

## ANNEXOS

### ANNEX I: SEQÜÈNCIES CONSENS

#### >ANG1 (ad)

GGGCCCCCATCACAGAAATCTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAAT  
CTTAGTTATTAAGTAGTCAATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGC  
GATCTAGAATTTTCGATTTATCACAAATCTAATACTAATATTATTAATAGTGATTGTAAA  
TATTGTTAATATTCTTTTATTTTCAATTATTTTCAATTTGAATTGAATGGTAAATATTAT  
TTTTTCATTTCTTTTTTTGGCATTAGAAATACTTTTTATTACAGTTCTATATTTGATTCTA  
TATTATATATCTATATCTCTCTCATTTCTATATTTAATTTATTTCAAATTTCTAATTTGTTA  
ATGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAAAGTTAAAAAA  
CAAGAATCGATCGTTCAAGTATTCCAAATGGATGGCAAAATGACAGGAAGCGAGACATA  
TAGATCGGGTATATATCCATCTATATTGAATTGCGGATTCGAAATGATAAAATCATTTT  
TGATTGGACAAAAAAGGGTCTCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAA  
CACGTTTTTCGAGATAGGAATCGGTATCTAATGAATTCATGGTTCCAGTATAAATGAAAG  
AAAAAGAAAAAGGAATGACATCCCAACGAGATCCTAATCTCAAAACAAAAAGAAAGGGGG  
ATATGGCGAAATGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAAACTT  
ACTAAGTGATCACTTTCAAATTTTCAGAGAAACCCTGGAATTAACAAAAATGGGCAATCCT  
GAGCCAAATCCTGTTTTCTCAAAACAAACAAAGGTTTCAGAAAAAAGGATAGTTGCAGAG  
ACTCAATGGAGGCTATTCTAACAAATGGAGTTAAATGCGTTGGGTAGAGGACTCTTTACA  
TCGGAAACTTCAGAAAGAAAAGAAATGAAGTGAAGATAAACGTATATTACATACGTTTTGA  
ATACTATATTCAAATGATTAATGACGACCGGATTCGGTATTTTTTCTTATAAAAATAGAG  
AATTGTGTGATCCATTCTACTTGAGAAGAATTCGATATTCATTGATCAAATCATTCACTC  
CATAGTCTGATAGATCTTTTGAAGAAGTGAATTAATCGGACGAGAATAAAGTTTTGAGTCCC  
GTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAAAATTC

#### >ANG1 (ef)

TTCAAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCCCT  
TTCCTTAACGGTCCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGGAT  
TTTTTTTTCTAAGAGTAAATGGTTTTCTCTTATCACAAGCCTTTTGATATCTATGATACAC  
ATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAAT  
ATCATTACTCATACTGAAACTTACAAAATCATTTTTTTGAAGATCGAAGAAATTCCCCGG  
CTTTGAGAAAGTTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCAA  
ATAAAAATATGATAGAATCAAAATAAATAAGGATACCACCCAAAGGACTCGAAATCCTCAT  
GTTAACGGTTCCAATTTCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCC  
AATCTAATCTGGGTTGGAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAA  
TCCTCGTGTACCAGTTCAAATA

#### >BC1M3xL2 (ad)

GGCCCCCATCACAGAATCTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCT  
TAGTTATTAAGTAGTCAATATTATATTGACTATTCTAGAGCATAAGGATTAATATAGCGA  
TCTAGAATTTTCGATTTATCACAAATCTAATACTAATACACAATTCTAATACTAATAATAG  
TGATTGTAAATATTGTTAATATTCTTTTTATTTTCAATTATTTTCAATTTGAATTGAATGG  
TAAATATTATTTTTTCAATTTCTTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATA  
TTTTGATTCTATATTATATATCTATATCTCTCTCATTCTATATTTAATTTATTTCAAATTC  
TAATTGTTAATGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAA  
AGTTAAAAACAAGAATCGATCGTTCAAGTATTCCAAATTTGAATGGCAAAATGACAGGAA  
GCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGATTCGAAATGATA  
AAATCATTTTTGATTGGACAAAAAAGGGTCTCTATAGAAGATAGTTAAGAAAATCAAA  
GAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATTCATGGTTCCAGTA  
TAAATGAAAGAAAAAGAAAAAGGAATGACATCCCAACGGGATCCTAATCTCAAAACAAAA  
AGAAAGGGGGATATGGCGAAATTTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGT  
ATGGAAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATG

GGCAATCCTGAGCCAAATCCTGTTTTCTCAAACAACAAAGGTTTCAGAAAAAAGGATAG  
GTGCAGAGACTCAATGGAAGCTATTCTAACAAATGGAGTTAAATGTGTTGGTAGAGGACT  
CTTTACATCGAAACTTCAGAAGGAAAAAAGATGAAGTGCAGAGAAACGTTTTTATACATA  
CGTTATTGAATACTATTATCCAATTGATTTAATGAACGACCCGGATCCGGTATTTTTCTA  
TAAAAAATAGAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCAT  
TGATCAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGA  
GAATAAAGATAGAGTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAA  
AGGAAAAATTC

**>BC1M3xL2 (ef)**

TTTAACTCCCCAACTATTTATCCGACCCCTTTTCTTAAACGGTTCCAAAATTCCTTATCT  
TTCTCATCCATTAATAAATTTTAGAAATGGATTTTTTTTTCTAAGAGTAAATGGTTTTCTC  
TTATCACAAAGCCTTTTGATATCTATGATACACGTAGAAATGAACATCTTTGAGCAAGGAA  
TCCCTAGTTGAATGATTCCCGATCAATACAATATCATTACTCATACTGAAACTTACAAAA  
TCATCTTTTTGAAGATCGAAGAAATCCCGGCTTTGAGAAAATTTGTTAATCGACTTAC  
TTGACATAGACCCAGTTCTATGATAGAATCAAATAAAATAAGGATACCACCCAAAGGACT  
CGAAATCCTCATGTTAACGGTTCCAATTTCCAATCCAGATTGGTAGGATAGAGGACTGGA  
AATCCTCGTTCCAATCTAATCTGGGTTGGAAATCGCCGGGATAGCTCAGTTGGTAGAGCA  
GAGGACTGAAAATCCTCGTGTACCAGTTCAA

**>BON (ad)**

GGCCCCATCACAGAAATCTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATC  
TTAGTTATTAAGTCAATATTTATATTGAATATTCTAGAGCATAAGGATTAATATAGCG  
ATCTATAATTTGATTTATCACAAATTCATTTATCACAAATCTAATACTAATATTATTA  
TAGTGATTGTAATATTGTTAATATCTTTTTATTTTCAATTTGAATTGAATGGTAATTTG  
AATTGAATGGTAAATATTCTTTTTTCAATTTCTTTTTTTGGCATTGGAATACTTTTTATTA  
CAGTTCTATATTTGATTCTATATTATATCTCTCTCATTCATATTTAATTTATTTCAA  
ATCCTAATTTGTTAATGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGCTTTTCAGG  
CGAAAGTTAAAAACAAGAATCGATCGTTCAAGTATTCCAAATGAATGGCAAAATGACA  
GGAAGCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGATTCCGAAAT  
GATAAAATCATTTTTGATTGGACAAAAAAGGGTCTCCTATATAAGATAGTTAAGAAAAAT  
CAAAGAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATTCAATGGTTCC  
AGTATAAATGAAAGAAAAAGAAAAAGGAATGACATCCCAACGAGATCCTAAATCTCAAAA  
CAAAAAGAAAGGGGATATGGCGAAATTTGGTAGACGCTACGGACTTAATTGGATTGAGCC  
TTGGTATGGAAACTTACTAAGTGATCACTTTTTCAAATTCAGAGAAACCCCTGGGAATTA  
CAAAAATGGGCCAATCCTGAGCCAAATCCTGTTTTCTCAAACAACAAAGGTTTCAGAA  
AAAAAAGGATAGGTGGCAGAGACTCCACGGGAAAGCCTATTCTAACAAATGGAAGTTAAA  
AGCGTTAGGTGAGGACTCTTTACATCGAAACTTCAGAAAAGAAAAAGAATGAAGTGAAGGA  
TAAACGTATATACATACGTATTGAATACTATATCAAATGATTAATGACGACCCGAATCCG  
TAGTTTTTCTATAAAAAATAGAAGAGAAGAATTGGTGTGAATCCATTCTACATTGAAGAA  
AGAATCGAATATTCATTGATCAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAA  
CTGATTAATCGGACGAGAATAAAGATAGAGTCCCGTTCTACATGTCAATACCGGCAACAA  
TGAAATTTATAGTAAAAGGAAA

**>BON (ef)**

GGTTCAAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCAACCC  
CTTTCTTAAACAGTTCCAAATTCCTTATCTTTCTCATTCCTCTATTCTTTTTAGAAATGG  
ATTTTTTTTTTCTAAGCGTAAATGGCTTTCTTATCACAAAGCCTTTTGATATCTATGAT  
ACACATAGACATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATA  
CAATATCATTACTCATACTGAAACGTACAAAGTCATCTTTTTGAAGATCGAAGAAATTC  
CCGGCTTTTATAAAATTTTTAATCGACTTACTTGACATAGACCCAGTTCTAGGATAGAA  
TCAAATAAAATAAGGATACCACCCAAAGGACTGGAAATCCTCAGGTTAACGGTTCCGATT  
TCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTG  
GAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACCAGT  
TCAAATA

**>CAM5 (ef)**

CTCTATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCCTTTCTTAAC  
GGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGGATTTTTTTCT  
AAGAGTAAATGGTTTTCTTATCACAAGCCTTTTGATATCTATGATACACATAGAAATG  
AACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAATATCATTACT  
CATACTGAACTTACAAAATCATCTTTTTGAAGATCGAAGAAATCCCCGGCTTTGAGAA  
AATTTGTTAATCGACTTATTTGACATAGACCCAGTTCTATGATAGAATCAAATAAAATAA  
GGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCAATCCAGATT  
GGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTGGAAATCGCCGGGA  
TAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTG

**>CAM7.1 (ad)**

CTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATCTTACCTATTAAGTAGTCA  
ATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTCGATTTA  
TCACAAATCTAATACTAATAATAGTGATTGTAAATATTGTTAATATTCTTTTATTTTCAA  
TTTTGAATTGAATGGTAAATATTATTTTTTCATTTCTTTTTTTGGCATTGGAAATACTTTTT  
ATTACAGTTCTATATTTGATTCTATATTATATATCTATATCTCTCTCATTCTATATTTAA  
TTTTATTTCAAATTTCTAATTTGTTTAAATGGAATGGTTAGTTATAACTAATGAGACATTCCTC  
CGTTTTTCAGGCGAAAGTTAAAAACAAGAATCGATCGTTCAAGTATTCCAAATTGAATGG  
CAAAATGACAGGAAGCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGG  
ATTCGAAATGATAAAATTTATTTTTGATTGGACAAAAAAGGGTCTCCTATAGAAGATAG  
TTAAGAAAATCAAAGAGGAGAAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATT  
CAATGGTTCCAGTATAAATGAAAAGAAAAGAAAAGGAATGACATCCCAACGGGATCCTA  
ATCTCAAAAACAAAAAGAAAAGGGGGATATGGCGAAATTGGTAGACGCTACGGACTTAAT  
TGGATTGAGCCTTGGTATGGAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCT  
GGAATTAACAAAATGGGCAATCCTGAGCCAAATCCTGTTTTCTCAAAAACAAAAGGT  
TCAGAAAAAAGGATAGGTGCAGAGACTCAATGAAGCTATTCTAACCAATGGAGGTAAT  
TGCGTTGGAAGAGGACTCTTTACATCGCAAACCTTCAGAAAAGAAAATAGAATGAAGTGCAA  
GGGATATCCGGTATATCACTACGTAATTGGCATACTTATATCAACTTGACTCAATGACCG  
ACCCCGTAACTCCGGTATTTTTCTCCTATTAAAAAATAGAAGAACTCTGTGAATCCATT  
CTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATTCCTCCATAGTCTGATAG  
ATCTTTTGAAGAATGATTAATCGGACGAGAATAAAGAAAAGAGTCCCCTTCTACATGTCA  
ATACCGCAACAATGAAATTTATAGTAAAAG

