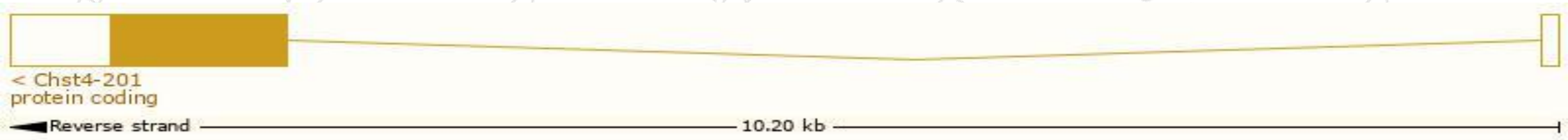
Official Symbol	Chst4 provided by MGI
Official Full Name	carbohydrate sulfotransferase 4 provided by MGI
Primary source	MGI:MGI:1349479
See related	Ensembl:ENSMUSG00000035930
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	GST-3; Gn6st-2; HEC-GlcNAc6ST
Expression	Biased expression in colon adult (RPKM 33.9), large intestine adult (RPKM 14.4) and 6 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

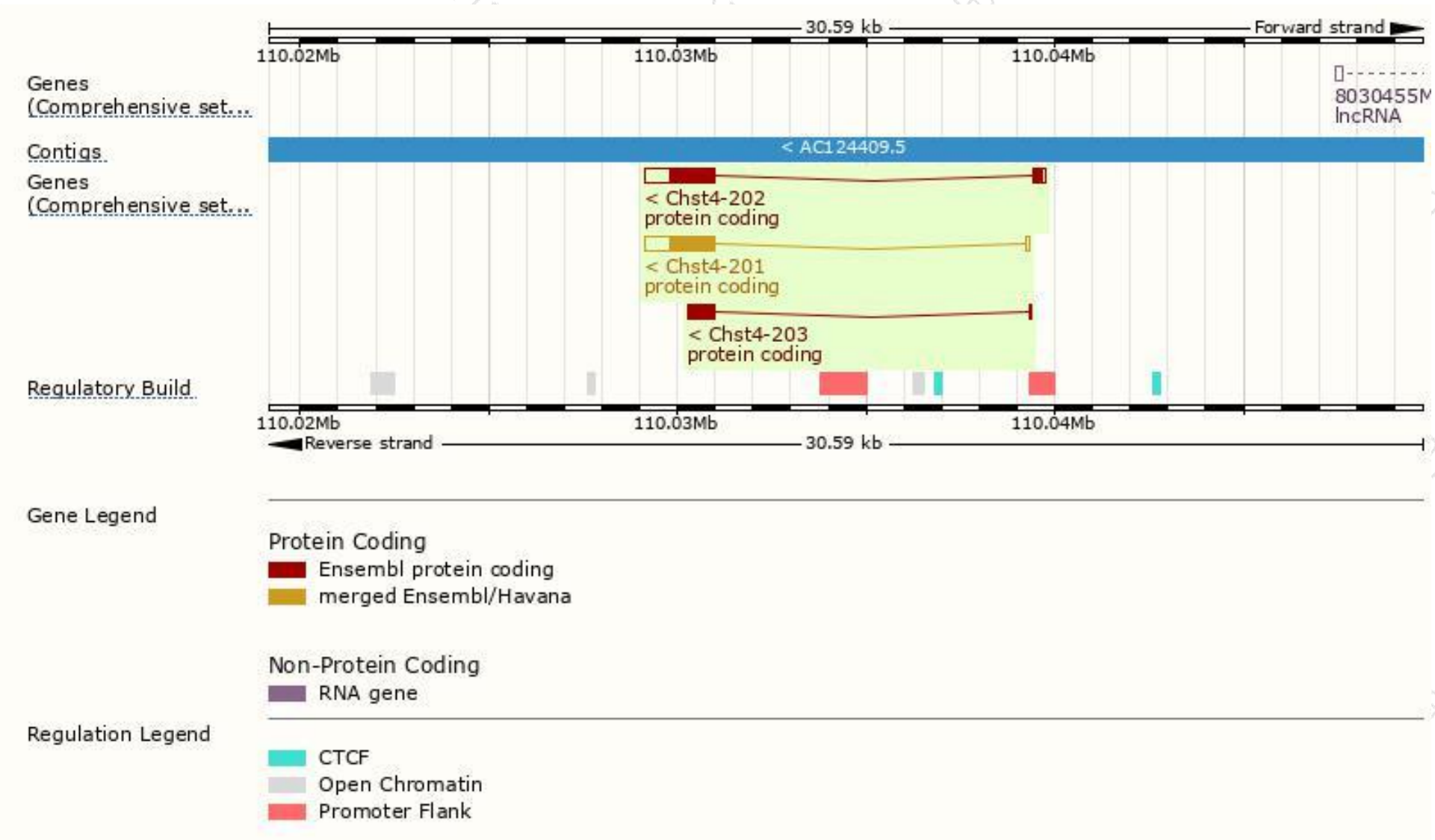
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chst4-201	ENSMUST00000109222.3	1942	388aa	Protein coding	CCDS22659	A0A0R4J1C9	TSL:1 GENCODE basic APPRIS P2
Chst4-202	ENSMUST00000211894.1	2146	471aa	Protein coding	-	A0A1D5RME2	TSL:1 GENCODE basic APPRIS ALT2
Chst4-203	ENSMUST00000212934.1	772	235aa	Protein coding	-	A0A1D5RMF5	CDS 3' incomplete TSL:3

