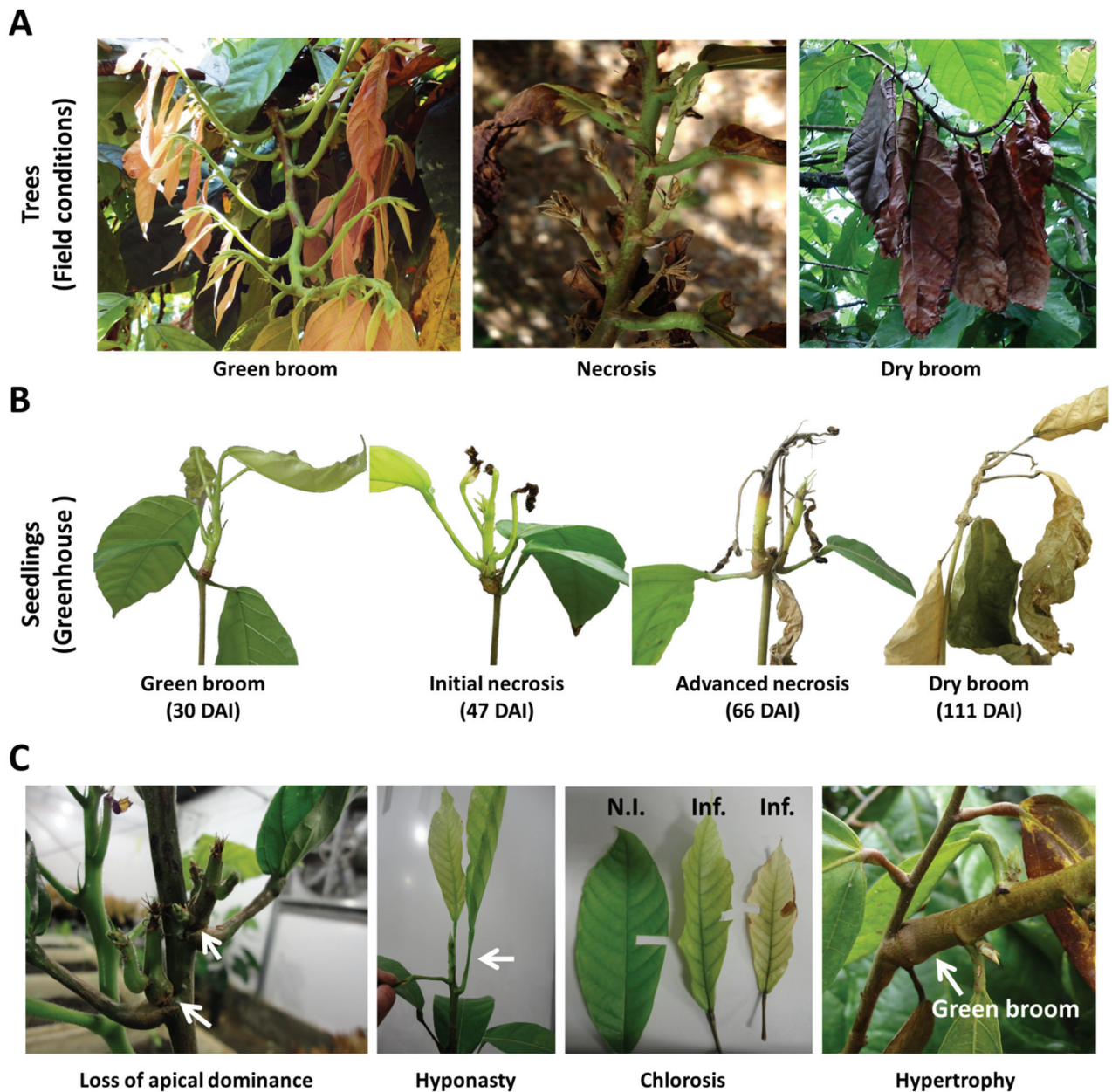
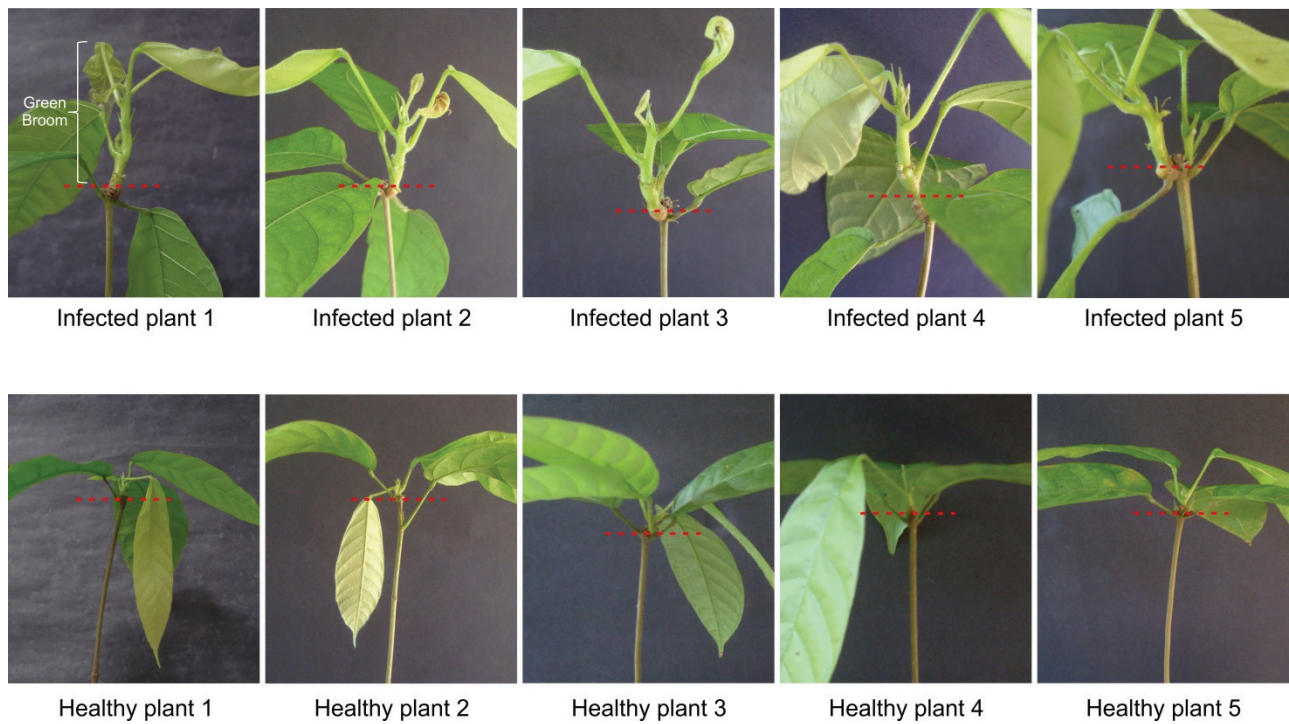


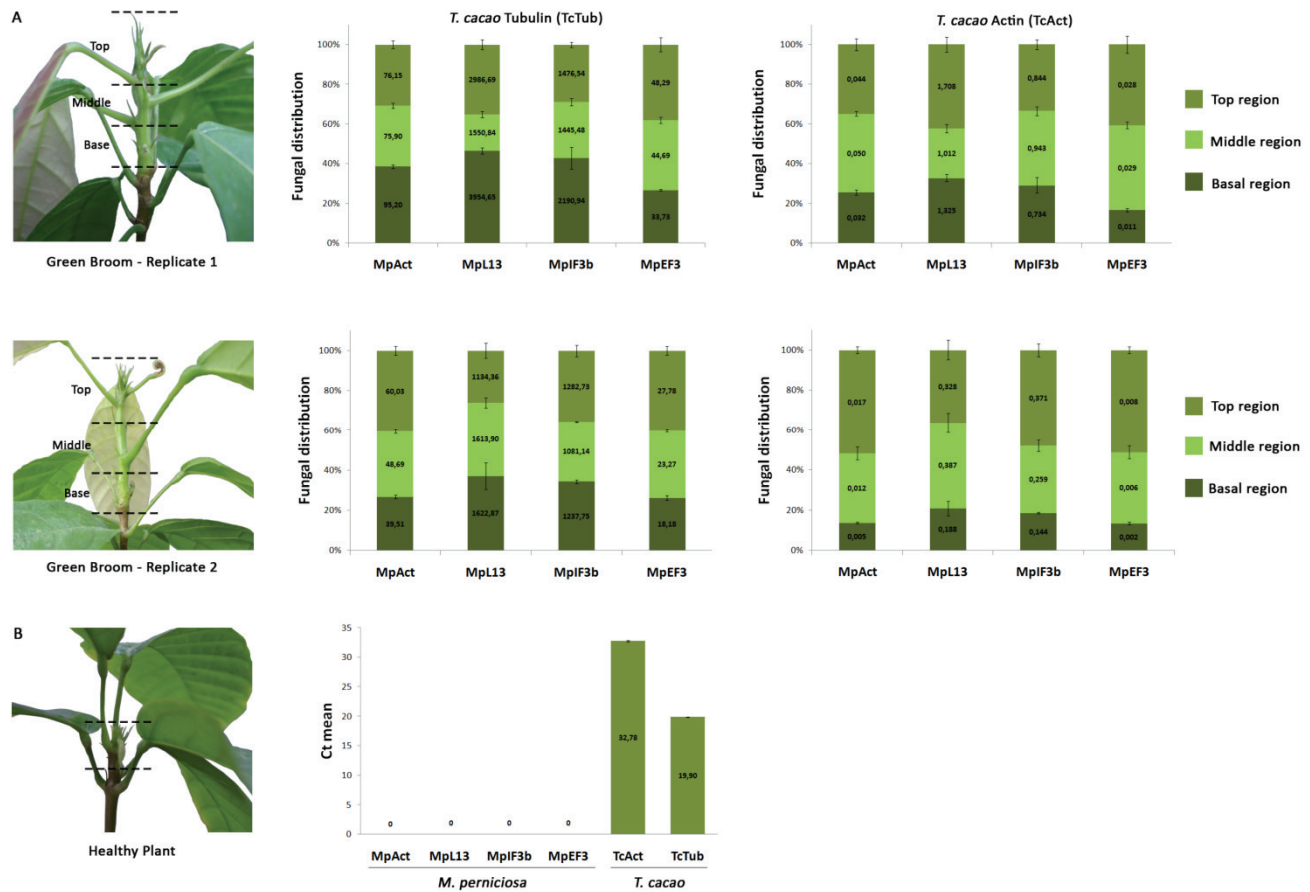
SUPPLEMENTAL FIGURES



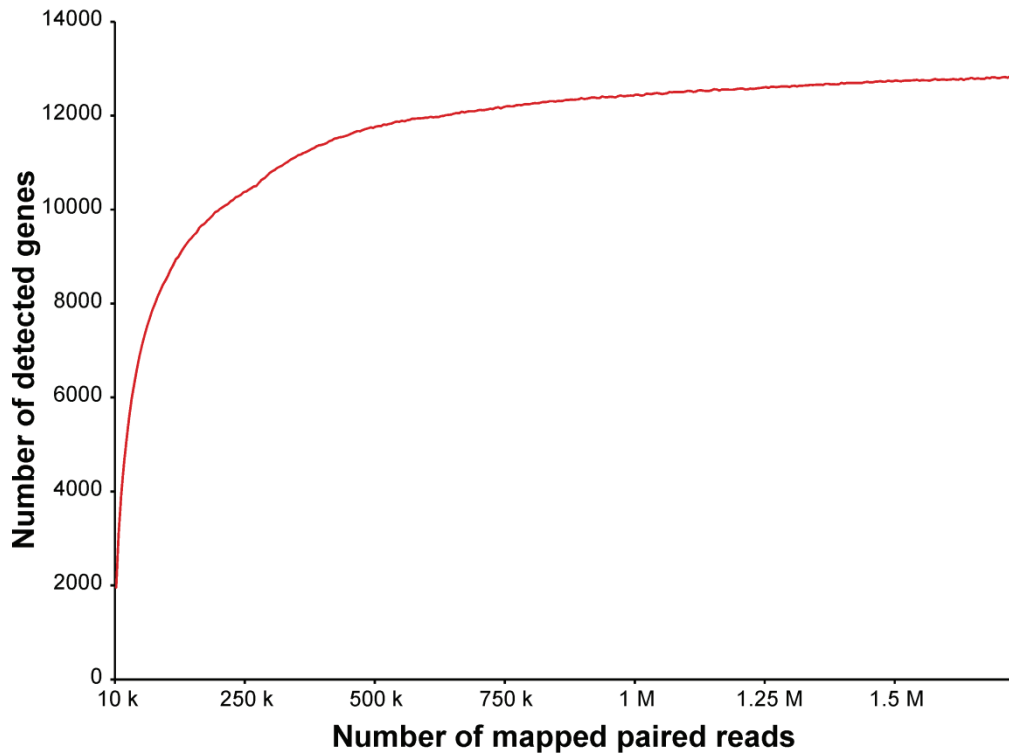
Supplemental Figure 1. Detailed view of WBD progression and the major symptoms observed in cacao plants during disease development. (A) Development of brooms in trees under field conditions. (B) Development of brooms in seedlings under greenhouse conditions. DAI, days after infection. (C) Major symptoms of WBD (indicated by arrows) include loss of apical dominance, hyponasty, chlorosis (N.I. = non-infected leaf; Inf. = infected leaf) and hypertrophy of the infected shoots.