**>CAM7.1 (ef)**

TGGTTCAAGTCCCTCTATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGACCC  
CCTTTCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATG  
GATTTTTTTTTCTAAGAGTAAATGGTTTTCTTATCACAAGCCTTTTGATATCTATGATA  
CACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATAC  
AATATCACTACTCATACTGAACTTACAAAATCATCTTTTTGAAGATCGAAGAAATCCC  
CGGCTTTGAGAAAATTTGTTAATCGACTTATTTGACATAGACCCAGTTCTATGATAGAAT  
CAAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTT  
CCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTGG  
AAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACAGTTC  
AA

**>DAS1 (ad)**

AAATCTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATCTTAGTTAATAACTA  
GTCAATATTATATTGAATATTCTAGAGCATAATGATTAATATAGCGATCTAGAATTTCGA  
TTTTATCACAATTTAATACTAATAATTACAATTTCTAATACTAATATTAATTCTAATAATTC  
TAATACTAATATTAATTCTAATACTAATATTATTAATAAGTATTGTTAATATTGTTAAT  
ATTCTTTTATTTTCAATTTATTTTCAATTTGAATTGAATGGTAAATATTATTTTTTCATTT

TTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATTTGATTCTATATTATATAT  
CTATATCTCTCTCATTCTATATTTAATTTATTTCAAATTCCTAATTGTTTAAATGGAATGGT  
TAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAAAAGTTAAAAACAAGAATCGA  
TCGTTCAAGTATTCCAAATTTGGATGGCAAATGACAGGAAGCGAGACATATAGATCGGGT  
ATATATCCATCTATATTGAATTGCGGATTCCGAAATGATAAAATCATTTTTTGATTGGACA  
AAAAAAGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTTTTCG  
AGATAGGAATTGGTATCTAATGAATTCATGGTTCCAGTATAAATGAAAGAAAAAGAAAA  
AGGAATGACATCCCAACGAGATCCTAATCTCAAACAAAAAGAAAGGGGGATATGGCGAA  
ATTGGTAGACGCTACGGACTTAATTGAATTGAGCCTTGGTATGGAACTTACTAAGTGAT  
CACTTTCAAATTCAGAGAAACCCTGGGAATTAACAAAAATGGGGCAATCCTGAGCCAAAT  
CCTGTTTTCTCAAACATAGGTTGAGAAAAAAGGATAGGTGCAGAGACTCAATGGAAAG  
CTATTCTACCAATGGGAGTTAATGCGTTGGTAGAGGACTCTTTACATCGGAACTTTC  
AGGAAAGAAAAAGGATGAAGTTGAAGGAATAAACGGTATATACATACGTTATGGAATACT  
TATATTCAATGGATTAATGGACCGAACCCGGATCGGTATTCTTTCTCTATTAAAAAATA  
GAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAGAATTGAATATTCATTGATCAAAT  
CATTCCTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGT  
TATATCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAAA

**>DAS1 (ef)**

TTTTGGTTCAAGTCCCTCTATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGA  
CCCCCTTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAA  
ATGGATTTTTTTTCTAAGAGTAAATGGTTTTCTTATCACAAGCCTTTTGATATCTATG  
ATACACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAA  
TACAATATCATTACTCATACTGAACTTACAAAATCATCTTTTGAAGATCGAAGAAAT  
CCCCGGCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAG  
AATCAAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTAAACGGTTCCAA  
TTTCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGT  
TGAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACCA  
GTTTCAA

**>EL (ad)**

CATCACAGAAATCTTATATGCATAGTAATTGACTAAACTATTGGAATTGGAATCTTAGTT  
AATAACTAGTCAATCTAGTCAATATTATATTGAATATTCTAGAGCATAAGGATTAATATA  
GCGATCTAGAATTTTCGATTTATCACAATTCTAATACTAATATTATTAATAGTGATTGTA  
AATATTGTTAATATTCTTTTATTTTCAATTATTTTCAATTTGAATTGAATGGTAAATATT  
ATTTTTCACTTTCTTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATTTAATTT  
ATTTCAAATTCATTTGTTTAAATGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGC  
TTTTAGGCGAAAAGTTAAAAACAAGAATCGATCGTTCAAGTATTCCAAATTGAATGGCAA  
AATGACAGGAAGCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGATT  
CCGAAATGATAAAATCATTTTTGGATTGGACAAAAAAGGGTCTCCTATAGAAGATAGTTA  
AGAAAATCAAAGAGAAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATTCAA  
TGGTTCAGTATAAATGAAAGAAAAAGAAAAAGGAATGACATCCCAACGAGATCCTAATC  
TCAAACAAAAAGAAAGGGGATATGGCGAAATTTGGTAGACGCTACGGACTTAATTGGAT  
TGAGCCTTGGTATGGAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAAT  
TAACAAAAATGGGCAATCCTGAGCCAAATCCTGTTTTCTCAAACAAACAAAGGTTTCA  
AAAAAAGGATAGGTGCAGAGACTCATGGAAGCTATTCTAACAAATGGAGTTAAATGCGTT  
GGTAGAGGACTCTTTACATCGAACTTCAGAAAGAAAAAGAAATGAAGTGAAGGATAAACG  
TATATACATACGTATTTGATACTATATCAAAGTTTTCTATAAAAAAATAGAAGAAATTG  
GTGTGAATCCATTCTACATTGGAAGAAAAGATCGGAATATTTTATGATCAAAGCCATTT  
ACCTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAAAGA  
GTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAA

**>EL (ef)**

TCAAGGTTCCCTCTATCCCCAAAAAGACTATTTAACTTCCCAACTATTTATCCGACCCCT  
TTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGTAT  
TTTTTTCTAAGAATAAATGGCTTTCTCTTATCACAAGCCTTTTGATATCTATGATACACA  
TAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAATA  
TCATTACTCATACTGAACTTACAAAGTCATCTTTTTGAAGATCGAAGAAATTCCCCGGC  
TTTGATAAAATTTTTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCAAA  
TAAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCGTTCCAATCTAATCTGGGTGGA  
AATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCGTGTACAGCTTC  
AA

**>INS1 (ad)**

CTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATCTTACCTTAATAACTAGTC  
AATATTATATTGACTATTCTAGAGCATAATTGATTAATATAGCGATCTAGAATTTTCGATT  
TATCACAATTCTAATACTAATAACACAATTCTAATACTAATAATAGTGATTGTAAATATTG  
TTAATAATCTTTTTATTTTCAATTATTTTCAATTTGAATTGAATGGTAAATATTATTTTTC  
ATTTCTTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATTTGATTCTATATTA  
TATATCTATATCTCTCTCATTCTATATTTAATTTATTTCAAATTCGAATTTGTTAATGGA  
ATGGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAAAGTTAAAAACAAGA  
ATCGATCGTTCAAGTATTCCAAATGGAATGGCAAAATGACAGGAAGCGAGACATATAGAT  
CGGGTATATATCCATCTATATTGAATTGCGGATTCCGAAATGATAAAATCATTTTTGATT  
GGACAAAAAAGGGTCTCCTATAGAAGATAGTTAAGAAAAATCAAAGAGGAGAAAAACAGT  
TTTTCGAGATAGGAATCGGTATCTAATGAATTTCAATGGTCCAGTATAAATGAAAGAAAA  
AGAAAAAGGAATGACATCCCAACGGGATCCTAATCTCAAAACAAAAAGAAAGGGGGATAT  
GGCGAAATTTGGTAGACGCTACGGACTTAATTTGGATTGAGCCCTTGGTATGGAACTTAC  
TAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATGGGCAATCCTGAG  
CCAAATCCTGTTTTCTCAAAACAAAACAAAGTTTCAGAAAAAAGGATAGGTGCAGAGACT  
CAATGGAAGCTATTCTAACAAATGGAGTTAAATGTGTTGGTAGAGGACTCTTTACATCGA  
AACTTCAGAAAGAAAAAGAATGAAGTGCAGGAGAAACGTATATACATACGTATTGAATAC  
TATATCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAAAAATAGAAGAATT  
GGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATTCACT  
CCATAGTCTGATAGATCTTTTTGAAGAACTGATTAATCGGACGAGAATAATTTTTTGAAGT  
CCGTTCTACATGTCAATACCGCAACAATGAAATTTATAGTAAA

**>INS1 (ef)**

TCAAGGTTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCT  
TTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATCCACTCTATTCTTTTAGAAATGGAT  
TTTTTTTCTAAGAGTAAATGGTTTTCTCTTATCACAAGCCTTTTGATATCTATGATACAC  
GTAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAAT  
ATCATTACTCATACTGAACTTACAAAATCATCTTTTTGAAGATCGAAGAAATTCCCCGG  
CTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCAA  
ATAAAAAAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCA  
ATCCAGATTGGTAGGATAGAGGACTGGAATCCTCGTTCCAATCTAATCTGGGTGGAAA  
TCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAAATCCTCGTGTAC

**>INS2 (ad)**

AGAAATCTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATCTTACTTATTAAC  
TAGTCAATATTATATTGACTATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTC  
GATTTATCACAATTCTAATACTAATAACACAATTCTAATACTAATAATAGTGATTGTAAAT  
ATTGTTAATATTCTTTTTATTTTCAATTATTTTCAATTTGAATTGAATGGTAAATATTATT  
TTTTCAATTTCTTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATTTGATTCTAT  
ATTATATATCTATATCTCTCTCATTCTATATTTAATTTATTTCAAATTCGAATTTGTTAA

TGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAAAGTTAAAAAAC  
AAGAATCGATCGTTCAAGTATTCCAAATTGAATGGCAAAATGACAGGAAGCGAGACATAT  
AGATCGGGTATATATCCATCTATATTGAATTGCGGATTCCGAAATGATAAAATCATTTTT  
GATTGGACAAAAAAGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAAAC  
ACGTTTTTCGAGATAGGAATCGGTATCTAATGAATTCAATGGTTCAGTATAAATGAAAGA  
AAAAGAAAAAGGAATGACATCCCAACGGGATCCTAATCTCAAACAAAAAGAAAGGGGA  
TATGGCGAAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTA  
CTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATGGGCAATCCTGA  
GCCAAATCCTGTTTTCTCAAACAAACAAAGGTTTCAGAAAAAAAGGATAGGTGCAGAGAC  
TCAATGGAAAGCTATTCTAACAAATGGAGTTTTAAATGTGTTGGTAAGAGGACTCTTTTAC  
ATCGAAACTTCAGAAAAGAAAAAGAATGAAGTGCAGGAGAAACGTATATACATACGTATT  
TGAATACTATATTCAAATGATTAATGACGAACCGATCCGTATTTTTTCTATTAAAAAATA  
GAAGAATTGGGGGTGATTCCATTTCTAATTTGGAAGAAAGAATCGGAAATCATTGAATCA  
ATCTGGCCACTTCTAATCTTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAA  
AGATAGAGTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAAA

**>INS2 (ef)**

TATGGTTC AAGTCCCTCTATCCCCAAATGACTATTTAACTCCCCAACTATTTATCCGAC  
CCCCTTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATCCACTCTATTCTTTTAGAAA  
TGGATTTTTTTTC-AAAGTAAATGGTTTTCACTTATCACAAGCCTTTTGATATCTATGA  
TACACGTA-AAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATA  
CAATAACATTACTCATACTGAAACTTACAAAATCATCTTTTTGAAGATCGAAAAAATTC  
CCGGCTTTGAGAAAATTTGTTAATCGACTTACTTGACAAAAACCCAGTTCTATGATAGAA  
TCAAATAAATTAAGGATACCACCCAAAGGACTCGAACTCCTCAAGGTTAACGGTTCCAATT  
TCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTG  
GAAATCGCCGGGATAGCTCAATTTGGTAGAGCAGAGGACTGAAAAAT

