

Sytl1 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-2-24

Project Overview

Project Name

Sytl1

Project type

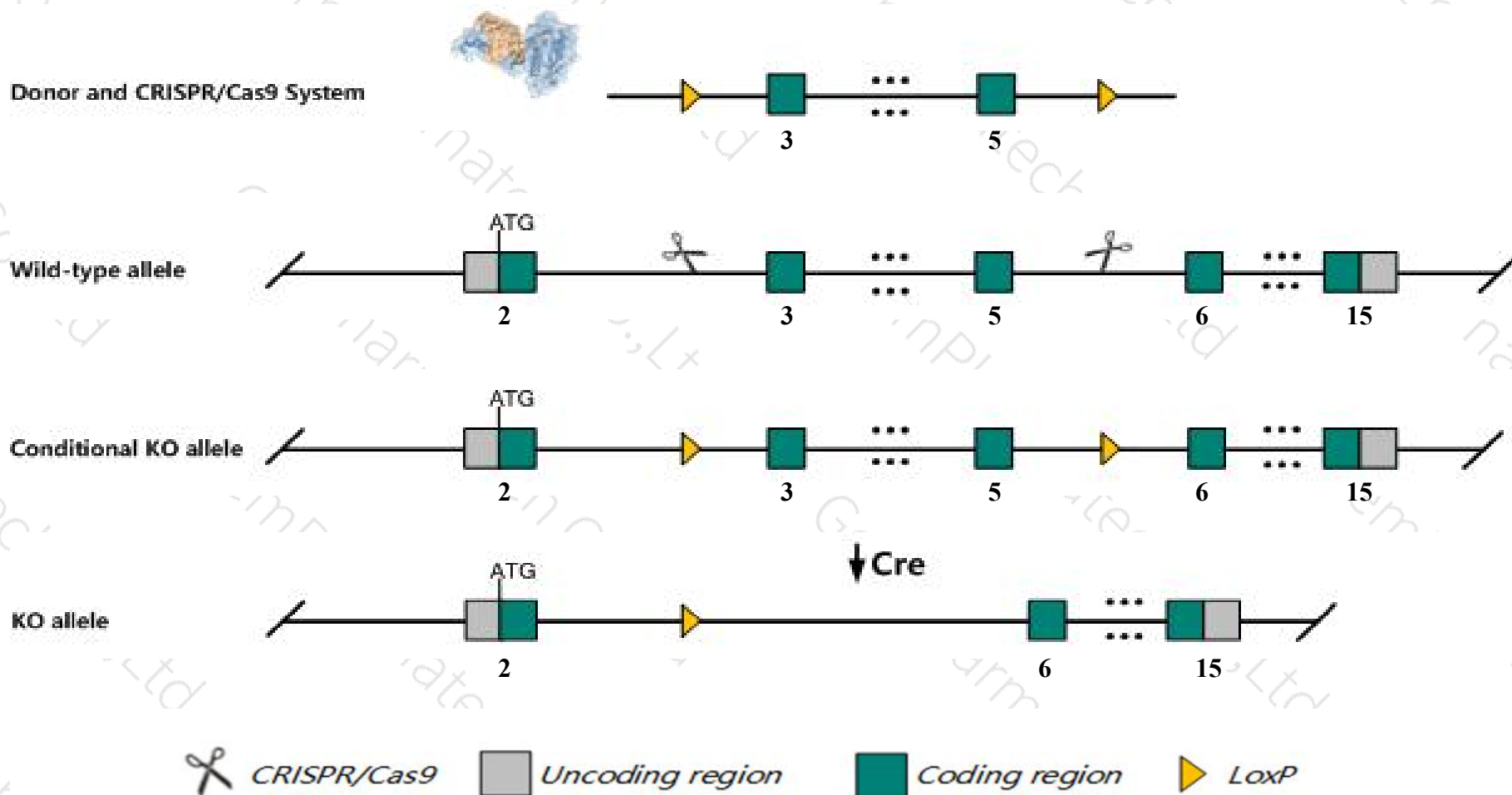
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sytl1* gene. The schematic diagram is as follows:



