

Gsto1 Cas9-KO Strategy

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Project Overview

Project Name

Gsto1

Project type

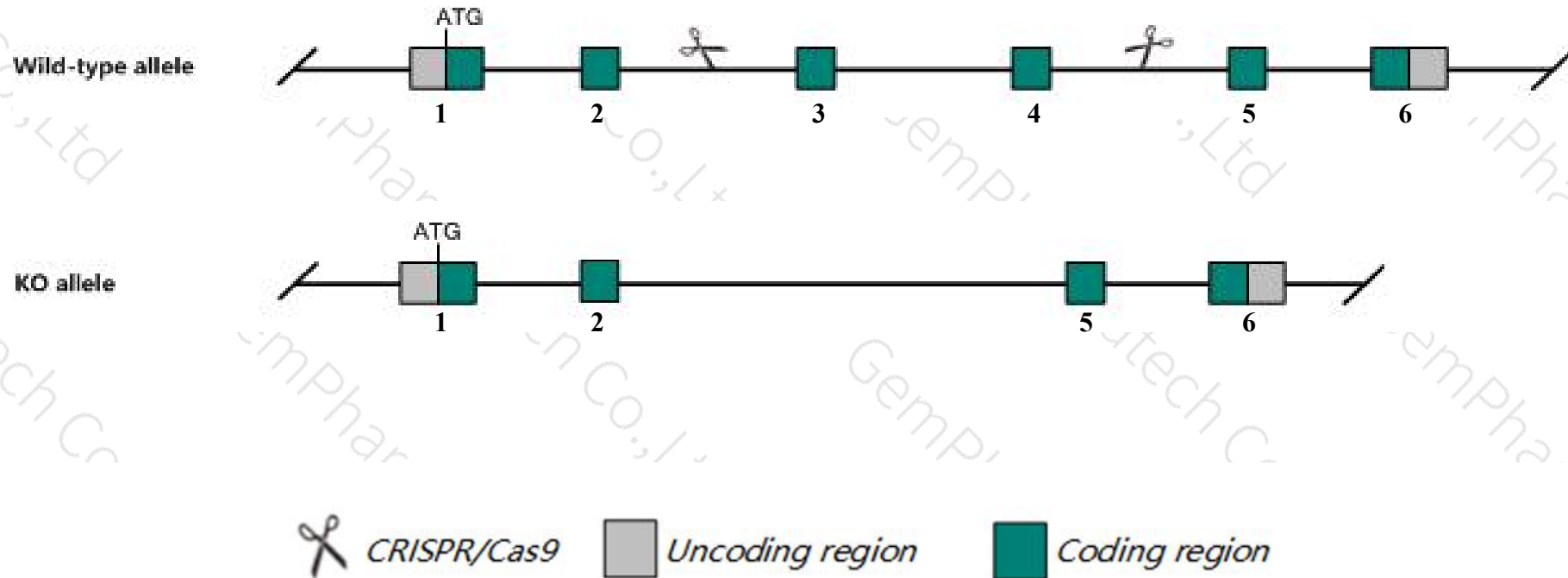
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gsto1* gene. The schematic diagram is as follows:



- The *Gsto1* gene has 6 transcripts. According to the structure of *Gsto1* gene, exon3-exon4 of *Gsto1-201* (ENSMUST00000026050.7) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gsto1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a mutant allele do not display abnormal arsenate metabolism following acute arsenate exposure.
- The knockout region is near to the N-terminal of *Gsto2* gene, this strategy may influence the regulatory function of the N-terminal of *Gsto2* gene.
- Transcript *Gsto1*-202&203 may not be affected.
- The partial sequence of intron of *Cfap43* gene will be deleted.
- The *Gsto1* gene is located on the Chr19. 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)

Gsto1 glutathione S-transferase omega 1 [*Mus musculus* (house mouse)]

Gene ID: 14873, updated on 10-Oct-2019

Summary

Official Symbol	Gsto1 provided by MGI
Official Full Name	glutathione S-transferase omega 1 provided by MGI
Primary source	MGI:MGI:1342273
See related	Ensembl:ENSMUSG00000025068
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	p28; Gstx; Spg-r; Gsto-1; AA407097; AI194287; AU018802
Summary	This gene encodes a member of the omega class of glutathione S-transferase (GST) proteins. GSTs are involved in the metabolism of xenobiotics and carcinogens. There is evidence that the encoded protein is involved in the biotransformation of arsenic. [provided by RefSeq, Dec 2015]
Expression	Broad expression in stomach adult (RPKM 297.2), bladder adult (RPKM 158.9) and 20 other tissues See more
Orthologs	human all