**>LID2 (ad)**

TCCTTATATGCATAGTAATTGACTAACTACTGGAATTTGGAATCTTAGTTATTAAGTCTAGTC  
AATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTCGATTT  
ATCACAATTTCTAATACTAATATTATTAATAGTGATTGTAAATATTGTTAATATTCTTTT  
ATTTTCAATTTATTTTCAATTTGAATTTGAATGGTAAATATTATTTTTTAATTTCTTTTTTTG  
GCATTGGAAATACTTTTTATTACAGTTCTATATTTGATTCTATATTATATATCTATATTCTC  
TCATTCTATATTTAATTTATTTCAAATTCCTAATTTGTTAATGGAATGGTTAGTTATAACTAA  
TGAGACATTCCTCCGTTTTTCAGGCGAAAGTTAAAAACAAGAATCGATCGTTCAAGTATTCC  
AAATTGAATGGCAAAATGACAGGAAGCGAGAAATATAGATCGGGTATATATCCATCTATATT  
GAATTGCGGATTCCGAAATGATAAAATCATTTTTGATTGGACAAAAAAGGGTCTCCTATAG  
AAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAAT  
GAATTC AATGGTTCAGTATAAATGAAAGAAAAAGAAAAAGGAATGACATCCCAACGAGATC  
CTAATCTCAAACAAAAAGAAAGGGGGATATGGCGAAATTTGGTAGACGCTACGGACTTAATT  
GGATTGAGCCTTGGTATGGAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGA  
ATTAACAAAAATGGGCACTCCTGAGCCAAATCCTGTTTTCTCAAACAAACAAAGGTTTCAGA  
AAAAAAGGATAGGTGCAGAGACTCAATGGAAGCTATTCTAACAAATGGAGTTAAATGCGTTG  
GTAGAGGACTCTTTACATCGAACTTCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTAT  
ATACATACGTATTGAATACTATATCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTA  
TAAAAAATAGAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTG  
ATCAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAAT  
AAAGATAGAGTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAA

**>LID2 (ef)**

GTTCAAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCC  
TTTCCTTAACGGTTCCAATTCCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGGAT  
TTTTTTTCTAAGAGTAAATGGTTTTCTCTTATCACAAGCCTTTTGATATCTATGATACAC  
ATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAAT  
ATCATTACTCATACTGAAACTTACAAAATCATCTTTTTGAAGATCGAAGAAATCCCCGG  
CTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCAA  
ATAAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCA  
ATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTGGAAA  
TCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACCAGTTCAA  
ATAA

**>LIN1 . 3 (ad)**

GCCCACATCACAGAATCTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCTT  
AGTTATTAAGTACTAGTCAATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGCGAT  
CTAGAAATTCGATTTATCACAATTCCTAATACTAATAATAGTGATTGTAAATATTGTTAAT  
ATTCTTTTATTTTCAATTATTTTCAATTTGAATTGAATGGTAAATATTATTTTTCATTTT  
TTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATTTGATTCTATATTATATAT  
CTATATCTCTCTCATTCTATATTTAATTTATTTCAAATTCCTAATTGTTAATGGAATGGT  
TAGTTATAACTAATGAGACATTCCCTCCGTTTTTCAGGCGAAAAGTTAAAAACAAGAATCGA  
TCGTTCAAGTATTCCAAATGAATGGCAAATGACAGGAAGCGAGACATATAGATCGGGT  
ATATATCCATCTATATTGAATTGCGGATTCCGAAATGATAAAATCATTTTTGATTGGACA  
AAAAAAGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTTTTCG  
AGATAGGAATCGGTATCTAATGAATTCATGGTTCCAGTATAAATGAAAGAAAAAGAAAA  
AGGAATGACATCCCAACGGGATCCTAATCTCAAAAACAAAAAGAAAGGGGGATATGGCGAA  
ATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAGGTGAT  
CACTTTCAAATTCAGAGAAACCTGGAATTAACAAAAATGGGCAATCCTGAGCCAAATCC  
TGTTTTCTCAAAAACAAAAGGGTTCAGAAAAAAGGATAGGTGCAGAGACTCAATGGA  
AGCTATTCTAACAATGGAGTTAAATGCGTTGGTAGAGGACTCTTTACATCGAACT  
TCAGAAAAGAAAAGAATGAAGTGCAGGAGAACCCTATATACATACGTATTGAATACT  
ATATCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAAAAATAGAAG  
AATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATT  
CACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGTTAGA  
GTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAAAATC

**>TOM1 (ef)**

TGGTTCAAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCC  
CCTTTCCCTTAACGGTTCCAATTCCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATG  
GATTTTTTTTTCTAAGAGTAAATGGTTTTCTCTTATCACAAGCCTTTTGATATCTATGATA  
CACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATAC  
AATATCATTACTCATACTGAAACTTACAAAATCATCTTTTTGAAGATCGAAGAAATCCC  
CGGCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAAT  
CAAAGAAAATATGATAGAATCAAAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCT  
CATGTTAACGGTTCCAATTTCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGT  
TCCAATCTAATCTGGGTTGGAAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGA  
AAATCCTCGTGTAC

**>TOR2 . 1 (ad)**

AATCTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCTTAGTTAATAACTAG  
TCAATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTCGAT  
TTATCACAATTCATTTATCACAATTCCTAATACTAATATTATTAATAGTGATTGTAAATA  
TTGTTAATATTCTTTTATTTTCAATTTGAATTGAATGGTAAATTTGAATTGAATGGTAAAT  
ATTCTTTTTTCATTTCTTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATTTGA

TTCTATATTATATATCTCTCTCATTCTATATTTAATTTATTTCTACAGTTCTATATTTGA  
TTCTATATTATATATCTCTCTCATTCTATATTTAATTTATTTCAAATCCTAATTGTTTAA  
TGGAATGGTTAGTTATAACTAATGAGACATTCCCTCCGCTTTCAGGCGAAAGTTCAAAAAC  
AAGAATCGATCGTTCAAGTATCCCAAATGAATGGCAAAATGACGGGAAGCGAGACATA  
TAGATCCGGGGATATATCCCATCTATATTGAATTGCGGATCCGAAATGATAAAATCATT  
TTTGATTGGACAAAAAAGGGTCTCCTATATAAGATAGTTAAGAAAATCAAAGAGGAGAA  
AACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATCAATGGTTCCAGTATAAATGAA  
AGAAAAAGAAAAAGGAATGACATCCCAACGAGATCCTAATCTCAAAACAAAAAGAAAGG  
GGATATGGCGAAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAAAC  
TTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATGGGCAATCC  
TGAGCCAAATCCTGTTTTCTCAAAACAAACAAAGGTTTCAGAAAAAAGGATAGGTGCAGA  
GACTCAATGGAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTCTTTACA  
TCGAAACTTCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTATATACATACGTATTGA  
ATACTATATCAAATGATTAATGACGACCCGAATCCGTAGTTTTTCTATAAAAAATAGAAG  
AATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATT  
CACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGATAGA  
GTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTAGAGTAAAAGGAAAATC

**>TOR2.1 (ef)**

TCAAGGGTCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCT  
TTCCTTAACAGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGGAT  
TCTTTTTCTAAGCGTAAATGGCTTTCTCTTATCACAAGCCTTTTGATATCTATGATACAC  
ATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATCCCGATCAATACAAT  
ATCATTACTCATACTGAAACGTACAAAGTCATCTTTTTGAAGATCGAAGAAATCCCCGG  
CTTTTCTAAAATTTTTTAATCGACTTACTTGACATAGACCCAGTTCTAGGATAGAATCAA  
ATAAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCA  
ATCCAGATTGGTAGGATAGAGGACTCGAAATCCTCAGGTTAACGGTTCCAATCTAATCTG  
GGTTGGCTGGATTGGTAGGATAGGGGACTGGAAATCCTCGTTCCAATCCAGATTGGTAGG  
GTAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTGGAAATCGCCGGGATAGCTC  
AGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACAGGTTCA

**>TOR3 (ad)**

AAAATCTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATCTTACTTATTA  
AGTCAATATTATATTGAATATTCTAGAGCATAATTGATTAATATAGCGATCTAGAATTT  
GATTTATCACAATTCATTTATCACAATTCCTAATACTAATATTATTAATAGTGATTGTAA  
ATATTGTTAATATTCTTTTATTTTCAATTTGAATTGAATGGTAATTTGAATTGAATGGTA  
AATATTCTTTTTTCACTTTCTTTTTTGGCATTGGAAATACTTTTTATTACAGTTCTATATT  
TGATTCTATATTATATATCTCTCTCATTCTATATTTAATTTATTTCTACAGTTCTATATT  
TGATTCTATATTATATATCTCTCTCATTCTATATTTAATTTATTTCAAATCCTAATTGTT  
TAATGGAATGGTTAGTTATAACTAATGAGACATTCCCTCCGCTTTCAGGCGAAAGTTCAA  
AACAAGAATCGATCGTTCAAGTATCCCAAATGAATGGCAAAATGACAGGAAGCGAGACA  
TATAGATCCGGGTATATATCCATCTATATTGAATTGCGGATCCGAAATGATAAAATCATT  
TTTGATTGGACAAAAAAGGGTCTCCTATATAAGATAGTTAAGAAAATCAAAGAGGAGAA  
AACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATCAATGGTTCCAGTATAAATGAA  
AGAAAAAG-AAAAAGGAATGACAT-CCCAACGAGATCCTAATCTCAAAACAAAA--GAA  
AGGGGGATATGGCGAAATTGGTAGACG-TACGGACTTAATT-GGATTGAGCCTTGGTAT  
GGAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATGGG  
AATCCTGAGCCAAATCCTGTTTTCTCAAAACAAACAAAGGTTTCAGAAAAAAGGATAGGT  
GCAGAGACTCAATGGAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTCT  
TTACATCGAACTTCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTATATACATACGT  
ATTGAATACTATATCAAATGATTAATGACGACCCGAATCCGTAGTTTTTCTATAAAAAAT  
AGAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAA  
TCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAATG  
ATAAAGTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTAGAGTAA

**>TOR3 (ef)**

TATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCTTTTCCTTAACAGT  
TCCAAATTCCTTATCTTTCTCATTCACCTATTCTTTTAGAAATGGATTCTTTTTCTAAG  
CGTAAATGGCTTTCTCTTATCACAAAGCCTTTTGATATCTATGATACACATAGAAATGAAC  
ATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAATATCATTACTCAT  
ACTGAAACGTACAAAGTCATCTTTTTGAAGATCGAAGAAATCCCCGGCTTTTCTAAAAAT  
TTTTTAATCGACTTACTTGACATAGACCCAGTTCTAGGATAGAATCAAATAAAAATAAGGA  
TACCACCCAAAGGACTCGAAATCCTCATGTAAACGGTTCCAATTTCCAATCCAGATTGGT  
AGGATAGAGGACTCGAAATCCTCAGGTAAACGGTTCCAATCTAATCTGGGTTGGCTGGAT  
TGGTAGGATAGGGGACTGGAAATCCTCGTTCCAATCCAGATTGGTAGGGTAGAGGACTGG  
AAATCCTCGTTCCAATCTAATCTGGGTTGGAAATCGCCGGGATAGCTCAGTTGGTAGAGC  
AGAGGACTGAAAATCCTCGTGTCAAAAGTTTCAAAAT

**>VIO1 (ef)**

TGGTTC AAGGTCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACC  
CCCTTTCCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACCTATTCTTTTAGAAAT  
GGATTTTTTTTTCTAAGAGTAAATGGTTTTCTTATCACAAAGCCTTTTGATATCTATGAT  
ACACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATA  
CAATATCATTACTCATACTGAAACTTCCAAATCATCTTTTTGAAGATCGAAGAAATTC  
CCGGCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAA  
TCAAATAAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTAAACGGTTCCAATT  
TCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTG  
GAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTG

## ANNEX II: BLASTs SILVESTRES vs *S. MELONGENA*

ANGLad)

