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                    5        10        15        20        25        30        35        40        45        50        55        60        65        70        75        80
conservation        ********** ********************* ********************* ********************* ********** **********
SPP1˙AM             ATGAAGGCCGCCATTGTTTTCGTGCTCCTCTTTGCCATAGTCTACTGTCGTCCTCTGAAGCGTTCAGTGAGCAGCTCAGA  80
SPP1˙CI             ATGAAGACTCTTATCGTTTTAACGCTCCTCGTTGCCACAGTCTTCTGCCTACCTGTCAAGCGCTCAGCTAGCAGTTCAGA  80
SPP1˙DR             ATGAAATCTATTATTGTTTTAACACTCCTCGTCGCCACAGTCTTCTGTGTACCTGTGAAGCGCTCAGCAAGCAGTTCAGA  80
SPP1˙IP             ATGAAGGCTGTCATTGTTTTCGTGCTCCTTTTCGCAGCGGTCTATTGTCACCCTGTGAAACGTTCAGCCAGCAGCTCAGA  80
SPP1˙LW             ATGAAGACCGTTATCGTTTTAACCCTCCTCATCGCCACAGTCTTCTGCCTGCCTGTCAAGCGCTCAGCCAGCAGTTCAGA  80
SPP1˙PN             ATGAAGGCCGTCATGATTTTCGGGCTCCTCTTCTGCTGTAGTCTACTGCCGTCCTGTAAAACGCTCAGCAAGCAGCTCAGA  80
SPP1˙PP             ATGAAGACTGTTATCGTTTTAACGCTTCTCATCGCCACAGTCTTCTGCCTACCTGTCAAGCGCTCAGCCAGCAGTTCAGA  80
SPP1-C1˙CC          ATGAAGACTGTCATCGTTTTAACGCTCCTCATCGCCACAGTTTTCTGTCTACCTGTGAAGCGCTCAGCTAGCAGTTCAGA  80
SPP1-C2˙CC          ATGAAGACTGTTTTCGTTTTAACGCTCCTCATCGCCACAGTCTTCTGTCTACCTGTGAAGCGCTCAGCTAGCAGTTCAGA  80
SPP1-C1˙SG          ATGAAGACTGTCATCGTTTTAACGCTCCTCATCGCCACAGTTTTCTGTCTACCTGTGAAGCGCTCAGCTAGCAGCTCAGA  80
SPP1-C2˙SG          ATGAAGACTGTTATCGTTTTAACGCTCCTCATCGCCACAGTCTTCTGTCTGCCTGTGAAGCGCTCAGCTAGCAGTTCAGA  80
SPP1-C1˙SR          ATGAAGACTGTCATCGTTTTAACGCTCCTCATCGCCACAGTTTTCTGTCTACCTGTGAAGCGCTCAGCTAGCAGTTCAGA  80
SPP1-C2˙SR          ................................................................................  0
SPP1-C1˙SA          ATGAAGACTGTCATCGTTTTAACGCTCCTCATCGCCACAGTTTTCTGTCTACCTGTGAAGCGCTCAGCTAGCAGTTCAGA  80
SPP1-C2˙SA          ATGAAGACTGTTATCGTTTTAACACTCCTCATCGCCACAGTCTTCTGTCTGCCTGTGAAGCGCTCGGCTAGCAGTTCAGA  80

                    85        90        95        100       105       110       115       120       125       130       135       140       145       150       155
conservation        ********** ** * ** ***** ********** * ********** ********** ******* ********* ****
SPP1˙AM             GAGTTCTGAGGAACAAGCCGCTGCCAAACCGGCGCCCCCAATTCTGCGGAAAGCCCCTGCAAAAGCAGTGCAGGCA....  156
SPP1˙CI             GAGCTCAGAAGAGCTTGTTGCTGTTCAACGGCCACCTCCTATTCTCCGAAAAGCTGCTGCTAATATGTTTGAGGCAGAAC  160
SPP1˙DR             GAGCTCAGAAGAGCTTGTAATTGTTCAACGGCCACCTCCTATTCTTCGAAAAGCTGCTGCCAATGTGTTCCAGGTAGAGC  160
SPP1˙IP             GAGTGCTGACCTGCAGCCTGTTGATACTCAGAGC......ATCAATGGAAAAAGAATCACAGTAGCCATATTCACAAAGC  154
