

# Mouse Tmprss2 Knockout Project (CRISPR/Cas9)

## Objective:

To create a Tmprss2 knockout Mouse model (C57BL/6J) by CRISPR/Cas-mediated genome engineering.

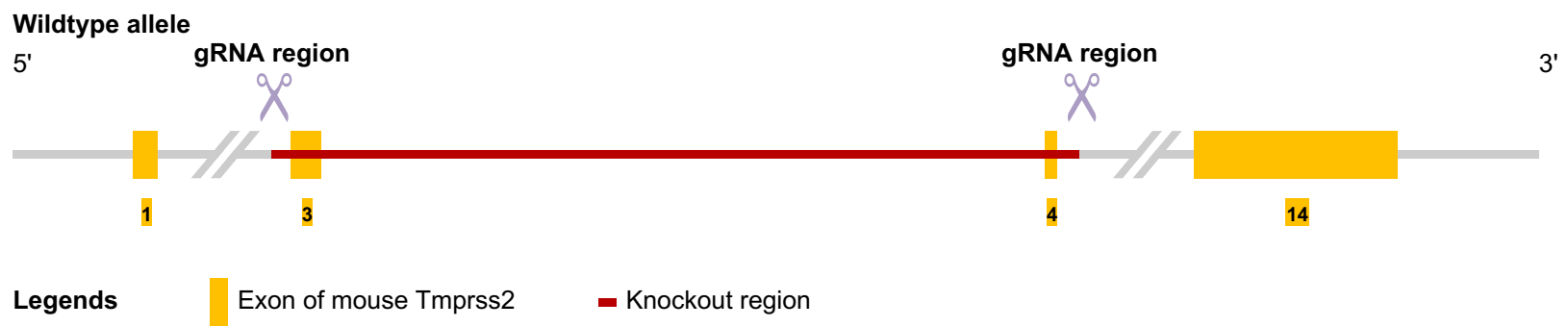
## Strategy summary:

- The Tmprss2 gene (NCBI Reference Sequence: NM\_015775 ; Ensembl: ENSMUSG00000000385 ) is located on Mouse chromosome 16.
- 14 exons are identified, with the ATG start codon in exon 2 and the TAA stop codon in exon 14 (Transcript: ENSMUST00000000395).
- Exon 3~4 will be selected as target site.
- Cas9 and gRNA will be co-injected into fertilized eggs for KO Mouse production.
- The pups will be genotyped by PCR followed by sequencing analysis.

**Note:** Mice homozygous for a disruption in this gene appear normal.

- Exon 3 starts from about 1.09% of the coding region. Exon 3~4 covers 20.88% of the coding region.
- The size of effective KO region: ~5536 bp.
- The KO region does not have any other known gene.

