

TextS2 - Alignment of homologous IESs found at non-homologous sites - page 1

CLUSTER 2

MUSCLE (3.7) multiple sequence alignment

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IESPGM.PTET51.1.25.381101 agtaagagtagatatactgatccttttgttatt--ataaatgtattagtttctcatttaa
IESPGM.PTET51.1.25.389332 -----catgt-ttgatatattattactcaaccaaatgctcctaataatgcattctt
                ** * **** * ** ** * **** * * ****
IESPGM.PTET51.1.25.381101 ttaatcttctgtatcatctttctcgattttaatatagcat-----aatatggcgat
IESPGM.PTET51.1.25.389332 taaaataaagtaggagatttcataatattatattatattataatcaatat-acaat
* ** * * **** * **** * ** * **** * ** **** * **
IESPGM.PTET51.1.25.381101 ctaaactat---atctcttattgaagttcataaatagtaaa---attcaaatt-----
IESPGM.PTET51.1.25.389332 ctaattaattttgaatttttatttgatcttgaatcatagggttattcaaaataatata
**** ** * * **** * ** * **** * ** **** *
IESPGM.PTET51.1.25.381101 ---attaattcttcttctgtgacttttcaaaattttcttattcatTATAGTGCTCACA
IESPGM.PTET51.1.25.389332 cgaattacttctcttctgtgtaac-----agattt-----aTATAGTGTTTACA
                **** **** * * **** * ** * **** * **** * ****
IESPGM.PTET51.1.25.381101 TAATACATTTTCGATGTTAAGAGTATATAT-AAGAGAAGGATTTAAATATATAAAGTAAAA
IESPGM.PTET51.1.25.389332 TAATAGATTTTGAATTAAGGATATATATAAAGTAAAGATTTAAATAGATTGAGTTAAA
**** * ** * **** * **** * **** * **** * **** * **** *
IESPGM.PTET51.1.25.381101 ATGTTTAA-----TTAAAATATGAAATCA-TAAAAAATTAATGTTATTA
IESPGM.PTET51.1.25.389332 ATATTTGAAATCAGAACTATACTTAAAATGTGAAAGCATTAAATCTTAAATTTTATA
** ** * **** * **** * **** * **** * **** * **** *
IESPGM.PTET51.1.25.381101 TTAATAATACCATTCATTAATTAATGTTTCATTCCTTCTATAAATTTATGATTTTCATATA
IESPGM.PTET51.1.25.389332 CTA-----TAATTAATCTTCATTCCTTCTATAAATTTATATATTTTCATATG
*** **** * **** * **** * **** * **** * **** *
IESPGM.PTET51.1.25.381101 TCCCTTCACATAAAAGATTTTATTTAATAAGTAtat-tagttgtttaacatatttacttt
IESPGM.PTET51.1.25.389332 TCCCTTCACATAAATGCTTTTATTTAACAATAatataatatttgaatcagttaaat
***** * **** * **** * **** * **** * **** * **** *
IESPGM.PTET51.1.25.381101 ttttctctattttattatctattcacaaattttctattctcagaataggattttgcatca
IESPGM.PTET51.1.25.389332 gttaacatcatcca--agctattcagcagtcgaatcgttattagaa-----tgtatca
** * ** * * **** * ** * **** * **** * **** *
IESPGM.PTET51.1.25.381101 ggatagttgc-ataaattttgaaaattgtttctgtctccctatcattttattcaagttt
IESPGM.PTET51.1.25.389332 ---aattgcaattaatatttagaa-----tgtcttatggatatttcttccaaatt
* **** * ** * ** * ** **** * **** * **** * **** *
IESPGM.PTET51.1.25.381101 ttaaatgaaatcatctttttattttaattg-----atcatcattatccttagc--aat
IESPGM.PTET51.1.25.389332 ttacttg-actctactattgaaatcaaataggattcaaaaaacatcatcttcagcagaat
*** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
IESPGM.PTET51.1.25.381101 aa-----ttag
IESPGM.PTET51.1.25.389332 aaaggagatcactcttga
** **
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TextS2 - Alignment of homologous IESs found at non-homologous sites - page 3

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IESPGM.PTET51.1.160.10020      GTTCTTTACTCTGCTTGCAAAATATGAAATTGTGAATTGCCAATAAATGAAATTCACCTCA
IESPGM.PTET51.1.117.944      ACTCCTTATT----TTCCAAAATATGAAATGGTGAATTGACAATAAAGGAAATTCACCAA
IESPGM.PTET51.1.44.7711      ATTCTTTGTT----TTGCAAAATATGAAATGGTAAATT-CCAATAAAGGTTATTCACCAA
          ** ** *      ** ***** ** ** *      ***** *      ***** *

IESPGM.PTET51.1.160.10020      TATAATAAAGA-----TATAAGATAAATTCACCTTGATATCAATTGGACCTA--TT
IESPGM.PTET51.1.117.944      TGTATATTTGGGTTAATTTCTAAACTGGAAATTCACGGGAGATAAAATGGGCCTATTTT
IESPGM.PTET51.1.44.7711      TATATATTTGAGTTAATTTCTATACTGAAAATTCACGAAAATAAAATGGCCTA--TT
          * ** **      ** *      ***** * ** *      ** ** *      **