Genomic context

Location: 19; 19 D1

See Gsto1 in [Genome Data Viewer](#)

Exon count: 6

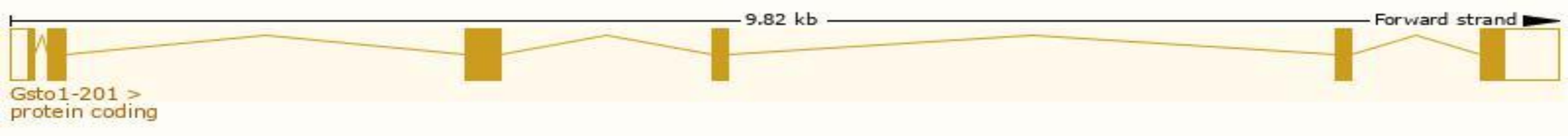
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (47854973..47864790)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (47929479..47939280)

Transcript information (Ensembl)

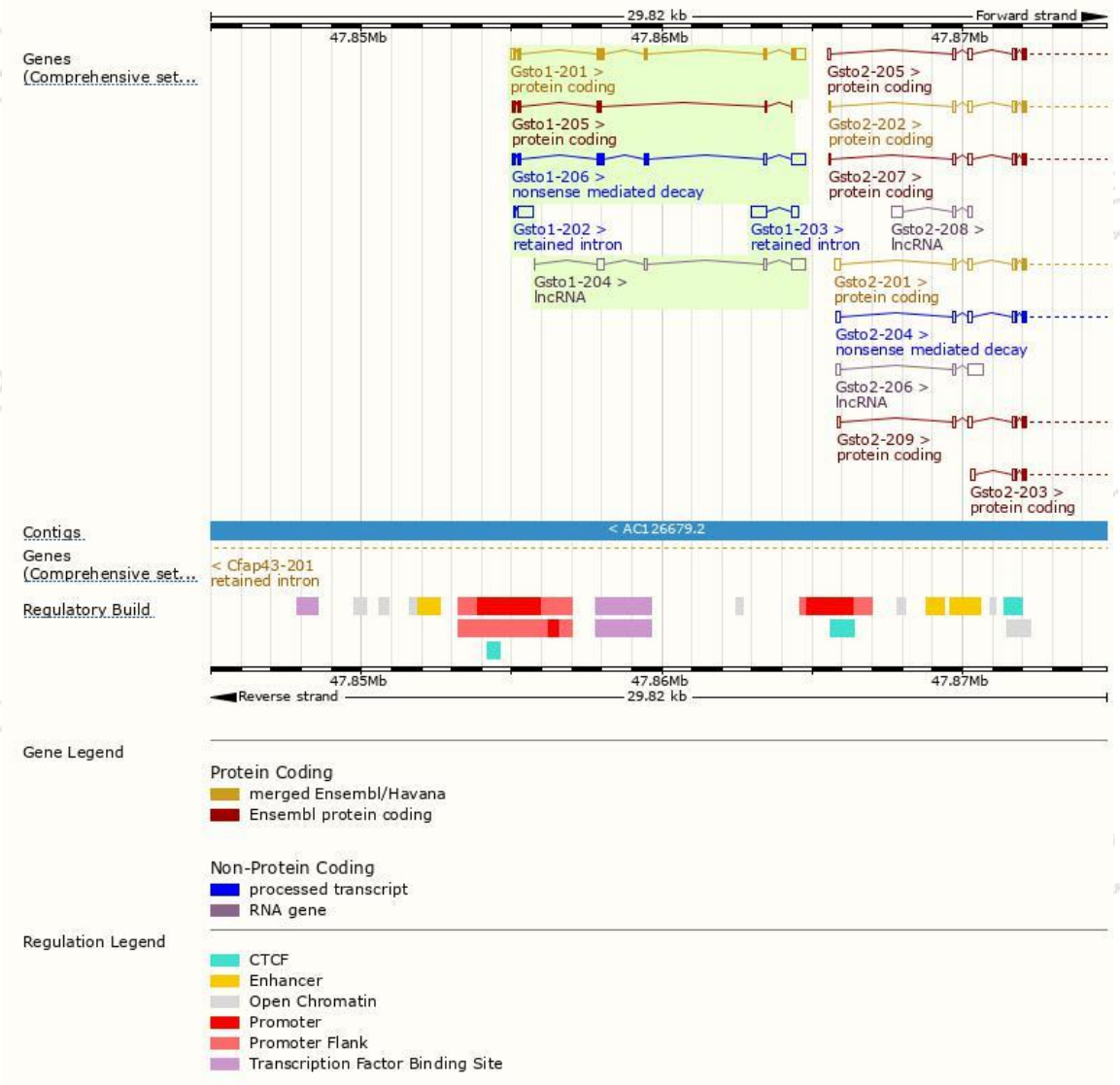
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gsto1-201	ENSMUST00000026050.7	1182	240aa	Protein coding	CCDS29893	O09131	TSL:1 GENCODE basic APPRIS P1
Gsto1-205	ENSMUST00000237121.1	384	108aa	Protein coding	-	-	CDS 3' incomplete
Gsto1-206	ENSMUST00000237472.1	1138	166aa	Nonsense mediated decay	-	-	
Gsto1-203	ENSMUST00000143694.1	759	No protein	Retained intron	-	-	TSL:2
Gsto1-202	ENSMUST00000130157.1	551	No protein	Retained intron	-	-	TSL:1
Gsto1-204	ENSMUST00000236902.1	950	No protein	lncRNA	-	-	

