

# *Chst8* Cas9-CKO Strategy

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# Project Overview

**Project Name**

***Chst8***

**Project type**

**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

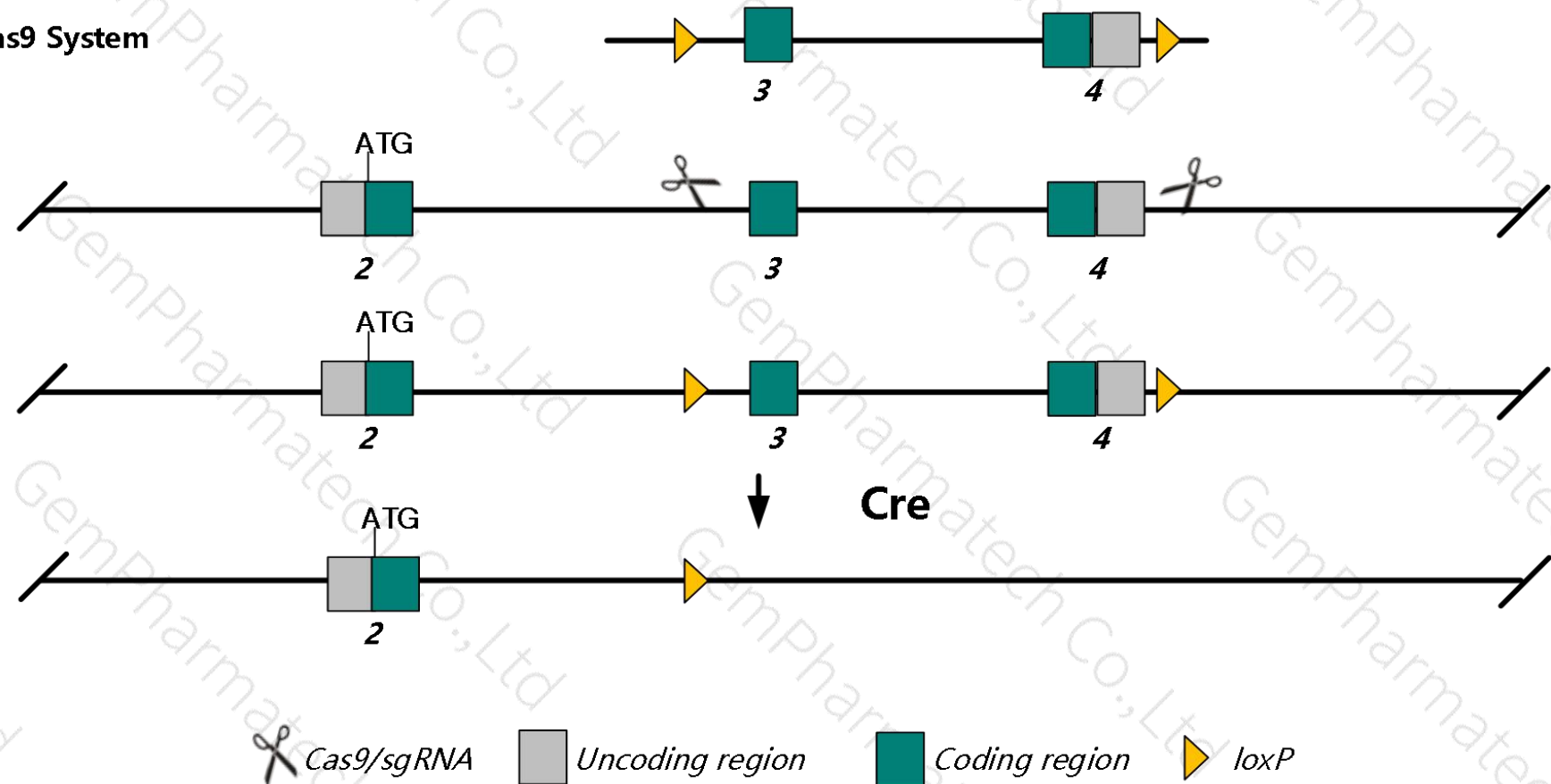
This model will use CRISPR/Cas9 technology to edit the *Chst8* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Floxed allele