Score	Expect	Identities	Gaps	Strand
2204 bits(1193)	0.0	1243/1265(98%)	12/1265(0%)	Plus/Plus
Query 1	GGGCCCCATCACAGAAATCTTATATGCATAGTAATGACTAAACTACTGGAATTGGAAT	60		
<b>Sbjct</b> 47691	..... <b>A</b> .....	47750		
Query 61	CTTAGTTATTAAGTAGTCAATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGC	120		
<b>Sbjct</b> 47751	..... <b>C</b> .....	47810		
Query 121	GATCTAGAATTCGATTTATCACAATCTAATACTAATA-----T-T-AT--T-A-AAT	168		
<b>Sbjct</b> 47811	..... <b>CACAAT.C.A.AC.A.T</b> ...	47870		
Query 169	AGTGATTGTAAAtattgttaaatattcttttattttcaattattttcaatttgaattgaat	228		
<b>Sbjct</b> 47871	.....	47930		
Query 229	ggtaaatattatttttcatttctttttttGGCATTAGAAATACTTTTATTACAGTtcta	288		
<b>Sbjct</b> 47931	..... <b>G</b> .....	47990		
Query 289	tatttgattctatattatataatctataatctctctcattctatatttaatttatttcaaat	348		
<b>Sbjct</b> 47991	.....	48050		
Query 349	tctaattGTTTAATGGAATGGTTAGTTATAACTAATGAGACATTCCCTCCGTTTTTCAGGCG	408		
<b>Sbjct</b> 48051	.....	48110		
Query 409	AAAGTTAAAAACAAGAATCGATCGTTCAAGTATTCCAAATTGGATGGCAAATGACAGG	468		
<b>Sbjct</b> 48111	..... <b>A</b> .....	48170		
Query 469	AAGCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGATTCCGAAATGA	528		
<b>Sbjct</b> 48171	.....	48230		
Query 529	TAAAATCATTTTTGATTGGACaaaaaaaaGGGTCTCTATAGAAGATAGTTAAGAAAAATCA	588		
<b>Sbjct</b> 48231	.....	48290		
Query 589	AAGAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATTCAATGGTTCCAG	648		
<b>Sbjct</b> 48291	.....	48350		
Query 649	TATaaatgaaagaaaaagaaaaaggaatgacatcccaacgagatcctaactctcaaaacaa	708		
<b>Sbjct</b> 48351	..... <b>G</b> .....	48410		
Query 709	aaagaaaGGGGGATATGGCGAAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTG	768		
<b>Sbjct</b> 48411	.....	48470		
Query 769	GTATGGAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCTGGAATTAACAAAAA	828		
<b>Sbjct</b> 48471	.....	48530		
Query 829	TGGGCAATCCTGAGCCAAATCCTGTTTTCTCAAAACAAACAAAGGTTTCAGaaaaaaaaGGA	888		
<b>Sbjct</b> 48531	.....	48590		
Query 889	TAGGTGCAGAGACTCAATGGAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGG	948		
<b>Sbjct</b> 48591	..... <b>T</b> .....	48650		
Query 949	ACTCTTTACATCGAACTTCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTATATACA	1008		
<b>Sbjct</b> 48651	..... <b>C</b> ..... <b>G</b> .....	48710		
Query 1009	TACGTATTGAATACTATATCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAA	1068		
<b>Sbjct</b> 48711	.....	48770		
Query 1069	AAAATAGAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGA	1128		
<b>Sbjct</b> 48771	.....	48830		
Query 1129	TCAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAA	1188		
<b>Sbjct</b> 48831	.....	48890		
Query 1189	TAAAGTTTGGAGTCCCGTTCTACATGTCAATACCGCAACAATGAAATTTATAGTAAAAGG	1248		

**Sbjct** 48891 ..... **A.A**..... 48950

Query 1249 AAAAT 1253

**Sbjct** 48951 ..... 48955

**ANG (ef)**

Score	Expect	Identities	Gaps	Strand
887 bits(480)	0.0	538/562(96%)	20/562(3%)	Plus/Plus
Query 1		TTCAAGTCCCTCTATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCT		60
<b>Sbjct</b> 48981		.....		49040
Query 61		TTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCCTTTAGAAATGGAt		120
<b>Sbjct</b> 49041		..... <b>C</b> .....		49100
Query 121		tttttttCTAAGAGTAAATGGTTTTCTCTTATCACAAGCCTTTTGATATCTATGATACAC		180
<b>Sbjct</b> 49101		.....		49160
Query 181		ATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAAT		240
<b>Sbjct</b> 49161		<b>G</b> .....		49220
Query 241		ATCATTACTCATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAGAAATTCCTCCG		300
<b>Sbjct</b> 49221		.....		49280
Query 301		CCTTGAGAAAGTTTGTAAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCAA		360
<b>Sbjct</b> 49281		..... <b>A</b> .....		49320
Query 361		ATAAAAATATGATAGAATCAAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCAT		420
<b>Sbjct</b> 49327		-----		49380
Query 421		GTTAACGGTTCCAATTTCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCC		480
<b>Sbjct</b> 49381		.....		49440
Query 481		AATCTAATCTGGGTTGGAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAA		540
<b>Sbjct</b> 49441		.....		49500
Query 541		TCCTCGTGTACCAGTTCAAAT 562		
<b>Sbjct</b> 49501		..... <b>G</b> ..... 49522		

**BC1M3XL2 (ad)**

Score	Expect	Identities	Gaps	Strand
2316 bits(1254)	0.0	1261/1264(99%)	1/1264(0%)	Plus/Plus
Query 1		GGCCCCATCACAG-AATCTTATATGCATAGTAATGACTAAACTACTGGAATTGGAATC		59
<b>Sbjct</b> 47692		..... <b>A</b> ..... <b>A</b> .....		47751
Query 60		TTAGTTATTAAGTACTAGTCAATATTATATTGACTATTCTAGAGCATAAGGATTAATATAGCG		119
<b>Sbjct</b> 47752		.....		47811
Query 120		ATCTAGAATTTTCGATTTATCACAATTCTAATACTAATACACAATTCCTAATACTAATAATA		179
<b>Sbjct</b> 47812		.....		47871
Query 180		GTGATTGTAAAtattgtaaatattcttttattttcaattattttcaatttgaattgaatg		239
<b>Sbjct</b> 47872		.....		47931
Query 240		gtaaatattatttttctttttttGGCATGGAAATACTTTTATTACAGTtctat		299
<b>Sbjct</b> 47932		.....		47991
Query 300		atttgattctatattatataatctataatctctctcattctatatttaatttattttcaaatt		359
<b>Sbjct</b> 47992		.....		48051
Query 360		ctaattGTTTAATGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGA		419
<b>Sbjct</b> 48052		.....		48111
Query 420		AAGTTAAAAACAAGAAATCGATCGTTCAAGTATTCCAAATGAATGGCAAAATGACAGGA		479
<b>Sbjct</b> 48112		.....		48171
Query 480		AGCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGATTCCGAAATGAT		539

Sbjct 48172 ..... 48231

Query 540 AAAATCATTTTTGATTGGACaaaaaaGGGTCTCCTTTAGAAAGATAGTTAAGAAAATCAA 599  
**Sbjct** 48232 ..... **A**..... 48291

Query 600 AGAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATCAATGGTTCCAGT 659  
**Sbjct** 48292 ..... 48351

Query 660 ATaaatgaaagaaaaagaaaaaggaatgacatcccaacgggatcctaatactcaaaacaaa 719  
**Sbjct** 48352 ..... 48411

Query 720 aagaaaGGGGGATATGGCGAAATGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGG 779  
**Sbjct** 48412 ..... 48471

Query 780 TATGAAACTTACTAAGTGATCACTTCAAATTCAGAGAAACCTGGAATTAACAAAAAT 839  
**Sbjct** 48472 ..... 48531

Query 840 GGGCAATCCTGAGCCAAATCCTGTTTTCTCAAACAAACAAAGGTTTCAGaaaaaaGGAT 899  
**Sbjct** 48532 ..... 48591

Query 900 AGGTGCAGAGACTCAATGGAAGCTATTTCTAACAAATGGAGTTAAATGTGTTGGTAGAGGA 959  
**Sbjct** 48592 ..... 48651

Query 960 CTCTTTACATCGAACTTCAGAAAGAAAAGAATGAAGTGCAGGAGAAACGTATATACAT 1019  
**Sbjct** 48652 ..... 48711

Query 1020 ACGTATTGAATACTATATCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAA 1079  
**Sbjct** 48712 ..... 48771

Query 1080 AAATAGAAGAATTGGTGTGAATCCATTTCTACATTGAAGAAAGAATCGAATATTCATTGAT 1139  
**Sbjct** 48772 ..... 48831

Query 1140 CAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAAAT 1199  
**Sbjct** 48832 ..... 48891

Query 1200 AAAGATAGAGTCCCGTTCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGA 1259  
**Sbjct** 48892 ..... 48951

Query 1260 AAAT 1263  
**Sbjct** 48952 .... 48955

### BC1M3XL2(ef)

Score	Expect	Identities	Gaps	Strand
902 bits(488)	0.0	505/513(98%)	1/513(0%)	Plus/Plus
Query 1	TTTAACTCCCAACTATTTATCCGACCCCTTTCCCTTAACGGTTCCAAAATTCCTTATCT			60
<b>Sbjct</b> 49010	.....-.....			49068
Query 61	TTTCTCATCCATTAATAAATTTTAGAAATGGAatTTTTTTCTAAGAGTAAATGGTTTTCTC			120
<b>Sbjct</b> 49069	..... <b>C.CT.TTC</b> .....			49128
Query 121	TTATCACAAGCCTTTTGATATCTATGATACACGTAGAAATGAACATCTTTGAGCAAGGAA			180
<b>Sbjct</b> 49129	.....			49188
Query 181	TCCCTAGTTGAATGATTCCCGATCAATACAATATCATTACTCATACTGAAACTTACAAAA			240
<b>Sbjct</b> 49189	.....			49248
Query 241	TCATCTTTTTGAAGATCGAAGAAATTCCCCGGCTTTGAGAAAATTTGTTAATCGACTTAC			300
<b>Sbjct</b> 49249	.....			49308
Query 301	TTGACATAGACCCAGTTCTATGATAGAATCAAATAAAATAAGGATACCACCCAAAGGACT			360
<b>Sbjct</b> 49309	.....			49368
Query 361	CGAAATCCTCATGTTAACGGTTCCAATTTCCAATCCAGATTGGTAGGATAGAGGACTGGA			420
<b>Sbjct</b> 49369	.....			49428
Query 421	AATCCTCGTTCCAATCTAATCTGGGTTGGAAATCGCCGGGATAGCTCAGTTGGTAGAGCA			480
<b>Sbjct</b> 49429	.....			49488

Query 481 GAGGACTGAAAATCCTCGTGTCCACCAGTTCAAA 513  
 Sbjct 49489 .....G..... 49521

**BON(ad)**

Score	Expect	Identities	Gaps	Strand	
2069 bits(1120)	0.0	1220/1264(97%)	24/1264(1%)	Plus/Plus	
Query 1		AAATCTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCTTAGTTATTAACTA			60
Sbjct 47706		.....G.....			47765
Query 61		GTCAATATTATATTGAATATTCCTAGAGCATAAGGATTAATATAGCGATCTATAAATTCGA			120
Sbjct 47766		.....C.....G.....			47825
Query 121		TTTATCACAATTCATTTATCAC-AATTC-TAATACTAATATTATTAATAGTGATTGTAA			178
Sbjct 47826		.....--.A.--.T...A.AC...T.....C..A.-.....			47881
Query 179		ATATTGTTAATATTCCTTTTatttttcaatttgaattgaatggtaatttgaattgaatggta			238
Sbjct 47882		.....-TC.....			47934
Query 239		aatattctttttcatttctttttttGGCATTGGAAATACtttttattacagttctatatt			298
Sbjct 47935		.....A.....			47994
Query 299		tgattctatatta-----tatatctctctcattctatatttaatttatttcAAATCCTA			352
Sbjct 47995		.....TATATC.....T...			48054
Query 353		ATTGTTTAAATGGAATGGTTAGTTATAACTAATGAGACATTCCTCCGCTTTCAGGCGAAAG			412
Sbjct 48055		.....T.....			48114
Query 413		TTAAAAACAAGAATCGATCGTTCAGTATTCCAAATTGAATGGCAAAATGACAGGAAGC			472
Sbjct 48115		.....			48174
Query 473		GAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGATTCGAAATGATAAA			532
Sbjct 48175		.....			48234
Query 533		ATCATTTTTGATTGGACaaaaaaGGGTCTCTATATAAGATAGTTAAGAAAATCAAAGA			592
Sbjct 48235		.....G.....			48294
Query 593		GGAGAAAACACGTTTTCGAGATAGGAATCGGTATCTAATGAATTCAATGGTTCCAGTATa			652
Sbjct 48295		.....			48354
Query 653		aatgaaagaaaaagaaaaaggaatgacatcccaacgagatcctaatactcaaaacaaaaag			712
Sbjct 48355		.....G.....			48414
Query 713		aaaGGGGGATATGGCGAAATGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTAT			772
Sbjct 48415		.....			48474
Query 773		GGAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATGGG			832
Sbjct 48475		.....			48534
Query 833		CAATCCTGAGCCAAATCCTGTTTTCTCAAACAACAAAGGTTTCAGaaaaaaGGATAGG			892
Sbjct 48535		.....			48594
Query 893		TGCAGAGACTCAACGGAAGCTATTTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTC			952
Sbjct 48595		.....T.....T.....			48654
Query 953		TTTACATCGAAACTTCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTATATACATACG			1012
Sbjct 48655		.....C...G.....			48714
Query 1013		TATTGAATACTATATCAAATGATTAATGACGACCCGAATCCGTAGTTTTTCTATAAAAA			1072
Sbjct 48715		.....T.....			48774
Query 1073		TAGAAGAGAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATG			1132
Sbjct 48775		-----			48829
Query 1133		ATCAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGA			1192
Sbjct 48830		.....			48889
Query 1193		ATAAAGATAGAGTCCGTTCTACATGTCAATACCGCAACAATGAAATTTATAGTAAAA			1252
Sbjct 48890		.....			48949

