

Table S1. GenBank accession numbers of reference isolates used in the phylogenetic analyses

Species	Type Strain	Host	County	GenBank No.					
				ITS	GAPDH	CHS-1	CAL	ACT	TUB2
<i>C. siamense</i>	ICMP 17795	Malus domestica	USA	JX010162	JX010051	JX009805	JX009703	JX009506	JX010393
<i>C. scovillei</i>	CBS 120708	Capsicum annuum	Thailand	JQ948269	JQ948599	JQ948930	-	JQ949590	JQ949920
<i>C. acutatum</i>	CBS 112996	Carica papaya	Australia	JQ005776	JQ948677	JQ005797	JQ005818	JQ005839	JQ005860
<i>C. boninense</i>	CBS 123755	Crinum asiaticum var. sinicum	Japan	JQ005153	JQ005240	JQ005327	JQ005674	JQ005501	JQ005588
<i>C. boninense</i>	CBS 128547	Camellia sp.	New Zealand	JQ005159	JQ005246	JQ005333	JQ005680	JQ005507	JQ005593

Table S2. Cluster analysis gene sequences of control strain CD and isolate strain C1

>CD ITS

AGGGATCATTACTGAGTTACCGCTCTATAACCCCTTTGTGAACATACCTAACCGTTGCTTCGGCGGGC
AGGGGAAGCCTCTCGCGGGCCTCCCCTCCCGGCGCCGGCCCCACACGGGGACGGGGCGCCC
GCCGGAGGAAACCAAACCTCTATTTACACGACGTCTCTTCTGAGTGGCACAAGCAAATAATTAAACT
TTTAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAAT
TGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCTCGCCAGCATTCTGGCGAGCATG
CCTGTTTCGAGCGTCATTTCAACCCTCAAGCACCGCTTGGTTTTGGGGCCCCACGGCACACGTGGG
CCCTTAAAGGTAGTGGCGGACCCTCCCGGAGCCTCCTTTGCGTAGTAACTAACGTCTCGCACTGGG
ATCCGGAGGGACTCTTGCCGTAAAACCCCCAAATTTTTTACAGGTTGACCTCGGATCAGGTAGGAAT
ACCCGCTGAA

>CD TUB2

ACGACGCGGCGATTTGACATTTGACACGATCTCGTACTGACCTCGGTACAGGCAAAACATCTCTG
GCGAGCACGGCCTCGACAGCAATGGCGTGTATGTCACCTTGTCTCCAGTGTGGCTTCCTCATGGAC
CCAGCAGCTAATCATACCACAGGTACAACGGCACTTCCGAGCTCCAGCTCGAGCGCATGAGCGTCT
ACTTCAACGAAGTTTGTATCCTAGTCCCCCAGTGTGCAGGCAATCCTATTGACGAATGCTGACCTT
CTCACCCAACCAGGCCTCCGGCAACAAGTACGTTCCCCGCGCCGTCTCGTCTGACTTGGAGCCCG
GTACCATGGACGCCGTCCGTGCCGGTCCCTTTGGCCAGCTTTTCCGCCCCGACAAC

>CD CHS-1

GATGCTTGGAAGAAGATTGTTGTCTGTGTCGTCAGCGACGGTCGTGGCAAGATCAACCCCAGAACG
CGAGCGCTGCTGGCTGGTATGGGTGTCTACCAGGAGGGTATCGCGAAGCAACAGGTCAACGGCAA
GGATGTCACGGCCCACATTTACGAATACACCTCTCAAGTCGGCATGACGATCAAGAATGACGTCGTC
ACTCTGGTCCCTAAACAGCAGCCTGTTTACAGATGCTGTTCTGCTTGAAGGAGAAGAACTCGAAGAAG
ATCAACTCTCACAGATGG

>CD ACT

GTTTCGCCGGTGACGATGCGCCCAGAGCTGTCTTCCGTAAGTTCCCCATCATCCGCAGACCGCAAT
CTTCTCCGTCAGGGGTATACGATTTTGGTCACCCATACCCTAGATTGTTGATTCTAACTGTTCTCTAG
CCTCCATTGTCGGTCGCCCCCGTCACCATGGGTAGGTCTATCTCTTGCTGCGGCAATGCCATCTCCT
GCGCCGCGACCTAACACGTGCACAGTATCATGATTGGTATGGGCC