SPP1˙LW             GAGCTCAGAAGAAATGATTGCTGTTCAACGGCCACCTCCTCTTCTACAAAAAGCTGCTGCTGATATGTTCCAGGCAGAAT  160
SPP1˙PN             GAGCTCTGAGGAACAGGCAGTTGCCAAACTGCCACTCCCAGTTCTTGATAAAGGCCCTGCAGATCCACTAAAGGCAGCAC  160
SPP1˙PP             GAGCTCAGAAGAAATGATTGCCGTTCAACGGCCACCTCCTATTCTA...AAAGCTGCTGCTGATATGTTCCAGGCAGAAC  157
SPP1-C1˙CC          GAGCTCAGAAGAACTTGTGGTTGCTCAACAACCAACTCCTATTCTACGAAAAGCTGCTGCTGTTATGTTCAAGGCAGAAC  160
SPP1-C2˙CC          GAGCTCAGAAGAACTTGTGACTGTTCAACAACCACCTCCTATTCTAGAAAAAGCTGCTGCTGTTATGTACAAGGCAGAAC  160
SPP1-C1˙SG          GAGCTCAGAAGAACTTGTGGTTGCTCAACAACCACCTCCTATTCTACGAAAAGCTGCTGCTGTTATGTTCAAGGCAGAAC  160
SPP1-C2˙SG          GAGCTCAGAAGAACTTGTGGTTGTTCAACGGCCACCTCCTATTCTGCAAAAAGCTGCTGCTGTTATGTTCAAGGCAGAAC  160
SPP1-C1˙SR          GAGCTCAGAAGAACTTGTGGTTGCTCAACGGCCACCTCCTATTCTACGAAAAGCTGCTGCTGTTATGTTCAAGGCAGAAC  160
SPP1-C2˙SR          ................................................................................  0
SPP1-C1˙SA          GAGCTCAGAAGAACTTGTGGTTGCTCAACGGCCACCTCCTATTCTACGAAAAGCTGCTGCTGTTATGTTCAAGGCAGAAC  160
SPP1-C2˙SA          GAGCTCAGAAGAACTTGTGGTTGTTCAACGGCCACCTCCTATTCTGCAAAAAGCTGCTGCT...ATGTTCAAGGCAGAAC  157

                    160       165       170       175       180       185       190       195       200       205       210       215       220       225       230
conservation        ******!****** ***** *!********** *!******!******* ****** ********** ********
SPP1˙AM             ..GTAGAGGTTGTACCTGCTCAGGCTGTTAAAGCAGCTCCAGAAGCTCCAGCAGATCCAGAAGCAGCAGCAGCGGCAGCA  234
SPP1˙CI             CTACACAGACCACGCCAACAGAATCTAATGAAAGCACA...GACAGTGCAGATGACACTGAGGAGGCATATGAGGAATCT  237
SPP1˙DR             CTACACAGACCACGCCAACAGAATCGAATGAAAGCACA...GACAGCGCAGATGACACTGAGGAGGCAGATGAGGAATCT  237
SPP1˙IP             CTACCTAATTTCAAGTGTTTTATAATTACTACTCGGCA...CATACTGTATTGAAAGTCACTGCGGTTGCTGATGTTAGC  231
SPP1˙LW             CTACACAGACCACACCAGCAGATTCCAATGAAAGCACA...GACAGTGAAGATGACACTGAGGAGGCAGATGAGAAATCT  237
SPP1˙PN             CTGCACAGGACAAAAACACAGAATCAGACACAGAGGGA...GACAGTGCAGACAGCGCAGACACGCAAGACACGCAAGAC  237
SPP1˙PP             CTACACAGACCACACCAGCAGATTCCAATGAAAGCACA...GACAGTGAAGATGACACTGAGGAGGAAGATGAGGAATCT  234
SPP1-C1˙CC          CTACACAGTCCACGCCAGGAGAATCCAATGAAAGCACA...GACAGTGCAGATGACAGTGAGGGTGCAGATGAGGAATCT  237
SPP1-C2˙CC          CCACACAGACCACACCAGTAGATTCCAATGAAAGCACA...GACAGTGCAGATGACAGTGAGGATGCAGATGAGGAATCT  237
SPP1-C1˙SG          CTACACAGACCACGCCAGCTGAATCCAATGAAAGCACA...GACAGTGCAGATGACAGTGAGGATGCAGATGAGGAATCT  237
SPP1-C2˙SG          CTACACAGACCACGCCAGCTGAATCCAATGAAAGCACA...GACAGTGCAGATGACAGTGAGGATGCAGATGAGGAATCT  237