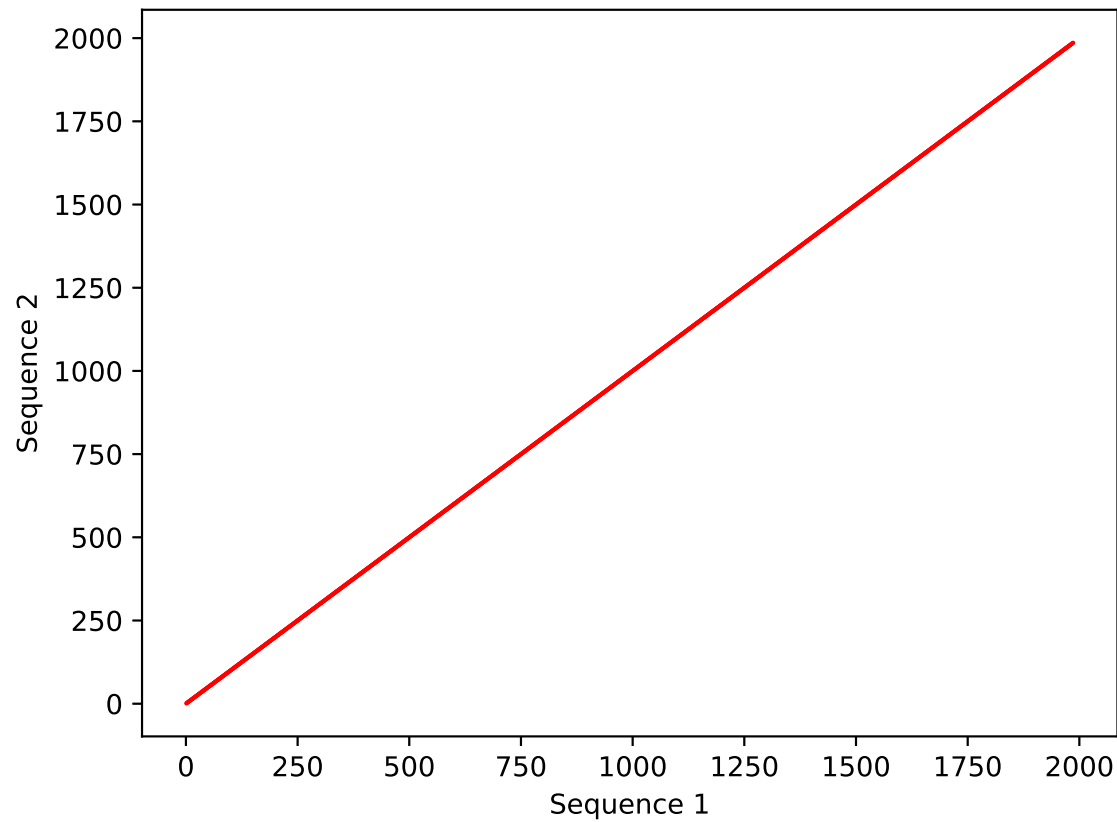
## Overview of the Targeting Strategy



### Overview of the Dot Plot (up)

Window size: 15 bp

● Forward ● Reverse Complement

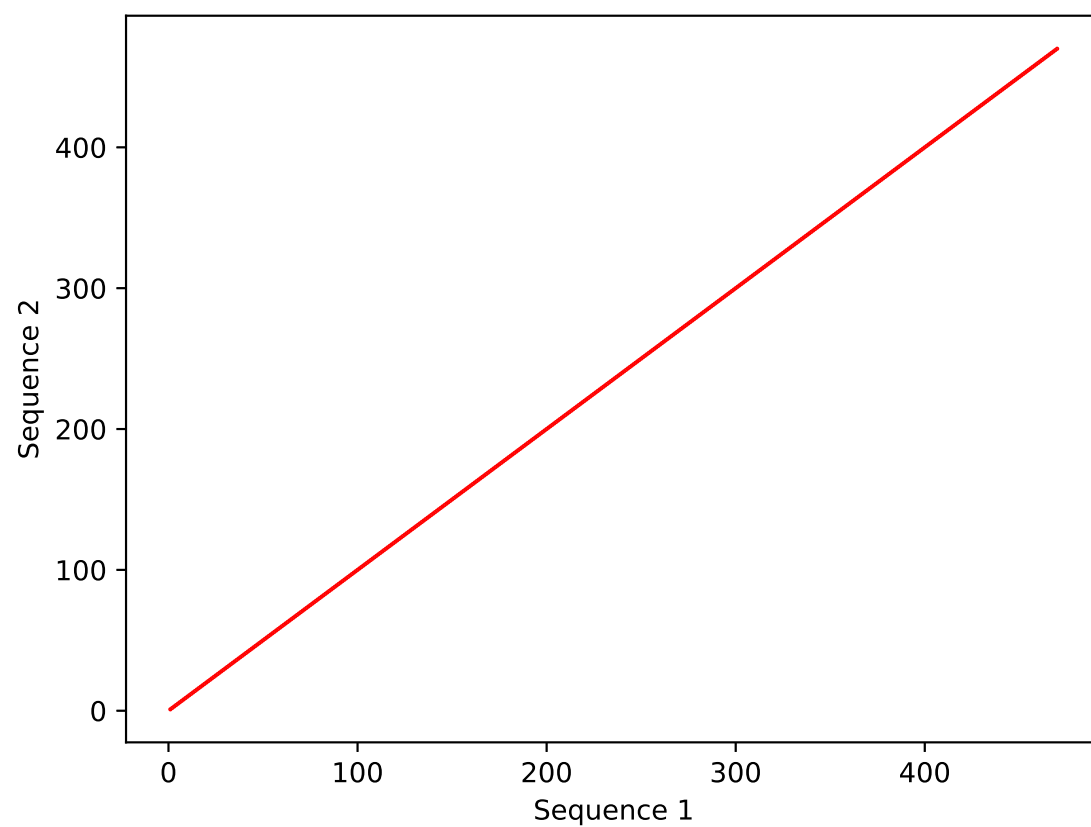


**Note:** The 2000 bp section upstream of Exon 3 is aligned with itself to determine if there are tandem repeats. No significant tandem repeat is found in the dot plot matrix. So this region is suitable for PCR screening or sequencing analysis.

