

Sting1 Cas9-KO Strategy

Designer: Daohua Xu

Reviewer: Yanhua Shen

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Overview

Target Gene Name

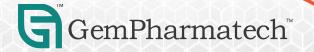
• Sting1

Project Type

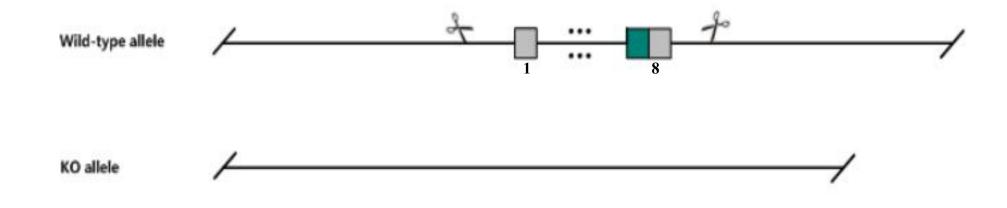
• Cas9-KO

Genetic Background

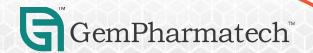
• C57BL/6JGpt



Strain Strategy





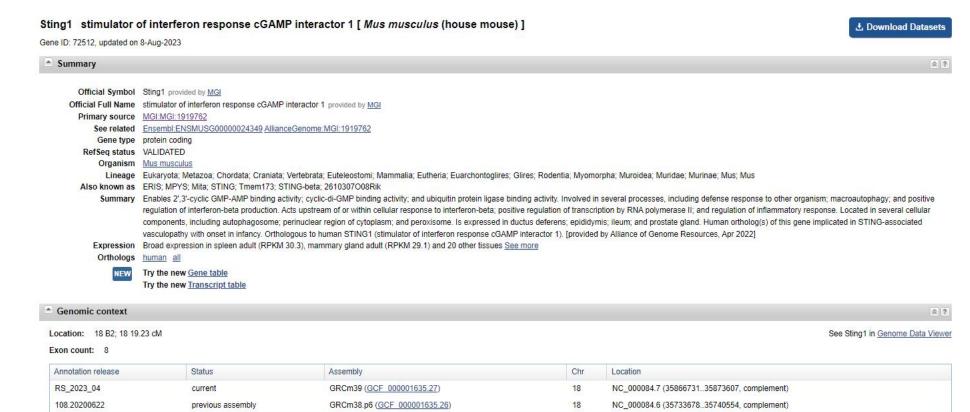


Technical Information

- The *Sting1* gene has 10 transcripts. According to the structure of *Sting1* gene, exon1-exon8 of *Sting1*-201 (ENSMUST00000115728.5) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Sting1* gene. The brief process is as follows: gRNAs were transcribed in vitro. 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 ontarget 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



Chromosome 18 - NC_000084.7

35940225

[35846139]

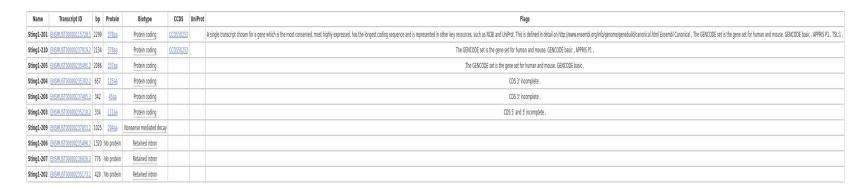
Ecser Sting1

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



Transcript Information

The gene has 10 transcripts, all transcripts are shown below:



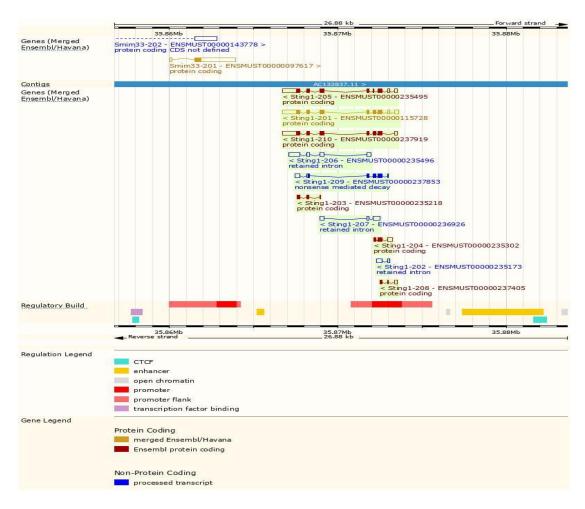
The strategy is based on the design of *Sting1*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



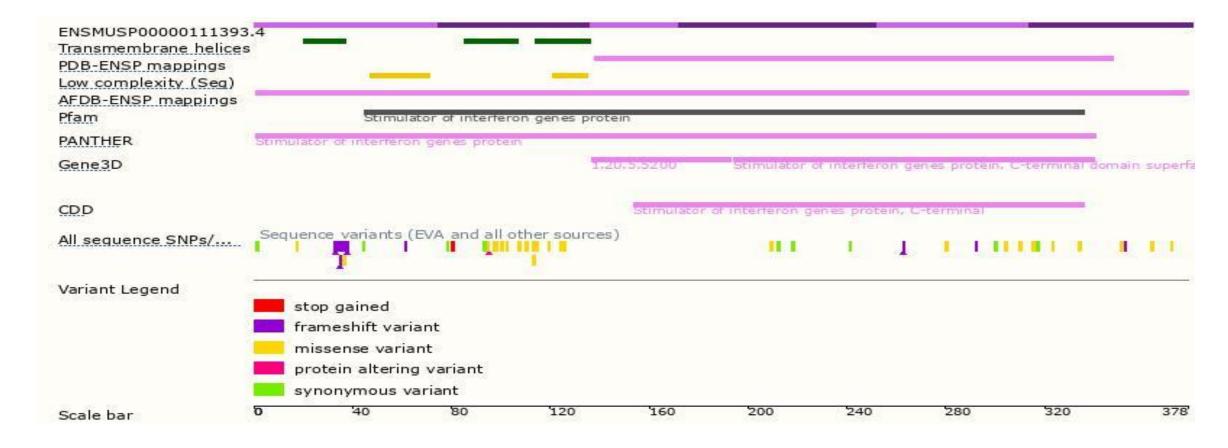
Genomic Information





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

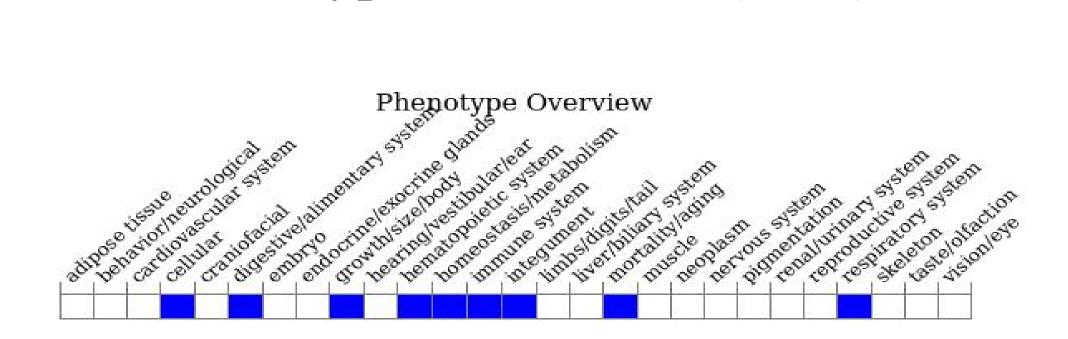
Protein Information





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

Mouse Phenotype Information (MGI)



• Mice homozygous for a knock-out allele exhibit increased susceptibility to viral infection and abnormal innate immunity. Mice homozygous for an ENU-induced allele exhibit altered response to bacterial and viral infection.



Source: https://www.informatics.jax.org

Important Information

- *Sting1* is located on Chr18. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