IESPGM.PTET51.1.160.10020      TTGCCTTCAAAACCTATAAATTATAATGATATAT-TTTTATTTATTTAATAAATTTCT
IESPGM.PTET51.1.117.944      TTATCTCCCAAACCTATAAATTATATCAATATATATTATAT---CTTTAAAATAATTTCT
IESPGM.PTET51.1.44.7711      CTATATCCCAAACCTGATAAATTATATTAATATATATTATAT---TTTATTAATAATTTCT
          * * * **** ***** ***** ** ** *      ** *****

IESPGM.PTET51.1.160.10020      AACATCAGCTATAtcattg---ttgattgttgagttgaaattatgatggataaataaa
IESPGM.PTET51.1.117.944      TATATCAGCTATA-----aattgttgatattacatttgggtgaaaa-----
IESPGM.PTET51.1.44.7711      GATATCAGCTATAttacagacaataattatataatttacaatttattgaata-----
          * *****      *** * * * * *      * * * *

IESPGM.PTET51.1.160.10020      actggcactaacattggtgaaggcacatatattggaatctgataaaggcaattctaataa
IESPGM.PTET51.1.117.944      -----cagcgttacttagaggaaatatttt-----aacttagttttggtgt
IESPGM.PTET51.1.44.7711      -----atctcttg----atctttt-----atctgaaaa
          ** *      ** * **      * *

IESPGM.PTET51.1.160.10020      agttgaa----cataagcaggtgcttactaaactgatgattgttaaattggttgttgaat
IESPGM.PTET51.1.117.944      aataaaaataaccattagttgtcgattatcat--actatctttgatttccttctgtat
IESPGM.PTET51.1.44.7711      actaaaag---cactgaaaatcaatcatttaac--aatataattgtacgatttgaatat
          * * **      **      * * * * ** **      ** **

IESPGM.PTET51.1.160.10020      tgcaggaatat-----attatt
IESPGM.PTET51.1.117.944      ctcaactctgttttctt-----tgtttcaatttactttatcttttggatatt
IESPGM.PTET51.1.44.7711      ttaaaattgttaacatacgaagaagaatgccttaat-----ataaaa
          *      * *      **

IESPGM.PTET51.1.160.10020      gctcttaacatcttgattctgct-----
IESPGM.PTET51.1.117.944      tgtcattaagattattattttt-----
IESPGM.PTET51.1.44.7711      agtagtagattgttatattatgcattgataaagcat
          * * *      *** *
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TextS2 - Alignment of homologous IESs found at non-homologous sites - page 4

CLUSTER 5

MUSCLE (3.7) multiple sequence alignment

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

```
-----  
-----  
-----catgagttaattaactta  
-----atgctaaaggcgctaattgatgat  
-----atggctcttattt-----tttgtagaaca  
ggccattaattggcagatttctctcttaaatattgaacttgaaaagaagaattttaata  
-----gtgcttccactaataaa  
-----
```

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

```
-----  
-----  
aatatat---ttcgaggataaacta-----atthtaaatat-aatataa-----aa  
aatttgggaaatcaaaataatgaa-----ataaggaatatcaaaataaaagtatcttg  
aacattc---ttcaaatacaaacta-----tcaaaaatat-gtattgatct-----aa  
gtgtttc---ccctaaataatagattattcgtactaacat-ttaaaatttg-----aa  
aatttgt---acctatgatcaagga---ttcgtataaaattt---gctaaattttaatat  
atcaggctttgttttaaggattgcttttttttaataaaattt-aataaattctacaagaa  
-----
```

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

```
-----  
-----  
tgaatattctgttgatattaataaaaaaatatttagttt----ctattatatttcat  
taaactcttttaactaattaaataaaactgattttgatt-----ga  
tggttgcattttaactctttcagacagttcatcatcagcacaatcctcataacaataaaa  
taagcatttatttagc-----aagatcatttgact-----agttaag  
tgtccatttatattcccagcaatcaaatatacttttagttctttccgataaca----aa  
tataactcctgttatattcaaaactcagatcataattagat----taattgatattaaa  
-----
```

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

```
-----  
-----  
taggtgatgaaaggctcttcttatatgagg-----aataatcgaaaattataaatcaa  
tttgtgattgtagtgattatttttgggaaa-----aacagtgtagaataata-----  
tacatcagcatcactataaatctcaagcttagcttaaaataggaagtattatcgc  
tatatcttcgacagtttaactattttata-----agaa-----aatttaaaaacga  
tagtttttaataagtttaactgcataataataaTACAATTAATTCGTACTGTAAATCA  
gatacttttcatatttattacttgatgta-----aaatgtagaggaaaaattgcaa  
-----
```