### Overview of the Dot Plot (down)

Window size: 15 bp

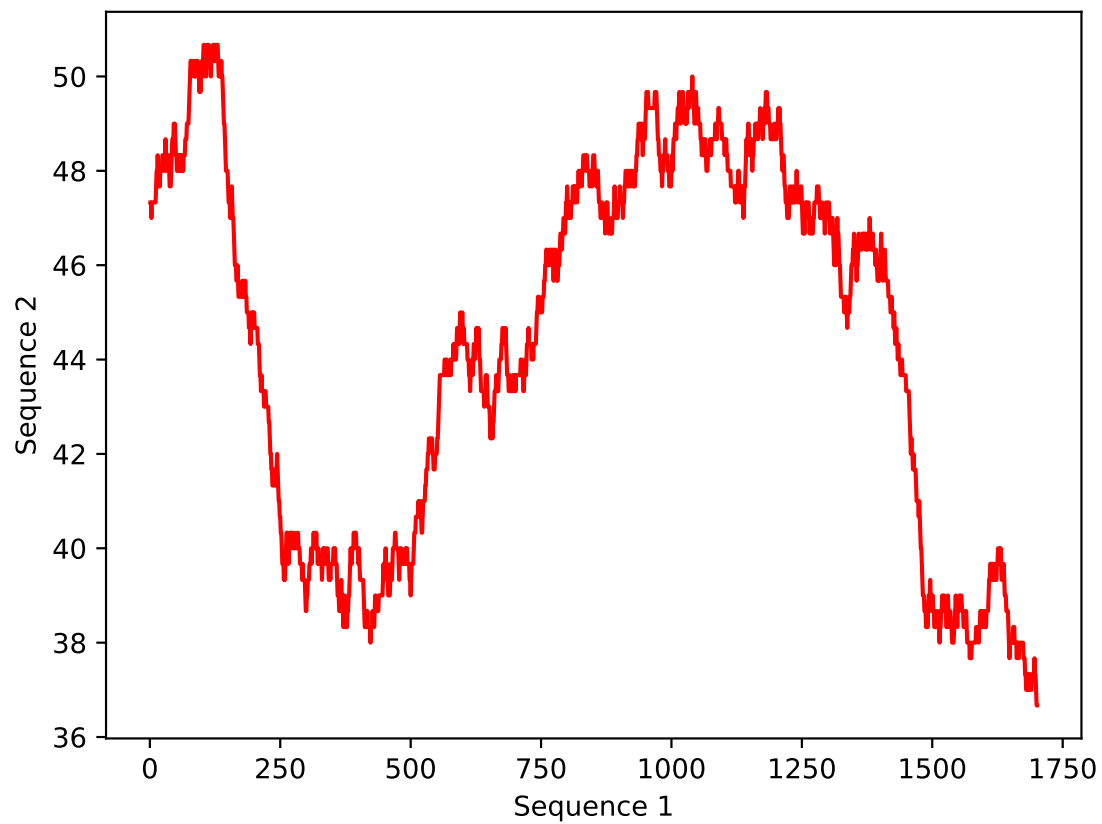
● Forward ● Reverse Complement



**Note:** The 484 bp section downstream of Exon 4 is aligned with itself to determine if there are tandem repeats. No significant tandem repeat is found in the dot plot matrix. So this region is suitable for PCR screening or sequencing analysis.

