

# Gsn Cas9-KO Strategy

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**Reviewer: Yumeng Wang** 

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## **Project Overview**

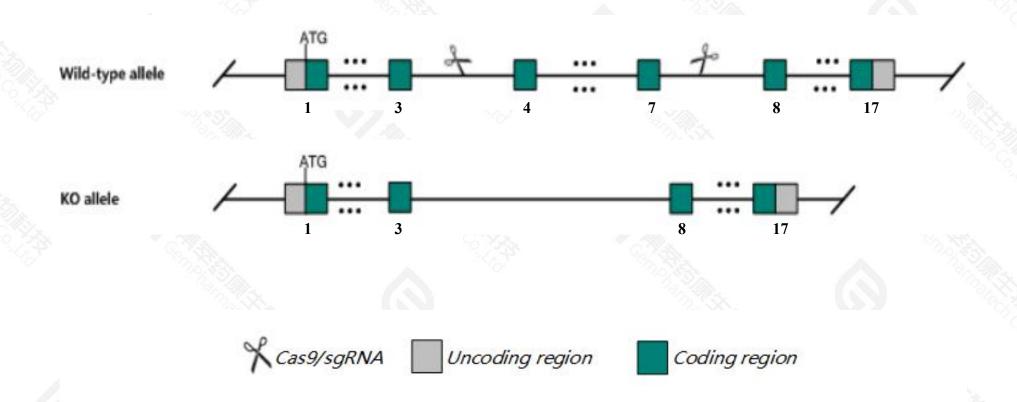


Project Name	Gsn			
Project type	Cas9-KO			
Strain background	C57BL/6JGpt			

## **Knockout strategy**



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



### **Technical routes**



- > The *Gsn* gene has 7 transcripts. According to the structure of *Gsn* gene, exon4-exon7 of *Gsn*201(ENSMUST00000028239.8) transcript is recommended as the knockout region. The region contains 535bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Gsn* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

### **Notice**



- > According to the existing MGI data, mice homozygous for disruptions in this gene display abnormalities in the immune system, platelet and platelet function, bone density, nervous and circulatory system. In addition, there are background related effects on viability and mammary gland development.
- > The *Gsn* gene is located on the Chr2. 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)



#### Gsn gelsolin [Mus musculus (house mouse)]

Gene ID: 227753, updated on 23-Feb-2021

#### Summary

☆ ?

Official Symbol Gsn provided by MGI

Official Full Name gelsolin provided by MGI

Primary source MGI:MGI:95851

See related Ensembl: ENSMUSG00000026879

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 ADF

Expression Biased expression in subcutaneous fat pad adult (RPKM 1628.5), bladder adult (RPKM 1379.3) and 12 other tissuesSee more

Orthologs <u>human</u> all

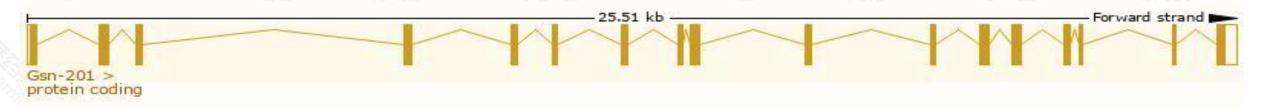
## Transcript information (Ensembl)