- The *Sytl1* gene has 4 transcripts. According to the structure of *Sytl1* gene, exon3-exon5 of *Sytl1-201* (ENSMUST00000030674.7) transcript is recommended as the knockout region. The region contains 271bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sytl1* 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, Mice homozygous for a null allele exhibit increased number of acinar zygomen granules in a fasted state that can be released by strong stimuli of the fed state.
- The *Syt11* gene is located on the Chr4. 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)

Syt11 synaptotagmin-like 1 [Mus musculus (house mouse)]

Gene ID: 269589, updated on 31-Jan-2019

Summary



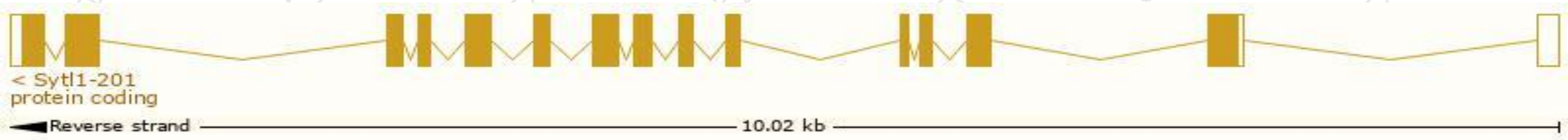
Official Symbol	Syt11 provided by MGI
Official Full Name	synaptotagmin-like 1 provided by MGI
Primary source	MGI:MGI:1933365
See related	Ensembl:ENSMUSG00000028860
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9030417L18, PSGL-1, Slp1
Expression	Biased expression in stomach adult (RPKM 54.8), colon adult (RPKM 46.3) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

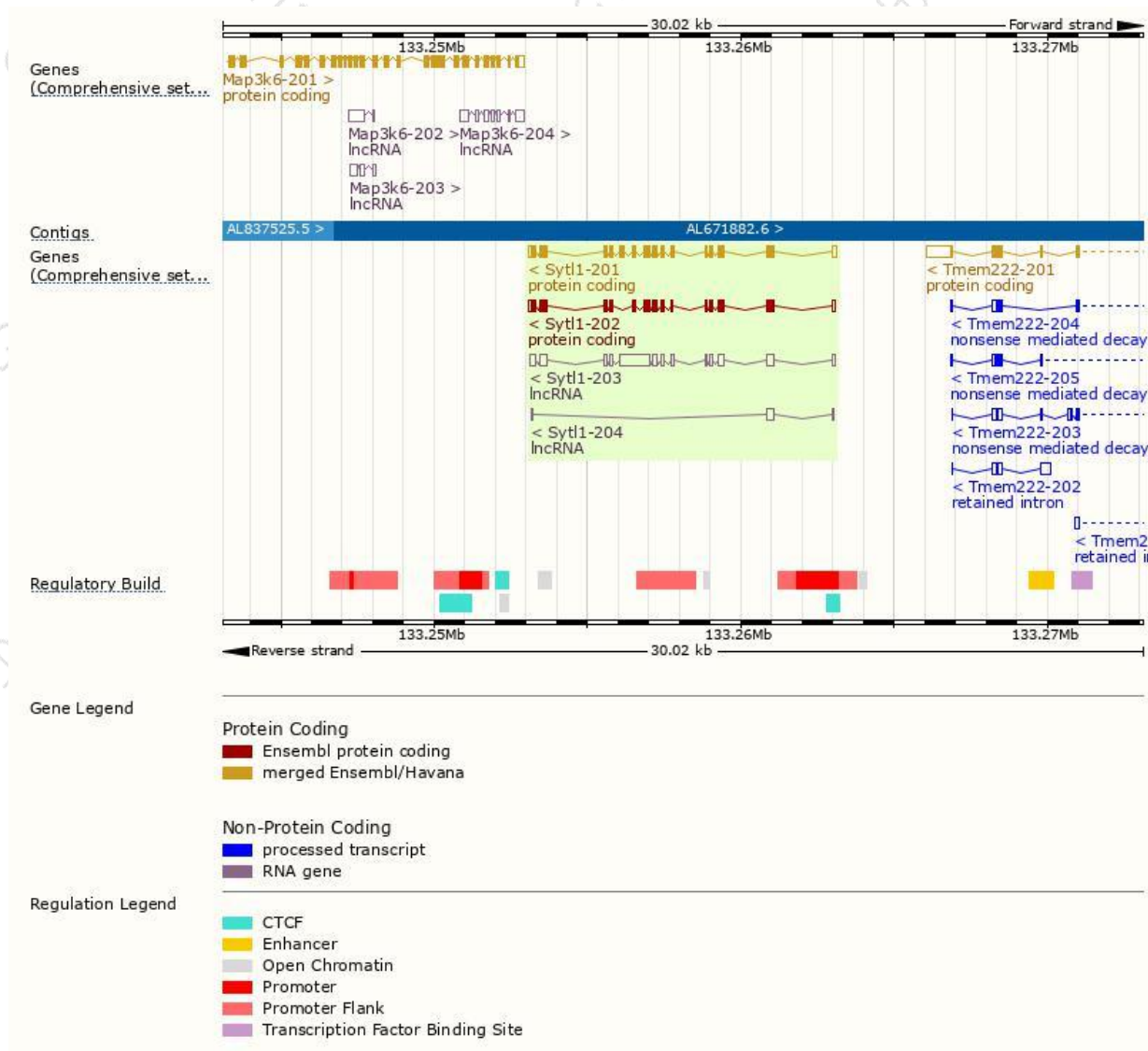
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sytl1-201	ENSMUST00000030674.7	1951	568aa	Protein coding	CCDS38902	A2AE94	TSL:1 GENCODE basic APPRIS P1
Sytl1-202	ENSMUST00000105908.9	1730	503aa	Protein coding	-	A2AE95	TSL:5 GENCODE basic
Sytl1-203	ENSMUST00000142039.7	2484	No protein	lncRNA	-	-	TSL:2
Sytl1-204	ENSMUST00000154911.1	367	No protein	lncRNA	-	-	TSL:3