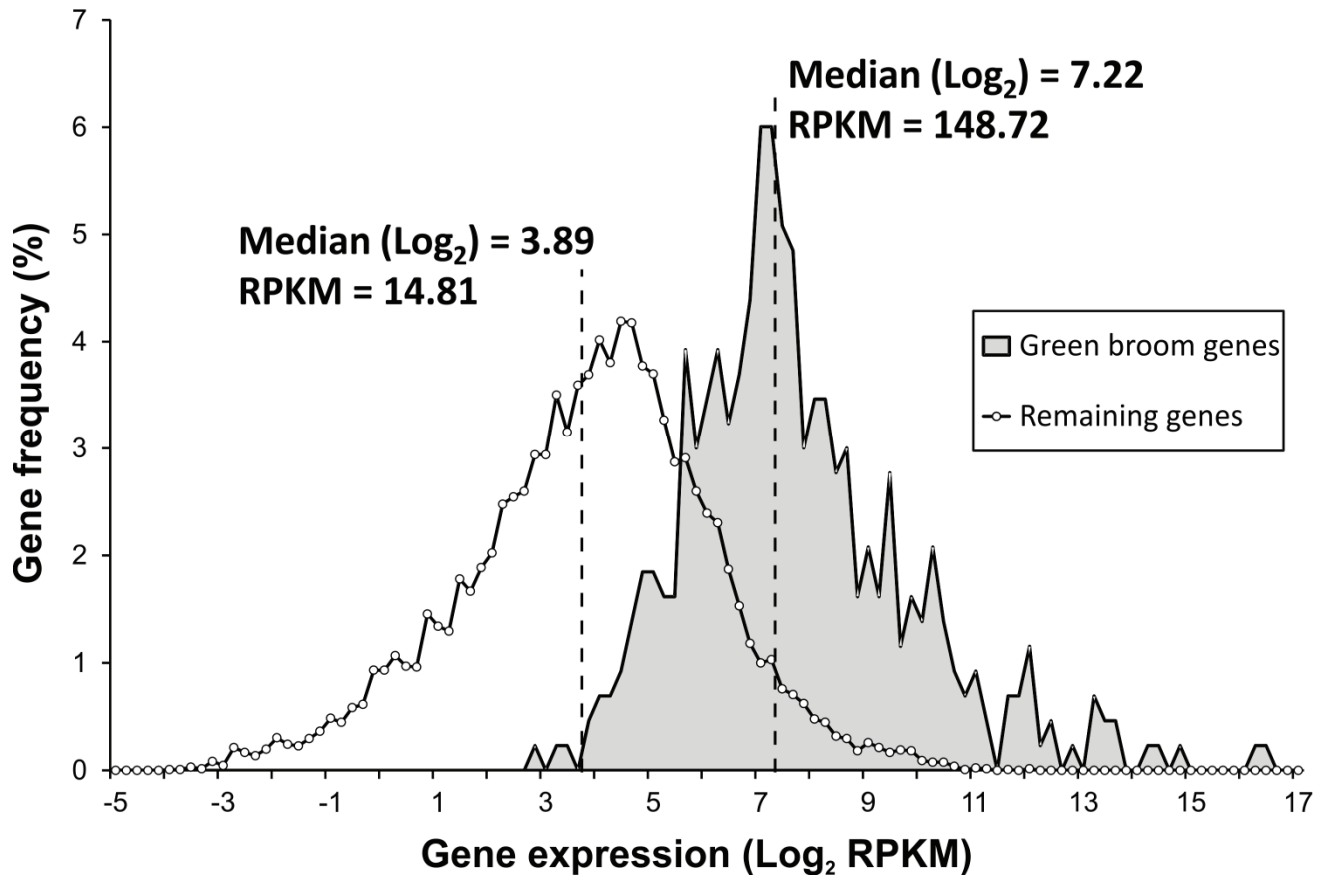
Supplemental Figure 2. Plant tissue collected for gene expression analysis. The apical portions of the ten cacao plants used in the experiment are shown. Dashed lines represent the sectioning position for sample harvesting. All plant tissue above this point, including shoots and leaves, was collected for RNA extraction.