Query 1253 GAAA 1256  
 Sbjct 48950 .... 48953

**BON(ef)**

Score	Expect	Identities	Gaps	Strand	
902 bits(488)	0.0	527/546(97%)	2/546(0%)	Plus/Plus	
Query 1		GGTTCAAGTCCCTCTATCCCCAAAAGACTATTTAACTCCCCA			60
Sbjct 48979		.....G.....			49038
Query 61		CTTTCCTTAACAGTTCCAAATTCCTTATCTTTCTCATTC			120
Sbjct 49039		.....G.....C.....			49098
Query 121		AttttttttttCTAAGCGTAAATGGCTTTCTTATCACAAG			180
Sbjct 49099		..--.....A.....T.....			49156
Query 181		ACACATAGACATGAACATCTTTGAGCAAGGAATCCCTAG			240
Sbjct 49157		....G....A.....			49216
Query 241		CAATATCATTACTCATACTGAAACGTACAAAGTCATCTT			300
Sbjct 49217		.....T.....A.....			49276
Query 301		CCGGCTTTTATAAAATTTTTAATCGACTTACTTGACATAG			360
Sbjct 49277		.....G.G.....G.....T.....			49336
Query 361		TCAAATAAAATAAGGATACCACCCAAAGGACTGGAAATC			420
Sbjct 49337		.....C.....T.....A...			49396
Query 421		TCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTC			480
Sbjct 49397		.....			49456
Query 481		GAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACT			540
Sbjct 49457		.....G..			49516
Query 541	TCAAAT	546			
Sbjct 49517	.....	49522			

**CAM5(ef)**

Score	Expect	Identities	Gaps	Strand	
942 bits(510)	0.0	516/519(99%)	0/519(0%)	Plus/Plus	
Query 1		CTCTATCCCCAAAAGACTATTTAACTCCCCA			60
Sbjct 48990		.....			49049
Query 61		GGTTCCAAATTCCTTATCTTTCTCATTC			120
Sbjct 49050		.....C.....			49109
Query 121		AAGAGTAAATGGTTTCTTATCACAAGCCTTTTGATATCT			180
Sbjct 49110		.....G.....			49169
Query 181		AACATCTTTGAGCAAGGAATCCCTAGTTGAATGATCCCG			240
Sbjct 49170		.....			49229
Query 241		CATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAG			300
Sbjct 49230		.....			49289
Query 301		AATTGTTAATCGACTTATTTGACATAGACCCAGTTCTAT			360
Sbjct 49290		.....C.....			49349
Query 361		GGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGG			420
Sbjct 49350		.....			49409
Query 421		GGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAAT			480
Sbjct 49410		.....			49469
Query 481	TAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTG	519			
Sbjct 49470	.....	49508			

**CAM7.1 (ad)**

Score	Expect	Identities	Gaps	Strand
2054 bits(1112)	0.0	1204/1242(97%)	31/1242(2%)	Plus/Plus
Query 1		CTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCTTACCTATTAACCTAGTCA		60
<b>Sbjct</b> 47710		..... <b>GT</b> .....		47769
Query 61		ATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTCGATTTA		120
<b>Sbjct</b> 47770		..... <b>C</b> .....		47829
Query 121		T-----CACAATTCTAATACTAATAATAGTGATTGTAAATATTGTT		161
<b>Sbjct</b> 47830		<b>.CACAATTCTAATACTAATA</b> .....		47889
Query 162		aatattcctt-----ttattttcaatttgaattgaatggtaaataattttttcat		211
<b>Sbjct</b> 47890		..... <b>TTATTTTCAA</b> .....		47949
Query 212		ttctttttttGGCATTGGAAACTTTTTATTACAGTtctatatttgattctatattata		271
<b>Sbjct</b> 47950		.....		48009
Query 272		tatctatatctctctcattctatatttaatttatttcaaattctaattGTTTAATGGAAAT		331
<b>Sbjct</b> 48010		.....		48069
Query 332		GGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAAAGTTAAAAACAAGAAT		391
<b>Sbjct</b> 48070		.....		48129
Query 392		CGATCGTTCAAGTATTCCAAATTGAATGGCAAATGACAGGAAGCGAGACATATAGATCG		451
<b>Sbjct</b> 48130		.....		48189
Query 452		GGTATATATCCATCTATATTGAATTGCGGATTCGAAATGATAAAATATTTTTGATTGG		511
<b>Sbjct</b> 48190		..... <b>C</b> .....		48249
Query 512		ACaaaaaaaaGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTT		571
<b>Sbjct</b> 48250		.....		48309
Query 572		TCGAGATAGGAATCGGTATCTAATGAATTCAATGGTCCAGTATAaatgaaagaaaaaga		631
<b>Sbjct</b> 48310		.....		48369
Query 632		aaaaggaatgacatcccaacgggatcctaattctcaaaacaaaaagaaaagGGGGATATG		691
<b>Sbjct</b> 48370		..... <b>-.-</b> .....		48427
Query 692		GCGAAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAA		751
<b>Sbjct</b> 48428		.....		48487
Query 752		GTGATCACTTTCAAATTCAGAGAAACCTGGAATTAACAAAAATGGGCAATCCTGAGCCA		811
<b>Sbjct</b> 48488		.....		48547
Query 812		AATCCTGTTTTCTCAAAACAAACAAAGGTTGAGAAAAAGGATAGGTGCAGAGACTCAA		871
<b>Sbjct</b> 48548		.....		48607
Query 872		<b>TGGAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTCTTTACATCGAAAC</b>		<b>931</b>
<b>Sbjct</b> 48608		..... <b>T</b> .....		48667
Query 932		TTCAGAAAAGAAAAGAATGAAGTGCAGGAGAACCCTATATACATACGTATTGAATACTAT		991
<b>Sbjct</b> 48668		..... <b>A</b> .....		48727
Query 992		ATCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAAAAATAGAAGAATTGGT		1051
<b>Sbjct</b> 48728		.....		48787
Query 1052		GTGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATTCACTCCA		1111
<b>Sbjct</b> 48788		.....		48847
Query 1112		TAGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGAAAGAGTCCCCT		1171
<b>Sbjct</b> 48848		..... <b>T</b> .....		48907
Query 1172		TCTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAAG	1213	
<b>Sbjct</b> 48908		.....	48949	

**CAM7.1 (ef)**

Score	Expect	Identities	Gaps	Strand	
972 bits(526)	0.0	537/542(99%)	1/542(0%)	Plus/Plus	
Query 2	GGTTC AAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCC				61
Sbjct 48979	.....				49038
Query 62	CTTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATCTTTTAGAAATGG				121
Sbjct 49039	.....C.....				49098
Query 122	AttttttttCTAAGAGTAAATGGTTTCTCTTATCACAAGCCTTTTGATATCTATGATAC				181
Sbjct 49099	.....				49158
Query 182	ACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATCCCGATCAATACA				241
Sbjct 49159	..G.....				49218
Query 242	ATATCATTACTCATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAGAAATCCCC				301
Sbjct 49219	.....				49278
Query 302	GGCTTTGAGAAAATTTGTTAATCGACTTATTTGACATAGACCCAGTCTATGATAGAATC				361
Sbjct 49279	.....C.....				49338
Query 362	AAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTAAACGGTTCCAATTC				421
Sbjct 49339	.....				49398
Query 422	CAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTGGA				481
Sbjct 49399	.....				49458
Query 482	AATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACAG-TTC				540
Sbjct 49459	.....C.G...				49518
Query 541	AA 542				
Sbjct 49519	.. 49520				

**DAS (ad)**

Score	Expect	Identities	Gaps	Strand	
1749 bits(947)	0.0	998/1021(98%)	10/1021(0%)	Plus/Plus	
Query 176	aattctaataactaatattaattctaataactaatattattaataatagtgattgtaaatattg				235
Sbjct 47834	.....--C--T.....C.A.-.....				47887
Query 236	ttaaatattcttttattttcaattattttcaatttgaattgaatgtaaatattatttttc				295
Sbjct 47888	.....				47947
Query 296	atctctttttttGGCATTGAAATACTTTTTATTACAGTtctatatttgattctatatta				355
Sbjct 47948	.....				48007
Query 356	tatatctatatctctctcattctatatttaatttatttcaaattctaattGTTTAATGGA				415
Sbjct 48008	.....				48067
Query 416	ATGGTTAGTTATAACTAATGAGACATTCCTCCGTTTTCAGGCGAAAGTTAAAAACAAGA				475
Sbjct 48068	.....				48127
Query 476	ATCGATCGTTCAAGTATTCCAAATGGATGGCAAAATGACAGGAAGCGAGACATATAGAT				535
Sbjct 48128	.....A.....				48187
Query 536	CGGGTATATATCCATCTATATTGAATTGCGGATTCGAAATGATAAAATCATTTTTGATT				595
Sbjct 48188	.....				48247
Query 596	GGACaaaaaaGGGTCTCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACCGT				655
Sbjct 48248	.....				48307
Query 656	TTTCGAGATAGGAATTGGTATCTAATGAATTCAATGGTTCAGTATaaatgaaagaaaa				715
Sbjct 48308	.....C.....				48367

```

Query 716 gaaaaaggaatgacatcccaacgagatcctaatactcaaaacaaaaagaaaGGGGGATATG 775
Sbjct 48368 .....G..... 48427

Query 776 GCGAAATTGGTAGACGCTACGGACTTAATTGAATTGAGCCTTGGTATGGAACTTACTAA 835
Sbjct 48428 .....G..... 48487

Query 836 GTGATCACTTTCAAATTCAGAGAAACCTTGAATTAACAAAAATGGGCAATCCTGAGCCA 895
Sbjct 48488 ..... 48547

Query 896 AATCCTGTTTTCTCA----AAACAAAGGTTGAGaaaaaaGGATAGGTGCAGAGACTCAA 951
Sbjct 48548 .....AAAC..... 48607

Query 952 TGGAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTCTTTACATCGAAAC 1011
Sbjct 48608 .....T..... 48667

Query 1012 TTCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTATATACATACGTATTGAATACTAT 1071
Sbjct 48668 .....C.....G..... 48727

Query 1072 ATCAAATGATTAATGACGACCCGAATCCGTATTCTTTCTATAAAAAATAGAAGAATTGGT 1131
Sbjct 48728 .....T..... 48787

Query 1132 GTGAATCCATTCTACATTGAAGAAAGAATTGAATATTCATTGATCAAATCATTCACTCCA 1191
Sbjct 48788 .....C..... 48847

Query 1192 T 1192
Sbjct 48848 . 48848

```

### DAS (ef)

Score	Expect	Identities	Gaps	Strand
979 bits(530)	0.0	539/543(99%)	1/543(0%)	Plus/Plus
Query 2	GGTTC AAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCCAAC TATTTATCCGACCCC	61		
<b>Sbjct</b> 48979	.....	49038		
Query 62	CTTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATCTTTTAGAAATGG	121		
<b>Sbjct</b> 49039	..... <b>C</b> .....	49098		
Query 122	AttttttttCTAAGAGTAAATGGTTTCTCTTATCACAAGCCTTTTGATATCTATGATAC	181		
<b>Sbjct</b> 49099	.....	49158		
Query 182	ACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATCCCGATCAATACA	241		
<b>Sbjct</b> 49159	.. <b>G</b> .....	49218		
Query 242	ATATCATTACTCATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAGAAATCCCC	301		
<b>Sbjct</b> 49219	.....	49278		
Query 302	GGCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTCTATGATAGAATC	361		
<b>Sbjct</b> 49279	.....	49338		
Query 362	AAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTC	421		
<b>Sbjct</b> 49339	.....	49398		
Query 422	CAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTGGA	481		
<b>Sbjct</b> 49399	.....	49458		
Query 482	AATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTCCAGTTT	541		
<b>Sbjct</b> 49459	..... <b>G</b> ...-	49517		
Query 542	CAA 544			
<b>Sbjct</b> 49518	... 49520			

