

Chst8 Cas9-KO Strategy

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Project Overview

Project Name

Chst8

Project type

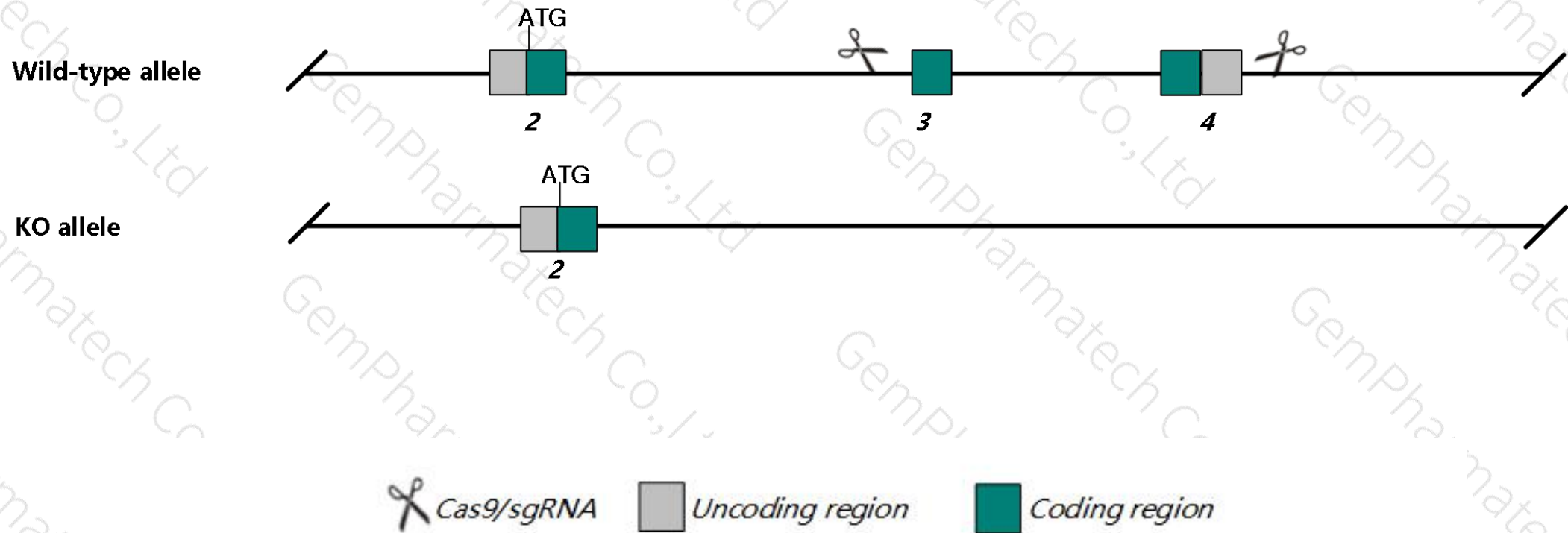
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chst8* gene. The schematic diagram is as follows:



- The *Chst8* gene has 7 transcripts. According to the structure of *Chst8* gene, exon3-exon4 of *Chst8-201* (ENSMUST00000078686.7) transcript is recommended as the knockout region. The region contains most 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 *Chst8* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Male mice homozygous for a null allele show higher luteinizing hormone and testosterone levels, early sexual maturation and enlarged seminal vesicles; females show higher LH, estrogen and progesterone levels, early sexual maturation, enlarged uteri, a prolonged estrous cycle and increased fecundity.
- The flox region contain part of the Gm12756 gene, which may delet it after Cre.
- The *Chst8* 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)

Chst8 carbohydrate sulfotransferase 8 [*Mus musculus* (house mouse)]