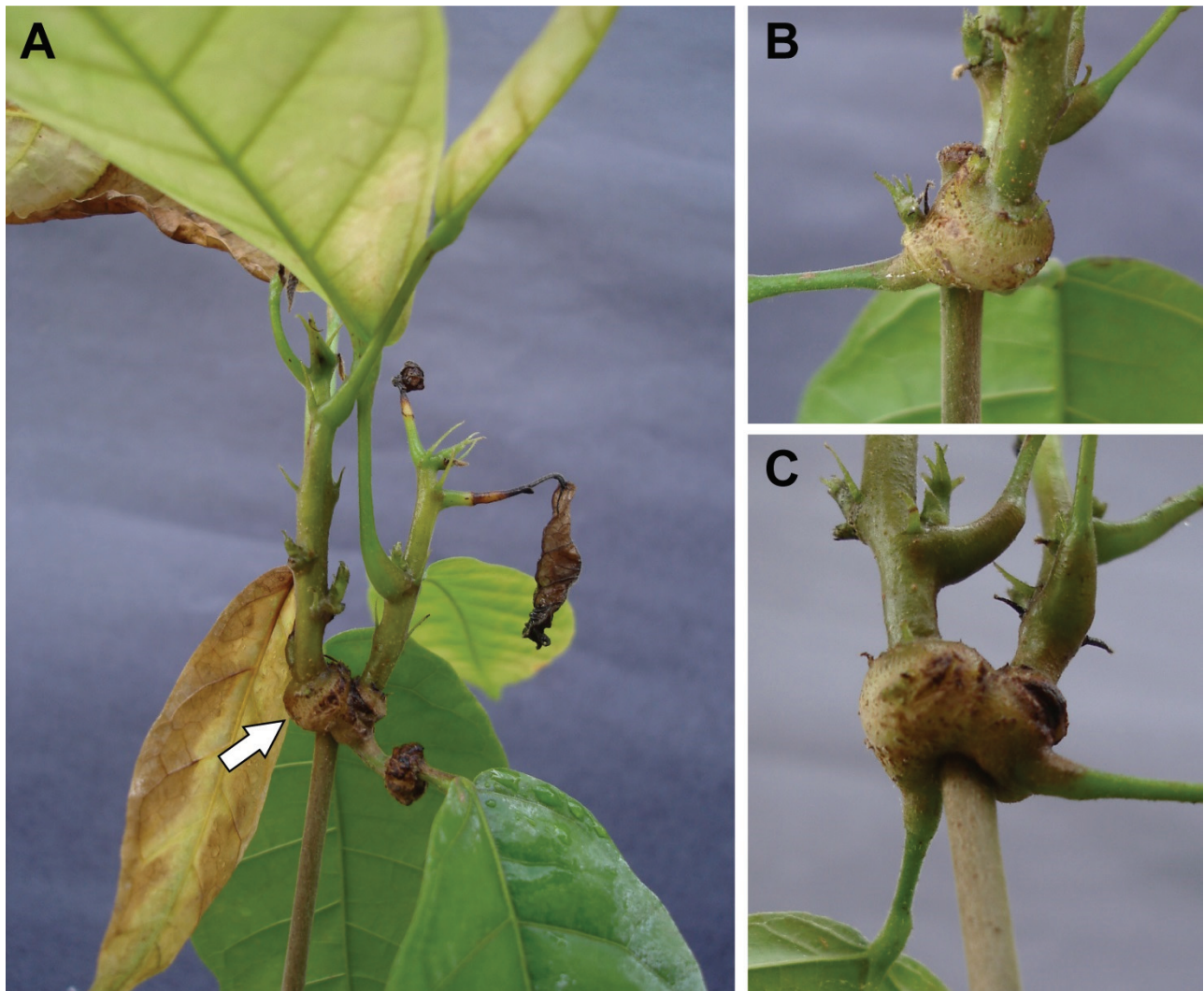
Supplemental Figure 3. *M. perniciosa* is uniformly distributed along the infected shoot. (A) Green brooms were sectioned into three different parts (dashed lines; basal, middle and top regions) and qPCR assays were performed to identify *M. perniciosa* transcripts. Four different constitutive fungal genes were analyzed (*MpAct*, *MpL13*, *MPIF3b* and *MpEF3*) and their expressions were normalized by either the cacao tubulin or actin genes. Relative expression levels are given as $2^{-\Delta Ct}$ and are shown in each bar. Fungal distribution represents the abundance of fungal transcripts in each sector of the green broom relative to the sum of the three sectors. (B) Amplification of fungal transcripts was not observed in healthy plants (numbers in the bars represent the cycle threshold – Ct). Error bars represent standard deviation of three measurements.



Supplemental Figure 4. Number of *Moniliophthora perniciosa* genes detected at different sequencing depths. Considering the 1.7 million paired reads mapping to *M. perniciosa* in our experiment, we identified approximately 13,000 fungal genes that were detected in at least one of the replicates. A total of 8,617 genes were detected in all five replicates. A gene was considered as being expressed if it had an expression value of at least 1 RPKM (reads per kilobase per million mapped reads).



Supplemental Figure 5. Distribution of expression levels of *M. perniciosa* genes in green brooms. Generally, the 433 fungal genes classified as ‘green broom-specific’ were strongly up-regulated during the biotrophic colonization of the cacao plant. Interestingly, other highly expressed genes that were not part of the green broom cluster encoded mostly housekeeping proteins, such as elongation factors or ribosomal proteins (see Supplemental Data Set 8 online).



Supplemental Figure 6. Callus-like structure formed on the basal region of infected shoots. (A) These structures (arrow) form during WBD progression and block the communication between healthy and infected parts of the plant. Note that the pattern of necrosis in infected shoots is similar to that of regular senescence. (B) and (C) Details of the callus-like structures. Photograph taken 50 days after infection.

SUPPLEMENTAL TABLES

Supplemental Table 1. Primer sequences used for cacao qPCR analyses.