KO allele



- 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 and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

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

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

### Summary

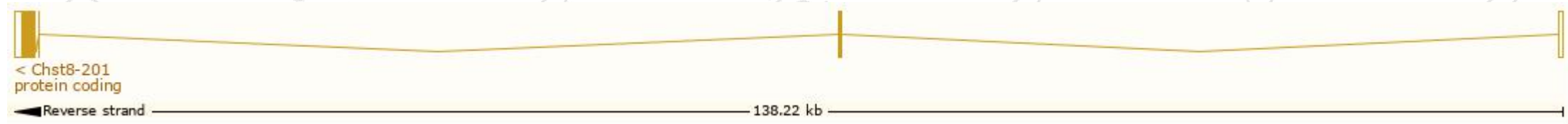
Official Symbol	Chst8 provided by <a href="#">MGI</a>
Official Full Name	carbohydrate sulfotransferase 8 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1916197</a>
See related	<a href="#">Ensembl:ENSMUSG00000060402</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
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 <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

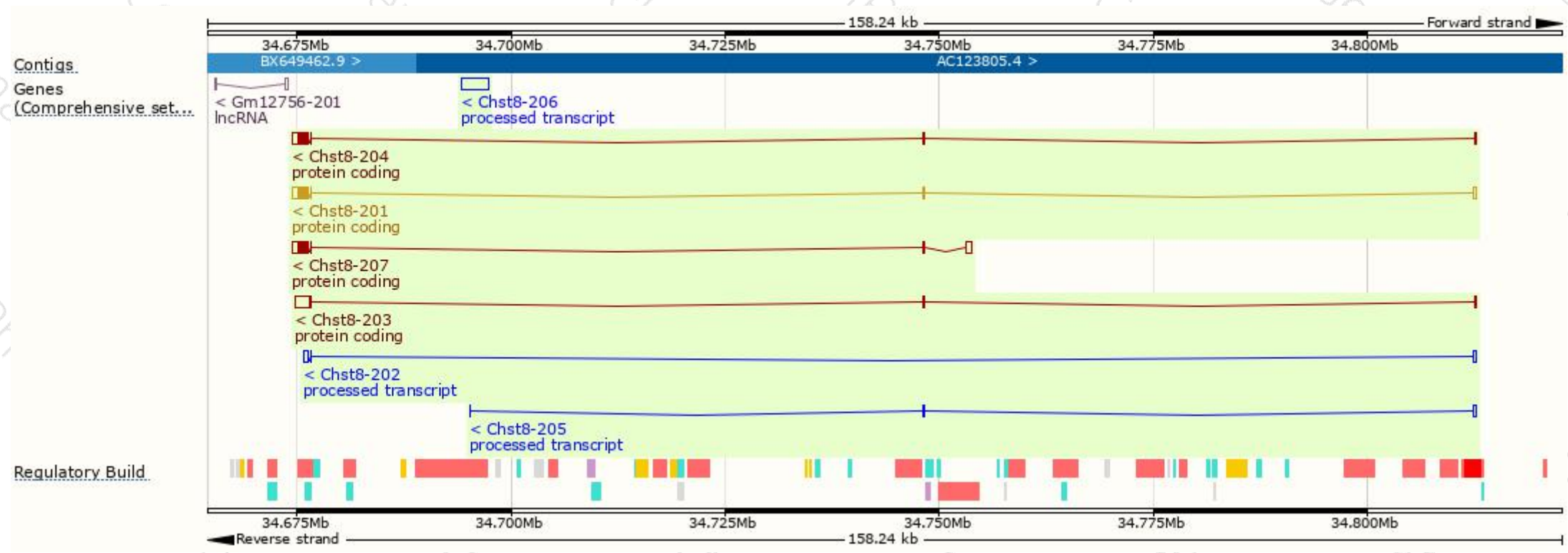
The gene has 7 transcripts,all transcripts are shown below:

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

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

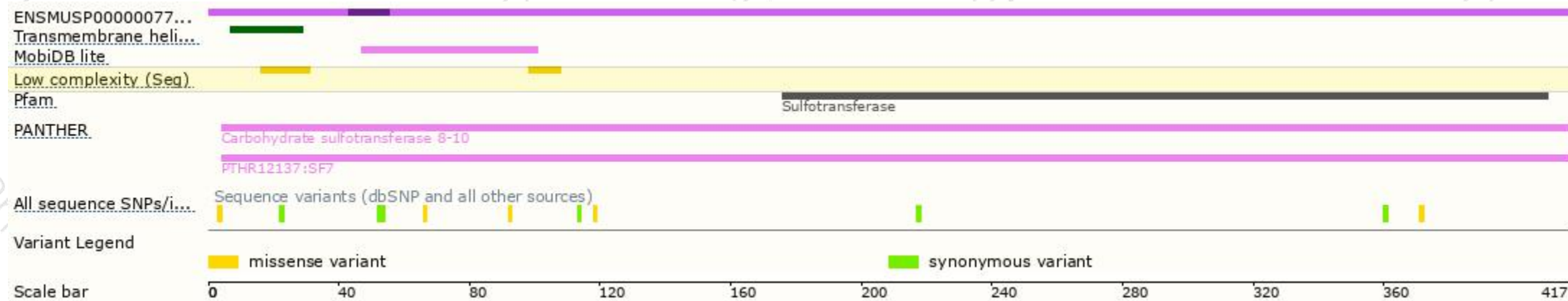


# Genomic location distribution

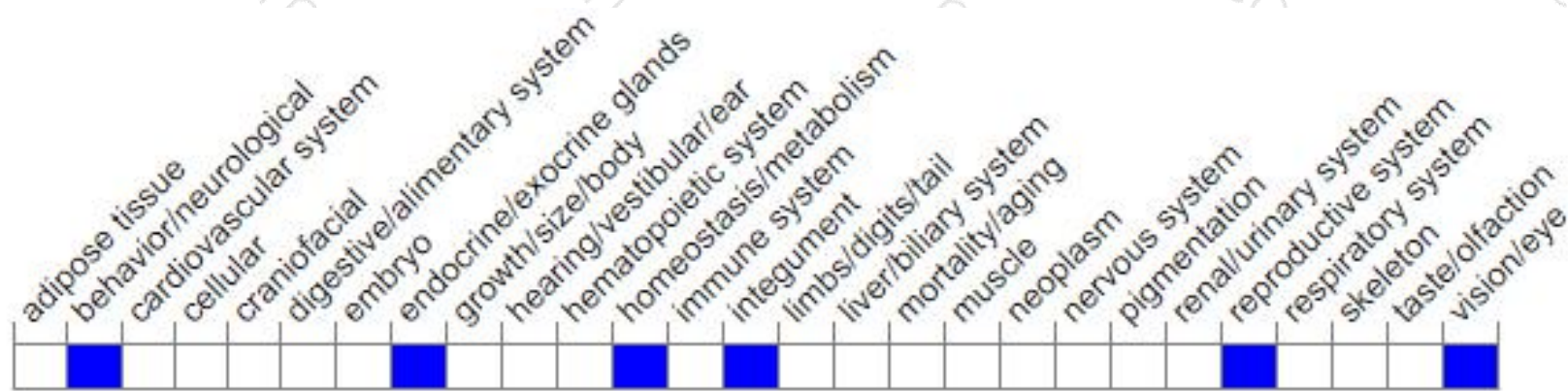




# Protein domain



# Mouse phenotype description(MGI)



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

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.

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

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