**EL (ad)**

Score	Expect	Identities	Gaps	Strand	
1397 bits(756)	0.0	832/864(96%)	24/864(2%)	Plus/Plus	
Query 258	TTCATATATTTAATTTATTTCAAATCTAATTGTTTAAATGGAATGGTTAGTTATAACTAAT				317
Sbjct 48027	.....				48086
Query 318	GAGACATTCCTCCGCTTTTAGGCGAAAGTTAAAAACAAGAATCGATCGTTCAAGTATTC				377
Sbjct 48087	..... <b>T</b> ..... <b>C</b> .....				48146
Query 378	CAAATTGAATGGCAAAATGACAGGAAGCGAGACATATAGATCGGGTATATATCCATCTAT				437
Sbjct 48147	.....				48206
Query 438	ATTGAATTGCGGATCCGAAATGATAAAATCATTTTTGATTGGACaaaaaaaaGGGTCTCC				497
Sbjct 48207	.....				48266
Query 498	TATAGAAGATAGTTAAGAAAATCAAAGAGAAGAAAACACGTTTTTCGAGATAGGAATCGGT				557
Sbjct 48267	..... <b>G</b> .....				48326
Query 558	ATCTAATGAATTC AATGGTTCCAGTATAaatgaaagaaaaagaaaaaggaatgacatccc				617
Sbjct 48327	.....				48386
Query 618	aacgagatcctaatactcaaaacaaaaagaaaGGGGGATATGGCGAAATGGTAGACGCTA				677
Sbjct 48387	..... <b>G</b> .....				48446
Query 678	CGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTGATCACTTTCAAATTC A				737
Sbjct 48447	.....				48506
Query 738	GAGAAACCCTGGAATTAACAAAAATGGGCAATCCTGAGCCAAATCCTGTTTTCTCAAAAC				797
Sbjct 48507	.....				48566
Query 798	AAACAAAGGTTTCAGaaaaaaaaGGATAGGTGCAGAGACTCAATGGAAGCTATTCTAACAAA				857
Sbjct 48567	.....				48626
Query 858	TGGAGTTAAATGCGTTGGTAGAGGACTCTTTACATCGAACTTCAGAAAGAAAAAGAATG				917
Sbjct 48627	..... <b>T</b> .....				48686
Query 918	AAGTGAAGGATAAACGTATATACATACGTATTGAATACTATATCAAA--A----G----				966
Sbjct 48687	..... <b>C</b> ..... <b>G</b> ..... <b>TG.TTAAT.ACGA</b>				48746
Query 967	-----TTTTCTATAAAAAATAGAAGAATTGGTGTGAATCCATTCTACATTG				1013
Sbjct 48747	<b>CCCGAATCCGTAT</b> .....				48806
Query 1014	AAGAAAGAATCGAATATTCATTGATCAAAGCATTCACTCCATAGTCTGATAGATCTTTTG				1073
Sbjct 48807	..... <b>T</b> .....				48866
Query 1074	AAGAACTGATTAATCGGACGAGAA 1097				
Sbjct 48867	..... 48890				

**EL (ef)**

Score	Expect	Identities	Gaps	Strand	
592 bits(320)	3e-170	339/348(97%)	1/348(0%)	Plus/Plus	
Query 1	CCGACCCCTTTCCCTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTT				60
Sbjct 49031	..... <b>C</b> .....				49090
Query 61	AGAAATGTA-tttttttCTAAGAATAAAATGGCTTTCTCTTATCACAAGCCTTTTGATATC				119
Sbjct 49091	..... <b>G.T</b> ..... <b>G</b> ..... <b>T</b> .....				49150
Query 120	TATGATACACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGA				179
Sbjct 49151	..... <b>G</b> .....				49210
Query 180	TCAATACAATATCATTACTCATACTGAACTTACAAAGTCATCTTTTTGAAGATCGAAGA				239
Sbjct 49211	..... <b>A</b> .....				49270
Query 240	AATTCCCCGGCTTTGATAAAATTTTTTAATCGACTTACTTGACATAGACCCAGTTCTATG				299

**Sbjct** 49271 ..... **G**.....**G**..... 49330

Query 300 ATAGAATCAAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTC 347

Sbjct 49331 ..... 49378

**INS1 (ad)**

Score	Expect	Identities	Gaps	Strand	
2109 bits(1142)	0.0	1165/1175(99%)	5/1175(0%)	Plus/Plus	
Query 1		TTGACTATTCTAGAGCATAATTGATTAATATAGCGATCTAGAATTTTCGATTTATCACAAT			60
<b>Sbjct</b> 47778		..... <b>-G</b> .....			47836
Query 61		TCTAATACTAATACACAATTCTAATACTAATAATAGTGATTGTAAAtattggttaaatattc			120
Sbjct 47837		.....			47896
Query 121		ttttattttcaattattttcaatttgaattgaatggtaaattattatttttcattttctttt			180
Sbjct 47897		.....			47956
Query 181		tttGGCATTGGAAATACTTTTTATTACAGTtctatatatttgattctatattatataatctat			240
Sbjct 47957		.....			48016
Query 241		atctctctcattctatatttcaatttatttcaaatttctaatGTTTAAATGGAATGGTTAGT			300
Sbjct 48017		.....			48076
Query 301		TATAACTAATGAGACATTCTCCGTTTTTCAGGCGAAAAGTTAAAAACAAGAATCGATCGT			360
Sbjct 48077		.....			48136
Query 361		TCAAGTATTCCAAATGAATGGCAAAATGACAGGAAGCGAGACATATAGATCGGGTATAT			420
Sbjct 48137		.....			48196
Query 421		ATCCATCTATATGAATTGCGGATTCGAAATGATAAAATCATTTTTGATTGGACaaaaa			480
Sbjct 48197		.....			48256
Query 481		aaGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTTTTCGAGAT			540
Sbjct 48257		.....			48316
Query 541		AGGAATCGGTATCTAATGAATTTCAATGGTTCCAGTATAaatgaaagaaaaagaaaaagg			600
<b>Sbjct</b> 48317		..... <b>-</b> .....			48375
Query 601		aatgacatcccaacgggatcctaattctcaaaaacaaaaagaaaGGGGGATATGGCGAAATT			660
Sbjct 48376		.....			48435
Query 661		GGTAGACGCTACGGACTTAATTTGGATTGAGCCCTTGGTATGGAACTTACTAAGTGATC			720
<b>Sbjct</b> 48436		..... <b>-</b> ..... <b>-</b> .....			48493
Query 721		ACTTCAAATTCAGAGAAACCCGGAATTAACAAAAATGGGCAATCCTGAGCCAAATCCT			780
Sbjct 48494		.....			48553
Query 781		GTTTCTCAAACAAACAAAGGTTTCAGaaaaaaaGGATAGGTGCAGAGACTCAATGGAAG			840
Sbjct 48554		.....			48613
Query 841		CTATCTAACAAATGGAGTTAAATGTGTTGGTAGAGGACTCTTTACATCGAACTTCAGA			900
Sbjct 48614		.....			48673
Query 901		AAGAAAAAGAAATGAAGTGCAGGAGAAACGTATATACATACGTATTGAATACTATATCAA			960
Sbjct 48674		.....			48733
Query 961		TGATTAATGACGACCCGAATCCGATTTTTTCTATAAAAAATAGAAGAATTGGTGTGAAT			1020
Sbjct 48734		.....			48793
Query 1021		CCATCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATCACTCCATAGTCT			1080
Sbjct 48794		.....			48853
Query 1081		GATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAATTTTTGAAGTCCCGTTCTAC			1140
<b>Sbjct</b> 48854		..... <b>AGA.A.-</b> .....			48912
Query 1141		ATGTCAATACCGCAACAATGAAATTTATAGTAAA 1175			

Sbjct 48913 ..... 48947

**INS1 (ef)**

Score	Expect	Identities	Gaps	Strand	
970 bits(525)	0.0	525/525(100%)	0/525(0%)	Plus/Plus	
Query 1		CCCTCTATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCTTTCCTTA			60
Sbjct 48988		.....			49047
Query 61		ACGGTTCCAAATTCCTTATCTTTCTCATCCACTCTATTCTTTTAGAAATGGAtttttttt			120
Sbjct 49048		.....			49107
Query 121		CTAAGAGTAAATGGTTTTCTTATCACAAGCCTTTTGATATCTATGATACACGTAGAAA			180
Sbjct 49108		.....			49167
Query 181		TGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAATATCATTA			240
Sbjct 49168		.....			49227
Query 241		CTCATACTGAAACTTACAAAATCATCTTTTTGAAGATCGAAGAAATTCCCCGGCTTTGAG			300
Sbjct 49228		.....			49287
Query 301		AAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCAAATAAAAT			360
Sbjct 49288		.....			49347
Query 361		AAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCAATCCAGA			420
Sbjct 49348		.....			49407
Query 421		TTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTGGAAATCGCCGG			480
Sbjct 49408		.....			49467
Query 481		GATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTCAC		525	
Sbjct 49468		.....		49512	

**INS2 (ad)**

Score	Expect	Identities	Gaps	Strand	
2290 bits(1240)	0.0	1242/1243(99%)	0/1243(0%)	Plus/Plus	
Query 1		<b>TTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCTTACTTATTAAGTCAA</b>			<b>60</b>
<b>Sbjct</b> 47711		..... <b>G</b> .....			47770
Query 61		TATTATATTGACTATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTCGATTTAT			120
Sbjct 47771		.....			47830
Query 121		CACAATTCTAATACTAATAACACAATTCTAATACTAATAATAGTGATTGTAAAatattgtta			180
Sbjct 47831		.....			47890
Query 181		atattccttttattttcaattattttcaatttgaattgaatggtaaataattatttttcatt			240
Sbjct 47891		.....			47950
Query 241		tctttttttGGCATTGGAAATACTTTTTATTACAGTtctatatttgattctatattatat			300
Sbjct 47951		.....			48010
Query 301		atctatatctctctcattctatatttaatttattttcaaattcctaattGTTTAATGGAATG			360
Sbjct 48011		.....			48070
Query 361		GTTAGTTATAACTAATGAGACATTCTCCGTTTTTCAGGCGAAAGTTAAAAACAAGAATC			420
Sbjct 48071		.....			48130
Query 421		GATCGTTCAAGTATTCCAAATGGAATGGCAAAATGACAGGAAGCGAGACATATAGATCGG			480
Sbjct 48131		.....			48190
Query 481		GTATATATCCATCTATATTGAATTGCGGATTCCGAAATGATAAAATCATTTTTGATTGGA			540
Sbjct 48191		.....			48250
Query 541		CaaaaaaaGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTTT			600
Sbjct 48251		.....			48310

```

Query 601 CGAGATAGGAATCGGTATCTAATGAATTCAATGGTCCAGTATaaatgaaagaaaaagaa 660
Sbjct 48311 ..... 48370

Query 661 aaaggaatgacatcccaacgggatcctaatctcaaaacaaaaagaaaGGGGGATATGGCG 720
Sbjct 48371 ..... 48430

Query 721 AAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAGTG 780
Sbjct 48431 ..... 48490

Query 781 ATCACTTTCAAATTCAGAGAAACCCTGGAATTAACAAAAATGGGCAATCCTGAGCCAAAT 840
Sbjct 48491 ..... 48550

Query 841 CCTGTTTTCTCAAAACAAACAAAGGTTTCAGaaaaaaaGGATAGGTGCAGAGACTCAATGG 900
Sbjct 48551 ..... 48610

Query 901 AAGCTATTCTAACAAATGGAGTTAAATGTGTTGGTAGAGGACTCTTTACATCGAAACTTC 960
Sbjct 48611 ..... 48670

Query 961 AGAAAGAAAAGAATGAAGTGCAGGAGAAACGTATATACATACGTATTGAATACTATATC 1020
Sbjct 48671 ..... 48730

Query 1021 AAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAAAAATAGAAGAATTGGTGTG 1080
Sbjct 48731 ..... 48790

Query 1081 AATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATTCACTCCATAG 1140
Sbjct 48791 ..... 48850

Query 1141 TCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGATAGAGTCCCGTCTT 1200
Sbjct 48851 ..... 48910

Query 1201 ACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAAA 1243
Sbjct 48911 ..... 48953

