>A. clavatus Aspergillus clavatus NRRL 1 1099423829800 genomic scaffold, wholegenome shotgun sequence.(contig_81.1) [DNA] 1545000-1546800 +

ATGAACTTTCCAAGGCTGTTCCTGCGTTCGAAAGCTCTCTCGTGTGCGACGGCAGCGGGGCGAGTATTTCGAGGTTGCGGGGTGTTCCCACACC
CATGTCCATCCTTCACCGGCAGCCCAAAATACTGCTCAACGATGCCCACTGCTGCGCCGTCGGGATCACTCGAAAATTTTGCGGAGGCGCATGC
CGGTGCTAATGATACACCATTTGCAGATAAATTCTCCATCTTACTGGCCAAGAACAAGGACTGGGCGGCCCAGACCTACAAGCAGCACCCTGAC
CTCCTCCCCCAGCTTGCCGTGGGCCAGCATCCTGAGATCCTCTGGATCGGCTGCTCCGACTCCCGGTGTCCCGAGACCACCATCTTGGGCCTCC
TACCCGGTGATGTCTTCACCCACCGCAACATCGCCAACGTCATCCACCCCGCCGATCTGAGTTCGGGCGCTGTTATCGAGTATGCCGTGCGCCA
TCTGCAGGTCAAGCATATCGTCATCTGCGGACACACCAAGTGCGGAGGCGTCGCCGCTGCTCTCGGCAACAAAGGCCTGGGCATCCTCGACCCC
TGGCTGTTGCCTCTGCGCCAGCTCCGGGAACAACACCACACGGAACTGGAGACTCTGCCGGGCGATGAGGCCACCGTGAAGCTGGCCGAGCTCA
ACGTCCGCGAGGGTCTGAAGACATTGAAGCAGAAGAGCGTAGTCCTAGAGGCGATACAGGAGCGTGGATTGCAGGTGCATGGAATGATTTATGA
TGTTGGCTCAGGTGTCCTTCGGGAACTGGATAGCAGCGAGCCGGAGGACGCGATCAAGGCACGGTATGCATCGTTCAAGACGGAGGCTTAA

>A. nidulans Aspergillus nidulans contig 1.98 [DNA] 12600-14000 + AN5611

ATGACAACCCAAGGTATGTATATAGTGCATGCCGATGTTCTCGGTATACGAGCATTCCATGTGTAGGGTACTGATGCAGTCGCCGTTCGCTGTT
TTATCCAATGTCATACTGGGACAGAATGTATCGTGTCGCTTGTTGCCGGGCATCAGCTTGTCAGGACTTTTGTTGCCATTTTCTGTGTTCTCCT
GTCGGCCCGTGAAGGAAAGCCCACCAAGGCCATGGGATTACTCGAAACCTATCCATGGGCTAGGTTGAAAACCGGTCATGGAAAAAGAGTGTCC
CATATTCCTGCGAGTCCTTCCATAACACTTAACATCTGAAATGTTGCACAGATCAGGGTGACACGTGCTGACAACAAACCCCAGATCCGTTCAC
CGCAGCCCTCAGCCAAAACAAAGCCTGGGCAGCCAAAGTAGCTAGAGAGCAGCCAGACCTTTTCCGCAAACTTTCCACCGGCCAGCACCCAGAG
ATCCTCTGGATAGGCTGTTCTGACTCTCGATGTCCCGAGACGACTCTGCTAGGCCTCAAGCCAGGTGATGTGTTTGTCCACCGAAACATCGCCA
ACATCTTGCAGCCCTCGGACCTCAGTTCCACCGCTGTTATAGAGTTCGCTGTTCGCCATCTGGGGGTCAAGCATGTTGTTGTCTGCGGACACAC
AAAATGTGGAGGCATCTCTGCCGTGATGGCAAACAAGAAGCTTGGTATTCTTGATTCATGGCTTTCGCCTCTGCGGAAGCTGCGTGACGATAAT
TCGGACTGCTTGAAGTCATTACCAACGGACGAGGCGCTCCTCAAACTAGTTGAACTGAATGTCCTTGCCGGGGTGAAGACGGTGAAGCAGAAGA
GTGTTGTGGTTGAGGCGATGCAGAAAGGGCTGAAGGTTCATGGACTCGTGTACGATGTCGGGAGCGGTGTTTTGCAGGAATTGGATACCAGTGC
TTCTGACAAGACCGTGAAGAAACGGTTGACATTGTTTAAGAAGGACTTTTAG

