

# S100g Cas9-KO Strategy

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### Overview

### Target Gene Name

• *S100g* 

**Project Type** 

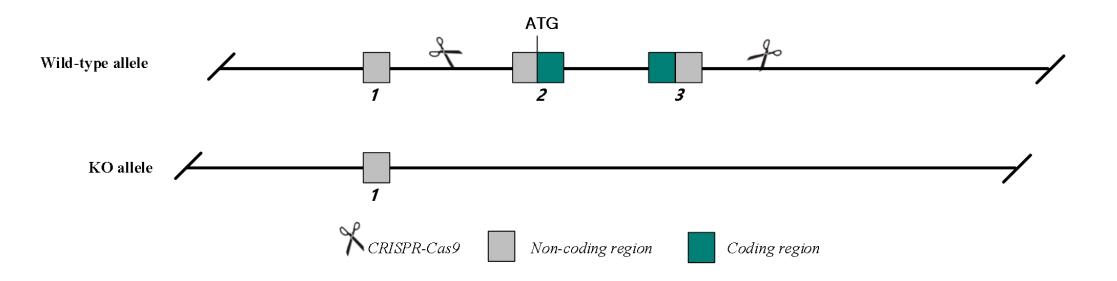
• Cas9-KO

**Genetic Background** 

• C57BL/6JGpt



## Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the S100g gene.

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### **Technical Information**

- The *S100g* gene has 1 transcript. According to the structure of *S100g* gene, exon2-3 of *S100g*-201 (ENSMUST0000038769.3) transcript is recommended as the knockout region. Knocking out the region will result in deletion all coding region of *S100g*, which may disrupt the function of *S100g*.
- In this project we use CRISPR-Cas9 technology to modify *S100g* gene. The brief process is as follows: Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



### Gene Information

#### S100g S100 calcium binding protein G [ Mus musculus (house mouse) ]

Gene ID: 12309, updated on 18-Aug-2023

#### Summary

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Official Symbol	S100g provided by MGI		
Official Full Name	S100 calcium binding protein G provided by MGI		
Primary source	MGI:MGI:104528		
See related	Ensembl:ENSMUSG00000040808 AllianceGenome:MGI:104528		
Gene type	protein coding		
<b>RefSeq status</b>	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	CABP1; Calb3; Cabp9k; CaBP-D9K		
Summary	Summary Predicted to enable calcium ion binding activity and calcium-dependent protein binding activity. Located in apical plasma membrane		
	basolateral plasma membrane. Is expressed in extraembryonic component; gut; metanephros; and ureter. Orthologous to human S100G		
	(S100 calcium binding protein G). [provided by Alliance of Genome Resources, Apr 2022]		
Expression	Biased expression in placenta adult (RPKM 553.0), kidney adult (RPKM 166.8) and 2 other tissues See more		
Orthologs	human all		
NEW	Try the new Gene table		
	Try the new Transcript table		

Source: https://www.ncbi.nlm.nih.gov/

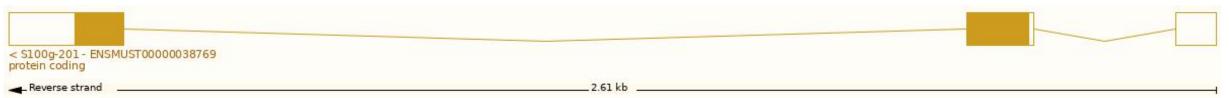


### **Transcript Information**

The gene has 1 transcript, the transcript is shown below:



### The strategy is based on the design of *S100g*-201 transcript, the transcription is shown below:

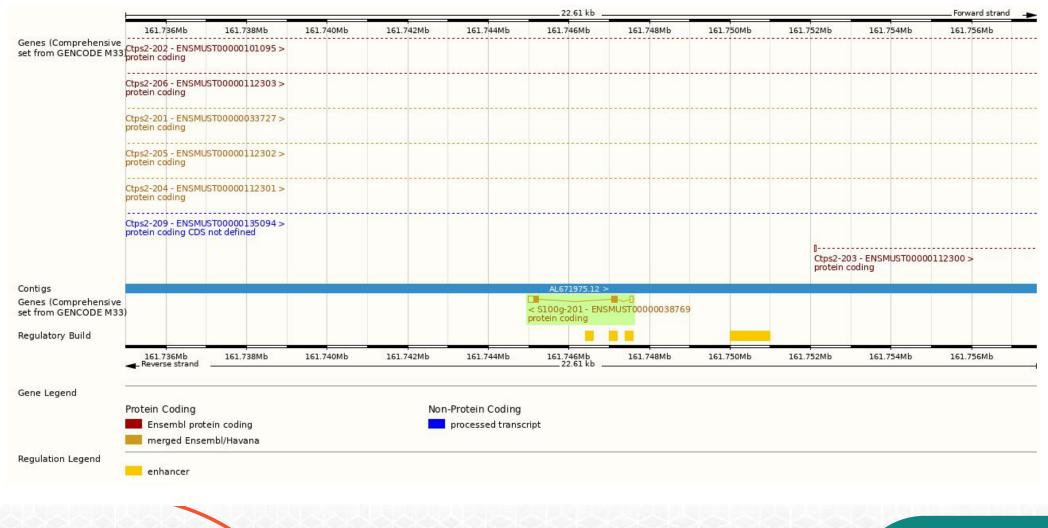


Source: https://www.ensembl.org



### Genomic Information

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Source: : https://www.ensembl.org

### Protein Information

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ENSMUSP0000004512 AFDB-ENSP mappings		
Superfamily	EP-hand domain pair	
SMART	S100/CaBP-9k-type, calcium binding, subdomain	EF-hand domain
Pfam	S100/CaBP-9k-type, calcium binding, subdomain	EF-hand domain
PROSITE profiles		Er-hand domain
PROSITE patterns		5100/Calcium binding protein 7/8-like, conserved site
PANTHER	PTAR11639	
Gene3D	1.10.238.10	
CDD	5-100	
All sequence SNPs/	Sequence variants (EVA and all other sources)	
Variant Legend	stop gained frameshift variant	missense variant
	synonymous variant	
Scale bar	<b>0</b> 8 16 24 32 40	48 56 64 79

Source: : https://www.ensembl.org

### **Important Information**

- Homozygous null mice do not exhibit any obvious abnormalities; in particular, these mice do not exhibit skeletal defects or any abnormalities of calcium homeostasis.
- The knockout region located in the intron of *Ctps1*, which may affect the regulation of this gene, the risk is unknown.
- *S100g* is located on ChrX. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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.