SPP1-C1˙SR          CTACACAGACCACGCCAGCTGAATCCAATGAAAGCACA...GAAAGTGCAGATGACAGTGAGGATGCAGATGAGGAATCT  237
SPP1-C2˙SR          .....CAGACCACGCCAGCTGAATCCAATGAAAGCACA...GACAGTTCAGATGACAGTGAGGATGCAGATGAGGAATCT  72
SPP1-C1˙SA          CTACACAGACCACGCCAGCTGAATCCAATGAAAGCACA...GACAGTGCAGATGACAGTGAGGATGCAGATGAGGAATCT  237
SPP1-C2˙SA          CTACACAGACCACGCCAGTAGAATCCAATGAAAGCACA...GACAGTGCAGATGACAGTGAGGATGCAGATGAGGAATCT  234
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                    235       240       245       250       255       260       265       270       275       280       285       290       295       300       305       310
conservation        *****!******* *!* * ****! ** ***!!***!**!!!***!  *!*****!!*!!* !** ** ******* **
SPP1˙AM             TCATCGGATGAGGACGACTCAGATGAAGCTGAGGACTCCAGTGAGAGTGCTGAGTCTGGAGAAACTGAGGCCACCACCAC  314
SPP1˙CI             GAAACAGATGAGAACAAAGAGGAGAACGACACTGATTCCAGTGAAAGT...GAATCTGGAGAAACTGAGACCACCGCAGT  314
SPP1˙DR             GAAACAGATGAGAAGGAAGAGGAGAATGAGACTGACTCCAGTGAGAGT...GAATCTGGAGAATCTGATACCACCATCAT  314
SPP1˙IP             TCTGAAGAGGATGATGATGATGATGATGACAGTGACAGCGATGAGTCTGATGAGAATGGCGAGCCCACCAGTTCT.....  306
SPP1˙LW             GAAACAGATGAGGATGAG...GAGAATGAGACTGACTCCAGTGAGAGT...AATTCTGGAGAAACTCAGAGCACCGTAGT  311
SPP1˙PN             ACTATAGATTTGTGCCAGGATTGGGACACAGATGACTCCAGTGAGAGTGCTGAATCAGGAGAGACTGAGGCCACTACCGT  317
SPP1˙PP             AAAACAGATGAGGATGAG...GAGAACGAGACTGACTCCAGTGAGAGT...AATTCTGGGGAAACTCAGAGCACCGTCGT  308
SPP1-C1˙CC          GAAATGGATGAGAACGAAAAGGAGAACGATACTGACTCCAGTGAGAGT...GAATCTGGAGAACCTGCGACCACCGTTGT  314
SPP1-C2˙CC          GAAACAGATGAGAAGGAAGATGAGAATGATACTGATACCAGTGAGAGT...GAATCTGGAGAAACTGCGATCACCGTTGT  314
SPP1-C1˙SG          AAAACAGTTGAGAACGAAAAGGAGAACGACACTGACTCCAGTGAGAGT...GAATCTGGAGAATCTGCGACCATCGTTGT  314
SPP1-C2˙SG          GAAACAGATGAGAGGGAAGATGAGAATGATACTGATTCCAGTGAGAGT...GAATCTGGAGAATCTGCGATCACCGTTGT  314
SPP1-C1˙SR          GAAACAGTTGAGAACGAAAAGGAGAACGATACTGACTCCAGTGAGAGT...GAATCTGGAGAATCTGCGACCGCCGTTGT  314
SPP1-C2˙SR          GAAACAGATGAGAGGGAAGATGAGAATGATACTGATACCAGTGAGAGT...GAATCTGGAGAATCTGCGATCACCGTTGT  149
SPP1-C1˙SA          AAAACAGCTGAGAATGAAAAGGAGAACGATACTGACTCCAGTGAGAGT...GAATCTGGAGAATCTGCGACCACCGTTGT  314
SPP1-C2˙SA          GAAACAGATGAGAGGGAAGATGAGAATGATACTGATTCCAGTGAGAGT...GAATCTGGAGAATCTGCGATCACCGTTGT  311

                    315       320       325       330       335       340       345       350       355       360       365       370       375       380       385       390
conservation        *   !! ***!**** !! *!!*! !!****!!**!*!!**!****!!*!!*!!!!!!!!***!*!*!!**!**!!*!!!!