Aspergillus oryzae Supercontig 6: 2980303-2981263 -

ATGCCAGGTATGTTCACGGGTTATGTTCCTTTTCGTTTTCCTTCTTGGCATTTTCGGATATCGTCGCTGAATGACGGGCCCTCTCTTTTCTACC
TTTTTCCCCTGTCTTCCTTTCGTGTTCAGTATCCTTTCTTTGGCGGGGTATCTTCATTTCTTCATTTTGTCGATAAGTCTTGACTTGAGCGCAT
CGTTGCAAAGAAAGGCTGAGGACTGGTGGTGACTGGACTCTGCTTGCTGGCCGCTTTTTGCTTTTTCTTTTTTCTTTTTCCTTTTTCCTTTTTT
TTTTTTTTGCCCCAACCCCTTCCCCGTCCCGTTGAGTCCGTTGAGTCATTCGCTGCCGGGCCCATCCTGACACCTTTTTTTTCCACCCTGCGAC
AACCTATCTGTAACATATCTGCCATCATGAAACTCGCAAGGCTGTTACCGCGGTCTCAAACATTGTTTCGTCCCCTAGCGGCGGTGAGGGAGTT
TCAAGGCTGCAGTGGAAGCGTCCATCTTCCTCCAGTCCGAGCCCGCACCAACCCCGTTATCGGCCAATCTCAGCGTCTTTCACTGTCAACCTCT
GCATCATTATTGTGCGACAAACGCAATATGTCGCAAGCGGAGACTAATTATTCTCCAGACCGATTCACTACCGCGCTGCAGGCAAACAAGGAGT
GGGCTGCCAGAACTGCCCTGGAACATCCGGACCTGTTCCCCACGCTTGCCAATGGCCAGTCCCCCGAAATTCTCTGGATCGGCTGCTCCGATTC
TCGATGCCCTGAGACGGTCGTTCTCGGACTAAAGCCTGGCGATGTCTTTGTCCATCGGAATATCGCCAATATCTTGCACGCCGGCGATCTCAGC
TCGAGTGCAGTCATTGAATATGCCGTCCGTCATCTGCGGGTCAACCACATCGTGCTCTCCGGCCACACCAAGTGTGGTGGTATCGCAGCTGCCC
TTGGTAACAAGCAACTCGGTATCCTGGATCCCTGGCTGTTGCCTCTGCGCCAGATCCGTGAGCAGAACCTTGCTGAGTTGCAGACATTGTCACC
GGAGGATGCGACCGTCAGGATGGCGGAGCTAAACGTCCGGGAAGGTGTCAAGTTATTGAAGTCGAAGGCTGTAGTGCTTGAAGCGATGCAAGAG
CGGGGTCTCCAGGTTCACGGACTCATTTATGATGTCGCCTGTGGTATGCTCCGGGATATCGACACCAAGGACTCGGAGGAAGAGATCAAGAGGA
GACTAGTGGCCTTCAAGACAGAGGCTTAG