>CD GADPH

CCTTCATTGAGACCAAGTACGCTGTGAGTATCACCCCACTTTACCCCTCTATCATGATATCACGTCTG
CCACGATAACACCAGCTTCGTCGATATCCACGGGAAAAGAGTCGGAGCTAGCACTCTCGATTCTTTT
GCCCCAAGGTTTCGATTGGGCTTGTGTAACGACACGACGTGACCCAATCATGCAGAAACAGCCGA
GACAAAATTTGCTGACAGACAATCCATCACAGGCCTACATGCTCAAGTAC

>CD CAL

CATCATTGGGATCTCCGGACGATGTCCTTTTGTCAAAAGGTATTTTTGAAGGTTAGCTGACCCATTC
ATATAGGACAAGGACGGCGATGGTCAGTACCTGGTCCCCCTTTCCCTTTCTCTCGACCCCGCGCC
CGTACAATTTGACTCCTGCGACCGCTTCGATACGAGAACAGCATTGGGACATTGTCGAGAATTGAT
CATGTGGATTTTCAAGGCACGGAGCTAAAGAATACGGACAGGACAAATTACAACCAAGGAGCTCGGC
ACCGTCATGCGCTCCCTGGGACAGAACCCTCCGAGTCTGAGCTTCAGGACATGATCAACGAGGTT
GACGCCGACAACAACGGAACGATCGACTTCCCTGGTAGGTCTACACAACAATACTGGCAATCACG
CACACGAAAGCGACTCACTGACGAATAACCTGACAGAGTTCCTCACCATGATGGCCCGCAAGATGA
AGGACACCGACTCCGAGGAGGAGATTTCGTGAAGCCTTCAAGGTAAGAAGAGCTAGTGCAACGCGC

AAGTGGATAATGCTGATCAGAGGAAGGTCTTTGACCGCGATAACAACGGCTTCATCTCCGCCGCCG
AGCTTCGCCACGTCATGACTTCAATCGGCGAGAAGCTCACCGACGATGAGGTTGATGAGATGATT
GCGAGGCTGACCAGGACGGCGATGGACGTATTGACTGTAAGAACGCGACATCCGTGTTACGCTG
CTCGTTGCTCACGTTGCTAACACACATTCCCAGACAACGAGTTCGCCATCGTGGAGGGGGAAAAA
AAAGGAAA

>C1 ITS

AGGGATCATTACTGAGTTACCGCTCTATAACCCCTTTGTGAACATACCTAACCGTTGCTTCGGCGGGC
AGGGGAAGCCTCTCGCGGGCCTCCCCTCCCGGCGCCGGCCCCACCACGGGGACGGGGCGCCC
GCCGAGGAAACCAAACCTCTATTTACACGACGTCTCTTCTGAGTGGCACAAGCAAATAATTAACCT
TTTAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAAT
TGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCTCGCCAGCATTCTGGCGAGCATG
CCTGTTTCGAGCGTCATTTCAACCCTCAAGCACCGCTTGGTTTTGGGGCCCCACGGCACACGTGGG
CCCTTAAAGGTAGTGGCGGACCCTCCCGGAGCCTCCTTTGCGTAGTAACCTACGTCTCGCACTGGG
ATCCGGAGGGACTCTTGCCGTAAAACCCCCAAATTTTTTACAGGTTGACCTCGGATCAGGTAGGAAT
ACCCGCTGAA

>C1 TUB2

ACGACGCGGCGATTTTCGACATTTGACACGATCTCGTACTGACCTCGGTACAGGCAAAACATCTCTG
GCGAGCACGGCCTCGACAGCAATGGCGTGTATGTCACTTGTCTCCAGTGTGGCTTCCTCATGGAC
CCAGCAGCTAATCATACCACAGGTACAACGGCACTTCCGAGCTCCAGCTCGAGCGCATGAGCGTCT
ACTTCAACGAAGTTTGTATCCTAGTCCCCAGTGTGCAGGCAATCCTATTGACGAATGCTGACCTT
CTCACCCAACCAGGCCTCCGGCAACAAGTACGTTCCCCGCGCCGTCTCGTCTGACTTGGAGCCCG
GTACCATGGACGCCGTCCGTGCCGGTCCCTTTGGCCAGCTTTTCCGCCCCGACAAC

