

Tmprss15 Cas9-KO Strategy

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Project Overview



Project Name

Tmprss15

Project type

Cas9-KO

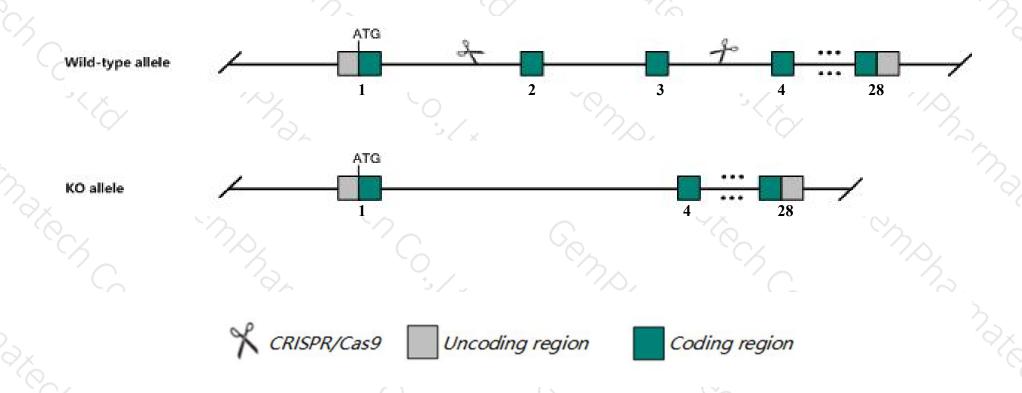
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Tmprss15* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Tmprss15* gene has 2 transcripts. According to the structure of *Tmprss15* gene, exon2-exon3 of *Tmprss15-201* (ENSMUST00000023566.10) transcript is recommended as the knockout region. The region contains 199bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Tmprss15* gene. The brief process is as follows: CRISPR/Cas9 sys

Notice



- The *Tmprss15* gene is located on the Chr16. 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)



Tmprss15 transmembrane protease, serine 15 [Mus musculus (house mouse)]

Gene ID: 19146, updated on 31-Jan-2019

Summary

↑ ?

Official Symbol Tmprss15 provided by MGI

Official Full Name transmembrane protease, serine 15 provided by MGI

Primary source MGI:MGI:1197523

See related Ensembl:ENSMUSG00000022857

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 Entk, Prss7

Summary This gene encodes an enzyme that proteolytically activates the pancreatic proenzyme trypsinogen, converting it into trypsin. The encoded

protein is cleaved into two chains that form a heterodimer linked by a disulfide bond. Alternatively spliced transcript variants encoding

multiple isoforms have been observed for this gene. [provided by RefSeq, Jan 2013]

Expression Biased expression in small intestine adult (RPKM 1.8) and duodenum adult (RPKM 0.4)See more

Orthologs <u>human all</u>

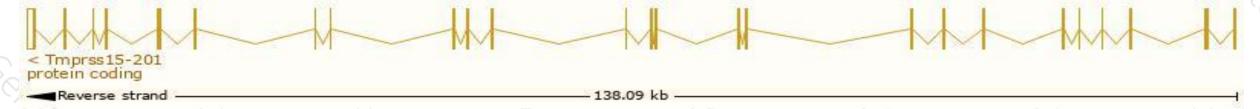
Transcript information (Ensembl)



The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tmprss15-201	ENSMUST00000023566.10	4177	<u>1069aa</u>	Protein coding	CCDS28280	P97435	TSL:1 GENCODE basic APPRIS P3
Tmprss15-202	ENSMUST00000060402.5	3681	<u>1054aa</u>	Protein coding	CCDS37380	E9Q6Y6	TSL:2 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Tmprss15-201* transcript, The transcription is shown below



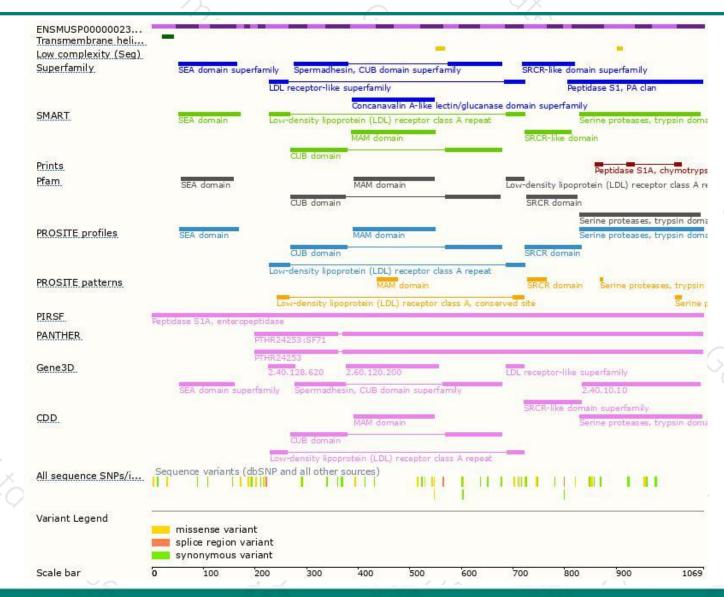
Genomic location distribution





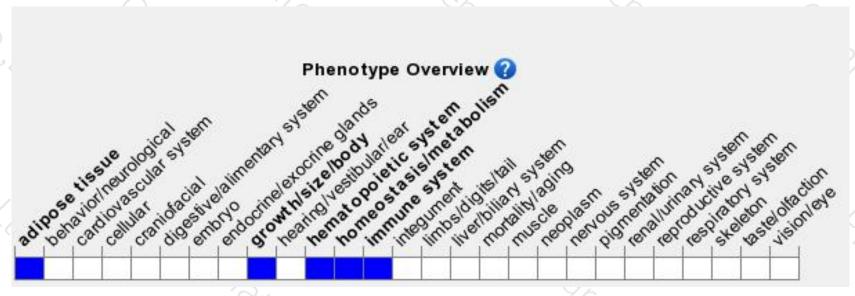
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).



If you have any questions, you are welcome to inquire. Tel: 400-9660890