>A. terreus supercont_1.5 of Aspergillus terreus [DNA] 1112500-1115000 -

ATGGCAGTCTCAGGTACGTGACGACGGTTTTCTCCCCCTTTTGCTCCTTCTTGGCATTCTGTCACGGCAGTTCAACATCTTTTTCCTTTCCTGT
TCTCCCATGACCCTTTTCCCATCATCACCATCCAACCGCACTTCTGCCCTGTCGTTGAGTTCACTCTCCATCGCGCGTGTTCGTAAAAGGGTCC
ATTGTCGCTGGCTTGGACAAGTGCGTTCGATCGCATCCTGGAACGGGTGTTGGCCGCGGGAAAAATTTTCCCCAACAATTTGGTGTCGCCCAGT
TTTGACTCACTCTTCCAACACCACCCACTGTCTCCCTCCTGCCTTCCACGGTCTCCCTTCAACATATTCCCATATATCAAAATTTCCTTGAAGC
ATCATGAATATCACAAGGCTGGTCCCACGGTCTCAAACGTTTTCGCGATCGCTTTCGACGGTCCGAGGGCCTTTGAGCCGCGGGGAAGGTATTC
GTTTTCCCTCCAGCCGAATCCCACACACTCAACCGCAACCTGTGATCGGCACCGCCCAGCATCGTTTTCTGACCAGCTCGGCGCCATCGTTATT
ACACCAACACAGTCACTCGTCGGATGGTGCTAATTGCTGCTCAGACCGATTCAACCTTGCCCTACAGAAGAACAAGGAGTGGGCCGACAAAGTT
TCCAAGGAGCAGCCCGACCTGTTTCCCCGACTGGCGGTTGGCCAGTCCCCTGAGATCCTCTGGATTGGCTGCTCTGACTCCCGCTGCCCTGAGA
CCAGCCTTCTCGGGCTGAACCCCGGTGATGTCTTCGTGCACCGTAACATCGCCAACATCCTGCATGCTGGTGACTTGAGTTCGGGGGCGGTGAT
CGAGTATGCCGTGCGTCATCTGCGGGTCAACCACGTTGTTCTGTGCGGCCACACTAGCTGCGGTGGTGTGGCGGCCGCCATGGGCAACAAGCAG
CTGGGCATCCTGGACCCCTGGTTGCTGCCTCTGCGGCAGATCCGCCAGCGTAATCTGGGCCTTCTGCAGACCCTCTCTCCCGACGAGGCGATGC
TGAAGATGGTCGAGTTGAATGTGCAGGAGGGTGTGGATATCCTGAAGCAGAAGAGCGTGGTGCTGGAGGCGATGCAGGAGCGAGGACTGCAGGT
GCACGCTCTCATTTATGATGTCGGATCCGGTGTGCTGCGGGAGCTGAATACCGATGAAACGGAAGAGTCCATCAAGGCTCGCCTGGTGTCCTTC
AAGACGGACGTTTAG

>C. globosum Chaetomium globosum supercontig 1.7 [DNA] 634600-636000

ATGGTCAACTCACGTGTCTGTACACCACTCCTGCGGTCGCTCACCCGACGCACAACCCCCCAACAACGAATCTTGTCATCGCCGATTTTCGCAA
CCACACCCCGGCACTCAAGCCTTTTCTCCTCATCATCCCGCCGCCCACAACACCCAACTCCAACTCCAACACACACCTGCGAGCTCC
AACTCCAATCACAACCCCAACCAGAGCAATAACAACAACAGCTGGCGCGTTATGGCCGAGAGAGACATCACCGACCACCTGCGCGAGACGCACG
ACCGCGTATTCGAGCACAACCGCTGTTGGGCGCGGGAGAAGCAGGCTAGCGACCCGGACTTCTTTGTCAAGCTCTCGGCGGGGCAGAACCCGGA
CTACCTCTGGATCGGATGCAGCGACTCGCGGATCCCGGCGGAGCAGATCACGGGCATGGAGCCCGGGCACGTGTTCGTGCACCGCAACATCGCC
AACCTGGTGTGCAACACGGACCTGAACGTCATGAGCGTCATCACGTACGCGGTGGAGCACCTCCAGGTCAAGCACATCGTCGTGTGCGGGCACT
ACGGCTGCGGCGGCGTGCAGGCGGCCATGACGGCCAAGAACCTCGGCATCCTGAACCCGTGGCTGCGTAACATCCGCGACGTCTACCGCCTGCA
CGAGAAGGAGCTCGACGCCATCCCCGACAAGGAGGCCCGCTACAACCGCCTCGTCGAGCTCAACGTCGAGGAGCAGGCCCGCAACGTCATCAAG
ACGGCCTGCGTGCAGCAGTCGTACGCCAAGAACCGCTTCCCCGTCGTTCACGGCTGGGTGTTTGGTTTCAACGACGGCCTGCTGAAGGACCTCA
AGATTGATTTTGAGGGGACTTTGAAGGATATTCAGAAGATCTATAATCTGACCGAGTAG