## Overview of the GC Content Distribution (up)

Window size: 300 bp

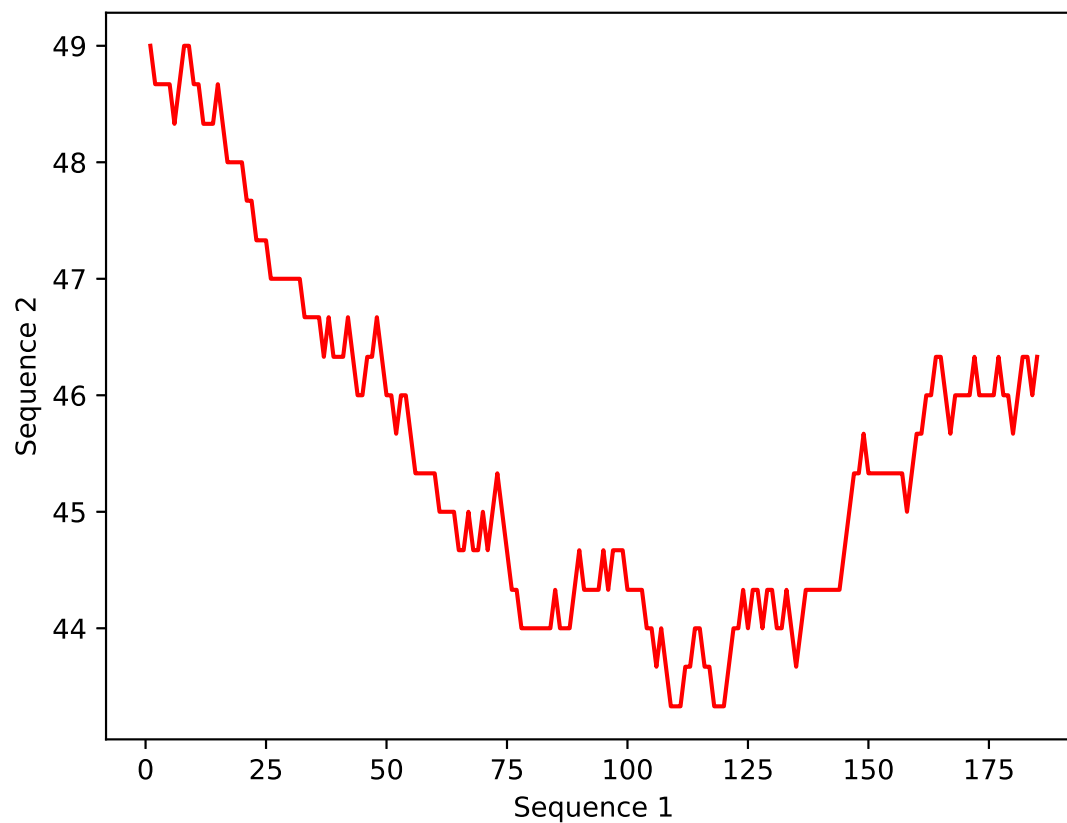


Summary: Full Length(2000bp) | A(28.3% 566) | C(20.65% 413) | T(27.75% 555) | G(23.3% 466)

**Note:** The 2000 bp section upstream of Exon 3 is analyzed to determine the GC content. No significant high GC-content region is found. So this region is suitable for PCR screening or sequencing analysis.

## Overview of the GC Content Distribution (down)

Window size: 300 bp



Summary: Full Length(484bp) | A(21.49% 104) | C(26.45% 128) | T(30.37% 147) | G(21.69% 105)

**Note:** The 484 bp section downstream of Exon 4 is analyzed to determine the GC content. No significant high GC-content region is found. So this region is suitable for PCR screening or sequencing analysis.

## BLAT Search Results (up)

| QUERY                           | SCORE   | START | END | QSIZE | IDENTITY | CHROM  | STRAND | START | END       | SPAN      |      |
|---------------------------------|---------|-------|-----|-------|----------|--------|--------|-------|-----------|-----------|------|
| <a href="#">browser details</a> | YourSeq | 2000  | 1   | 2000  | 2000     | 100.0% | chr16  | -     | 97596960  | 97598959  | 2000 |
| <a href="#">browser details</a> | YourSeq | 50    | 53  | 110   | 2000     | 93.2%  | chr15  | +     | 77047520  | 77047577  | 58   |
| <a href="#">browser details</a> | YourSeq | 49    | 50  | 111   | 2000     | 90.2%  | chr9   | -     | 9271190   | 9271252   | 63   |
| <a href="#">browser details</a> | YourSeq | 48    | 51  | 111   | 2000     | 90.2%  | chr5   | -     | 108776105 | 108776166 | 62   |
| <a href="#">browser details</a> | YourSeq | 47    | 10  | 111   | 2000     | 98.0%  | chr1   | +     | 24631041  | 24631465  | 425  |
| <a href="#">browser details</a> | YourSeq | 46    | 854 | 916   | 2000     | 85.8%  | chrX   | -     | 158995662 | 158995722 | 61   |
| <a href="#">browser details</a> | YourSeq | 43    | 29  | 111   | 2000     | 95.8%  | chr12  | +     | 110075841 | 110075992 | 152  |
| <a href="#">browser details</a> | YourSeq | 42    | 51  | 111   | 2000     | 77.4%  | chr15  | -     | 33372990  | 33373044  | 55   |
| <a href="#">browser details</a> | YourSeq | 40    | 61  | 111   | 2000     | 90.0%  | chr8   | -     | 56538970  | 56539021  | 52   |
| <a href="#">browser details</a> | YourSeq | 40    | 67  | 127   | 2000     | 93.5%  | chr6   | -     | 47823553  | 47823931  | 379  |
| <a href="#">browser details</a> | YourSeq | 39    | 52  | 108   | 2000     | 84.3%  | chr9   | +     | 83043787  | 83043843  | 57   |
| <a href="#">browser details</a> | YourSeq | 38    | 51  | 101   | 2000     | 88.0%  | chr14  | -     | 71505116  | 71505167  | 52   |
| <a href="#">browser details</a> | YourSeq | 36    | 50  | 91    | 2000     | 92.9%  | chr12  | +     | 118879687 | 118879728 | 42   |
| <a href="#">browser details</a> | YourSeq | 35    | 69  | 111   | 2000     | 90.7%  | chr1   | -     | 108028420 | 108028462 | 43   |
| <a href="#">browser details</a> | YourSeq | 35    | 67  | 110   | 2000     | 94.9%  | chr1   | -     | 71759319  | 71759363  | 45   |
| <a href="#">browser details</a> | YourSeq | 34    | 71  | 113   | 2000     | 90.5%  | chr18  | -     | 67763150  | 67763193  | 44   |
| <a href="#">browser details</a> | YourSeq | 34    | 75  | 111   | 2000     | 97.3%  | chr11  | -     | 37907444  | 37907481  | 38   |
| <a href="#">browser details</a> | YourSeq | 34    | 75  | 111   | 2000     | 97.3%  | chr13  | +     | 96218652  | 96218689  | 38   |
| <a href="#">browser details</a> | YourSeq | 34    | 62  | 102   | 2000     | 92.5%  | chr1   | +     | 26732325  | 26732365  | 41   |
| <a href="#">browser details</a> | YourSeq | 33    | 75  | 109   | 2000     | 97.2%  | chr7   | -     | 57085759  | 57085793  | 35   |