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

```
-----TATAGCTGA  
tttgaatttataatacgttggcaattctctttgaattcctaataattttataTATAGCCAA  
tttccctatatagatcaacttcaatg-----caatcaacataTATAGCCAA  
ttttatcatata-----TATAGCCAA  
tttaatgttttaacacaactactcta-----aagttcattgaagtaaTATAGCCGA  
TTTATTTATATTTGAC-----TATATAGCCAA  
ttgataaatacaat-----TATAGCCAA  
-----TATAGCCAA  
***** *
```

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

```
TTTCATCAGCAAAATATACTTAATATTACTACAATATATATAAATTCAT-ATTAAAAATTT  
ACT-ATTTGCCAAATAAAAATATATAAATAAATAACAATATTTAATAGAAAA-----  
TCTCATTTACAAAATATAAATAATTTTATATCAATATACAATAATTAACAGAAAACACTCA  
TCTCATTTGCAAAAATATAAATAATATTATATCAATATACAATAATTAACAGAAAACACTCA  
TCTCATTTGCAAAAATATAAATAATATTATATCAATATACAATAATTAACAGAAAACACTCA  
TCTCATTTGCAAAAATATAAATAATATTACGTCAATATAAAGAATTAACAGAAAACACTCA  
TCTCATTTGCAAAAATATAAATAATATTATATCAATATACAATAATTAACAGAAAACACTCA  
TCTCATTTGCAAAAATATAAATAATATTATATCAATATACAATAATTAACAGAAAACACTCA  
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TextS2 - Alignment of homologous IESs found at non-homologous sites - page 5

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus
GAATTAAGTTAATATATTGATA--ATGTATTAAGTCAATAAAAATCAACTATTTTATTG
-----CAAATATTTGA--ACATATTAAGTCAATAAAAATCAACTATTTTATTA
TAATTTAACTAATATATTGAA--ATATATTAAGTCAATAAAAATCAACTATTTTATTG
TAATTTAATTAATATGTTTGAAAAATATATTAAGTCAATAAAAATCAACTATTTTATTG
TAATTTAATTAATATATTGAA--ATATATTAAG-CAATAAAAATCAACTATTTTATTG
TAAATTTAATTAATAATTTGAAATATATATTAAGTCAATAAAAATCAACTATTTTATTG
TAATTTAATTAATATATTGAA--ATACATTAAGTCAATAAAAATCAACTATTTTATTG
TAATTTAATTAATATATTGAA--ATATATTAAGTCAATAAAAATCAACTATTTTATTG
*** * ** ** * * * ***** ***** *****

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus
ACTTAATATAAAGTTTCTATTGGTGAAAAGATAAATA--TCTTTCACGGTGAAAAGAAAA
ACTT-GTATATAATTAACATGGT-----GAAAGAAAT
ACTTAGTATATAATTAACACTGG-----TGAAAAGAAAT
ACTTAATATAAATTTACACTGG-----TGAAAAGAAAT
ATTTAGTATATAATTAACACTGGTGAAGGAAAAATATCTTTTGTGTGAAAAGAAAT
ACTTAGTATATAATTAACACTGGTGAAGGAAAAATATCTTTTGTGTGAAAAGAAAT
ACTTAGTATATAAT-----CTTTTATGTTGAAAAGAAAT
ACTTAGTATATAATTAACACTGGTGAAGGAAAAATATCTTTTGTGTGAAAAGAAAT
* * * **** * * *****

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus
TTTTCTTTTCAACTACT-----TT
ATTTT-TTTTACCTTCCAAGTTATTTGTAATTGTAATAAGTTTCTACCTGAACCTCT
ATTTCTTTTACATGCCA-----TT
ATTTCTTTTACATACCA-----TT
ATTTCTTTTCAACATACCA-----TT
ATTTCTTTTACATACCA-----TT
ATTTCTTTTACATACCA-----CT
ATTTCTTTTACATACCA-----TT
*** ** * *

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus
TTTACACAAAACCAAGAACAATTTTTGATTTGTAATAATAATAATAAAAATTATG-
TAAAGAGAAAAGAAGATCATAATTTTGTATT-----TAATATAAACTTATGT
TCAAGAGAAAA-----GATTTTGTATT-----TAATAT-AAATTTATAT
TCAAGAGAAATGAAGATTAATAATTTTGTATT-----TAACAT-AAATTTATAT
TGAAGAGAAAATGAAGATTAATAATTTTGTATT-----TAATAT-AAATTTTAT
TCAAGAGAAAATGAAGATTAATAATTTTGTATT-----TAATAT-AAATTTTAT
TCAAGAGAAAATGAAGATTAATAATTTTGTATT-----TAATAT-AAATTTTAT
TCAAGAGAAAATGAAGATTAATAATTTTGTATT-----TAATAT-AAATTTTAT
* * * * * ***** ** ** ** *

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus
-----GTGAAAAGAAAAATTTCTTTTACCAATAAT-ATGCTTTTATAGAAACC