→ Translation beginning with the ATG leads to the production of a MTS, but this start codon is not in frame with the ORF. A nucleotide might be missing.

F. graminearum supercont3.2 of Gibberella zeae PH-1 [DNA] 386000-388000

ATGCCCATAATGTTTTCCTCTCGGCTCGCTTCATTTTCTCTCCGCTCATCGGCCATTTGTTCCTCTCCCATCGCTTCAACTCTTTCTTCTCGCT
CCATTTCAGCCGCTGCTGCTTGTTTCTCACAAACGCGCTTCCATTCTTCTTGTTCCTCTTCTTCTTCTTCTTCGTCATCATCATCCTCCTCCGC
TTCAAAACCCACCTCGTGGCGCAACATGGCCGAAAAGGACATCACAAAGTACCTCCAGCAGAGCCACGACCGGCTGTTCGTCAACAACCGCGAG
TGGGCTGAGAACAAGGCCAAGGTCAACCCCGACTTCTTCAAGAACCTCGTTGCCGGCCAGGCTCCCGAGTACCTCTGGATCGGATGCGCCGACT
CGCGCATCCCCGCCGAGCAGATCTGCGGCCTCGAGCCCGGCGAGGCATTTATCCACCGCAACATCGCCAACCTCGTCTGCAACACTGACCTCAA
CGCCATGGGCGTCATCAACTACGCCGTCAAGCACCTCGGCGTCAAGCACATCATCGTCTGCGGCCACTACGGCTGCGGCGGTGTCAAGGCCGCC
ATGACACCCCAGGACCTGGGTCTGCTGAACCCCTGGCTGCGAAACATCCGCGACGTGTACCGCCTTCACGAGAAGGAGCTCGATGCCATTGCCG
ACGAGAGCGAGCGATATGACCGGCTCGTCGAGCTCAACGTCATTGAGCAATGCCGCAACGTCATCAAGTCTGCCGACGTTCAACAGTCATGGCA