**Note:** The 2000 bp section upstream of Exon 3 is BLAT searched against the genome. No significant similarity is found.

## BLAT Search Results (down)

| QUERY                           | SCORE   | START | END | QSIZE | IDENTITY | CHROM  | STRAND | START | END       | SPAN      |     |
|---------------------------------|---------|-------|-----|-------|----------|--------|--------|-------|-----------|-----------|-----|
| <a href="#">browser details</a> | YourSeq | 484   | 1   | 484   | 484      | 100.0% | chr16  | -     | 97590940  | 97591423  | 484 |
| <a href="#">browser details</a> | YourSeq | 68    | 244 | 327   | 484      | 90.5%  | chr11  | +     | 105582567 | 105582650 | 84  |
| <a href="#">browser details</a> | YourSeq | 66    | 247 | 328   | 484      | 90.3%  | chr3   | -     | 144731198 | 144731279 | 82  |
| <a href="#">browser details</a> | YourSeq | 63    | 247 | 327   | 484      | 88.9%  | chr4   | -     | 22399587  | 22399667  | 81  |
| <a href="#">browser details</a> | YourSeq | 61    | 247 | 327   | 484      | 87.7%  | chr12  | +     | 86609532  | 86609610  | 79  |
| <a href="#">browser details</a> | YourSeq | 60    | 187 | 301   | 484      | 79.5%  | chr1   | -     | 32844594  | 32844683  | 90  |
| <a href="#">browser details</a> | YourSeq | 58    | 250 | 327   | 484      | 87.2%  | chr8   | +     | 83107336  | 83107413  | 78  |
| <a href="#">browser details</a> | YourSeq | 58    | 247 | 327   | 484      | 92.7%  | chr10  | +     | 66823594  | 66823674  | 81  |
| <a href="#">browser details</a> | YourSeq | 57    | 247 | 306   | 484      | 98.4%  | chr7   | -     | 126612866 | 126612926 | 61  |
| <a href="#">browser details</a> | YourSeq | 57    | 247 | 327   | 484      | 85.2%  | chr2   | +     | 6067111   | 6067191   | 81  |
| <a href="#">browser details</a> | YourSeq | 56    | 54  | 293   | 484      | 75.0%  | chr10  | -     | 91323891  | 91324049  | 159 |
| <a href="#">browser details</a> | YourSeq | 56    | 248 | 323   | 484      | 90.7%  | chrX   | +     | 89962293  | 89962367  | 75  |
| <a href="#">browser details</a> | YourSeq | 56    | 247 | 310   | 484      | 93.8%  | chr10  | +     | 36156783  | 36156846  | 64  |
| <a href="#">browser details</a> | YourSeq | 55    | 38  | 301   | 484      | 67.3%  | chr13  | -     | 114801405 | 114801465 | 61  |
| <a href="#">browser details</a> | YourSeq | 55    | 247 | 303   | 484      | 98.3%  | chr2   | +     | 74180657  | 74180713  | 57  |
| <a href="#">browser details</a> | YourSeq | 54    | 244 | 301   | 484      | 96.6%  | chr5   | -     | 138693439 | 138693496 | 58  |
| <a href="#">browser details</a> | YourSeq | 54    | 247 | 309   | 484      | 93.7%  | chr3   | -     | 26020609  | 26020689  | 81  |
| <a href="#">browser details</a> | YourSeq | 54    | 247 | 304   | 484      | 96.6%  | chr1   | -     | 95254454  | 95254511  | 58  |
| <a href="#">browser details</a> | YourSeq | 53    | 247 | 301   | 484      | 98.2%  | chr5   | -     | 37402985  | 37403039  | 55  |
| <a href="#">browser details</a> | YourSeq | 53    | 247 | 301   | 484      | 98.2%  | chr18  | -     | 3248804   | 3248858   | 55  |