ATAATATGAGTAAAAAGAAATGTTTCTTTTCAACATTTAATAATGTTTCTCAAAAATC
ATATTAAGTGTG-----ACCGTTGAATAATG-TTTCTTAAAAATC
-TATTAGGCATGAAAAGAAAAATTTCTT-TCACCTTTGAATAATTTTCT-----
ATATTAAGCGTGAAAAGAAAAATTTCTTTTACCATTAAATAATGTTTCTCAAAAAT
ATATTAAGCGTGAAAAGAAAAATTTCTTATCACCATTTAATAATGTTTCTCAAAAAT
ATATTAAGCGTGAAAAGAAAAATTTCTTTTACCAATTTAATAATGTTTCTCAAAAAT
ATATTAAGCGTGAAAAGAAAAATTTCTTTTACCATTTAATAATGTTTCTCAAAAAT
* * * * * ** ** **

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus
AAAAATAACACATAGAAATGTGTTAATACTATTTCTTCTAT--ATATAATCAAAAAT
G-----ATTCATTCTATTTGGAACCTAATCTATTGAGATG-----
G-----ATTCATTTGATTTAAAACCTGAATATATTAATAATGGAATCGTAAGT
-----CATTCGATTTAAAACCTGAATATATTTAATGAAAGAGTCGTAAGT-
G-----ATTCATTTGATTTAAAACCTGAATATATTTAATGATAGAGTCGTAAGT-
G-----ATCCATTTGATTTAAAACCTGAATATATTTAATGATAGAGTCGTAAGT-
G-----ATCCATTTGATTTAAAACCTGAATATATTTAATGATAGAGTCGTAAGT-
G-----ATTCATTTGATTTAAAACCTGAATATATTTAATGATAGAGTCGTAAGT-
* * * * * ** ** **

TextS2 - Alignment of homologous IESs found at non-homologous sites - page 6

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

AAGATG-----TTTGTAAATGATTCTGAACTTTTAGAAAAATAAACGAATTAT
GAAGGTATAAAGTAAATCTT-----ACTTT
AAAAGAAAACCGCAAATTTTAGAGCCATTTCTGAA----TAATAGAAAATAACGAATTTT
AAAAGAATACCGCAAATTTTAGAGCCATTTTCTGAA----TAGTAGAAAATAACTAATTTT
AGAAGAATACCGCAAATTTTAGAGCCATTTCTGAA----TAATAGAAAATAACTAATTTT
AGAAGAATACCTCAAATTTTAGAGCCATTTCTGAA----TAATAGAAAATAACTAATTTT
AGAAGAATACCGCAAATTTTAGAGCCATTTCTGAA----TAATAGAAAATAACTAATTTT
AAAAGAATACCGCAAATTTTAGAGCCATTTCTGAA----TAATAGAAAATAACTAATTTT
** * * *

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

T-GGTGAAAAGAAATTTTTCTTTTACCATAATTTTATATTATCATATATACAAATCA
TCTATGTAAAAAGATTATTTT-----
TTGGTTAAAAGAAATTTTTCTTTTACGCTTA-ATATATATAAATTTATATTTAAATCA
TTGGTAAAAGAAATTTTTCTTTTCTTATTT-----
TTGGTGAAAAGAAATTTTTCTTTTACGCTTA-ATATATA-AAATTTATATTTAAATCA
TTGGCGAAAAGAAATTTTTCTTTTACACTTA-ATATATAAAAATTTATATTTAAATCA
TTGGTGAAAAGAAATTTTTCTTTTACACTTA-ATATATAAAAATTTATATTTAAATCA
TTGGTGAAAAGAAATTTTTCTTTTACACTTA-ATATATAAAAATTTATATTTAAATCA
TTGGTGAAAAGAAATTTTTCTTTTACACTTA-ATATATAAAAATTTATATTTAAATCA
* ** * ** * ** *

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

AAAAATTGTTCTTTGTTTTGTGTA AAAAAGTATTGTGAAAAGAAAATTTTTCTTTTAC

AA-----TGGTATGTTTAAAGAAAATATTTCTTTTAC

AAAATTTTAA-----
AAAAATTTAATCTTCATTTTCTCTTGAAATGGTATGTA AAAAAGAAAATATTTCTTTTAC
AAAAATTTAATCTTCATTTTCTCTTGAAATGGTATGTA AAAAAGAAAATATTTCTTTTAC
AAAAATTTAATCTTCATTTTCTCTTGAAATGGTATGTA AAAAAGAAAATATTTCTTTTAC

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

CGTGAAAGA--TATTTATCTTTTACCA-----
-----CCTTTACCAGTGTTAATTATCTACTAATTAATAAATTAATA
CTTAAAATGATAATTTT-TCTTTACCAGTGTTAATTATATAC-----TAAGTCAATA
-----CCTTTACCAGTGTTAATTATATAT-----TAAGTCAATA
-----TCTTCCATCAGTGTTAATTATATAC-----TAAATCAATA
CATAAAAAGATAATTTTTCTTTTACCAGTGTTAATTATATAC-----TAAGTCAATA
CATAAAAAGATAATTTTTCTTTTACCAGTGTTAATTATATAC-----TAAGTCAATA
CATAAAAAGATAATTTTTCTTTTACCAGTGTTAATTATATAC-----TAAGTCAATA
** * * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

AAATAG-----TTTTATTTTATTGACTAAATATA--TTTCTTATATATTAATTAA
AAATAT-----TTTTATTCTATTGACTTAATATC--TTTCAAATATATGAATTAC