CGAGAACAAGTACCCCATCGTTCACGGATGGGTGTTTGGGTTCAAGGACGGTCTGCTCAAGGATCTTAAGATTGACTTTGAGGCGGTGCTGGGC
GATATCCAAAAGATTTACAACCTTGTTGACAAGAAATAA
>F. verticillioides supercont_3.16 of Fusarium verticillioides [DNA] 420700-421800
ATGCCTCTAATGTTTTCCTCTCGGCTCCCTTCCTTTTCTCTCCGCTCCTCCTCTGCCTCCCTCACATCTTTATCTTTATCCTCATCATCTCAAC
GCCTTGCCTCTCGCTCCATACTCACCAGCTTCAAACCCCGTTTCTCTTCTTCATCTTCATCCTCCTCCACACAAGACCCAATACCCGCTCCAAA
ACCAGAGTGGCGCACAATGGCCGAAAAGGACATCACAAAGTATCTCCAGCAGAGCCACGATCGGCTCTTCCACAACAACCGCGCCTGGGCCGAG
AACAAGGCCAAGGTCAACCCCGACTTCTTCAAGAACCTCGCCGCCGGCCAGGCACCCGAGTATCTCTGGATTGGATGCGCCGACTCTCGCATCC
CCGCCGAGCAGATCTGCGGCCTTGAGCCCGGCGAGGCATTTATCCACCGCAACATCGCCAACCTCGTGTGCAACACGGACCTCAACGCCATGGG
CGTCATCAACTACGCCGTCAAGCACCTCGGCGTCAAGCACATCATCGTCTGTGGTCACTACGGCTGCGGAGGTGTCAAGGCGGCTATGACCCCC
CAGGACCTCGGCCTGCTGAACCCGTGGCTTCGCAACATCCGCGACGTGTACCGCCTCCACGAGAAGGAGCTCGATGCTATCGAGGACGAGAGCG
CCCGCTACGACCGCTTGGTCGAGCTGAATGTCGTCGAGCAGTGCCGCAACGTCATCAAGTCTGCTGATGTCCAGCAGTCGTGGCACGAGAACAA
GTATCCCATTGTTCACGGATGGGTGTTTGGTTTCAAGGATGGACTTCTCAAGGATCTTAAGATTGACTTTGAGGCTGTGTTGGCTGACATCCAA
AAGATTTACAACCTTGTTGACAAGAAATAA
>F. oxysporum supercont2.20 of Fusarium oxysporum f. sp. lycopersici [DNA] 271600-272700 +
ATGCCTCTAATGTTTTCCTCTCGGCTCCCTTCCTTTTCTCTCCGCTCCTCCTCTTCCTCCTTCACATCTTTATCCTTATCATCTCAACGTCTTG
CCTCTCGCTCCATACTCACCAGCTTCCAAACACGCTTCTCTTCTTCCTCCTCCACACAAGACCCAAAACCCGCTCCAAAACCAGAGTGGCGCAC
AATGGCCGAACAGGACATCACAAAGTATCTCCAGCAAAGCCACGACCGGCTCTTCCACAACAACCGCGCCTGGGCCGAGAACAAGGCCAAGGTC
AACCCCGACTTCTTCAAGAACCTCGCCGCCGGCCAAGCACCCGAGTACCTCTGGATCGGATGCGCCGACTCTCGCATCCCCGCCGAGCAGATCT
GCGGCCTTGAGCCGGGCGAGGCATTTATCCACCGCAACATCGCCAACCTCGTGTGCAACACGGACCTCAACGCCATGGGCGTCATCAACTACGC
CGTCAAGCACCTCGGCGTCAAGCACATCATCGTCTGTGGTCACTACGGCTGCGGAGGTGTCAAGGCGGCTATGACCCCCCAGGACCTCGGCCTG
CTGAACCCATGGCTTCGCAACATCCGCGACGTCTACCGCCTTCACGAGAAGGAGCTCGATGCAATTGAGGACGAGAGCGCTCGCTACGACCGCT
TGGTCGAGCTGAATGTCGTTGAGCAGTGTCGCAACGTCATCAAGTCTGCTGATGTTCAGCAGTCGTGGCACGAGAACAAGTACCCTATTGTTCA
CGGATGGGTGTTTGGTTTCAAGGATGGCCTTCTCAAGGATCTTAAGATTGACTTTGAGTCTGTGTTGGCCGACATCCAAAAGATTTACAACCTT
GTTGACAAGAAGAAATAA
>N. fischeri Neosartorya fischeri NRRL 181 1099437636245 genomic scaffold, wholegenome shotgun
sequence. [DNA] 1093700-1094900 +