**Note:** The 484 bp section downstream of Exon 4 is BLAT searched against the genome. No significant similarity is found.

## Gene and protein information:

Tmprss2 transmembrane protease, serine 2 [ *Mus musculus* (house mouse) ]

Gene ID: 50528, updated on 12-Aug-2019

## Gene summary

|                           |   |
|---------------------------|---|
| <b>Official Symbol</b>    | Tmprss2 provided by <a href="#">MGI</a>   |
| <b>Official Full Name</b> | transmembrane protease, serine 2 provided by <a href="#">MGI</a>  |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1354381</a>   |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000000385</a>  |
| <b>Gene type</b>          | protein coding  |
| <b>RefSeq status</b>      | PROVISIONAL   |
| <b>Organism</b>           | <a href="#">Mus musculus</a>  |
| <b>Lineage</b>            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| <b>Also known as</b>      | D16Erd61e   |
| <b>Expression</b>         | Biased expression in bladder adult (RPKM 149.8), colon adult (RPKM 109.6) and 8 other tissues <a href="#">See more</a>  |
| <b>Orthologs</b>          | <a href="#">human all</a>   |

## Genomic context

Location: 16 C4; 16 57.53 cM

See Tmprss2 in [Genome Data Viewer](#)

Exon count: 16

| Annotation release  | Status            | Assembly                                       | Chr | Location                                     |
|---------------------|-------------------|--|-----|--|
| <a href="#">108</a> | current           | GRCm38.p6 ( <a href="#">GCF_000001635.26</a> ) | 16  | NC_000082.6 (97564682..97659541, complement) |
| Build 37.2          | previous assembly | MGSCv37 ( <a href="#">GCF_000001635.18</a> )   | 16  | NC_000082.5 (97786289..97832802, complement) |