```

**INS2 (ef)**

Score	Expect	Identities	Gaps	Strand
909 bits(492)	0.0	513/523(98%)	1/523(0%)	Plus/Plus
Query 4	GGTTC AAGTCCCTCTATCCCCAAAATGACTATTTAACTCCCAACTATTTATCCGACCCC			63
<b>Sbjct</b> 48979	..... <b>A</b> .....			49038
Query 64	CTTTCCTTAACGGTTCAAATTCCTTATCTTTCTCATCCACTCTATTCTTTTAGAAATGG			123
Sbjct 49039	.....			49098
Query 124	AttttttttCTAAGAGTAAATGGTTTTCACTTATCACAAGCCTTTTGATATCTATGATAC			183
<b>Sbjct</b> 49099	..... <b>T</b> .....			49158
Query 184	ACGTA-AAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACA			242
<b>Sbjct</b> 49159	..... <b>G</b> .....			49218
Query 243	ATAACATTACTCATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAAAATCCCC			302
<b>Sbjct</b> 49219	... <b>T</b> ..... <b>G</b> .....			49278
Query 303	GGCTTTGAGAAAATTTGTTAATCGACTTACTTGACAAAAACCCAGTTCATGATAGAATC			362
<b>Sbjct</b> 49279	..... <b>T.G</b> .....			49338
Query 363	AAATAAATTAAGGATACCACCCAAAGGACTCGAATTCCTCATGTTAACGGTTCCAATTC			422
<b>Sbjct</b> 49339	..... <b>A</b> ..... <b>A</b> .....			49398
Query 423	CAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTGGA			482
Sbjct 49399	.....			49458
Query 483	AATCGCCGGGATAGCTCAATTGGTAGAGCAGAGGACTGAAAAT			525
<b>Sbjct</b> 49459	..... <b>G</b> .....			49501

LID2 (ad)

Score	Expect	Identities	Gaps	Strand
2170 bits(1175)	0.0	1223/1244(98%)	12/1244(0%)	Plus/Plus
Query 1	TCTTATATGCATAGTAATTGACTAAACTACTGGAATTGGAATCTTAGTTATTAAC TAGTC	60		
Sbjct 47709	.....	47768		
Query 61	AATATTATATTGAATATTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTTCGATTT	120		
Sbjct 47769	..... <b>C</b> .....	47828		
Query 121	ATCACAATTCTAATACTAATA-----T-T-AT--T-A-AATAGTGATTGTAAAtattgt	168		
Sbjct 47829	..... <b>CACAAT.C.A.AC.A.T</b> .....	47888		
Query 169	taatattcttttattttcaattattttcaatttgaattgaatggtaaatattatttttaa	228		
Sbjct 47889	..... <b>C</b> .....	47948		
Query 229	tttctttttttGGCATTGGAAACTTTTTATTACAGTtctatatttgattctatattat	288		
Sbjct 47949	.....	48008		
Query 289	atatctatatctctctcattctatatttaattttattttcaaattctaattGTTTAATGGAA	348		
Sbjct 48009	.....	48068		
Query 349	TGGTTAGTTATAACTAATGAGACATTCCCTCCGTTTTTCAGGCGAAAGTAAAAACAAGAA	408		
Sbjct 48069	.....	48128		
Query 409	TCGATCGTTCAAGTATTCCAAATTGAATGGCAAATGACAGGAAGCGAGAAATATAGATC	468		
Sbjct 48129	..... <b>C</b> .....	48188		
Query 469	GGGTATATATCCATCTATATTGAATTGCGGATTCCGAAATGATAAAATCATTTTTGATTG	528		
Sbjct 48189	.....	48248		
Query 529	GACaaaaaaaaGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTT	588		
Sbjct 48249	.....	48308		
Query 589	TTTCGAGATAGGAATCGGTATCTAATGAATTC AATGGTTCCAGTATAaatgaaagaaaaag	648		
Sbjct 48309	.....	48368		
Query 649	aaaaaggaatgacatcccaacgagatcctaatactcaaaacaaaaagaaaGGGGGATATGG	708		
Sbjct 48369	..... <b>G</b> .....	48428		
Query 709	CGAAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAAG	768		
Sbjct 48429	.....	48488		
Query 769	TGATCACTTTAAAAATTCAGAGAAACCCTGGAATTAACAAAAATGGGCACTCCTGAGCCAA	828		
Sbjct 48489	..... <b>C</b> ..... <b>A</b> .....	48548		
Query 829	ATCCTGTTTTTCTCAAAAACAAACAAAGGTTTCAGaaaaaaaaGGATAGGTGCAGAGACTCAAT	888		
Sbjct 48549	.....	48608		
Query 889	GGAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTCTTTACATCGAAACT	948		
Sbjct 48609	..... <b>T</b> .....	48668		
Query 949	TCAGAAAGAAAAAGAATGAAGTGAAGGATAAACGTATATACATACGTATTGAATACTATA	1008		
Sbjct 48669	..... <b>C</b> ..... <b>G</b> .....	48728		
Query 1009	TCAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAAAAATAGAAGAATTGGTG	1068		
Sbjct 48729	.....	48788		
Query 1069	TGAATCCATTCTACATTGAAGAAAGAATCGAATATTCATTGATCAAATCATTCACTCCAT	1128		
Sbjct 48789	.....	48848		
Query 1129	AGTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGATAGAGTCCCGTT	1188		
Sbjct 48849	.....	48908		
Query 1189	CTACATGTCAATACCGGCAACAATGAAATTTATAGTAAAAGGAA	1232		
Sbjct 48909	.....	48952		

## LID2 (ef)

Score	Expect	Identities	Gaps	Strand	
987 bits(534)	0.0	540/543(99%)	0/543(0%)	Plus/Plus	
Query 1		GTTC AAGTCCCTCTATCCCCAAAAGACTATTTAACTCCCAACTATTTATCCGACCC			60
Sbjct 48980		.....			49039
Query 61		TTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGGA			120
<b>Sbjct</b> 49040		..... <b>C</b> .....			49099
Query 121		tttttttttCTAAGAGTAAATGGTTTTCTCTTATCACAAGCCTTTTGATATCTATGATACA			180
Sbjct 49100		.....			49159
Query 181		CATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCGGATCAATACAA			240
<b>Sbjct</b> 49160		<b>.G</b> .....			49219
Query 241		TATCATTACTCATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAGAAATCCCCG			300
Sbjct 49220		.....			49279
Query 301		GCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAATCA			360
Sbjct 49280		.....			49339
Query 361		AATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCC			420
Sbjct 49340		.....			49399
Query 421		AATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTGGAA			480
Sbjct 49400		.....			49459
Query 481		ATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTGTACCAGTTCA			540
<b>Sbjct</b> 49460		..... <b>G</b> .....			49519
Query 541	AAT	543			
Sbjct 49520	...	49522			

## LIN1.3 (ad)

Score	Expect	Identities	Gaps	Strand	
2152 bits(1165)	0.0	1223/1247(98%)	19/1247(1%)	Plus/Plus	
Query 1		CTTATATGCATAGTAATTGACTAACTACTGGAATTGGAATCTTAGTTATTAAGTAGTCA			60
Sbjct 47710		.....			47769
Query 61		ATATTATATTGAATATTTCTAGAGCATAAGGATTAATATAGCGATCTAGAATTTGATTTA			120
<b>Sbjct</b> 47770		..... <b>C</b> .....			47829
Query 121		T-----CACAACTCTAATACTAATAATAGTGATTGTAAAtattggtt			161
<b>Sbjct</b> 47830		<b>.CACAATTCTAATACTAATA</b> .....			47889
Query 162		aatattccttttattttcaattattttcaatttgaattgaatggtaaatattatttttcat			221
Sbjct 47890		.....			47949
Query 222		ttctttttttGGCATTGGAATACTTTTTATTACAGTtctatatttgattctatattata			281
Sbjct 47950		.....			48009
Query 282		tatctatatctctctcattctatatttaatttatttcaaattctaattGTTTAATGGAAAT			341
Sbjct 48010		.....			48069
Query 342		GGTTAGTTATAACTAATGAGACATTCCTCCGTTTTTCAGGCGAAAGTAAAAACAAGAAT			401
Sbjct 48070		.....			48129
Query 402		CGATCGTTCAAGTATTCCAAATGGAATGGCAAAATGACAGGAAGCGAGACATATAGATCG			461
Sbjct 48130		.....			48189
Query 462		GGTATATATCCATCTATATTGAATTGCGGATTCGAAATGATAAAATCATTTTTGATTGG			521
Sbjct 48190		.....			48249

Query	522	ACaaaaaaaaGGGTCTCCTATAGAAGATAGTTAAGAAAATCAAAGAGGAGAAAACACGTTT	581
Sbjct	48250	.....	48309
Query	582	TCGAGATAGGAATCGGTATCTAATGAATTCAATGGTTCAGTATaaatgaaagaaaaaga	641
Sbjct	48310	.....	48369
Query	642	aaaaggaatgacatcccaacgggatcctaatactcaaaacaaaaagaaaGGGGATATGGC	701
Sbjct	48370	.....	48429
Query	702	GAAATTGGTAGACGCTACGGACTTAATTGGATTGAGCCTTGGTATGGAACTTACTAGGT	761
<b>Sbjct</b>	48430	..... <b>A</b> .....	48489
Query	762	GATCACTTTCAAATTCAGAGAAACCTGGAATTAACAAAAATGGGCAATCCTGAGCCAAA	821
Sbjct	48490	.....	48549
Query	822	TCCTGTTTTCTCAAAACAAACAAAGGTTTCAGaaaaaaaaGGATAGGTGCAGAGACTCAATG	881
Sbjct	48550	.....	48609
Query	882	<b>GAAGCTATTCTAACAAATGGAGTTAAATGCGTTGGTAGAGGACTCTTTACATCGAACTT</b>	941
<b>Sbjct</b>	48610	..... <b>T</b> .....	48669
Query	942	CAGAAAGAAAAAGAAATGAAGTGCAGGAGAACCCTATATACATACGTATTGAATACTATAT	1001
<b>Sbjct</b>	48670	..... <b>A</b> .....	48729
Query	1002	CAAATGATTAATGACGACCCGAATCCGTATTTTTTCTATAAAAAATAGAAGAATTGGTGT	1061
Sbjct	48730	.....	48789
Query	1062	GAATCCATTCTACATTGAAGAAAGAAATCGAATATTCATTGATCAAATCATTCACTCCATA	1121
Sbjct	48790	.....	48849
Query	1122	GTCTGATAGATCTTTTGAAGAACTGATTAATCGGACGAGAATAAAGTTAGAGTCCCGTTC	1181
<b>Sbjct</b>	48850	..... <b>A</b> .....	48909
Query	1182	TACATGTCAATACCGCAACAATGAAATTTATAGTAAAAGGAAAATC	1228
Sbjct	48910	.....	48956

### TOM1 (ef)

Score	Expect	Identities	Gaps	Strand
883 bits(478)	0.0	532/554(96%)	20/554(3%)	Plus/Plus
Query	2	GGTTC AAGTCCCTCTATCCCCAAAAAGACTATTTAACTCCCAACTATTTATCCGACCCC	61	
Sbjct	48979	.....	49038	
Query	62	CTTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGG	121	
<b>Sbjct</b>	49039	..... <b>C</b> .....	49098	
Query	122	AttttttttCTAAGAGTAAATGGTTTTCTTATCACAAGCCTTTTGTATCTATGATAC	181	
Sbjct	49099	.....	49158	
Query	182	ACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATCCCAGATCAATACA	241	
<b>Sbjct</b>	49159	.. <b>G</b> .....	49218	
Query	242	ATATCACTACTCATACTGAAACTTACAAAATCATCTTTTGAAGATCGAAGAAATTCCCC	301	
Sbjct	49219	.....	49278	
Query	302	GGCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTCTATGATAGAATC	361	
<b>Sbjct</b>	49279	.....-----	49326	
Query	362	AAAGAAAATATGATAGAATCAAATAAAAATAAGGATACCACCCAAAGGACTCGAAATCCTC	421	
<b>Sbjct</b>	49327	-----.....	49378	
Query	422	ATGTTAACGGTTCCAATTTCCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTT	481	
Sbjct	49379	.....	49438	
Query	482	CCAATCTAATCTGGGTTGGAAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAA	541	
Sbjct	49439	.....	49498	

