

zgc92349

Genomic Sequence



Coding Sequence



For help interpreting these results, view the [PARSENP Introduction](#) page.

| # | View On Sequence | Nucleotide Change | Effect | Restriction Enzyme Differences from REBASE | | Description | Zygoty |
|---|-------------------------------------|-------------------|-------------|---|---|-------------|--------|
| | | | | Gained in Variant | Lost from Reference | | |
| 1 | G | A101T | Non-coding | | BccI , FokI , Hpy178III | 2446 | Homo |
| 2 | G C | T155A | C16S | Eco57MI , GsuI | | 7762 | Homo |
| 3 | G C | T170G | S21A | Eco47III , HaeII , HhaI | AluI , BpII , CviJI | 5127 | Homo |
| 4 | G C | T170G | S21A | Eco47III , HaeII , HhaI | AluI , BpII , CviJI | 5187 | Homo |
| 5 | G C | G181T | S24= | Ksp632I , MboII | | 2732 | Homo |
| 6 | G C | C290T | Q61* | MaeI | | 7003 | Homo |
| 7 | G C | C306T | T66I | | | 999 | Homo |
| 8 | G | C355T | Intron | MseI | | 6986 | Homo |
| 9 | G | C355T | Intron | MseI | | 6988 | Homo |

[Download Tab-Separated table](#)

No [protein homology model](#) was submitted. You may add one using any or all of the fields below.

Blocks Families:

Blocks File: no file selected

Sequence Alignment: no file selected

-OR-

Genomic Sequence

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                                                                                               72

                                                                 M  V  L  Q  V  L  G  L      8
aaacaatatacagagtgtgtgtttcaggatggcggtg atg gtg ctg cag gtg ctg ggc ttg      133
                                                                 t[1]

F  L  G  I  V  G  W  C  L  E  S  S  S  I  N  S  S  V      26
ttt ctg ggg atc gtg ggc tgg tgt ttg gag tcc agc tct ata aac tcg tct gtg      187
                                                                 aC16S[2]
                                                                 gS21A[3]
                                                                 tS24=[5]
                                                                 gS21A[4]

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G  L  W  F  S  C  A  S  N  S  L  G  A  I  H  C  Q  R      62
ggc ctc tgg ttc tcc tgc gcc tca aac tca ctg gga gcc att cac tgc cag agg      295
                                                                 tQ61*[6]

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                                                                 t[8]
                                                                 t[9]

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| gtcgtcattattggacatcaaaataacatcgtctTTtagacgctggctagatgTTgaattTTtagtcacctgac | 12742 |
| | 71 |
| atcacaacctaaatctaaactaatTTTTTTTTTtacataattactaataattactaataattaataatttt | 12814 |
| | 71 |
| tttgggattTTTcaagaagaaacgcacacaaacacacacacactTggcactgtctcggacaaatcccatac | 12886 |

| | |
|---|-------------|
| aataagtcaatgaacaaataacaatgacaacagtttagcaatcgacaaaagaaaatagaataaacaagtgag | 71 12958 |
| taaaaatgaataattaaatgatgaaaataagtaaatttagaatcataagagggttaagtggctggtttgctca | 71 13030 |
| tctagacacactcaaaaaaaaaaatttggtgaatgaacatgatttaatccaatcaagtaaacctgaactgctt | 71 13102 |
| tgaacatggtgtatgaacacaaagcacatttgtagataaaacatggtttcaatatgtcagtcctaacttcttt | 71 13174 |
| gcaactaattgactcaaaatgtttgattgtgttattctaattaaaatgattctaatttactcgatgtaaca | 71 13246 |
| ctaaagctttacttttaacaaaattatgtcttgataaatcagctagtaaatttcttgttcaatattggtgttt | 71 13318 |
| aaattacatTTTTTaaatgacaataactatgaagcaagaataaaattaagtaattcaacacaaaaaggacaga | 71 13390 |
| aaacatgtta | 71 13462 |
| ta | 71 13534 |
| tatatatatatatatatatatatatatatatatattcacggtacggttaaacctcgggtatgaatgtcacggt | 71 13606 |
| acggtatttattgaatcatttacaggaaaaaacaaaacttatgaaaatactcaaaaaagtgccaaaagtgt | 71 13678 |
| caatgatatacaaattagccatctatctgtaagctttgaaacaggaacttcaattttaataacaaaaaaatc | 71 13750 |
| attaaaccatgtaaaaaaataaagtttcaatttagtattggtgaaaactcatcacattcaacatttaacac | 71 13822 |
| tcactcacttagatagagatgggtttaaggaaaattatcatataaatataatctggtaaaagctggtatct | 71 13894 |