ATGAACATAACGAGGCTGTTACCGCGCTCCAATGCTCTGTCTTCGCCGACAGCAGCAGCACGAGCATTTCGGGGTCGCGGGGCATGCGTATATC
CTCCATCATCACAGACCGTATATATGTGTCCAACCTCCACCGTCAGCTTAATGCATCGCTCGCCCTGTTCCACATCTGCGCCATTGCGATCGAG
TCAGAAGTCGGCGGCCCAGACGAGTGCTAATAGTGACTCACTTTCAGACAAATTCTCTGCCGCGCTTGCCAAGAACAAGGAATGGGCTGCGAAG
TGCTCCCAAGAGCACCCTGAGCTGCTTCCCACACTTGCTGTCGGTCAACACCCGGAAATTCTGTGGATCGGCTGCTCCGACTCCCGCTGCCCCG
AGACCACCATCTTAGGCCTTCTGCCCGGTGATGTCTTCACCCACCGTAACATTGCCAACGTGATCCACCCTGCCGATCTCAGCTCGGGCGCCGT
CATCGAGTTTGCCGTGCGTCATCTTCGCGTTAAGCACGTCGTAATCTGCGGTCACACCAAGTGCGGAGGTGTGGCCGCTGCCCTGGGCAACAAA
GGCCTGGGCATCCTCGACCCCTGGCTGATTCCTCTGCGTCAGCTCCGTGAGCAGCACCTCGCTGACCTGCAATCTCTGTCCCAGGACGAGGCCG
TCGTCAAGCTGGCCGAGTTGAACGTCAAGGAGGGCCTGAAGGCATTGACGCAGAAGAGCGTCGTGCTGGAGGCGATGCAGGAGCGAGGCCTTCA
GGTGCACGGGCTCATCTACGATGTCGGATCTGGCGTCCTTCGGGAGCTGGACGCCGCTGAACCCGAGGATGCGATCAAGGCACGGTTGACATCG
TTCAAGACCGATGCTTAG
>N. crassa Neurospora crassa contig 7.52 [DNA]
ATGCTTAGCACACGTCTGGGTCTTTCTCCCCTGCTTCACTCCTCCAAGCAAGCATCATCAGCCCTATCACGCCTCGCCGTCCCGAGAACGACGT
CGACTCCCCTGCCACGCCGCCGTCTCACCATCGTCCCGAGTGCTACCCCGCGCCGAAGCTTCTGCAGCTCCCACACCGCCGACGATAAAGACCG
CAGCAAGAAGGACATCACCATGTATCTCCAGGAGACGCACGACAAGGTCTTTGAGAACAACAAGTCCTGGGCCGCCGAGCAGGTTGCCAAGGAC
CCCGACTTCTTCAAGAAGCTCGCCGCCGGCCAGAACCCCGAGTACCTCTGGATCGGATGCTCCGACTCGCGCATCCCCGCCGAGCAGATCACGG
GCCTGCAGCCCGGCGACGCCTTTGTGCACCGCAACATTGCCAACCTGGTCTGCAACACGGACCTCAACGTTATGAGCGTCATTGAGTATGCCGT
CAAGCACCTCCAGGTCAAGCACATTGTCGTCTGCGGCCACTACGGCTGCGGCGGTGTCAAGGCGGCCATGACCCCCAAGGACCTGGGCCTCATG
AACCCCTGGCTGCGCAACATCCGCGACGTCTACCGCCTGCACGAGAAGGAGCTCGACGCCATCGCCGACGAGGAGGCCCGCTACGAGCGCCTCG
TCGAGCTCAACGTCTACGAGCAGTGCCGCAACGTGGTCAAGACGGCCGCCCTCCAGCAGTCGTATGCCGAGAACGGCTTCCCCATTATCCACGG
CTGGGTCTTCAACTTCCGCGACGGCATGCTCAAGGACCTCAACGTCGACTTCAAGACCATCCTCAAGGATATTCAGAAGATCTACAACCTGACC
AACTAA
>P. brasiliensis Pb18 supercont1.12 of Paracoccidioides brasiliensis (Pb18) [DNA] 315800-
316950 +
ATGTTCCGACCCCGCCAGGTATCAACCCTATCGACCCTCAGAACTCAATGCACTGCCATCACCACACCTACACGAAGTAGCATCAACAAATCCA
GCCTCCTATTCAACCACCAGAACCACCTCGTCAATAAACCCCTCCCGCGTTTTCCCCATCCCTGCACCACCCGCCGAACAATAAGCCAGATGGC
CCCAAGCGACGTCTCCAAATATCTCCAGGAAACACACGAGCGTGTCTTCGAGAACAACAGGAAATGGGCAGCAGAAAAGGCCGCCAAGGACCCG
CACTTCTTCGAGAAGCTCTCCATCGGACAGAACCCCGACTACCTGTGGATTGGCTGCAGTGACAGCCGTATTCCTGCCGAGCAGATAACAGGCC