Query 542 AATCCTCGTGTAC 555  
 Sbjct 49499 ..... 49512

**TOR2.1(ad)**

Score	Expect	Identities	Gaps	Strand
1683 bits(911)	0.0	958/979(98%)	9/979(0%)	Plus/Plus
Query 344	tacagttctatatttgattctatatta-----tatactctctcattctatatttaatt			397
<b>Sbjct</b> 47981	..... <b>TATATC</b> .....			48040
Query 398	tatttcAAATCCTAATTGTTTAAATGGAATGGTTAGTTATAACTAATGAGACATTCTCCG			457
<b>Sbjct</b> 48041	..... <b>T</b> .....			48100
Query 458	CTTTCAGGCGAAAGTTCAAAAACAAGAATCGATCGTTCAAGTATTCCCAAATTGAATGGC			517
<b>Sbjct</b> 48101	<b>T</b> ..... <b>A</b> .....-			48159
Query 518	AAAAATGACGGGAAGCGAGACATATAGATCCGGGGATATATCCCATCTATATTGAATTGCG			577
<b>Sbjct</b> 48160	..... <b>A</b> .....-... <b>T</b> .....-			48217
Query 578	GATTCGAAATGATAAAATCATT'TTTGATTGGACaaaaaaaGGGTCCTATATAAGATA			637
<b>Sbjct</b> 48218	..... <b>G</b> .....			48277
Query 638	GTTAAGAAAATCAAAGAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAAT			697
Sbjct 48278	.....			48337
Query 698	TCAATGGTTCCAGTATAaatgaaagaaaaagaaaaggaatgacatcccaacgagatcct			757
<b>Sbjct</b> 48338	..... <b>G</b> .....			48397
Query 758	aatctcaaaaacaaaaagaaaGGGGGATATGGCGAAATTGGTAGACGCTACGGACTTAATT			817
Sbjct 48398	.....			48457
Query 818	GGATTGAGCCTTGGTATGGAAACTTACTAAGTGATCACTTTCAAATTCAGAGAAACCCTG			877
Sbjct 48458	.....			48517
Query 878	GAATTAACAAAAATGGGCAATCCTGAGCCAAATCCTGTTTTCTCAAAACAAACAAAGGTT			937
Sbjct 48518	.....			48577
Query 938	CAGaaaaaaaGGATAGGTGCAGAGACTCAATGGAAGCTATTCTAACAAATGGAGTTAAAT			997
Sbjct 48578	.....			48637
Query 998	GCGTTGGTAGAGGACTCTTTACATCGAACTTCAGAAAAGAAAAGAATGAAGTGAAGGAT			1057
<b>Sbjct</b> 48638	<b>.T</b> ..... <b>C</b> ..... <b>G</b>			48697
Query 1058	AAACGTATATACATACGTATTGAATACTATATCAAATGATTAATGACGACCCGAATCCGT			1117
Sbjct 48698	.....			48757
Query 1118	AGTTTTTCTATAAAAAATAGAAGAATGGTGTGAATCCATTCTACATTGAAGAAAGAATC			1177
<b>Sbjct</b> 48758	<b>.T</b> .....			48817
Query 1178	GAATATTCATTGATCAAATCATTCACTCCATAGTCTGATAGATCTTTTGAAGAACTGATT			1237
Sbjct 48818	.....			48877
Query 1238	AATCGGACGAGAATAAAGATAGAGTCCCGTTCTACATGTCAATACCGGCAACAATGAAAT			1297
Sbjct 48878	.....			48937
Query 1298	TTAGAGTAAAAGGAAAATC 1316			
<b>Sbjct</b> 48938	... <b>T</b> ..... 48956			

**TOR2.1(ef)**

Score	Expect	Identities	Gaps	Strand
749 bits(405)	0.0	433/447(97%)	0/447(0%)	Plus/Plus
Query 9	CCTCTATCCCCAAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCTTTCCTTAA			68
Sbjct 48989	.....			49048
Query 69	CAGTTCCAAATTCCTTATCTTTCTCATTCACTCTATCTTTTAGAAATGGATTCTTTTTC			128
<b>Sbjct</b> 49049	<b>.G</b> ..... <b>C</b> ..... <b>T</b> .....			49108

Query	129	TAAGCGTAAATGGCTTTCTCTTATCACAAGCCTTTTGATATCTATGATACACATAGAAAT	188
<b>Sbjct</b>	49109	..... <b>A</b> ..... <b>T</b> ..... <b>G</b> .....	49168
Query	189	GAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATCCCGATCAATACAATATCATTAC	248
<b>Sbjct</b>	49169	.....	49228
Query	249	TCATACTGAAACGTACAAAGTCATCTTTTTGAAGATCGAAGAAATCCCCGGCTTTTCTA	308
<b>Sbjct</b>	49229	..... <b>T</b> ..... <b>A</b> ..... <b>GAG</b> .....	49288
Query	309	AAATTTTTTAATCGACTTACTTGACATAGACCCAGTTCTAGGATAGAATCAAATAAAATA	368
<b>Sbjct</b>	49289	..... <b>G</b> ..... <b>T</b> .....	49348
Query	369	AGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCAATCCAGAT	428
<b>Sbjct</b>	49349	.....	49408
Query	429	TGGTAGGATAGAGGACTCGAAATCCTC	455
<b>Sbjct</b>	49409	..... <b>G</b> .....	49435

### TOR3 (ad)

Score	Expect	Identities	Gaps	Strand
1640 bits(888)	0.0	947/973(97%)	14/973(1%)	Plus/Plus
Query	343	tacagttctatatttgattctatatta-----tatactctctcatctatatttaatt	396	
<b>Sbjct</b>	47981	..... <b>TATATC</b> .....	48040	
Query	397	tatttcAAATCCTAATTGTTTAATGGAATGGTTAGTTATAACTAATGAGACATTCTCCG	456	
<b>Sbjct</b>	48041	..... <b>T</b> .....	48100	
Query	457	CTTTCAGGCGAAAGTTCAAAAACAAGAATCGATCGTTCAAGTATCCAAATTGAATGGCA	516	
<b>Sbjct</b>	48101	<b>T</b> ..... <b>A</b> .....	48160	
Query	517	AAATGACAGGAAGCGAGACATATAGATCGGGTATATATCCATCTATATTGAATTGCGGAT	576	
<b>Sbjct</b>	48161	.....	48220	
Query	577	TCCGAAATGATAAAATCATTTTTGATTTGGACaaaaaaaaGGGTCTCTATATAAGATAGTT	636	
<b>Sbjct</b>	48221	..... <b>G</b> .....	48280	
Query	637	AAGAAAATCAAAGAGGAGAAAACACGTTTTTCGAGATAGGAATCGGTATCTAATGAATCA	696	
<b>Sbjct</b>	48281	.....	48340	
Query	697	ATGGTTCCAGTATAAATGaaagaaaaagaaaaaGGAATGACATCCCCAACGAGATCCTA	756	
<b>Sbjct</b>	48341	.....-.....-..... <b>G</b> .....	48398	
Query	757	ATCTCAAAACAAAAAGAAAGGGGGATATGGCGAAATTGGTAGACGCTTACGGACTTAA	816	
<b>Sbjct</b>	48399	.....-.....-.....-.....	48455	
Query	817	TTGGGATTGAGCCTTGGTATGGAAACTTACTAAGTGATCACTTTTCAAATTCAGAGAAAC	876	
<b>Sbjct</b>	48456	..-.....-.....	48513	
Query	877	CCTGGAATTAAC-AAAATGGGCAATCCTGAGCCAAATCCTGTTTTCTCAAAACAAACAAA	936	
<b>Sbjct</b>	48514	..... <b>A</b> .....	48573	
Query	936	GGTTCAGaaaaaaaaGGATAGGTGCAGAGACTCAATGGAAGCTATTCTAACAAATGGAGTT	996	
<b>Sbjct</b>	48574	.....	48633	
Query	996	AAATGCGTTGGTAGAGGACTCTTTACATCGAACTTCAGAAAGAAAAAGAATGAAGTGAA	1056	
<b>Sbjct</b>	48634	..... <b>T</b> ..... <b>C</b> .....	48693	
Query	1056	GGATAAACGTATATACATACGTATTGAATACTATATCAAATGATTAATGACGACCCGAAT	1116	
<b>Sbjct</b>	48694	... <b>G</b> .....	48753	
Query	1116	CCGTAGTTTTTCTATAAAAAATAGAAGAATTGGTGTGAATCCATTCTACATTGAAGAAAG	1176	
<b>Sbjct</b>	48754	..... <b>T</b> .....	48813	
Query	1176	AATCGAATATTCATTGATCAAATCATTCCTCCATAGTCTGATAGATCTTTTGAAGAACT	1236	
<b>Sbjct</b>	48814	.....	48873	
Query	1236	GATTAATCGGACGAGAATAATGATAAAGTCCCGTTCTACATGTCAATACCGGCAACAATG	1296	
<b>Sbjct</b>	48874	..... <b>A</b> ..... <b>G</b> .....	48933	

Query 1296 AAATTTAGAGTAA 1308  
**Sbjct** 48934 .....**T**..... 48946

**TOR3 (ef)**

Score	Expect	Identities	Gaps	Strand
741 bits(401)	0.0	429/443(97%)	0/443(0%)	Plus/Plus
Query 1	TATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGACCCCTTTCCTTAACAGT			60
<b>Sbjct</b> 48993	..... <b>T</b> .....			49052
Query 61	TCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATGGATTCTTTTTCTAAG			120
<b>Sbjct</b> 49053	..... <b>C</b> ..... <b>T</b> .....			49112
Query 121	CGTAAATGGCTTTCTCTTATCACAAGCCTTTTGATATCTATGATACACATAGAAATGAAC			180
<b>Sbjct</b> 49113	<b>A</b> ..... <b>T</b> ..... <b>G</b> .....			49172
Query 181	ATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATACAATATCATTACTCAT			240
<b>Sbjct</b> 49173	.....			49232
Query 241	ACTGAAACGTACAAAGTCATCTTTTGAAGATCGAAGAAATCCCCGGCTTTTCTAAAAAT			300
<b>Sbjct</b> 49233	..... <b>T</b> ..... <b>A</b> ..... <b>GAG</b> .....			49292
Query 301	TTTTTAATCGACTTACTTGACATAGACCCAGTTCTAGGATAGAATCAAATAAAATAAGGA			360
<b>Sbjct</b> 49293	.. <b>G</b> ..... <b>T</b> .....			49352
Query 361	TACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTTCCAATCCAGATTGGT			420
<b>Sbjct</b> 49353	.....			49412
Query 421	AGGATAGAGGACTCGAAATCCTC 443			
<b>Sbjct</b> 49413	..... <b>G</b> ..... 49435			

**VIO1 (ef)**

Score	Expect	Identities	Gaps	Strand
946 bits(512)	0.0	525/531(99%)	1/531(0%)	Plus/Plus
Query 2	GGTTC AAGGGT CCTCTATCCCCAAAAGACTATTTAACTCCCCAACTATTTATCCGACCC			61
<b>Sbjct</b> 48979	.....- <b>TC</b> .....			49037
Query 62	CCTTTCCTTAACGGTTCCAAATTCCTTATCTTTCTCATTCACTCTATTCTTTTAGAAATG			121
<b>Sbjct</b> 49038	..... <b>C</b> .....			49097
Query 122	GATtttttttttCTAAGAGTAAATGGTTTCTCTTATCACAAGCCTTTTGATATCTATGATA			181
<b>Sbjct</b> 49098	.....			49157
Query 182	CACATAGAAATGAACATCTTTGAGCAAGGAATCCCTAGTTGAATGATTCCCGATCAATAC			241
<b>Sbjct</b> 49158	.. <b>G</b> .....			49217
Query 242	AAATCATTACTCATACTGAAACTTCCAAAATCATCTTTTGAAGATCGAAGAAATCCC			301
<b>Sbjct</b> 49218	..... <b>A</b> .....			49277
Query 302	CGGCTTTGAGAAAATTTGTTAATCGACTTACTTGACATAGACCCAGTTCTATGATAGAAT			361
<b>Sbjct</b> 49278	.....			49337
Query 362	CAAATAAAATAAGGATACCACCCAAAGGACTCGAAATCCTCATGTTAACGGTTCCAATTT			421
<b>Sbjct</b> 49338	.....			49397
Query 422	CCAATCCAGATTGGTAGGATAGAGGACTGGAAATCCTCGTTCCAATCTAATCTGGGTTGG			481
<b>Sbjct</b> 49398	.....			49457
Query 482	AAATCGCCGGGATAGCTCAGTTGGTAGAGCAGAGGACTGAAAATCCTCGTG 532			
<b>Sbjct</b> 49458	..... 49508			