| | |
|---|-------------|
| ctgggtatttacaatgtcccctgcaacagaaaaaacccctctcatttgggactgaggtttctgggacagaga | 71 13966 |
| gatatgacttggcccagggtgacagcagtgggtaacggtgtgcattgtctttccccacttgagaggacaaa | 71 14038 |
| ccatgagtgagatagaggtctcatgtctgcatcaatctgaacagtggtgtgtgtttctgcagtccccatgac | 71 14110 |
| tgattattagtcgtattccccaaacttgcaggcacgtgcacacacagtgctcaacctgtgcagtgcacatgcc | 71 14182 |
| cttttttagtcttggatagaaaagttcccttccaaaatgatcaaaagtgccccgcgacgacataccctccg | 71 14254 |
| tccccgctttacagtacgcgcgacaacacagctgataagaactcgcgcgacaacaccgctattcagtacg | 71 14326 |
| cgcgcgcgacaacacagctgataagaactcgcgcgacaacaccactattcagtacgcgcgggcgacaaca | 71 14398 |
| cccgctttagggttttccagctctttttgatccccgcttctagcagcacactccatttccgcattactggat | 71 14470 |
| ctgtagcgacaacagaccgcaagggattatggccaagcctgcgctgatgggaattgtagttttcgtacctc | 71 14542 |
| ccgttcgcttcattcgcctgagcaaattttctcagaagacctatagttttaccgagtcatgcgactacggta | 71 14614 |
| atatcgaaaaaattaatattgcggtatgacggatatttacaataccgttacatccctaataatatatatat | 71 14686 |
| atatatttcttttattatagcctttagcaggcatcaatcacatttaacaaatttcttctttaatattctga | 71 14758 |
| tacaaaatgatataataatccaaaattgcaatatgtaataaaaatgtataagaacatttagccaacaaa | 71 14830 |
| ataaccttggctcttaagaaaactgatccccaagcaatattttagtagcgtaaacatcatttttttttacca | 71 14902 |

| | |
|--|-------------|
| attgagtttaaacagctttcttcacttttggtactcctattcaaaatgtaaaagtataaaatgtataggaac | 71 14974 |
| atntagccaacaacataacatgcataacattcaagctcttgaaaaaccaatcccaaactgtgccgaaaac | 71 15046 |
| acgcggtgatacttcttcttgccgttttcgtatggtgacatccaaacgcactaccgccacctactgatatgc | 71 15118 |
| gtgaagtgactctccagagtgagagttgtcgatttgaagcgtctcagtcctcattgaatcaacatgttctgat | 71 15190 |
| caaattcatttgattatcttcttgattcagtttcatataacatgaattaatcatttaacatgagtaaaacttga | 71 15262 |
| tttgttcttttcaatctgacaaaatctttttgtaaatccaatacatgcctagttgatttttttgagtgtgta | 71 15334 |
| gttaagaaaaatcaaacctaataattaacgtctaatgacgtgtgcctgctgggcaagaactaaatgcactaca | 71 15406 |
| gaatgttacgtttacacacacattcacaaattacatgtgaatccatcaactttttacagcataataactcact | 71 15478 |
| actcttgagtacttctgaaagctctactttttacttttgagtaatatttaaaacaggtacttttactctactt | 71 15550 |
| gcactacatcttttgggcaagtgacggtacttttactttgagtatgactattcagtcctctttccaccactgtg | 71 15622 |
| tgtatgtttgcacgtgtaataatctagctgctgatgtttatagagtgtagtagtattgagagatgggtattgtttg | 71 15694 |
| Y I Q A C R A L M I I A | 83 |
| tttgtgctgtgtgattgtag ga tat atc cag gct tgt cgg gct ctg atg atc atc gct | 15752 |
| L I L G L L S V V L A S M G L K C T | 101 |
| ctg att ctg ggt ctg ctg tct gtg gtt ctg gcc tcg atg gga ctc aag tgc act | 15806 |
| K L G S T S E E A K G K I S L T A G | 119 |
| aaa ctg ggc agc acg tct gag gag gcc aag ggc aaa atc agc ctg act gca gga | 15860 |
| I M F I L S G | 126 |