AAATAG-----TTGTATTTTATTGACTTAATATATTTTCAAATATATTAATCAA
AAATAG-----TTGTATTTTATTGACTTAATATA--TTTCAAATATATTAATTAA
AAATAGTTGCATTTTATTGTATTTTATTGACTTAATATA--TTTCAAATATATTAATTAA
AAATAG-----TTGTATTTTATTGACTTAATATA--TTTCAAATATATTAATTAA
AAATAG-----TTGTATTTTATTGACTTAATATA--TTTCAAATATATTAATTAA
AAATAG-----TTGTATTTTATTGACTTAATATA--TTTCAAATATATTAATTAA
***** ** * ** * ** * ** * ** * ** * ** * ** * ** *

ThonS6b:1..566
IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

AA-----ATATATCTTTGCG
AATTATGTGTTTTTC---TGTTCAATTATTGTATATTGATATAATGTTATTTATATTTTGT
AATTATGAGTTTTTC---TGTTAAATATTGTATATTGATTAATATTTTATATTTTGC
AATTATGAGTTTTTC---TGTAATTTA--GTATATTGATATAATATTTTATATTTTGC
AATTATGAGTTTTTC---TGTTAATTATTGTATATTATATAATATTTTATATTTTGC
AATTATGAGTTTTTC---AGTTAATTATTGTATATTGATATAATATTTTATATTTTGC
AATTATGAGTTTTTC---TGTTAATTATTGTATATTGATATAATATTTTATATTTTGC
***** *

TextS2 - Alignment of homologous IESs found at non-homologous sites - page 7

ThonS6b:1..566

IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

AAATGAAATTGGCTATA-----tttc-catacttcttatttttaacaaaattttg
AAGTGAGATTGGCTATA-----atat-ctaatttgtttttaaaagggaattctcaa
AAATGAGATTGGCTATA-----taat-----tataaaaaaaaaattcgaa
AAATGAGATCGGCTATA-----ttgt-----aaaatacgc
AAATGAGATTGGCTATA-----atttgcagaattttaatagttcaagaaaccttaa
AAATGAGATTGGCTATAtgagctaatttatgaaagcatttgaatttcaataaaaactgaa
AAATGAGATTGGCTATA-----
** ** * * **

ThonS6b:1..566

IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

ttcaattagaga-----aaagaatgattaatatgact-----tttgaatattttg
ttttttgttata-----tgtaatgtcatagatatatttc-----gtttattttggaa
t---cgaattagcttaccaaaatttgaggagtactt-----
ttacttaatacaatttgaaaaaatgtcatalctattg-----tcattagtac
t-----aagtgctcctgaataactaataccctaaagtctaaatttcta
tcatataatata-----atatcagtgatatttgt-----

ThonS6b:1..566

IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

gttgtttacaat-----tttcaacagtaaa-----attcaca
ttcatttcaaataggaatgaatttaatgagtatatatt-----tta-----atta
tgcaattccaacaatacatatatttcgctcattatttaac-----ctataatttattcaaa
taattcaaaaattcacaataatttatacagatgaaggat-----ata-----gtaggaa
attagttagattataactagaaaatttatcgatataagatggcccttttaagctataaca
---atttgaacataagtaaatagctattttataaatt-----cataagggatttgtac

ThonS6b:1..566

IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

aaaatatatatatatatttt-----tatattgt-----atlttgggaatc
atcatat-----tatatcct-----catactgc-----caattctaaggaag
aaatatggaacatatatatttttggttacatacttttcta-----cttttgtttaattgat
aacatttttaaaagcattt-----catatctaataaaagataggagtttttcta
attgttcaatgtcaaatctcctaattacaatttaa-----ttgaattttaaattatc
atgaactaattgaatagttg-----tatattac-----attcttaattatt

ThonS6b:1..566

IESPGM.PTET51.1.34.280841
IESPGM.PTET51.1.131.262422
IESPGM.PTET51.1.109.40673
IESPGM.PTET51.1.58.302214
IESPGM.PTET51.1.18.127217
IESPGM.PTET51.1.128.266698
consensus

ttttactc-----
cgatactgaattaaaggcttgtttgcctctgtcaa
ctttacttcatcctaatttatatgtgcttttctcg
ttataaacattagagatgaatgtaaaaaaaacaa
gtttagatagagca-----
aaatagacttttaataataacttttcatgcaata

TextS2 - Alignment of homologous IESs found at non-homologous sites - page 8

CLUSTER 9

MUSCLE (3.7) multiple sequence alignment