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

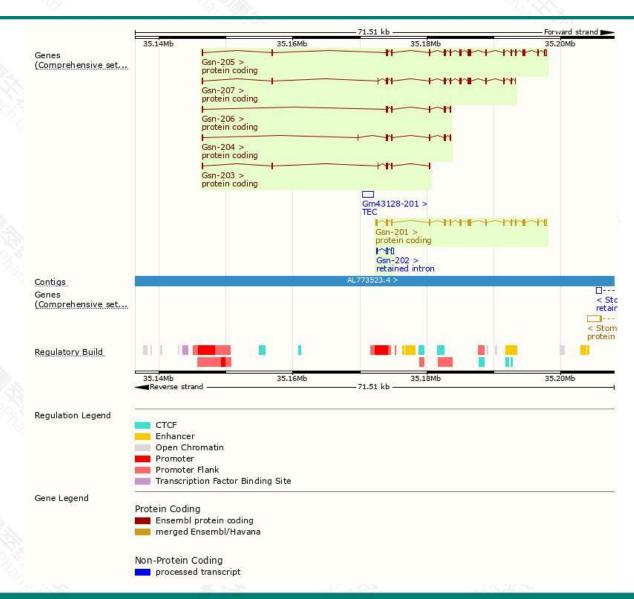
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000028239.8	2653	<u>780aa</u>	Protein coding	CCDS15960		TSL:1 , GENCODE basic ,
ENSMUST00000201185.4	2607	<u>731aa</u>	Protein coding	CCDS79785		TSL:1, GENCODE basic, APPRIS P1,
ENSMUST00000202990.4	1925	<u>568aa</u>	Protein coding	-		CDS 3' incomplete , TSL:5 ,
ENSMUST00000142324.8	883	<u>251aa</u>	Protein coding	-		CDS 3' incomplete , TSL:5 ,
ENSMUST00000202899.4	842	<u>251aa</u>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
ENSMUST00000139867.5	646	<u>166aa</u>	Protein coding	-		CDS 3' incomplete , TSL:5 ,
ENSMUST00000124323.5	646	No protein	Retained intron	-		TSL:2,
	ENSMUST00000028239.8  ENSMUST00000201185.4  ENSMUST00000202990.4  ENSMUST00000142324.8  ENSMUST00000202899.4  ENSMUST00000139867.5	ENSMUST00000028239.8 2653 ENSMUST00000201185.4 2607 ENSMUST00000202990.4 1925 ENSMUST00000142324.8 883 ENSMUST00000202899.4 842 ENSMUST00000139867.5 646	ENSMUST00000028239.8       2653       780aa         ENSMUST00000201185.4       2607       731aa         ENSMUST00000202990.4       1925       568aa         ENSMUST00000142324.8       883       251aa         ENSMUST00000202899.4       842       251aa         ENSMUST00000139867.5       646       166aa	ENSMUST00000028239.8         2653         780aa         Protein coding           ENSMUST00000201185.4         2607         731aa         Protein coding           ENSMUST00000202990.4         1925         568aa         Protein coding           ENSMUST00000142324.8         883         251aa         Protein coding           ENSMUST00000202899.4         842         251aa         Protein coding           ENSMUST00000139867.5         646         166aa         Protein coding	ENSMUST00000028239.8         2653         780aa         Protein coding         CCDS15960           ENSMUST00000201185.4         2607         731aa         Protein coding         CCDS79785           ENSMUST00000202990.4         1925         568aa         Protein coding         -           ENSMUST00000142324.8         883         251aa         Protein coding         -           ENSMUST00000202899.4         842         251aa         Protein coding         -           ENSMUST00000139867.5         646         166aa         Protein coding         -	ENSMUST00000028239.8         2653         780aa         Protein coding         CCDS15960           ENSMUST00000201185.4         2607         731aa         Protein coding         CCDS79785           ENSMUST00000202990.4         1925         568aa         Protein coding         -           ENSMUST00000142324.8         883         251aa         Protein coding         -           ENSMUST00000202899.4         842         251aa         Protein coding         -           ENSMUST00000139867.5         646         166aa         Protein coding         -

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



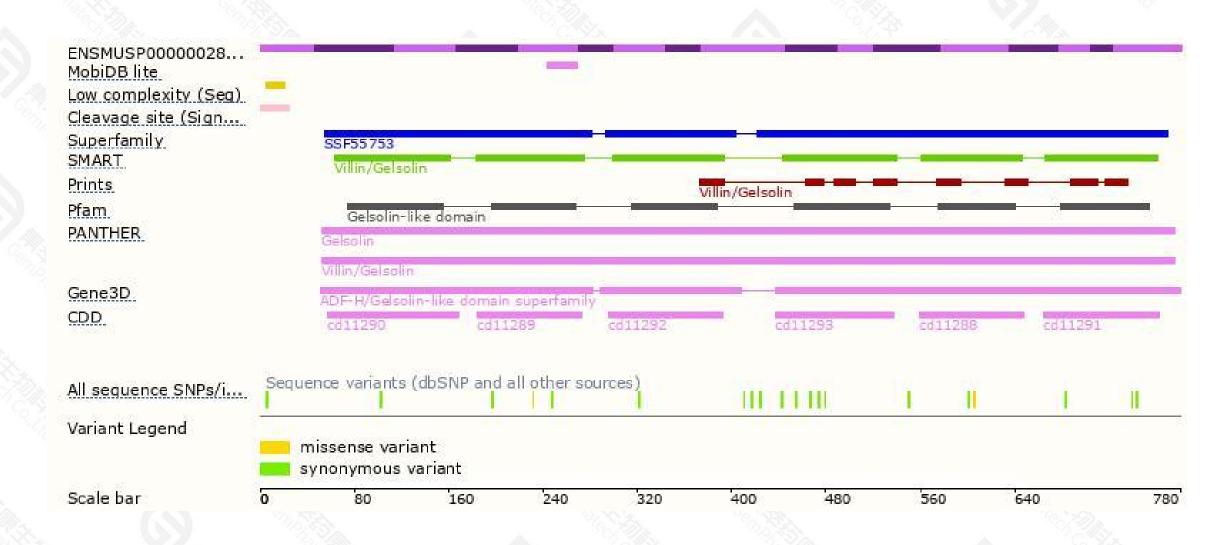
### Genomic location distribution





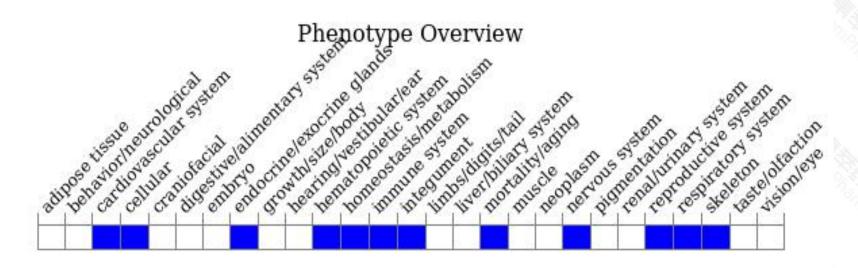
### Protein domain





## 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 display abnormalities in the immune system, platelet and platelet function, bone density, nervous and circulatory system. In addition, there are background related effects on viability and mammary gland development.



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

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