SPP1˙AM             CCCACCTTTCACCGAGGAGCCCACCCTGGGCCCTATTATTAACGACGGCCGCGGAGACAACATGGGCTACCCCAGCGACT  394
SPP1˙CI             C...CCATCCACAGTAGAGCCCTCACTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTACCCTAGCGACT  391
SPP1˙DR             C...CCAGTCACAGTCGATCCCACGCTGGGTCCCATTATCAACACAGGCCGGGGAGACAGTTTGGGCTACCCTAGCGACT  391
SPP1˙IP             ....CCTCCTATCATAGAGACCACTCTGATCCCTGTTATTAATT...GGCCGTGGAGACAGCATTGGCTTCCAGAGTGACT  379
SPP1˙LW             C...CCATCCACAGTCGAGCCCTCGCTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTACCCCAGCGACT  388
SPP1˙PN             CCCACCTGTAACCGTGGAGCCCACCCTGGACCCTATTATTGACAACGGTCGTGGAGACAGCATGGGCTACCCCAGCGACT  397
SPP1˙PP             C...CCATCCACAGTCGAGCCCTCGCTGGACCCCATTATCCACACAGGCCGGGGAGACAACATGGGCTACCCAAGCGACT  385
SPP1-C1˙CC          C...CCATTCACAGTGGAACCCCCACTGGACCCCATCATCAACACAGGCCGGGGAGACAACATGGACTATCCTAGCGACT  391
SPP1-C2˙CC          C...CCCTCCACAGTAGAACCCTCACTAGATCCCATCATCAACACAGGCCGGGGAGACAACATGGGCTACCCTAGCGACT  391
SPP1-C1˙SG          C...CCCTCCACAGTGGAACCCTCACTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTATCCTAGCGACT  391
SPP1-C2˙SG          C...CCCTCCACAGTAGAACCCTCACTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTACCCTAGCGACT  391
SPP1-C1˙SR          C...CCCTCCACAGTGGAACCCTCACTGGACCCCATCATCAACACTGGCCGGGGAGACAGCATGGGCTATCCTAGCGACT  391
SPP1-C2˙SR          C...CCCTCCACAGTAGAACCCTCACTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTACCCTAGCGACT  226
SPP1-C1˙SA          C...CCCTCCACAGTGGAACCCTCACTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTATCCTAGCGACT  391
SPP1-C2˙SA          C...CCCTCCACAGTAGAACCCTCACTGGACCCCATCATCAACACAGGCCGGGGAGACAGCATGGGCTACCCTAGCGACT  388
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               395  400  405  410  415  420  425  430  435  440  445  450  455  460  465  470
conservation   !!*******  ***  *****  !!**!  ***!!*  !**!*!!*!!*  **!!*!*  *!**!*!!*!!!*!*******!!!**!*
SPP1˙AM        ACAAGAAGACCATCATCTACGTAGATGCCAACGAAATCGAGAAGATACCTTCTCCCTACAAGTCCTACGTGCCTGAGCAC   474
SPP1˙CI        ACAAAAAAACCATCGTCTATGTGGACGCAAACGACTTTGAAAAGCTACCTTCTCCATACAAGTCCTACAGCAGTGACAAG   471
SPP1˙DR        ACAAAAAATCCATCGTCTATGTGGACGCAAAAGACTTTGAGAAACTTCCTTCACCATACAAATCCTACAGCAGTGACAAA   471
SPP1˙IP        ACAAGAAACCCGTTTATTATGTGGATGGCAACAACATTGAGAAAGGACCTTCTTCTCATAAATCCTATGGATCTGACAAG   459
SPP1˙LW        ACAAAAAAACCATAGTCTATGTGGACGCAAACAACATTGAAAAACTACCTTCACCATACAAGTCCTACAGCAGTGACAAG   468
SPP1˙PN        ACAAGAAGACCATCATCTATGTGGATGCCAACGACATTGAGAAAATTCCTTTTCCCTACAAGTCCAACGGACCTGACAAA   477
SPP1˙PP        ACAAAAAAAGCATTGTTTATGTGGACGCAAACAACTTTGAAAAACTACCTTCCCCATACAAGTCCTACAGCAGTGACAAG   465
SPP1-C1˙CC     AC..................GTGGACACAAACAACCTTGAAAAAATACCTTCACCATACAAGTCCTACAGCAGTGACAAG   453
SPP1-C2˙CC     ACAAAAAAAACATTGTCTACGTGGACGCAAACAACTTCGAAAAAATACCTTCCCCATACAAGTCCTACAGCAGTGACAAG   471
SPP1-C1˙SG     ACAAAAAAAACATTGTCCACGTGGACTCAAACGACTTTGAAAAAATACCGTCCCCATACAAGTCCTACAGCAGTGACAAG   471