```
IESPGM.PTET51.1.19.475992    taat-aacttgaatagtgcttttaaacctttctttcaatatctatttatcataaaaaacat
IESPGM.PTET51.1.96.236752    aaataaaaaagacaaaatgatcataa-----ttagatcaccatt-----caaaaacct
                               *** **  * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    aaaggcagaccta----aatttag----tctaactctatttgctagatccactttta---
IESPGM.PTET51.1.96.236752    ata----acttatttacaatttaactatttctaactcctctccttcatgttttcttaaga
                               * *   * * * * * * * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    -tctaot-tgatagccaaattaagta-ataagtttttcttatattaaatta----aga
IESPGM.PTET51.1.96.236752    ttctactataatacataaaaatagtatgccatttatttttgatgatactttatagttata
                               **** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    attgtttatttcaattgtgttttttcttttagaaccaacacTACAGTCTCGCAGAAGAT
IESPGM.PTET51.1.96.236752    aaagctttccttaattttcctttgactatc---ttactgcTACAGTCTCGCAGGGAAT
                               * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    TATTTGGAAAAATAATATTACATGCCATTCTATCGATATAATAATGGCATAGGGATCC
IESPGM.PTET51.1.96.236752    TATTTAAAAAATAATATTACATGCCATTCTATAGATACAAAATGGCATAGGGATCC
                               ***** *****
IESPGM.PTET51.1.19.475992    CTAACAGTCATCTTCGATGAATATACATACTAATTAATTTAATTTTTTTTATAAGAAT
IESPGM.PTET51.1.96.236752    TAAAAAGTGATCTTCGATGAATATACATACTAATTA-----TTTATAAGAAT
                               ** ** *****
IESPGM.PTET51.1.19.475992    TCAATTTCTTTTAATAATAGAAATAGGGGAGCATATAAATTGAGAAAAAGATGTCTTAAC
IESPGM.PTET51.1.96.236752    TCAA-TACCTTTTAATAATAGAAATAGGGGAGTATATATTGAGAAAAAGATGTCTTAGT
                               **** * * *****
IESPGM.PTET51.1.19.475992    TTAGCTT--TTAATTTAAGATTTTTGTATTGATAATGAGGTGGAGTAAACAATTTAATA
IESPGM.PTET51.1.96.236752    TTGACCTAGCTAATTAATGA-TATTGCATTGATAATGAAGTGGAGTAAA-AAGTTTAATG
                               ** * * *****
IESPGM.PTET51.1.19.475992    ATATTTGGAATAACATAACTTTATTAATAAATAAATTAACATCTATTTAAAAATAAGA--
IESPGM.PTET51.1.96.236752    ATAATTGGAAT-ATATACCTTGATCAAATTAATTTAAATATCTATTTAAAAATACAAGG
                               *** ***** * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    ----ATTTCAATATATAAATATTCAAAGCCTTCA-----ATCACAATAAAAAAATT
IESPGM.PTET51.1.96.236752    TTTGATTTCAAGTATAGAAATATTAAAAAGCCTTCAATATATTCATCACAAT-AAAAAATT
                               ***** * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    TAAATTTCACTTTGGAAATATGAATCTATATTGTGCGCTTAAAGTCTCAATTTAACC
IESPGM.PTET51.1.96.236752    GATATTTCTG-TCTGGAAATATGAGTTCTATATTGTGAACCTTAAAGTCTCAATTTAAAA
                               * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    TTATAGAAAACATTTTGGGAATAATGAAATAAAGTGTATAAAAATGGGACAGAGAATAA
IESPGM.PTET51.1.96.236752    CAATAGAAAACATTTGGGAATAATCAAATGAAGTATATAAAAAGTGAACCGAGAACAA
                               ***** ***** * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    ATTAAGCTTTCTAA-ATTTAATTATAAAACACTGACAGCGATGAAACCATTTAGTATTTA
IESPGM.PTET51.1.96.236752    ATTAAGCTTTGTAACATTCAATTAAGGCACTTATAGCGATGAAGCCATTTGTGTTTA
                               ***** * * * * * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    GAGAACCATAAAGGATTAATTCAAATAGTTTTAAATAATTGCTGAAAAATTGAATTTT
IESPGM.PTET51.1.96.236752    GAGAATCATAAATGATAAATCACATTAA-TTTAGAATAATTGCTGAGAAAAATGAATATT
                               ***** ***** * * * * * * * * * * * * * * * * * * * *
IESPGM.PTET51.1.19.475992    AAATCAATTTAATTATCTAATCTATCTGAATATTCCAGTATGCAAATAATCCCTGCGAG
IESPGM.PTET51.1.96.236752    AAATCAATTTAATTATCTAATCTATCTGAATATTCCATTTTGCAAACAATCCCTTCGAG
                               ***** ***** * * * * * * * * * * * * * * * * * * * *
```


TextS2 - Alignment of homologous IESs found at non-homologous sites - page 11