>C1 CHS1

GATGCTTGGAAGAAGATTGTTGTCTGTGTGTCGTCAGCGACGGTCGTGGCAAGATCAACCCCAGAACG
CGAGCGCTGCTGGCTGGTATGGGTGTCTACCAGGAGGGTATCGCGAAGCAACAGGTCAACGGCAA
GGATGTCACGGCCCACATTTACGAATACACCTCTCAAGTCGGCATGACGATCAAGAATGACGTCGTC
ACTCTGGTCCCTAACAGCAGCCTGTTTCAGATGCTGTTCTGCTTGAAGGAGAAGAACTCGAAGAAG
ATCAACTCTCACAGATGG

>C1 ACT

GTTTCGCCGGTGACGATGCGCCCAGAGCTGTCTTCCGTAAGTTCCCCATCATCCGCAGACCGCAAT
CTTCTCCGTACAGGGGTATACGATTTTGGTCACCCATACCCTAGATTGTTGATTCTAACTGTTCTCTAG
CCTCCATTGTGCGTCGCCCCCGTCACCATGGGTAGGTCTATCTCTTGCTGCGGCAATGCCATCTCCT
GCGCCGCGACCTAACACGTGCACAGTATCATGATTGGTATGGGCC

>C1 GADPH

CCTTCATTGAGACCAAGTACGCTGTGAGTATACCCCCACTTTACCCCTCTATCATGATATCACGTCTG
CCACGATAACACCAGCTTCGTCGATATCCACGGGAAAAGAGTCGGAGCTAGCACTCTCGATTCTTTT
GCCCCAAGGTTTCGATTGGGCTTGTTGTAACGACACGACGTGACCCAATCATGCAGAAACAGCCGA
GACAAAATTTGCTGACAGACAATCCATCACAGGCCTACATGCTCAAGTAC

>C1 CAL

CATCATTGGGATCTCCGGACGATGTCCTTTTGCTCAAAAGGTATTTTTGAAGGTTAGCTGACCCATTC
ATATAGGACAAGGACGGCGATGGTCAGTACCTGGTCCCCCCTTTCCCTTTCTCTCGACCCCGCGCC
CGTACAATTTGACTCCTGCGACCGCTTCGATACGAGAACAGCATTGGGACATTGTGAGAATTGAT
CATGTGGATTTAGGGCACGGAGCTAAAGAATACGGACAGGACAAATTACAACCAAGGAGCTCGGC

ACCGTCATGCGCTCCCTGGGACAGAACCCCTCCGAGTCTGAGCTTCAGGACATGATCAACGAGGTT
GACGCCGACAACAACGGAACGATCGACTTCCCTGGTAGGTCTACACAACAACACTACTGGCAATCACG
CACACGAAAGCGACTCACTGACGAATAACCTGACAGAGTTCCTCACCATGATGGCCCGCAAGATGA
AGGACACCGACTCCGAGGAGGAGATTCTGTGAAGCCTTCAAGGTAAGAAGAGCTAGTGCAACGCGC
AAGTGGATAATGCTGATCAGAGGAAGGTCTTTGACCGCGATAACAACGGCTTCATCTCCGCCGCCG
AGCTTCGCCACGTCATGACTTCAATCGGCGAGAAGCTCACCGACGATGAGGTTGATGAGATGATT
GCGAGGCTGACCAGGACGGCGATGGACGTATTGACTGTAAGAACGCGACATCCGTGTTACGCTG
CTCGTTGCTCACGTTGCTAACACACATTCCCAGACAACGAGTTCGCCATCGTGGAGGGGGGAAAAA
AAAGGAAA