TAGACCCCGGCGAGGCCTTTATTCACCGCAACATCGCCAACCTGGTCTGCAACACCGATCTCAATGTGATGAGCGTGATAAACTATGCCGTGCG
GCACCTGCACGTCAAGCACATCATTGTCTGCGGGCATTACGAGTGCGGCGGCGTCAAGGCTGCTCTGACACCGGCAGACCTGGGCTTGTTGAAC
CCCTGGCTGCGAAATATCCGCGACGTCTACCGGCTCCATGAGGCGGAGCTGGATGCCCTGGATGAGAACAAGCGCTATGACAGGCTTGTAGAGC
TGAATGTGATTGAGCAGTGTCGGAACATCATTAAGACGGCAGCTGTGCAGAAGATGTATTCGAAAAACCAGTATCCGATTGTGCACGGGTGGGT
GTTTAACATCAAGAATGGGCTGTTGACGGATTTGAAGATTGATTTTGAGAAAGTGTTAACGGGTATCCAGAAGATTTACGATTTGACGGGGAAG
TGA
>Trichoderma atroviride; Triat1/scaffold_4
ATGGCCGCGTCCCGACCCCGGGTTGGTCACCGGCCGTCGTCGCTGACCAGCTCGCCGGCGCGCTCAAATACTGGCGGAAGCCGCTCGGTTTCGT
CCTCTTCATCCGCCAATCCTTCTGGCACCGCAAAAGTCAAAGTTGCTCCTCCTCGTTTGCCCGGCATGTCTGAAGACGACCACGATGTCGAGAA
GTACCTGCGCGAGAACCACCAGCGCCTCTTTGAGAACAACAAGAAATGGGCCGCCGACCGGCTGCAGCAAGACCCCGACTTCTTTTCTCGCCTG
GCTGCCGGCCAGTCGCCCGAGTATCTCTGGGTGGGATGCAGTGACTCTCGCATCCCCGCCGAGCAAATCACTGGCCTAGAGGCCGGCGAGGCCT
TTGTCCACCGAAACATCGCCAACATGGTCATCAGCACCGACCTCAACGTCATGAGCGTCATCAACTATGCTGTCAACCACCTCAAGGTCAAGCA
CATTGTAGTCTGCGGCCACTACGGCTGCGGTGGTGTCAAGGCCGCCATGACGCCCAAGGACATGGGCCTGCTCAACCCCTGGCTGCGAAACATT
CGCGATGTCTACAGAATCTACGAAAAGGAGCTGGATACCATCACCGATGATCACCAGCGGTACAACCGCCTGGTCGAGCTCAACGTCATCGAGC
AGTGCCGTAACATCCTCAAGACTGCAGATGTGCAGCACTCGTTTGAAACGAACCGATTCCCCATCATTCACGGCTGGGTCTTCAACTTTGAGGA
CGGCTCTATCAAGGATTTGCAGGTCGACATGAAGCAGATGCTGGGTAACATCCAGAAGATTTACAACTTGACCGATTAA
>Trichoderma reesei; Trire2/scaffold_25
ATGCTCCCGTCGCGAATTGGAGGTCAATCCTTGCGTCTGGCCGCTTTCCGTTCCAGTTCTGCCCGGTCCTCGTCGCTGACCTTTTCTCCCGCCC
ACCGCCCTGCTGCTGCTGGGAACCGATACTGCGCTTCATCCTCCTCCTCCTCCTCCTCCAGCAACAACAACAACACCACCACCACCACTTCTGG
CTCAGTCCCTGGTACCGTCTCTGGAACAAACGCAAAGACACCCGCTCGTCTGCCCGGCATGCCTGAACACGACCACGACGTTGAGCGCTACCTG
CGCGAAAACCACCAGCGCCTCTTCGAGAACAACAGGAAATGGGCTGCCGAGAGGCTCAAGCAGGACCCCGAGTTCTTCACTCGCCTGTCCGCCG
GCCAGTCGCCCGAGTACCTCTGGATCGGCTGCAGTGATTCGCGCATCCCCGCCGAGGCCATCACGGGGCTCGGGGCCGGCGAGGCCTTTGTGCA
CCGCAACATCGCCAACATGGTCATCAGCACCGACCTCAACGTCATGAGCGTCATCAACTACGCCGTGCGCCACCTCAAGGTCAAGCACATTGTC
GTCTGCGGCCACTACGGCTGCGGCGGTGTCAAGGCCGCCATGACCCCCAAGGACATGGGCCTGCTCAACCCGTGGCTGCGCAACATTCGCGACG
TCTACCGCCTCCACGAGAAGGAGCTGGATGCCATCCCCGACGAGAAGAAGCGCTACGACCGCCTGGTCGAGCTCAACGTCTTTGAGCAGTGCCG