Gene ID	Gene description	Forward primer	Reverse primer
CGD0027635	Pathogenesis-related protein 1	5' ACCTTATGGCGAGAACCTTG 3'	5' GGAGTAATCATAGTCGGCCTTC 3'
CGD0015104	Malate synthase	5' TTCTCATCAGGACATGCCATAGG 3'	5' CCTCATTGCTGCTGGATCATCT 3'
CGD0012378	Isocitrate lyase	5' ACTGTCCAGGGAGGCATCTCATC 3'	5' CCTCACCTCCAACGCCCGT 3'
CGD0019988	Beta xylosidase	5' TTACAATCAAGTCAATGGGAAGC 3'	5' CAACCGAATCACAACTGACAC 3'
CGD0008202	Endochitinase I	5' AACCCCGCTGATTACTGC 3'	5' TTCCACACTGCCCATAGTTG 3'
CGD0013652	Aquaporin	5' GCTCTTAGGTGCTATTGTGGC 3'	5' AACTCCCAACTCCAGACG 3'
CGD0023677	Similar to protease inhibitors	5' GCGTCTAGCTCTTAGTGATGTGC 3'	5' AGTGAGAATGGTGTGGGTAAAT 3'
CGD0010241	SAG29 (Senescence-associated protein 29)	5' CCTTAAACATTGTGGCACGAG 3'	5' TGAATAGTCCATAGGCAAACCAC 3'
CGD0034897	Peroxidase IV	5' TTTGTCTGGTGTAGTTTCTCG 3'	5' GCTTAACATCCCAGTCAGGTC 3'
CGD0034326	Asparagine synthetase (ASN1)	5' TACATCTTCCCTCACAATACCCC 3'	5' GGACAGTCAATCTAGCGGAGTT 3'
CGD0020178	Integral membrane protein	5' ACGCCTGCATATCCAAAAGC 3'	5' TCCGATATACGCAACACCCC 3'
CGD0020550	4-hydroxyphenylpyruvate dioxygenase	5' CCTCTTCCACTGCTTCCATCC 3'	5' GTTTCGGCGTCTTCCACTTCG 3'
CGD0003335	Triacylglycerol lipase	5' ACTCCACCATCTCAGGCAATTAG 3'	5' GATCTACCAATGCCATCACTAGC 3'
CGD0025812	ACC oxidase 1	5' AAAGATGCCTGTGAGAATTGGG 3'	5' ACTTCTGTAGTGCTCCTTTGTC 3'
CGD0003150	Gibberellic acid receptor	5' GTGGGAAGGATTCTAAAGTCTATG 3'	5' GTTACCTAATACCTCAACATCTGC 3'
CGD0030359	Alpha-amylase	5' CCCTTCCCATCTGACAAAAGTC 3'	5' TCTCATCCTTCAAACCCCAATC 3'
CGD0014936	NADPH oxidase	5' TCAGAGCCGATAACAAGCCAGA 3'	5' CAACCCACTAGCAAAACCACTTC 3'
CGD0030866	Acyl-CoA-binding protein (acbp)	5' AGTTCATTTCCAGATCAGCAGAC 3'	5' TCAGTGCTTGTGCTCTCAGTTA 3'
CGD0029727	Alpha tubulin 1	5' ACCAATCTTAAACCGCCTTGCTC 3'	5' GTTAGTCTGGAACCTCAGTCACAT 3'
CGD0021775	60S ribosomal protein L35	5' CGAGCGCTTACTAAACACCAG 3'	5' GAGAACACTTGGCTCCATTACAC 3'
CGD0001967	60S ribosomal protein L11	5' TTACCCCTCCATTTTCATCCAG 3'	5' GCTTCTGTACCTTGATTCCCTC 3'
CGD0023921	Actin	5' TACTATTTGATTGTAGAAGCATTG 3'	5' TTGGTCTTGTGATTATATGAAGG 3'
CGD0026243	Magnesium-chelatase subunit chlI	5' GTCTCTCGTTACACCTTCCTCG 3'	5' CTGAACCCCAAACCTCCATAAA 3'
CGD0018362	Ribulose biphosphate carboxylase small chain	5' CAATAAGTGGGTTCCGTGCTTGG 3'	5' GTTCCACATGATCCAGCAGCG 3'
CGD0003251	PSI reaction center subunit II (PsaD)	5' ACAATCAGCACCCGAAATCC 3'	5' AGCCCTAATGGTACTGTGAGC 3'
CGD0034137	PSAO (photosystem I subunit O)	5' GCTAGGAACCCCTTTGATGCTG 3'	5' CCACCCAATCAGCCCAAATC 3'
CGD0002031	Rhamnose synthase	5' TCTAGGGTCAGGAATTGGGTTC 3'	5' CATTGTCTACTCCCTCAGAAGC 3'
CGD0011230	Polygalacturonase	5' ACTCATAATCCACTAAACAGC 3'	5' CTCCCGTAAACCTAAGTGC 3'
CGD0003164	Histone H2AX	5' TGTCTTGTAGTATCTCGCCG 3'	5' TTCATCGTTTCTCACAGCCAAC 3'
CGD0006481	Lipid binding protein	5' CATTCTGATCGTCTGTGG 3'	5' GGGTACTTCTAATGGTAGGCAC 3'
CGD0003215	Fantastic four 2 like	5' GACCAAGCCTTCGCCCTATAATG 3'	5' TCCACCCACCCGTGCAACAT 3'
CGD0011230	Polygalacturonase	5' ACTCATAATCCACTAAACAGC 3'	5' CTCCCGTAAACCTAAGTGC 3'

Supplemental Table 2. Primer sequences used for *M. pernicioso* qPCR analyses.