SPP1-C2˙SG     ACAAAAAAAACATTGTCTACGTGGATGCAAACAACTTTGAAAAATTACCTTCCCCATACAAGTCCTACAGCAGTGACAAG   471
SPP1-C1˙SR     ACAAAAAAACCATCGTCCACGTGTACTCAAACGACTTTGAAAAAATACCGTCCCCGTACAAGTCCTACAGCAGTGACAAG   471
SPP1-C2˙SR     ACAAAAAAAACATTGTCTACGTGGATGCAAACAACTTTGAAAAATTACCTTCCCCATACAAGTCCTACAGCAGTGACAAG   306
SPP1-C1˙SA     ACAAAAAAAACATCGTCCACGTGGACTCAAACGACTTTGAAAAAATACCGTCCCCATACAAGTCCTACAGCAGTGACAAG   471
SPP1-C2˙SA     ACAAAAAAAACATTGTCTACGTGGATGCAAACAACTTCGAAAAATTACCTTCCCCATACAAGTCCTACAGCAGTGACAAG   468

               475  480  485  490  495  500  505  510  515  520  525  530  535  540  545  550
conservation   *****  !*****!!****  ************  *  ***     **      ***!!*******!***!**!****!!*********
SPP1˙AM        ATCGAGGGTCTGAACACCATCAGTAAGAAGACCTCCCACTACGACGGGCAGGAAGCCAATGACGTGGAGAAGCATCTGAA   554
SPP1˙CI        TTGGGCGGTTTGACATTCGTGAGCAAGAAGACATCTGCTTATGATGATCAGAGCATCAATGATGTGGAGAAAGAGATTAA   551
SPP1˙DR        CTGGGCGGCTTGACATTTGTGAGCAAGAAGACGTCTGCCTATGATGATCAGAGCATCAATGACGTGGAGAAAGAGATTAC   551
SPP1˙IP        ACCAAGGGTGAGAATAGTACTTTATATCCTGATGCATGCCAAACTAAACAATCCAGAAGGAATATCTCAAAGGGAACATT   539
SPP1˙LW        TTAGGCGGTTTGACATTTGTGAGCAAGAAGACGTCTGCTTAT...GATCAGAGCTTCAATGATGTGGAGAAAGAGATTCA   545
SPP1˙PN        ACTGATGACCTGAACAGCATCAGCATGAAGACATCTCATTTTGATGGCCAGGAAGCTAATGATGTGGAGAAGCATCTGAA   557
SPP1˙PP        TTAGGCGGTTTGACATTTGTGAGCAAGAAGTCGTCTGCTTATGATGACCAGAGCTTCAATGACGTGGAGAAAGAGATTCA   545
SPP1-C1˙CC     TTGGGCGGCTTGACATTCGTGAGCAAGAAGTCCTATGCTTATGATGACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   533
SPP1-C2˙CC     TTGGGCGGCTTGACATTTGTGAGCAAGAAGTCCTCT.........GACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   542
SPP1-C1˙SG     TTGGGCGGCTTGACATTCGTGAGCAAGAAGTCCTCTGCCTATGATGACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   551
SPP1-C2˙SG     TTGGGCGGCTTGACATTTGTGAGCAAGAAGTCCTCT.........GACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   542
SPP1-C1˙SR     TTGGGTGGCTTGACATTCGTGAGCAAGAAGTCCTCTGCCTATGATGACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   551
SPP1-C2˙SR     TTGGGTGGCTTGACATTTGTGAGCAAGAAGTCCTCT.........GACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   377
SPP1-C1˙SA     TTGGGTGGCTTGACATTCGTGAGCAAGAAGTCCTCTGCCTATGATGACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   551
SPP1-C2˙SA     TTGGGCGGCTTGACATTTGTGAGCAAGAAGTCCTCT.........GACCAGAGCATCAATGATGTGGAGAAAGAGATTAA   539

               555  560                 565  570  575  580            585  590  595  600  605  610  615
conservation   *******!*******  *****!*******   **  ****     ******!*********!*****!*****************
SPP1˙AM        GGTTTACAAG.........GTGCACAATGATGTTCTG......GAGGAGGACACCAGCACCCCTGAGGAGGAGAGC....   615
SPP1˙CI        ACTGTACAAGGCTCTACAGGTGCATGATGCTCCTCTG...GAGGAGGAGGACACCAGCACCCCAGAGGTGGAAAACATGG   628
SPP1˙DR        ACTGTACAAGGCTCTCCAGGTACATGATCTG.........GAGGACGGGAACACCAGCACCTCAGAGATAGACAACATCG   622