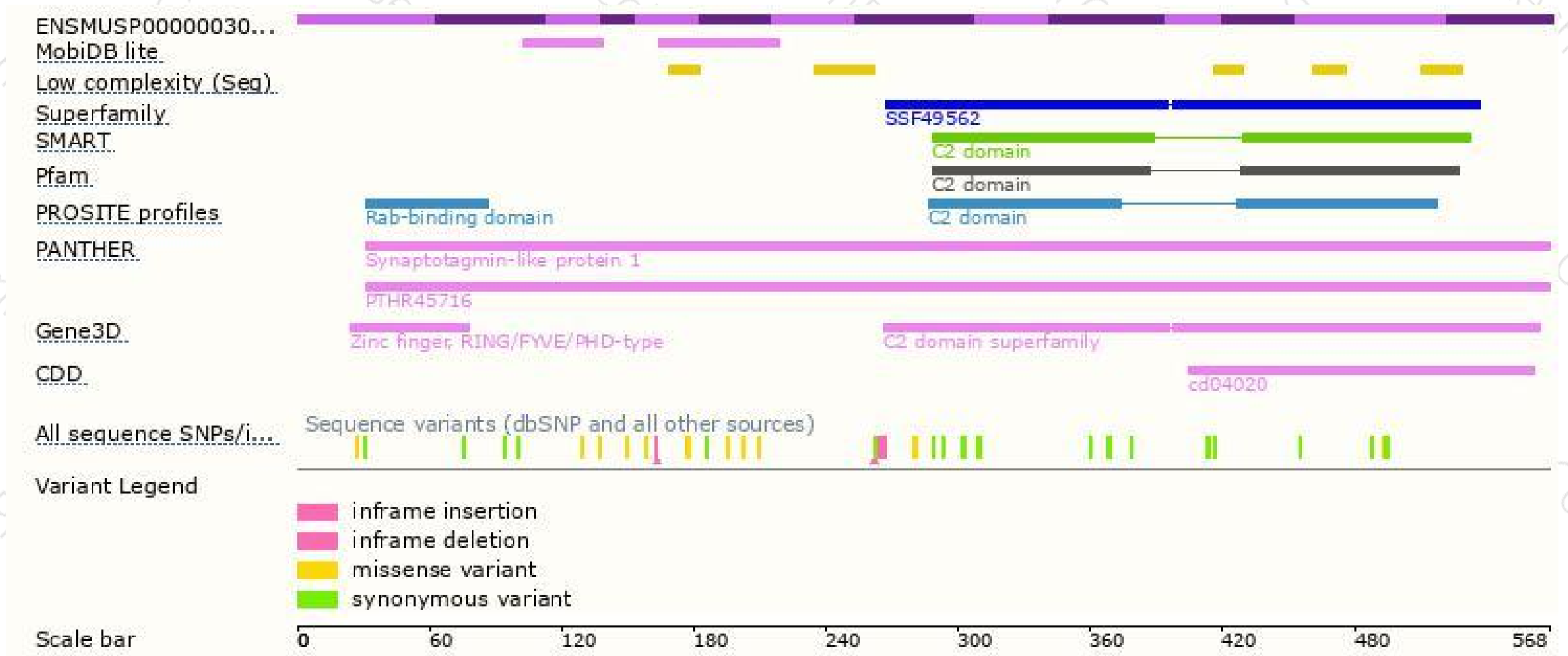
The strategy is based on the design of *Sytl1-201* transcript,The transcription is shown below