Gene ID: 68947, updated on 13-Mar-2020

Summary

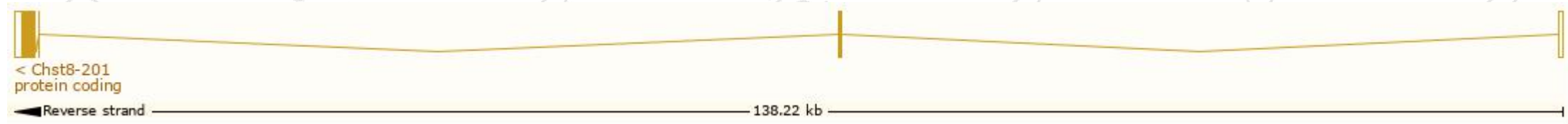
Official Symbol	Chst8 provided by MGI
Official Full Name	carbohydrate sulfotransferase 8 provided by MGI
Primary source	MGI:MGI:1916197
See related	Ensembl:ENSMUSG00000060402
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI426009; 1500011J21Rik
Expression	Biased expression in ovary adult (RPKM 27.2), adrenal adult (RPKM 7.4) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

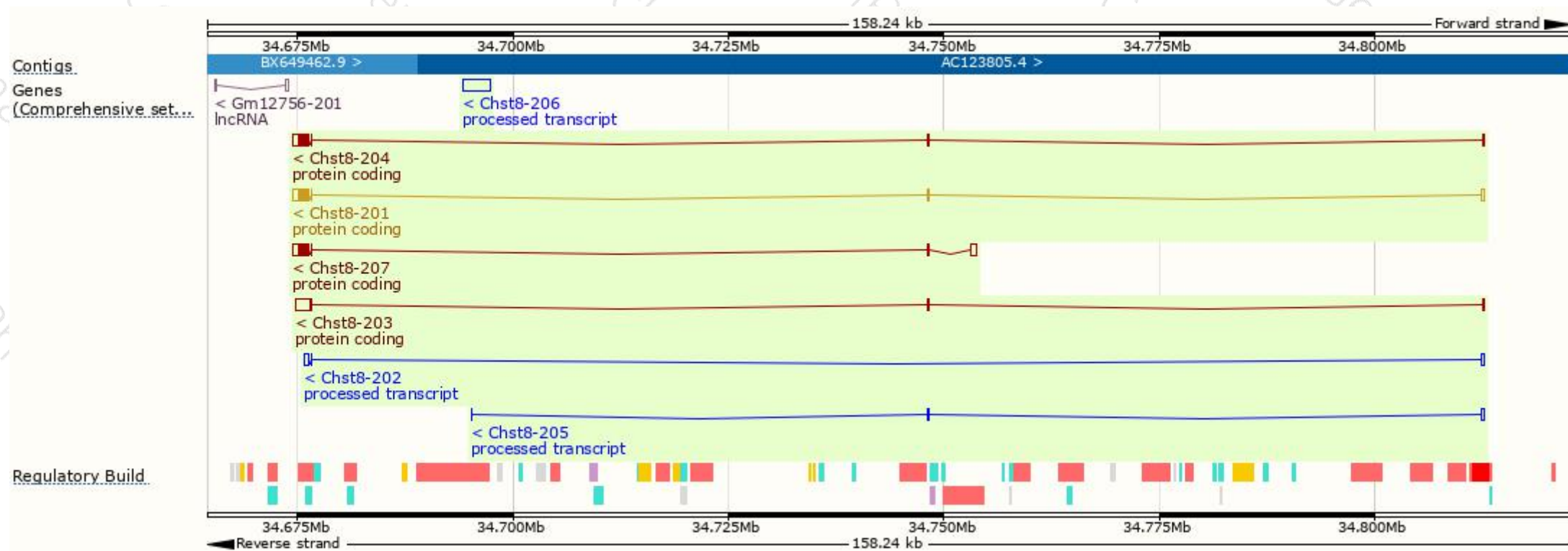
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chst8-207	ENSMUST00000238947.1	2699	417aa	Protein coding	CCDS21142	-	GENCODE basic APPRIS P1
Chst8-201	ENSMUST00000078686.7	2372	417aa	Protein coding	CCDS21142	Q8BQ86	TSL:1 GENCODE basic APPRIS P1
Chst8-204	ENSMUST00000205259.1	1980	417aa	Protein coding	CCDS21142	Q8BQ86	TSL:5 GENCODE basic APPRIS P1
Chst8-203	ENSMUST00000154629.2	2079	123aa	Protein coding	-	D6RCV4	TSL:5 GENCODE basic
Chst8-206	ENSMUST00000206207.1	3179	No protein	Processed transcript	-	-	TSL:NA
Chst8-202	ENSMUST00000135295.1	830	No protein	Processed transcript	-	-	TSL:3
Chst8-205	ENSMUST00000205390.1	569	No protein	Processed transcript	-	-	TSL:3

