GemPharmatech™

Elane Cas9-KO Strategy

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Reviewer:Ruirui Zhang

Design Date:2023-12-4

Overview

Target Gene Name

- Elane

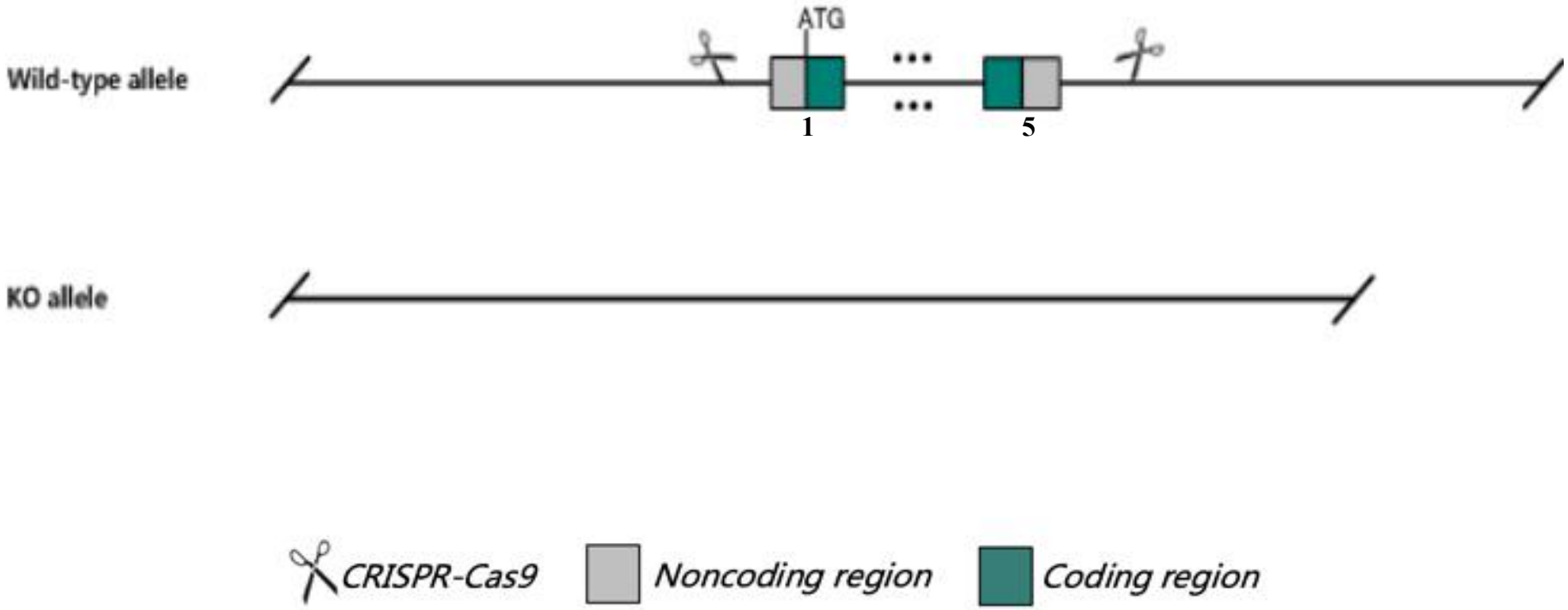
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Technical Information

- The *Elane* gene has 1 transcript. According to the structure of *Elane* gene, exon1-exon5 of *Elane*-201 (ENSMUST00000046091.7) 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 *Elane* 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 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

Elane elastase, neutrophil expressed [Mus musculus (house mouse)]

Gene ID: 50701, updated on 31-May-2023

Summary

Official Symbol	Elane provided by MGI
Official Full Name	elastase, neutrophil expressed provided byMGI
Primary source	MGI:MGI:2679229
See related	Ensembl:ENSMUSG00000020125
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	Ela2, F430011M15Rik, NE
Summary	This gene encodes a member of the chymotrypsin-like family of serine protease enzymes that hydrolyzes a broad range of protein substrates including elastin. This gene is expressed by neutrophils where the encoded enzyme is stored in azurophil granules. Upon neutrophil activation, the active enzyme is released into the extracellular mileu. Mice lacking the encoded protein exhibit increased susceptibility to sepsis and death following intraperitoneal infection with Gram negative bacteria. This gene is located adjacent to a related proteinase gene on chromosome 10. [provided by RefSeq, Jul 2016]
Expression	Biased expression in liver E18 (RPKM 61.1), liver E14.5 (RPKM 36.1) and 2 other tissuesSee more
Orthologs	human all