### Chromosome 16 - NC\_000082.6



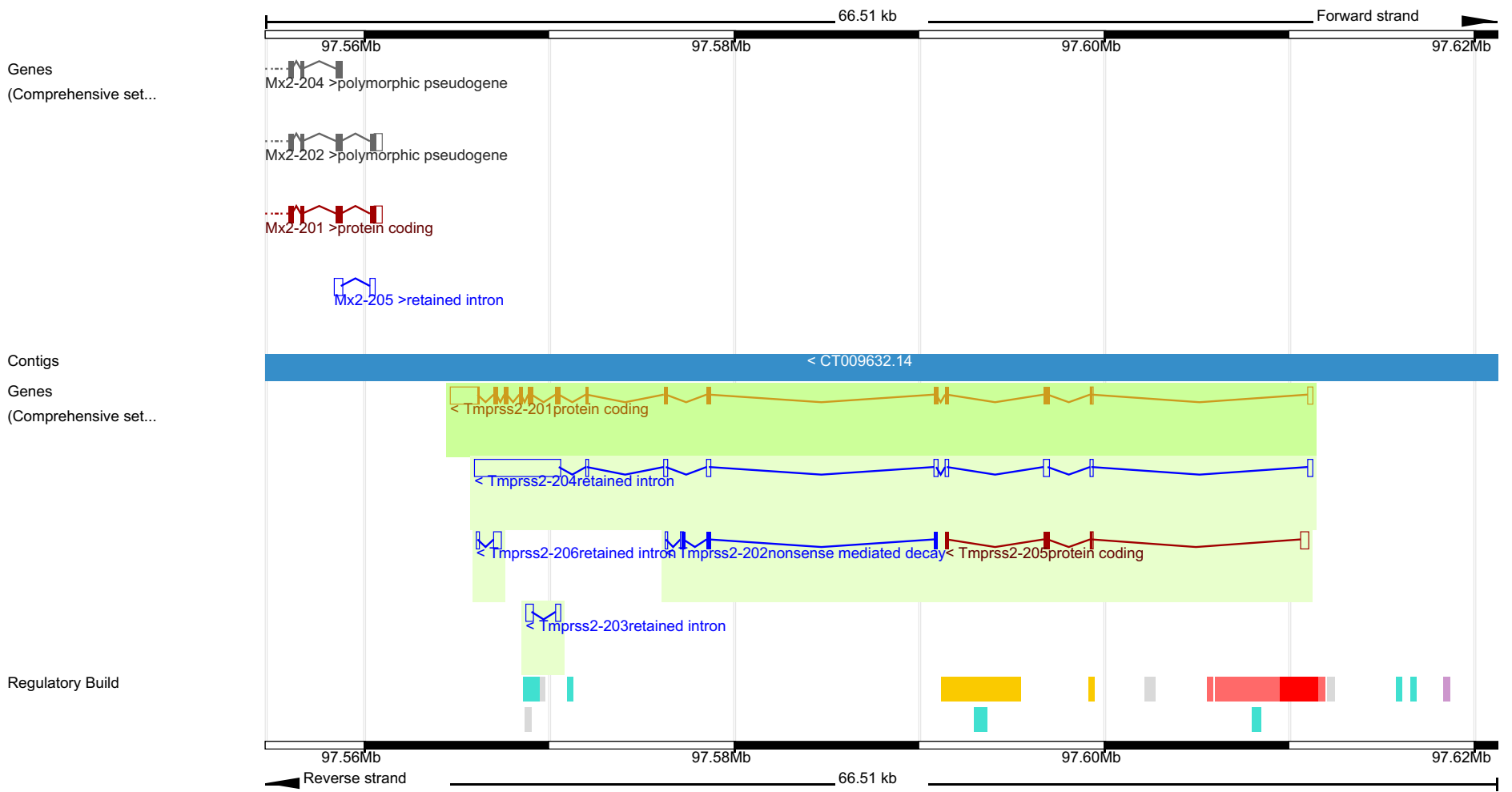
## Transcript information: This gene has 6 transcripts

### Gene: Tmprss2 ENSMUSG0000000385

**Description** transmembrane protease, serine 2 [Source:MGI Symbol;Acc:[MGI:1354381](#)]  
**Gene Synonyms** D16Ert61e, epitheliasin  
**Location** [Chromosome 16: 97,564,682-97,611,195](#) reverse strand.  
 GRCm38:CM001009.2  
**About this gene** This gene has 6 transcripts ([splice variants](#)), [231 orthologues](#), [20 paralogues](#), is a member of [1 Ensembl protein family](#) and is associated with [7 phenotypes](#).

#### Transcripts

| Name        | Transcript ID                        | bp   | Protein               | Translation ID                       | Biotype                 | CCDS                      | UniProt                    | Flags                                  |
|-------------|--------------------------------------|------|-----------------------|--------------------------------------|-------------------------|---------------------------|----------------------------|--|
| Tmprss2-201 | <a href="#">ENSMUST00000000395.7</a> | 3161 | <a href="#">490aa</a> | <a href="#">ENSMUSP00000000395.6</a> | Protein coding          | <a href="#">CCDS37417</a> | <a href="#">Q9JIQ8</a>     | TSL:1<br>GENCODE<br>basic<br>APPRIS P1 |
| Tmprss2-205 | <a href="#">ENSMUST00000232141.1</a> | 695  | <a href="#">103aa</a> | <a href="#">ENSMUSP00000156304.1</a> | Protein coding          | -                         | <a href="#">A0A338P779</a> | CDS 3'<br>incomplete                   |
| Tmprss2-202 | <a href="#">ENSMUST00000231544.1</a> | 391  | <a href="#">96aa</a>  | <a href="#">ENSMUSP00000156007.1</a> | Nonsense mediated decay | -                         | <a href="#">A0A338P6L7</a> | CDS 5'<br>incomplete                   |
| Tmprss2-204 | <a href="#">ENSMUST00000231908.1</a> | 5503 | No protein            | -                                    | Retained intron         | -                         | -                          | -                                      |
| Tmprss2-203 | <a href="#">ENSMUST00000231715.1</a> | 475  | No protein            | -                                    | Retained intron         | -                         | -                          | -                                      |
| Tmprss2-206 | <a href="#">ENSMUST00000232599.1</a> | 380  | No protein            | -                                    | Retained intron         | -                         | -                          | -                                      |