CAACGTCATCAAGACGGCCGATGTGCAGTACTCGTTTGAGCACAACCGTTATCCCATTGTCCACGGCTGGGTCTTTGGCTTCGAGGACGGCCTC
ATCAAGGACCTCAACATTGACATGAGGAAGATTCTTGCAGATATCCAGAAGATTTACAACCTCACTGATGAGTAA
>Trichoderma virens; Trive1/scaffold_4
ATGAGCTTTAAGCCGGCTCGCCGCCCTGCCACCGGAGGGAACCGACACTGCTCATCATCTTCCAACGCTGGCTCTGGCTCTGGCTCTGGCTCTG
GTGCAAACCCAAACGCAAAGATTCCTGCTCGTCTGCCTGGCATGTCTGAGAACGACCACGACGTTGAGCGCTACCTGCGCGAGAACCACCAGCG
TCTCTTTGAGAACAACAAGAAGTGGGCCGATGAGAGGCTCAAGCAGGACCCCGACTTCTTCAAGCATCTCGCTGCTGGCCAGTCCCCCGAGTAT
CTCTGGATTGGATGCAGTGACTCTCGTATTCCCGCCGAGGCAATCACTGGTCTCCAGGCTGGTGAGGCCTTTGTCCACCGAAACATTGCCAACC
TGGTCATCAGCACCGACCTCAACGTCATGAGTGTCATCAACTACGCTGTGCGCCATCTCAAGGTCAAGCACATTGTCGTCTGCGGCCACTACGG
CTGCGGAGGTGTCAAGGCCGCCATGACCCCCAAGGACATGGGCCTGCTCAACCCCTGGCTGCGAAACATCCGCGACGTCTACAGGCTCTACGAG
AAGGAGCTGGATGCCATTGAGGATGAGAAGAAGCGATACGACCGCCTGGTCGAGCTCAACGTCATGGAGCAGTGCCGCAACGTCATCAAGACGG
CTGACGTGCAGTACTCGTTTGAGGAGAACCGATATCCCATTGTTCACGGCTGGGTCTTTGGCTTCGAGGATGGCCGCATTACCGACTTGAACGT
CGACATGAAGAAGATGCTTGGAGACATTCAGAAGATTTACAACTTGACTGACTAA

Figure S3: Novel annotation of *cas1*- and *cas2*-homologues from several filamentous ascomycetes. The annotated ORFs were taken from NCBI and are starting with an ATG (or CTG in case of *N. crassa*) and ending with a stop codon (indicated in green). The translation starting with newly identified ATGs (highlighted by green boxes) upstream of the previously annotated start-codons (indicated in red) or inside predicted introns results in putative mitochondrial target sequences. Introns are marked as red sequence in annotated genes. All genes encoding for mitochondrial localized CAs are not interrupted by introns after modification of the genomic sequence.