SPP1˙IP        ATACTGAAAAAAAAAAAGCATTACA...............ATATCTGAGACTCAGTGAGTTCCTTTTGTTTCTCAG....   600
SPP1˙LW        ACTGCACAGTGCTCTACAGGTGCATGATCTTCTG......GAGGAGGAGGACACCAGCACCCCCGAGATGGAGAACATGG   619
SPP1˙PN        GGTGTACAAGGCTCTGCAGGTGCACAATGAAGTCCTG......GAGGAGGATACTAGCACTCCAGAGGAGGAGAGC....   627
SPP1˙PP        ACTGCACAAGGCTCTGCAGGTGCATGATCTTCTG.........GAGGAGGACAGCAGCACTCCCGAGATGGAGAACATGG   616
SPP1-C1˙CC     ACTGTACAAGGCTCTGCAGGTGCATGATACTCCTCAG...GAGGAGGACAACACCAGCACCCCAGAGGTGGAGAACATGG   610
SPP1-C2˙CC     ACTGTACAAGGCTCTACAGGTGCATGATACTCCTCTGGAGGAGGAGGAGGACACCAGCACCCCAGACGTGGAGAACATGG   622
SPP1-C1˙SG     ACTGTACAAGGCTCTGCAGGTGTATGATACTCCTCTG...GAGGAGGACGACACCAGCACCCCAGAGGTGGAGAACATGG   628
SPP1-C2˙SG     ACTGTACAAGGCTCTGCAGGTGCATGATACTCTTCTG...GAGGAGGAGGACACCAGCACCCCAGAGGTGCAGAACATGG   619
SPP1-C1˙SR     ACTGTACAAGGCTCTGCAGGTGCATGATACTCTTCTG...GAGGAGGACGACACCAGCACCCCAGAGGTGGAGAACATGG   628
SPP1-C2˙SR     ACTGTACAAGGCTCTGCAGGTGCATGATACTCTTCTG...GAGGAGGAGGACACCAGCACCCCAGAGGTGCAGAACATGG   454
SPP1-C1˙SA     ACTGTACAAGGCTCTGCAGGTGTATGATACTCCTCTG...GAGGAGGACGACACCAGCACCCCAGAGGTGGAGAACATGG   628
SPP1-C2˙SA     ACTGTACAAGGCTCTGCAGGTGCATGATACTCTTCTG...GAGGAGGAGGACACCAGCACCCCAGAGGTGCAGAACATGG   616

                        620  625  630  635  640  645  650  655  660  665  670  675  680  685  690
conservation   *******  *************!***********!**!  ***!**!****  **********   ***  *  *    ***
SPP1˙AM        .....CAGGGTCTGGAGGCTTCCAGCGGTACTGAGGAAGAGGAGCCCAATGCAAAGCAGGCGTCTCTGGATGATCAACAG   690
SPP1˙CI        AGCCAAGCGATCGCCAGGTTGCTCTGGGAAGCCAAGAGATCGTTCCCGCCGAGAACCAA............GAG......   690
SPP1˙DR        AGGCAAATGAGCGCCAGGCTGCCCTGGGAGCCCAAGAGATTGTTCCCGTTGGGGACCAGGCAGCTACAGAAGAG......   696
SPP1˙IP        ....................GCTCTGCAGGTGCACAATGTTGGGCTGGACCAGGGAGTGGACGCCTCCAGTGGC......   654
SPP1˙LW        AGCCAGGAGACCGCCAGGCGGCTCTGGGAGGCCAAGAGATCGTTCCCGCCGGGAACCAA............GAG......   681
SPP1˙PN        .....CAGGGTCTGGAGGTTGCCAGCAGAACAGAGGACGAGGGGCCCAGTGCAAAGCAGGCATCCCTG............   690
SPP1˙PP        AGCCAGGAGACCGCCAGGCGGCTCTGGGAAGCCAAGAGATCGTCCCTGCCGGCAACCAA............GAG......   678
SPP1-C1˙CC     AGCCAAACGACCGCCAGGCTGCTCTGGGAAACCAAGAGATCGTTCCCACCGGAAACCAGGATGCTACAGAAGAG......   684
SPP1-C2˙CC     AGCCAAACGACCGCCAGGCTCCTCTGGGAAGCCAAGAGATCGTTCCCACTGGAAACAAGGATGCTACAGCAGAG......   696
SPP1-C1˙SG     AGCCAAACGACCGCCAGGCTGCTCTGGGAAGCCAAGAGATCGTTCCCACCGGAAACCAGGATGCTACAGCAGAG......   702
SPP1-C2˙SG     AGCCAAACGACCGCCAGGTTGCTCTGGGAAGCCAAGATATCGTTCCCACTGGAAACCAGGATGCTACAGCAGAG......   693
SPP1-C1˙SR     AGCCAAACGACCGCCAGGCTGCTCTGGGAAGCCAAGAGATCGTTCCCACCGGAAACCAGGATGCTACAGCAGAG......   702
SPP1-C2˙SR     AGCCAAACGACCGCCAGGCTGCTCTGGGAAGCCAAGATATCGTTCCCACCGGAAACCAGGATGCTACAGCAGAG......   528
SPP1-C1˙SA     AGCCAAACGACCGCCAGGCTACTCTGAGAAGCCAAGAGATCGTTCCCACCGGAAACCAGGATGCTACAGCAGAG......   702