The strategy is based on the design of *Gsto1-201* transcript,The transcription is shown below



Genomic location distribution



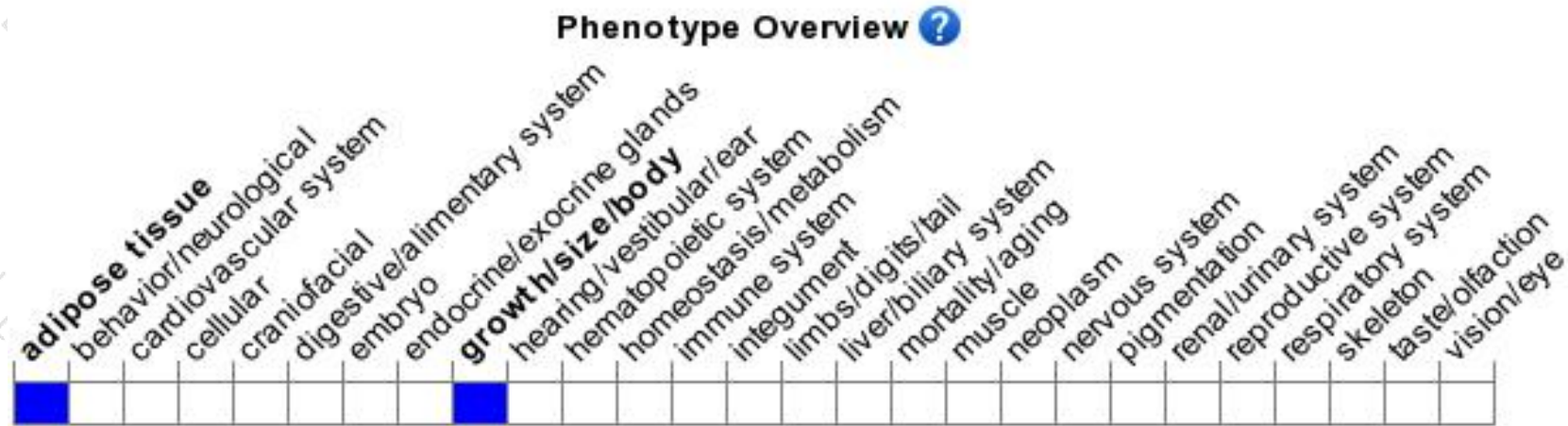
Protein domain



集萃药康
GemPharmatech



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 a mutant allele do not display abnormal arsenate metabolism following acute arsenate exposure.

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

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