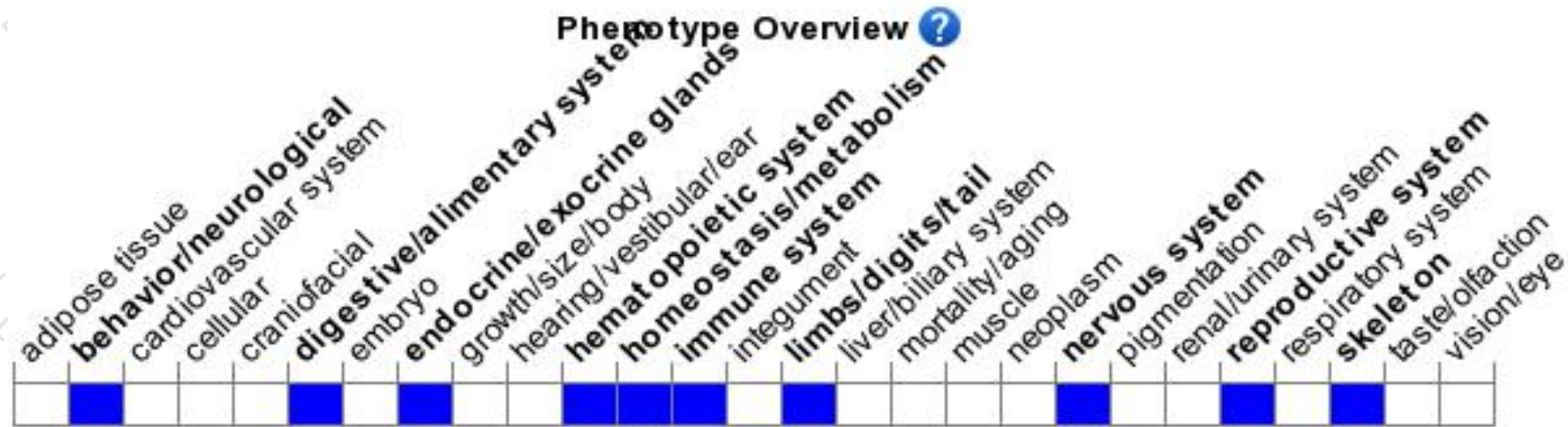
Genomic location distribution



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 a null allele exhibit increased number of acinar zygomen granules in a fasted state that can be released by strong stimuli of the fed state.

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

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