SPP1-C2˙SA     AGCCAAACGACCGCCAGGCTGCTCTGGGAAGCCAAGATATCGTTCCCACTGGAAACCAGGATGCTACAGCAGAG......   690

                   695  700  705  710  715  720  725  730  735  740  745  750  755  760  765  770
conservation    ************  !!*!!******  !!*  **  ***  *!*******  ***********************  *  !*****!*
SPP1˙AM        GGGGAGAGTGATGGTGCCAGTGCCAGTGAAGCCGCCGGTGAGAGTGCCAGTGCCAGCGCCAGCCAGGAGGAGACGGCAGC   770
SPP1˙CI        TCAGATAGCGAGGGGGCGAGTGCTGGTGACGCTCCCACCGACAGCGCAAGCGCCAGTGCCAGCCAGGAGGAAAATGAAGA   770
SPP1˙DR        ............GGGGCAAGTGCTAGGGACTCTCCCAGCGACAGCGCCAGTGCAAGTGCCAGCCAGGAGGAGAATGAAGA   764
SPP1˙IP        ACGGACAGTGATGACGCGAGCCAGCAAGAGCAGAAGGCAGCTTCTTCTTCCAGTGCCAGTGATGCCGTTCCCAGTCAGGA   734
SPP1˙LW        TCAGACGGCGAGGGTGCAAGTGCTGGAGACACTGCCACCGACAGCGCCAGCGCCAGCGCCAGCCAGGAGGAGAATGAAGA   761
SPP1˙PN        GGTAGTGAGGAGAGTGCCAGTGCCAGCGATGCCAATGGTGAGAGCGCAAGTGCTAGTGCCAGCCAGGAGGAGACGGAAGA   770
SPP1˙PP        CCAGACAGCGAGGGAGCGAGTGCTGGAGACTCC...ACCGACAGCGCTAGCGCAAGC.........CAGGAGAAAGAAGG   746
SPP1-C1˙CC     TCAGACAGCGAGGGCGCAAGTGCTGGCGACACTCCCAATGACAGCGTGAGCGCCAGTGCCAGCCAGGAGCAAAATGAAGA   764
SPP1-C2˙CC     ............GGGGCAAGTGCTGGCGACACATCCAGCGACAGTGCAAGCGCCAGCGCCAGCCAGGAGCAAAATGAAGA   764
SPP1-C1˙SG     TCAGACAGCGAGGGGGCAAGTGCTGGCGACACTCCCAACGACAGCGCGAGCGCCAGTGCCAGCCAGGAGCAAAATGAAGA   782
SPP1-C2˙SG     TCAGACAGCGAGGGGGCAAGTGCTGGCGACACTCCCAACGACAGCACAAGTGCCAGTGCCAGCCAGGAGCAAAATGAAGA   773
SPP1-C1˙SR     TCAGACAGCGAGGGGGCAAGTGCTGGCGACGCTCCCAACGACAGCGCGAGCGCCAGTGCCAGCCAGGAGCAAAATGAAGA   782
SPP1-C2˙SR     TCAGACAGCGAGGGGGCAAGTGCTGGCGACACTCCCAATGACAGCGTGAGCGCCAGTGCCAGCCAGGAGCAAAATGAAGA   608
SPP1-C1˙SA     TCAGACAGCGAGGGGGCAAGTGCTGGCGACACTCCCAACGACAGCACAAGCGCCAGTGCCAGCCAGGAGCAAAATGAAGA   782
SPP1-C2˙SA     TCAGACAGCGAGGGGGCAAGTGCTGGCGACACTCCCAACGACAGCACAAGCGCCAGTGCCAGCCAGGAGCAAAATGAAGA   770
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                          775  780  785  790  795  800  805  810  815  820  825  830  835  840  845
conservation  *******!!******** ****!!*!!*!!***!!!**!**! *!*****!**!*!!******* **************
SPP1˙AM       G...TCCGACAGCAGCCAAAGCAGCGAGGAGGCCACCGCCACCCCCGGTGCCGCCGACGGCGAGAGCGACTCCTCTCAG.   846
SPP1˙CI       GGAGTCAGATAGCAGCCCGAGCAGCGAGGATACCACAACCACGCCTGGAGCTGCAGACAGCGATGAAGACTCCTCACAG.   849
SPP1˙DR       AGAGTCGGAT............AGTGAGGAGACCACATCGACGCCGGGAGCTGCAGACAGCGAGTCCAACTCCTCTCAGA   832
SPP1˙IP       GAGTGAGGAGGACAGCCAGAGCAGTGAGGAGAACACAACCGCGGCTACCGCGACCGACAGC......AACTCCTCCGAG.   807
SPP1˙LW       GCAGTCAGAT.........AGCAGCGAGGAGACCACAGCCACCCCTGGAGCTGCAGACAGCGAGAGCGACTCCTCACAG.   831
SPP1˙PN       G...TCTGACAGCAGCAAGAGCAGCGAGGAGGCCACTGCCACCCCTGGGGCTGCAGACACAGAGAATGACTCCTCTCAG.   846
SPP1˙PP       GGAGTCGGAT.........AGCAGCGAGGAGACCACAGCCACCCCCGGAGCTGCAGACAGCGACAGCGACTCCTCACAG.   816
SPP1-C1˙CC    GGAGTCAGACAGCAGCCCGAGCAGCGAGGAGACCACAGCCACACCTGGAGCTGCAGACAGAGAGGACGACTCCTCACAG.   843