Gene ID	Gene description	Forward primer	Reverse primer
MP04381	Protein kinase	5' CAAACGCGAGCTACGAGCAC 3'	5' CTGGGCCTTTAAACGGAGACG 3'
MP05620	Hypothetical protein	5' TCTACTGTGATCCGCATAGCAAG 3'	5' GATCCTCAAGGGAGCTTCAGGTG 3'
MP05651	Cell wall glucanase	5' AGATTCAAACCGCCACCAAACC 3'	5' TCAATTCATCCCTTCGGACCTG 3'
MP08861	Fruit-body specific gene a	5' TCTCTTCTCGTTACTGGCTCTTG 3'	5' TGGATGTGTTGCTCAAGTCTAGC 3'
MP11703	No hits	5' GATGCCATTGCGCCTAAAAGGG 3'	5' GAGGGTAAGCAGCAGGAATAAAGTCCTTTA 3'
MP03904	Fasciclin-like	5' CAGTCGGTCGCACGCTCTTG 3'	5' GATACCAATCCCGTATCGACCATAC 3'
MP07491	No hits (CSEP)	5' AACATCCAGGACTATGATTATGACTACACTTATT 3'	5' TTAGTCGTTCTGGTGTGGGTCGG 3'
MP08165	No hits (CSEP)	5' ATCAAGCTACGTGTGAAACCGA 3'	5' CCAGTCTGGTAGCCGTCACC 3'
MP10355	Chitin deacetylase 9	5' TATGGCCGTCGATGGGCTATGTA 3'	5' CTGTGGCAGTATCATTCCGGCATGTT 3'
MP12416	No hits (CSEP)	5' GACGTTGTGCGCGAGACAAAGTC 3'	5' CCAAGTTGTAGTTGGTTTTACGATTGTTA 3'
MP01616	No hits (CSEP)	5' CGTTTTTGTATAGATCAGTTACACCCT 3'	5' GAGTCACGGTATTTAGCCGGTAAAC 3'
MP05440	Gamma-aminobutyric acid transporter	5' TCGCAAACCAATGTATCTGGCT 3'	5' ATGGTGACGGCTCCGAAAATAAC 3'
MP05573	No hits (CSEP)	5' GCGATAACAAGATAGGCGGTTGGG 3'	5' GGTTTTGTATCGTCTGGCAGGGTC 3'
MP07624	Hypothetical protein (CSEP)	5' GAACACCCAGCTACGGTCTAGG 3'	5' GTGGTATCGGCACAGGTGATAGG 3'
MP07720	No hits (CSEP)	5' CAACCAAGGGGTGCAGAGCTTTG 3'	5' TCGGGTTTTGTACCAATCAGCG 3'
MP09116	Catalase	5' TGACCACGAAAATATCCCTGAACG 3'	5' TGAGATTAGACCAGTCACCATACGATT 3'
MP09913	No hits (CSEP)	5' CAACCAGTAACAGCACATGGCTG 3'	5' CACAACATCCGCCCTGAAGGC 3'
MP10165	No hits (CSEP)	5' CTGGGTATGATTGCACACTACAC 3'	5' CAAACTGGTCGCTCCTTCTACAC 3'
MP10658	No hits (CSEP)	5' CCATTCCAGCCGACTTAGAGC 3'	5' GGTGTTGTACGCCACACGATC 3'
MP02381	Amino acid transporter	5' CGATTTTACTCGGGCCTTAAAGCAC 3'	5' CCTTCAGGAACACATTCCAGCCAC 3'
MP12254	Terpene cyclase	5' CTTGTTTGGTATTTTACTTGTGGGA 3'	5' GTCGTATAGAATTTTATAGGAGTAATCGTGA 3'
MP12302	Asparaginase homolog	5' TAGAGGATCTCGGGAAGACAGTC 3'	5' GTAGCGTCATTCCTCAGTTGAGAA 3'
MP13732	C6 transcription factor	5' TGAAATAGCCAAAATCCCTATATTGG 3'	5' TGGTCTCACGGCTAGCGTACA 3'
MP14639	CFEM domain	5' GAACACAGAGGGCTGTGGTG 3'	5' CGGGTCTGCTCTGGGGGAG 3'
MP14755	No hits (CSEP)	5' CCATCATCTTGGGCGACATAGC 3'	5' AGACGATTTGGACAGCAGTTTGG 3'
MP15342	Endo-polygalacturonase	5' GCTGGGAATGGAGTATCGCTCAA 3'	5' GTTCCATTTGCCTGAGCAGTTAG 3'