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

Transcript Information

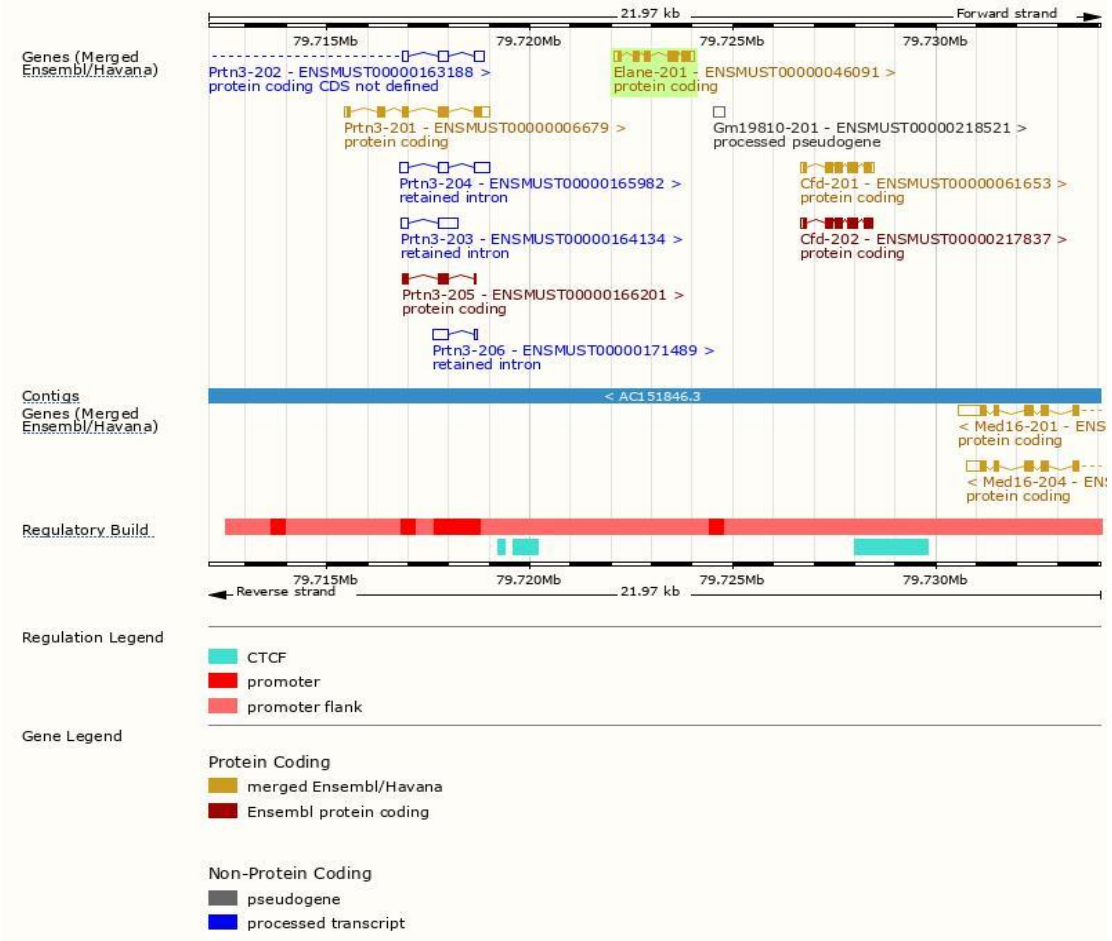
The gene has 1 transcript,and the transcript is shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000046091.7	Elane-201	984	265aa	Protein coding	CCDS23994	Q3UP87	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1