SPP1-C2˙CC    GGAGTCAGATAACAGCCTGAGCAGCGAGGAGACCACAGCCACACCTGGAGCTGCAGACAGCGAGGAG.............   831
SPP1-C1˙SG    GGAGTCAGATAGCAGCCCGAGCAGTGAAGAGACCACAGCCACGCCTGGAGCTGCAGACGGTGAGGACGACTCCTCACAG.   861
SPP1-C2˙SG    GGAGTCAGATAGCAGCCCGAGCAGCGAGGAGACCACAGCCACGCCTGGAGCTGCAGACAGCGAGGACGACTCCTCACAG.   852
SPP1-C1˙SR    GGAGTCAGACAGCAGCCCGAGCAGCGAGGAGACCACAGCCACGCCTGGAGCTGCAGACAGCGAGGACGACTCCTCACAG.   861
SPP1-C2˙SR    GGAGTCAGATAGCAGCCCGAGCAGCGAGGAGACCACAGCCACACCTGGACCTGCAGACAGCGAGGACGACTCCTCACAG.   687
SPP1-C1˙SA    GGAGTCAGATAGCAGCCCGAGCAGCGAGGAGACCACAGCCACGCCTGGAGCTGCAGAGAGCGAGGACAACTCCTCACAG.   861
SPP1-C2˙SA    GGAGTCAGATAGCAGCCCGAGCAGCGAGGAGACCACAGCCACGCCTGGAGCTGCAGACAGCGAGGACGACTCCTCACAG.   849

                   850  855  860  865  870  875  880  885  890  895  900  905  910  915
conservation          !!!***!!*!!***!!!!****!**!** *!!********* ************      *** ** * **
SPP1˙AM       ........AGCTCCGAGAGCCTGGAGGACGACTCCGCCGAGCAGACAGTGGAGGCAACGTCCGACATCCCTGACGTCATC   918
SPP1˙CI       ........AGCACAGAAAGCCAGGAGAGCGATTCGGATGAGGAGACCACCCAGACCACCGAG......GCTTCCATCGTA   915
SPP1˙DR       GCACAGAAAGCACAGAAAGCCAGGAGAGCGACTCAGATGAGGAGACCACTCAGACCACTGAG......GCCTCCATCATC   906
SPP1˙IP       ........AGCGATGAGAGTGAGGAGACCAACACAGCGGAT.......................................   840
SPP1˙LW       ........AGCACAGAAAGCCAGGAGAGCGATTCGGCTGAGGAGAACACACAGACCACCGAG......GCTTCCATCATA   897
SPP1˙PN       ........AGCTCTGAGAGTCAGGAGGATGACTCCGCCGAGCAGGCCATGGAAACCACGACCGATGTCCCTGACGTCATA   918
SPP1˙PP       ........AGCACAGAAAGCCAGGAGAGCGATTCGGATGAGCAGAACACACAGACCACCGAG......GCTTCCATCATA   882
SPP1-C1˙CC    ........AGCACAGAGAGCCAGGAGAGCGATTCGAGTGAGGATACCACCCAGACCACCGAC......GCTACTGTTATC   909
SPP1-C2˙CC    ........AGCACAGAGAGCCAGGAGAGTGATTCGAGTGAGGGGACCACCCAGACCACCGAC......CCTACTATTATC   897
SPP1-C1˙SG    ........AGCACAGAGAGCCAGGAGAGCGATTCGGATGAGGAGACCATCCAGACCACCGAC......GCTACTGTTATC   927
SPP1-C2˙SG    ........AGCACAGAGAGCCAGGAGAGCGATTCGGATGAGGAGACCACCCAGACCACCGAC......GCTACCGTTATC   918
SPP1-C1˙SR    ........AGCACAGAGAGCCAGGAGAGCGATTCGGATGAGGAGACCACCCAGACCACCGAC......GCTACCGTTATC   927
SPP1-C2˙SR    ........AGCACAGAGAGCCAGGAGAGCGATTCGGATGAGGAGACCACCCAGACCACCGAC......GCTACCGTTATC   753
SPP1-C1˙SA    ........AGCACAGAGAGCCAGGAGAGCGACTCGGATGAGGAGACCACCCAGACCACCGAC......GCTACTGTTATC   927
SPP1-C2˙SA    ........AGCACAGAGAGCCAGGAGAGTGATTCGGATGAGGAGACCACCCAGACCACCGAC......GCTACCGTTATG   915

               920
conservation  *
SPP1˙AM       ATC   921
SPP1˙CI       ACC   918
SPP1˙DR       ATC   909
SPP1˙IP       ...   840
SPP1˙LW       AGC   900
SPP1˙PN       ATC   921
SPP1˙PP       AAC   885
SPP1-C1˙CC    AAA   912
SPP1-C2˙CC    ACA   900
SPP1-C1˙SG    ATA   930
SPP1-C2˙SG    ATA   921
SPP1-C1˙SR    ATA   930
SPP1-C2˙SR    ATA   756
SPP1-C1˙SA    ATA   930
SPP1-C2˙SA    ATA   918
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X non conserved
X ≥55% conserved
X ≥85% conserved