```
IESPGM.PTET51.1.124.248174    taaagattaataactaataacgccatcattaacttt---attatt-aacatctctaggta
IESPGM.PTET51.1.27.275392    -----ctaatctttttttattagttttcaataattgaataagtctagata
                               *****      *  ***  ***      *  ***  ** *  ***** **
```

```
IESPGM.PTET51.1.124.248174    aagggtataatcagttgtgtcaccgtttattttgtaaatttatca---tttgaatt
IESPGM.PTET51.1.27.275392    aatatttattctca-----tattt-taagtttgtaaatattaagaa
**      ***  ***                               *****  ***  ***  *  *      ** **
```

```
IESPGM.PTET51.1.124.248174    tattttaatctatt
IESPGM.PTET51.1.27.275392    catttt-----
                               *****
```

TextS2 - Alignment of homologous IESs found at non-homologous sites - page 12

CLUSTER 13

MUSCLE (3.7) multiple sequence alignment

```
IESPGM.PTET51.1.155.211807 -----tatcagtttctaagaatattcacctcctatctagac
IESPGM.PTET51.1.20.46790 ataa---agaaggtatcttactttttttatttta-----catttttgtttcag-t
IESPGM.PTET51.1.27.294496 ataacctataaacta-atgatattttttatttgaagaaattgatcatccctaatccaact
                               * * *** ** * *
aggaaataagagatttagtattttatttcattgt-----ctagagtaaacccaaaaaaa
IESPGM.PTET51.1.155.211807 acagtttgaatcagttaagctttctttcttttggaatatgacaatagtctctt-----
IESPGM.PTET51.1.20.46790 agtgactataaaaaataagatgtgtatatatt--taatattgaagtgtgatatagaaaa
IESPGM.PTET51.1.27.294496 * * * ** * * * * * * * *
ttagataaagtgatagga---tgaaa---taaaaaaattattttgtagttaata-----g
IESPGM.PTET51.1.155.211807 -tttattcttg-gttgaa---ggactctttcacatatattcatggacctagtttttacg
IESPGM.PTET51.1.20.46790 gtatatgcaagaattgaaaattggac-----tgttcttagattaagtgt---g
IESPGM.PTET51.1.27.294496 * ** * * * * * * * * * *
ctcagaagatgttagatcatatagaattcctaatttaggaagatttatgaaataattgtta
IESPGM.PTET51.1.155.211807 ccgatcacactttcactgctattcatttaagattt-----atattttata
IESPGM.PTET51.1.20.46790 ttaaccagaagataagagtcgtaagttgcaatgt-----at-----
IESPGM.PTET51.1.27.294496 * * * * * * * * * *
aTATAGCTGATATCAGAAATTATTTTAAA-----ATATAATAT-----ATCA
IESPGM.PTET51.1.155.211807 tTATAGCTGTTATTAGAAAATATTTA-AAAATATATTGAAATATATAATATAATTAATCA
IESPGM.PTET51.1.20.46790 tTATGGCTGGTATTAGAAAATATTTATAAAATATAATGAA--ATATAATATAATTAATCA
IESPGM.PTET51.1.27.294496 *** **** * * * * * * * * * * * * * *
GTTTGGAGGATAAAA-TAGGCCATTTTATTTCTTG-----TGAAT
IESPGM.PTET51.1.155.211807 GTTGAGGAGATAAAAATTATTCCTAT-----TATAT
IESPGM.PTET51.1.20.46790 GTTGATGA-ATTAATTATGCCTATTTAATAACCGTATTATAAAATTTATATTAGTGAAT
IESPGM.PTET51.1.27.294496 *** ** * * * * * * * *
TTCCAGTTTAGGAAATTAACCCAAATATATATTGGTGAATTCCTTTATTTACAATTCAC
IESPGM.PTET51.1.155.211807 CTCCCCT-----TATTATC---AAA--ATATTGGTGAAGATGCTGAATTGAAATTCAC
IESPGM.PTET51.1.20.46790 TTCCACTTTTGGATATTCAC---AAAATATATTGGTGAAGATCCTGAATTGAAATTCAC
IESPGM.PTET51.1.27.294496 *** * * * * * * * * * * * * * *
CATTTCATATTTTGTAAAACAAGAATAATTTTGTATTTTAAATTATAAAATGTAAA
IESPGM.PTET51.1.155.211807 T-TTTTTCATTTTGTAGTTTAAAGATTAATTTTGTGTA--TTTGTATATAA-TTTTATA
IESPGM.PTET51.1.20.46790 --TTTTTCATTTTGTAGTTTAAAGATTAATTTTGTGTA--TTTGTATATAATTTTATA
IESPGM.PTET51.1.27.294496 *** * * * * * * * * * * * * * *
TATATTGGTGAATTCCT-AATTAAGAAATTCACCAATATATTT-----
IESPGM.PTET51.1.155.211807 TAATAGCTTGAATTTGACAAATGAAATATTTTTTATTATATTCAATAGAAGCTGGTAA
IESPGM.PTET51.1.20.46790 CAATAGTGTG-----AATGAAGTATTATTC-TTAGATTACATAGTAGATGGTAT
IESPGM.PTET51.1.27.294496 * ** * * * * * * * *
-TACATTTTAAATTA---ATA--CAAAAAATTATCTTTGTTTTACAAAATATG
IESPGM.PTET51.1.155.211807 ATACATCAAAAAAGAAACAATTGATAG-TGAGAGGCAGACGTATAATTTTAAATGAATA
IESPGM.PTET51.1.20.46790 GTATAT--AAAAAAGAAATAATTGATAGTTAGAGACTGACCTATAATTTATAATGAATA
IESPGM.PTET51.1.27.294496 ** ** * * * * * * * * * *
A-----AATGGTGAATTGT-----
IESPGM.PTET51.1.155.211807 AGTCAGTATTTTAGTGAAATTTGCTTATTATAATTTTATAATTCAATATTAATCTG
IESPGM.PTET51.1.20.46790 AG-----TTTAG---AATTTGT-----
IESPGM.PTET51.1.27.294496 * * * * *
-----AAATAAGGAAATTCACCAATATATATTTGGGTTAATTCCTAAACTGGAATT
IESPGM.PTET51.1.155.211807 AATATCCAAAAGTGGAATCCACTTATATATAT-----ATTTTATAA-----
IESPGM.PTET51.1.20.46790 -----GTGGAATTCACTTATATATA-----TTTATAA-----
IESPGM.PTET51.1.27.294496 ***** * * * * * * * * * * * *
```


TextS2 - Alignment of homologous IESs found at non-homologus sites - page 16