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

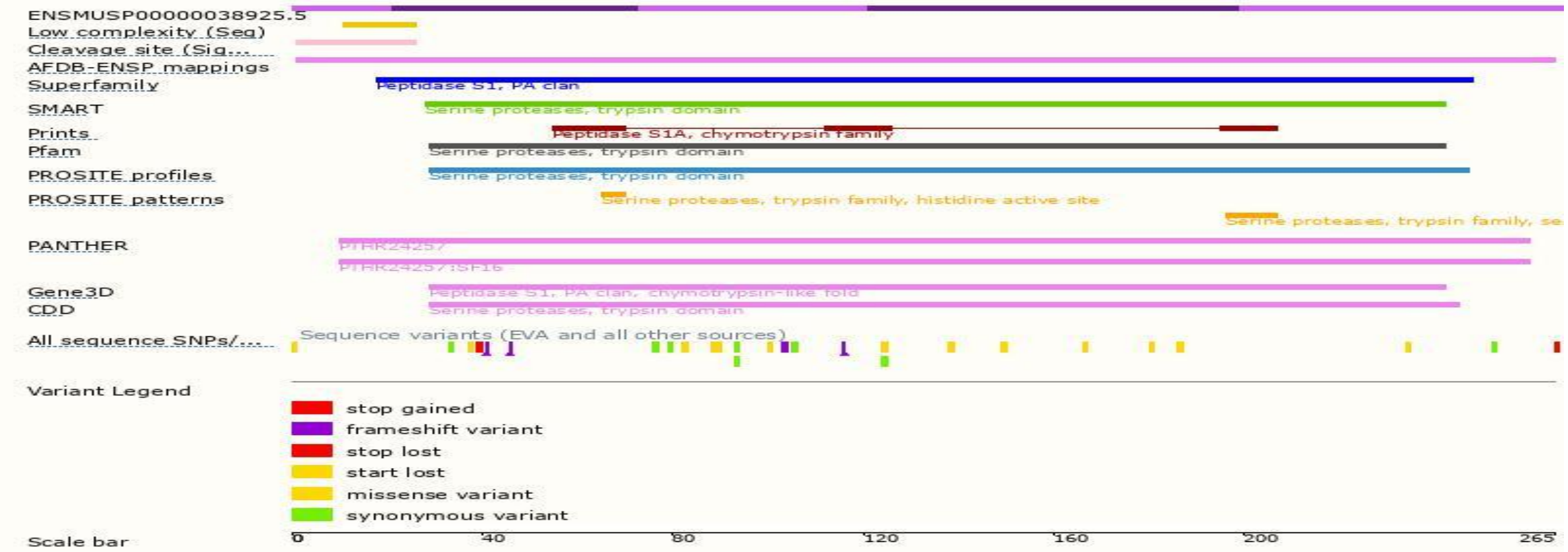
Source: https://www.ensembl.org

Genomic Information



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

Protein Information



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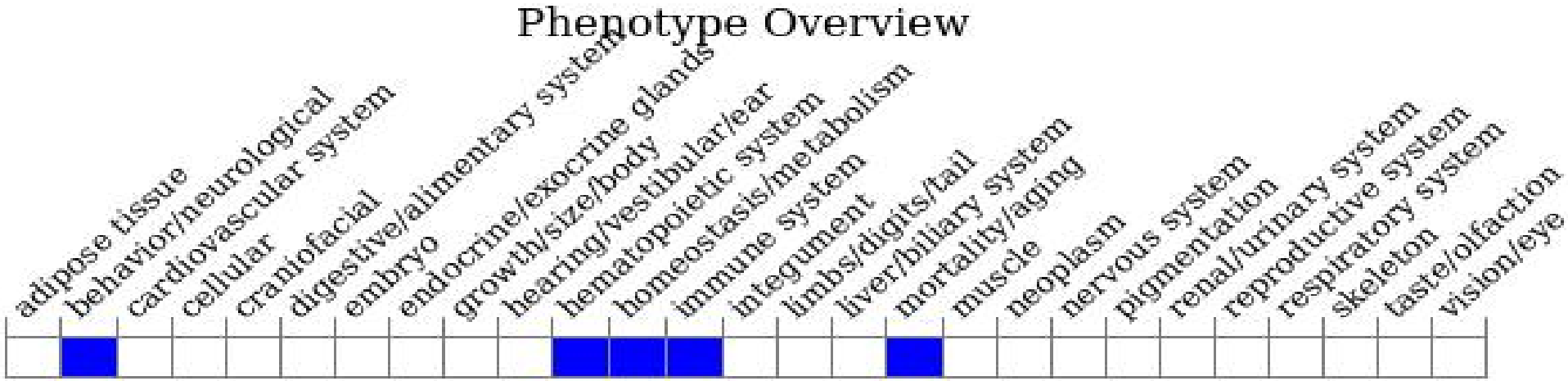
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Homozygotes for a null allele show impaired neutrophil physiology, susceptibility to Gram (-) bacterial infection, reduced sensitivity to xenobiotics, and abnormal local Shwartzman responses. Homozygotes for a knock-in allele show susceptibility to fungal infection and resistance to endotoxic shock.

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

Important Information

- According to the existing MGI data,homozygotes for a null allele show impaired neutrophil physiology, susceptibility to Gram (-) bacterial infection, reduced sensitivity to xenobiotics, and abnormal local Shwartzman responses. Homozygotes for a knock-in allele show susceptibility to fungal infection and resistance to endotoxic shock. *Gm19810* gene may be destroyed.
- The knockout region is near to the N-terminal of *Cfd* gene and the C-terminal of *Prtn3* gene,the strategy may have effect on the function of the N-terminal of *Cfd* gene and the C-terminal of *Prtn3* gene.
- *Elane* is located on Chr10. 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.