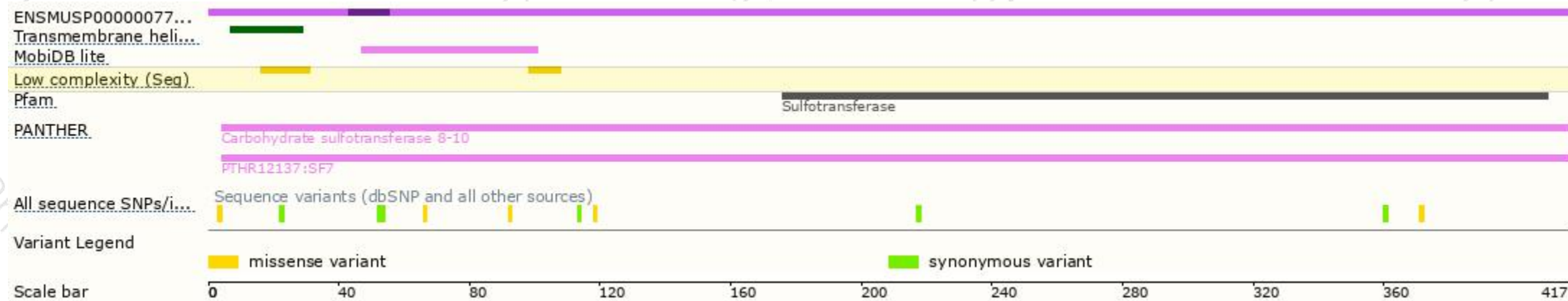
The strategy is based on the design of *Chst8-201* transcript,The transcription is shown below



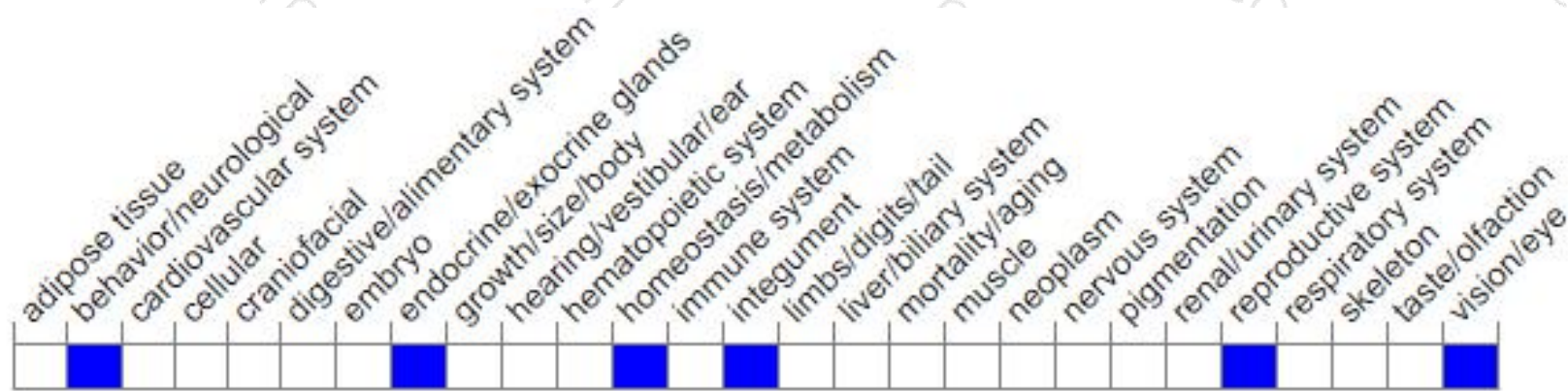
Genomic location distribution



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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