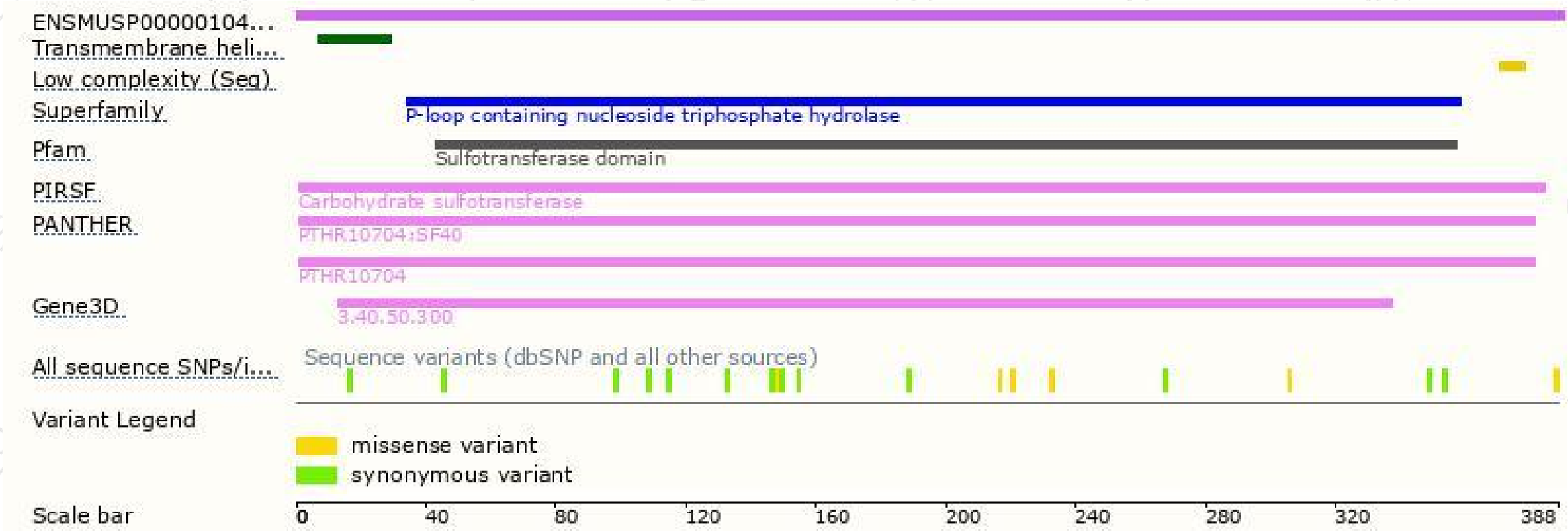
The strategy is based on the design of *Chst4-201* transcript,The transcription is shown below



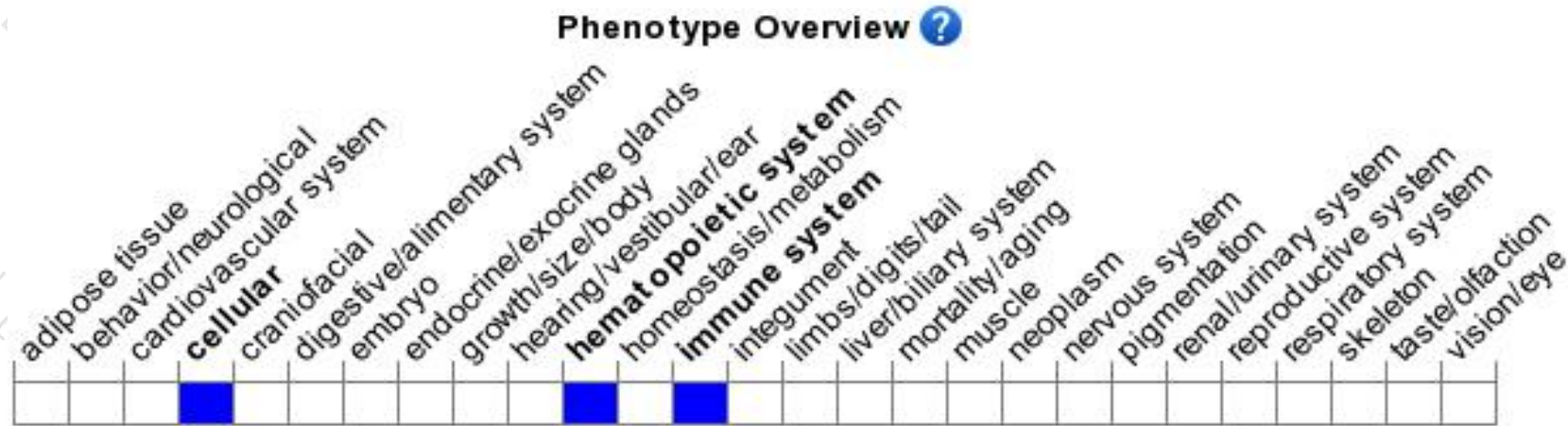
Genomic location distribution



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 disruptions in this gene do not accumulate lymphocytes in peripheral lymph nodes to as great an extent as normal. The animals are phenotypically normal otherwise.

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

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