```
IESPGM.PTET51.1.184.21279      acaataatagcaagcgaggatcccatatatttcagattagta--  
IESPGM.PTET51.1.21.430950     gcatttctatttgtttattttttatagattccaattt-----  
IESPGM.PTET51.1.58.200038     acaattcaagta-----cagttttacagtttatcttt  
                               ** *  *                               *  **  **  **
```


TextS2 - Alignment of homologous IESs found at non-homologous sites - page 17

CLUSTER 15

MUSCLE (3.7) multiple sequence alignment

```
IESPGM.PTET51.1.28.278632      gtcccatgaattgaccttaataagataaaaactaccctcctgattcgtgtatgagtaagtat
IESPGM.PTET51.1.4.361312      -----gcatgatgttgtaataacttatcttc-----ggaataaatatc
                               * * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      tt-----ccaacattgtgctttattgtttatacatattgtggtaa-----atcatt
IESPGM.PTET51.1.4.361312      ttcctaaccaacaaaatgatgcatttgtataatcttccttaataatctttttccatcagt
**          * * * * *      *          * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      tacaatctgaatagatatatcctctttag-----cgt-tgtaaaatcctata--agggg
IESPGM.PTET51.1.4.361312      tccaatactatcagctgggtctacagtaggagctatgtgtatcacattcgaactaaagg
* * * * *      * * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      ttatcttaaaatattgtcaaaataacaataaaacattatccat--TATAGTTGATATCAG
IESPGM.PTET51.1.4.361312      ttaaagcagttcatttgggaacttcatatggtacccaatttattaTATGTTGATATCTG
***          *          * * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      AAATTATTATTTAAAATATAATATATATTAATATAATTTATCAGTTTAGGAGATAAAATAG
IESPGM.PTET51.1.4.361312      AAATTTAAAATAAAATTTAATAGATATTAATATAATTTATCATTTTGGGAGATAAAATAG
*****      * * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      GCCATTTTATCTCCCGTGAATTTCCAGCTTAGGAAATTAACCAAAGGAAATTCACCAATA
IESPGM.PTET51.1.4.361312      GTTCATTTACCTCTTGTGAATTT-CAGTTTCTGAAATT--CCTA---AATTCATT--TA
*          * * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      TATATAAATAAGCTAATCTCCTAAACTGGAAATCCACGAGTGATAAATTGGGCCCTAATT
IESPGM.PTET51.1.4.361312      TCTACATCTTAGTAAATTTCCAGATATTGGAAA-----GGTAAATGAG--CCTATTT
* * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      TATCTCTCAAACGATAAAATTATATTAATATATGTTATATTTAATAATAATTTCTGATT
IESPGM.PTET51.1.4.361312      TATCTCCCAAATGATAAAATTATGTGAATATACAGAATATTTAATTA-AATTTCAGGTA
*****      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      TCAGCTATA---tccttcatataaaaatattatcaaattcaaatgacaa-agtggttagtt
IESPGM.PTET51.1.4.361312      TCAGCTATAtagatccagtttattagtgcagtaactactgtgattaatggtagtgta---
*****      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      aaagttttgaaagagtaaaaacttttgggtaattattttatttttggatCTATATCA
IESPGM.PTET51.1.4.361312      aaatttctg-----tatatattgtacctcatt-----tacattccaCATTGAGCT
*** * * * *      * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      gcagaacaaccaaccaattcaccttatcattggc-----acgttcaatggaa
IESPGM.PTET51.1.4.361312      gttgaaattcc-----ttcacataaattttgacctccagttgatgatggttctgttaa
* * * * *      *          * * * * *      * * * * *      * * * * *
IESPGM.PTET51.1.28.278632      ta----gataaattgtgtccttgtataataatttaatcttttaataatac
IESPGM.PTET51.1.4.361312      tatccttaagagtttcttaattttttattctatttctgtattttaatcaat
**          * * * * *      * * * * *      * * * * *      * * * * *
```