| | |
|---|--------------|
| ctgatgagtctccatcttctgctgacacattcggatggtcgggtcagaatttgggggtcaacatcacgagagca | 153 17985 |
| tgagtcaatgtttttgcagtgatgaaagtctttaacaacaatttattccttagtgtggagaatatttatct | 153 18057 |
| gatctaaaaaacttttttctaatttaataatattttgtggaaggaacagatttgacgaatgttaaaatttg | 153 18129 |
| ttcattgagccagttcagtcgatagagaactaataaagaccattaaaactgctgaggaacaatgacaaagag | 153 18201 |
| aacaaattgtttcagaaaattaaatattcctcaaaagtttagagaagttttataggctttggaagattattt | 153 18273 |
| caccactgaggaacagagaaatcaaatgttctgaatataaatgttcctcaaatgatttgagaacttttataaa | 153 18345 |
| gctttggaagatcatttcacctctgaggaacagagatatgaagggttctggaaataaatgttcctcaaaaga | 153 18417 |
| ttgtgaactttttaaagctttggaagatcatttcaccacggaggaacagagatacgaagggttctggaata | 153 18489 |
| aatgttcctcaaaagattgtgaactttttaaagctttggaagatcatttcacctctgaggaacagagatagc | 153 18561 |
| aagggttctggaataaatgttcctcaaaagttttgagaagttttaatggcctttggaagatcatttcaccg | 153 18633 |
| ctgaggaacagagaaatcaaaggttctagaaataaatcttcatcagtagcctgacggtcataatttagttctg | 153 18705 |
| atctcttcttttttgtttgttaattatthaaggaataatttaatgaccatatagttattagaaaacaatg | 153 18777 |
| caaacctgattatgcggttattatgcatgtcattttaatagtaatatctgtgcggttatctaatatctgatta | 153 18849 |
| ctaataatgcatctaaaaccacttaagtttactttataaagggcagtaaaaagacatgattcatgagctttaaat | 153 18921 |

| | |
|--|-------|
| tacatgtgagtgcaataccttggatttcttttaagtagtttagtatataattgctgtaatacaacaataaat | 19960 |
| | 190 |
| agcaaagtaccatactattattatgaaaaaaaaataagtttaggacataaaaagagactattttgcattattat | 20032 |
| | 190 |
| gttgcaaaaacattactataaattgtaattataaagtttatttcgttaaattaagtaagagatactcgatgac | 20104 |
| | 190 |
| aggctgctgaattattagaaaataatgcacaccacatccccacgtcaggtgtgcattgtttttaataattca | 20176 |
| | 190 |
| gcagcatgcggtcaaataccactgaggaatagtgaaattaaagttctggaaatattataccttcatcaaaa | 20248 |
| | 190 |
| gactgacagtcacatttagttctgatttctttttatataagaaattattaatgttcctcaaaagttttgaga | 20320 |
| | 190 |
| agttttaaaggctttgtaaggtaatttcaccgctgaggaacagagatatgaaagttctggaaatatatgtt | 20392 |
| | 190 |
| tctcaaaagatttatttttaaggctttggaagataatttaaccactgaggaacagagatatgaaaggttaaa | 20464 |
| | 190 |
| aaatattcatcaaaatattcgagatgttttaaggctttggaagatcattttactgctgaggaacagagat | 20536 |
| | 190 |
| cttaaaggttctggaaataaatgtttcttaaaagttttgagaagttttaaaggatttggaagaccatttcac | 20608 |
| | 190 |
| cactgaggaacagagaaatgaaagttctggaaatagaccttaatcaaaagcctaacagtcatgttttagttc | 20680 |
| | 190 |
| agatttttgtatttatttaaggaataattaatgtgcgatggatttattagaaaataatgcacacactaggat | 20752 |
| | 190 |
| gcattattacgcaggtaatttttattgggttattatcttactaatttacttcagtccgctgaattccctg | 20824 |
| | 190 |
| ttaagatgttgtatttcagacatttgtcaggcttttgtttttaaacgatcctgtgtgttgactagtttct | 20896 |
| | 190 |
| ttcacatctcctccaaagccctctgttgtgttttgatgtaatttttgatgattgtagctgtgaaataactca | 20968 |