Table S3. Functional annotation of genes with insertion and deletion mutations

Gene ID	Functional Annotation
CscA186g00989	Lysine methyl transferase
CscA186g01084	Zinc finger
CscA186g01085	Belongs to the AAAATPase family
CscA186g01086	Belongs to the Ca (2) cation antiporter (Ca CA)(TC2.A.19)family
CscA186g01087	Oxidoreductase molybdopterin binding domain-containing protein
CscA186g01088	Fungal specific transcription factor domain-containing protein
CscA186g01089	FAD dependent oxidoreductase superfamily
CscA186g01090	2-haloalkanoic acid dehalogenase
CscA186g01091	Belongs to the class-III pyridoxal-phosphate-dependent amino transferase family (UGA1)
CscA186g01092	Belongs to the aldehyde dehydrogenase family (UGA2)
CscA186g01093	-
CscA186g01096	Major Facilitator Superfamily
CscA186g01097	Pectin lyase
CscA186g01099	Phosphoglycerate mutase (PMU1)
CscA186g01100	DNA mismatch repair protein (MLH3)
CscA186g05230	Fungal specific transcription factor domain
CscA186g05231	Major Facilitator Superfamily
CscA186g05232	Dihydrodipicolinate synthetase family
CscA186g05233	Protein of unknown function (DUF3830)
CscA186g05234	Taurine catabolism dioxygenase TauD, TfdA family
CscA186g05235	Fungal specific transcription factor domain
CscA186g09598	Transcription factor
CscA186g09599	Serine carboxy peptidase S28
CscA186g09600	Sulfatase-modifying factor enzyme1
CscA186g09601	Belongs to the eIF-2B alpha beta delta subunits family (GCN3)
CscA186g09602	Adapt in ear-binding coat-associated protein
CscA186g10640	Conserved hypothetical protein
CscA186g10641	Belongs to the peptidase C2 family
CscA186g10643	Belongs to the Ni Co T transporter (TC2. A. 52) family
CscA186g10644	Xaa-pro dipeptidase (PEPP)

Table S4. KEGG pathway enrichment gene information (p<0.05)

Term	ID	Gene Number	P-Value	Gene Ratio	Gene ID
Glyoxylate and dicarboxylate metabolism	mgr00630	5	0.000338	0.151515152	CscA186g07289
					CscA186g02661
					CscA186g00132
					CscA186g04854
					CscA186g02318
					CscA186g06678
Carbon metabolism	mgr01200	7	0.000413	0.064814815	CscA186g00132
					CscA186g07289
					CscA186g06650
					CscA186g02661
					CscA186g02318
					CscA186g04854
					CscA186g07503
					CscA186g06678
					CscA186g06681
					CscA186g06679
					CscA186g00132
					CscA186g05282
					CscA186g04257
Metabolic pathways	mgr01100	19	0.004456	0.019812304	CscA186g07289
					CscA186g06650
					CscA186g08484
					CscA186g08395
					CscA186g08536
					CscA186g01151
					CscA186g06036
					CscA186g02798
					CscA186g02661
					CscA186g10311
					CscA186g02318
Vitamin B6 metabolism	mgr00750	2	0.009019	0.25	CscA186g04854
					CscA186g10411
					CscA186g10412
Biosynthesis of secondary metabolites	mgr01110	8	0.027366	0.023460411	CscA186g06678
					CscA186g00132
					CscA186g07289
					CscA186g08536
					CscA186g06036
					CscA186g02661

Amino sugar and nucleotide sugar metabolism	mgr00520	3	0.027366	0.056603774	CscA186g02318
					CscA186g04854
					CscA186g06678
					CscA186g06679
					CscA186g06681

Table S5. Functional annotation table of differentially expressed genes

Gene ID	Functional Annotation
CscA186g00004	-
CscA186g00132	Belongs to the malate synthase family
CscA186g00305	FAD binding
CscA186g00381	Transferrin receptor-like dimerization domain
CscA186g00838	Amino acid adenylation domain-containing protein
CscA186g00901	Taurine catabolism dioxygenase TauD
CscA186g00976	Methyl transferase domain
CscA186g00977	CytochromeP450
CscA186g00980	CytochromeP450
CscA186g01024	OPT oligo peptide transporter
CscA186g01151	Major facilitator super family transporter
CscA186g01168	Ribonuclease III family
CscA186g01397	Protein of unknown function (DUF4246)
CscA186g01455	GAL4-like Zn (II) ₂ Cys ₆ (or C6 zinc) binuclear cluster DNA-binding domain
CscA186g01666	Integral membrane protein
CscA186g02181	Fungal specific transcription factor
CscA186g02318	Interconversion of serine and glycine
CscA186g02661	Occurs in almost all aerobically respiring organisms and serves to protect cells from the toxic effects of hydrogen peroxide
CscA186g02798	Plasma-membrane proton-efflux P-type ATPase
CscA186g02811	Short chain dehydrogenase
CscA186g03947	-
CscA186g03948	Cation transporter
CscA186g04034	ABC transporter transmembrane region
CscA186g04189	Fungal specific transcription factor domain
CscA186g04282	-
CscA186g04737	permease
CscA186g04854	Belongs to the isocitrate lyase PEP mutase superfamily. Isocitrate lyase family (ICL1)
CscA186g05240	Alpha methyl acyl-CoA racemase
CscA186g05241	3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
CscA186g05282	GMP synthase
CscA186g05586	Belongs to the multi copper oxidase family
CscA186g05630	-
CscA186g06034	Bacterial protein of unknown function (DUF924)
CscA186g06035	Belongs to the glycosyl hydrolase11(cellulase G) family
CscA186g06036	Copper amine oxidase
CscA186g06037	Amino acid
CscA186g06038	Fungal specific transcription factor
CscA186g06039	Fungal specific transcription factor
CscA186g06040	Belongs to the DEAD box helicase family (MSS116)