MP13831	No hits (CSEP)	5' GGTTAGCACACGGGACTGTCAGG 3'	5' GCCATTGCCGAACCTTAGTCGATTC 3'
MP15672	Cytochrome p450	5' CATTGTGCCCGCAGGAACATCA 3'	5' ACCAAAAGTTATATACTCGGGGTTGG 3'
MP16298	Hexose transporter protein	5' CCTTAAATTGCTTGGTGCTTGATAAT 3'	5' CACGACCAGCTATAAGCATCCC 3'
MP16558	No hits (CSEP)	5' AATATCCGAGGTTACATCGGGCA 3'	5' GGACAAAATAATAGATCAGCGTGTGA 3'
MP00102	Asparagine amidase a	5' CCCTTGATACTCGCATCCACTAC 3'	5' AGGTATCCAGATCGCTCCTTG 3'
MP07852	F-box protein	5' TCTCACACATAACTTGGTCTACG 3'	5' ATCCTGGACAGCTATACAGCGGT 3'
MP10524	No hits (CSEP)	5' CAAGGGACACAATTAAGTACACAGC 3'	5' TGTTGAGAACGACGACTACACAGG 3'
MP13717	No hits (CSEP)	5' GCAAAGATACTTCGCACTGGTTGTC 3'	5' TCTTCTTCTCCAGTCTCGGGC 3'
MP02311	Exoglucanase 3 precursor	5' TCGCTGTCGGAGAGATCGATAGG 3'	5' CAATATCGGGGTGTGCCTCGACA 3'
MP07531	Hypothetical protein	5' CAACAACATGACTTCTGGCGAGC 3'	5' ATCGTATTCTGCCTGACCACGGG 3'
MP10673	No hits	5' TGACACCACAGATTACTGTACAG 3'	5' CAGATGGTCTGTAGCTGGAATGCTT 3'
MP14969	Extracellular protease	5' TCAGGTTTATACCAACAGCTCTTACG 3'	5' TGCCAAACCAGTTTCATAGCGA 3'
MP07692	Thaumatococin-like protein	5' CGTCTGGTACTGAGGTGTCTTT 3'	5' AAGAAGTCGGTCTGGGTTAG 3'
MP12125	MpPR-1h	5' CCGCGGTTACAGTATGGC 3'	5' CACGTGGAGCGTAGTGGG 3'
MP05107	MpEF3	5' GGAGAACTACCTTACCAGCTTG 3'	5' ATTGCCACGGTATCTCTTGGAG 3'
MP05317	MpIF3b	5' CCCTGTAGAAGTCGTGGAATTG 3'	5' GACAATGGCAAATCGTTCTCC 3'
MP07289	MpL13	5' ATGGACAAGAAACCGGAAGAG 3'	5' GCCAACTACGATGACATTAG 3'
MP12536	MpActin	5' CCCTTCTATCGTCGGTCTG 3'	5' AGGATACCACGCTTGGATTG 3'

Supplemental Table 3. Identification of *NEP* genes in basidiomycetes. The table consolidates the results from Blast searches against the NCBI nr and the JGI Mycocosm databases.

Species	Subphylum	Lifestyle	# of <i>NEP</i> genes
<i>Moniliophthora perniciosa</i>	Agaricomycotina	Cacao pathogen	5
<i>Moniliophthora roreri</i>	Agaricomycotina	Cacao pathogen	3
<i>Pseudozyma flocculosa</i>	Ustilaginomycotina	Mycoparasite	2
<i>Agaricostilbum hyphaenes</i> ATCC MYA-4628 v1.0	Pucciniomycotina	Mycoparasite	1
<i>Exidia glandulosa</i> v1.0	Agaricomycotina	Saprotroph	2
<i>Ganoderma</i> sp. 10597 SSI v1.0	Agaricomycotina	Saprotroph	1
<i>Lentinus tigrinus</i> ALCF2SSI-6 v1.0	Agaricomycotina	Saprotroph	2
<i>Naiadella fluitans</i> ATCC 64713 v1.0	Pucciniomycotina	Mycoparasite	5
<i>Polyporus arcularius</i> v1.0	Agaricomycotina	Saprotroph	1
<i>Sistotrema brinkmannii</i> HHB7604 ss-1 v1.0	Agaricomycotina	Saprotroph	1