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aatcattcattcaaatcgcaaaaatatggagctgtaatgCGctcgaaatctacctgaactacttttagctgtg      190
                                                                21040

cccaaacacttttagaatgctcgttagccaatcagaatcaaacattttaaacagaactgtagcaaaacaacttg      190
                                                                21112

                                G P G Y N Y S A      198
attgatcatgaaattaaatatgtttgtgtctttctcag g ggc ccg ggc tac aac tac agc gct      21175

A Q P Q K I Y R S A P S D N S I T K      216
gca cag cct cag aag att tac aga tct gct cca tca gac aac agc atc acc aaa      21229

A Y V *      220
gca tat gtt taa gactgactttatTTTTgagctgtccttcatgTTTTTgtacatggaccccatgtaatt      21297

gcacTcttaaagTcaacacacttaacctttgaaaaaaaaactgt      220
                                                                21341
    
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Coding Sequence

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M V L Q V L G L F L G I V G W C L E      18
atg gtg ctg cag gtg ctg ggc ttg ttt ctg ggg atc gtg ggc tgg tgt ttg gag      54
                                                                aC16S[2]

S S S I N S S V W K S S S H G E A V      36
tcc agc tct ata aac tcg tct gtg tgg aag agc agc agt cat ggg gaa gcg gtg      108
    gS21A[3]          tS24=[5]
    gS21A[4]

V T A S S Q F E G L W F S C A S N S      54
gtg acg gcc agc tcg cag ttc gaa ggc ctc tgg ttc tcc tgc gcc tca aac tca      162

L G A I H C Q R F K T T L G L P G |      71
ctg gga gcc att cac tgc cag agg ttc aag acc act ctg ggt ctg cca g | ga      213
    tQ61*[6]          tT66I[7]

Y I Q A C R A L M I I A L I L G L L      89
tat atc cag gct tgt cgg gct ctg atg atc atc gct ctg att ctg ggt ctg ctg      267

S V V L A S M G L K C T K L G S T S      107
tct gtg gtt ctg gcc tcg atg gga ctc aag tgc act aaa ctg ggc agc acg tct      321
    
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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| E | E | A | K | G | K | I | S | L | T | A | G | I | M | F | I | L | S | 125 | |
| gag | gag | gcc | aag | ggc | aaa | atc | agc | ctg | act | gca | gga | atc | atg | ttc | atc | ctg | tca | 375 | |
| G | | L | C | V | I | V | A | V | S | W | Y | A | A | R | V | V | Q | 142 | |
| g | | gt | ttg | tgt | gtt | atc | gtg | gcc | gtg | tcg | tgg | tac | gct | gct | cga | gtc | gtc | cag | 426 |
| E | F | N | D | P | F | Y | G | G | T | K | | Y | E | L | G | A | G | 159 | |
| gaa | ttt | aat | gac | ccg | ttt | tat | gga | ggc | aca | aa | | g | tat | gaa | ctg | ggc | gcg | ggt | 477 |
| L | Y | L | G | W | A | A | A | A | L | C | I | L | G | G | G | T | L | 177 | |
| ctg | tat | ctg | gga | tgg | gcg | gca | gct | gct | ctg | tgt | ata | tta | gga | gga | gga | act | ctc | 531 | |
| C | T | S | F | K | G | S | S | P | A | Q | T | R | | G | P | G | Y | 194 | |
| tgc | act | tcc | ttt | aaa | ggt | tca | tct | cct | gca | caa | aca | cg | | g | ggc | ccg | ggc | tac | 582 |
| N | Y | S | A | A | Q | P | Q | K | I | Y | R | S | A | P | S | D | N | 212 | |
| aac | tac | agc | gct | gca | cag | cct | cag | aag | att | tac | aga | tct | gct | cca | tca | gac | aac | 636 | |
| S | I | T | K | A | Y | V | * | | | | | | | | | | | 220 | |
| agc | atc | acc | aaa | gca | tat | gtt | taa | | | | | | | | | | | 660 | |