Regulation Legend

- CTCF
- Enhancer
- Open Chromatin
- Promoter
- Promoter Flank
- Transcription Factor Binding Site

Gene Legend

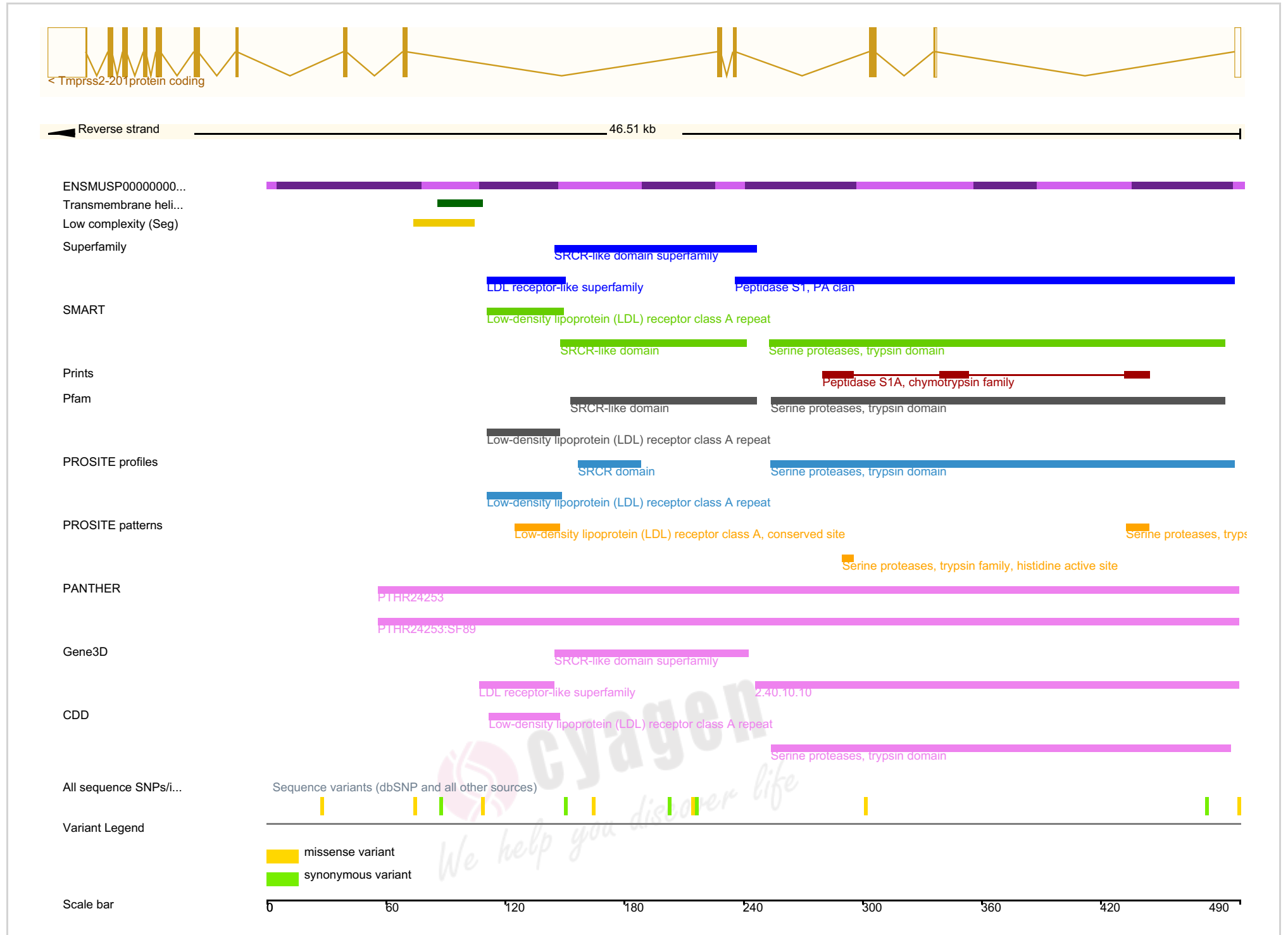
- Protein Coding
- Ensembl protein coding
  - merged Ensembl/Havana
- Non-Protein Coding
- pseudogene
  - processed transcript





*We help you*

**Transcript: ENSMUST00000000395**



We wish to acknowledge the following valuable scientific information resources: Ensembl, MGI, NCBI, UCSC.