CscA186g06650	Amino transferase class I and II(ALT1)
CscA186g06678	Belongs to the hexokinase family (NAG5)
CscA186g06679	Glucosamine-6-phosphate isomerase (NAG1)
CscA186g06680	N-acetylglucosamine-6-phosphate deacetylase (NAG2)
CscA186g06681	N-acetylglucosamine-6-phosphate deacetylase (NAG2)
CscA186g06741	Toxin biosynthesis protein
CscA186g06845	This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the transport of calcium (PMC1)
CscA186g06970	-
CscA186g07164	Heter okaryon incompatibility protein (HET)
CscA186g07289	Belongs to the malate synthase family
CscA186g07459	Phospholipase c
CscA186g07495	Major Facilitator Superfamily
CscA186g07498	-
CscA186g07499	FAD binding domain
CscA186g07503	FAD binding domain
CscA186g07505	Belongs to the purine-cytosine permease (2.A.39) family
CscA186g07506	Phytanoyl-CoA dioxygenase (Phy H)
CscA186g07508	-
CscA186g07511	-
CscA186g07582	Major Facilitator Superfamily
CscA186g08289	Sulfate transporter
CscA186g08289	Sulfate transporter
CscA186g08395	Inositol oxygenase
CscA186g08483	Uncharacterized alpha/beta hydrolase domain (DUF2235)
CscA186g08483	Uncharacterized alpha/beta hydrolase domain (DUF2235)
CscA186g08484	Linoleate diol synthase
CscA186g09807	permease
CscA186g09816	Belongs to the iron ascorbate-dependent oxidoreductase family
CscA186g09956	Response to estrogen
CscA186g10089	Ccc h zinc finger DNA binding protein
CscA186g10411	Belongs to the Pdx SSNZ family (SNZ1)
CscA186g10412	SNO glutamine amido transferase (SNO1)
CscA186g10644	Xaa-pro dipeptidase (PEPP)
CscA186g10662	Belongs to the mitochondrial carrier (TC2. A. 29) family (SFC1)
CscA186g10679	Lys M domain-containing protein
CscA186g10768	Belongs to the type-B carboxylesterase lipase family
CscA186g10915	Extra cellular serine-rich protein
CscA186g10929	Ankyrin repeat
CscA186g10930	-
CscA186g11291	-
CscA186g11471	domain-containing protein
CscA186g11584	Amidohydrolase
CscA186g11675	-

CscA186g11683	CytochromeP450
CscA186g11685	Transporter
CscA186g11692	GAL4-like Zn (II)2Cys6(orC6zin c) binuclear cluster DNA-binding domain
CscA186g11694	Serine hydrolase (FSH1)
CscA186g12527	Major facilitator superfamily transporter
CscA186g12532	-
CscA186g12579	Major facilitator superfamily transporter
CscA186g12905	-
CscA186g12960	Isomerase (EC11)
CscA186g13054	C6zincfinger protein
CscA186g13056	Respiratory chain complex III assembly
CscA186g13061	-
CscA186g13062	Protein tyrosine kinase
CscA186g13062	Protein tyrosine kinase
CscA186g13063	Protein kinase domain
CscA186g13217	Lip A and NB-ARC domain-containing protein
CscA186g13662	Clathrin is the major protein of the polyhedral coat of coated pits and vesicles (CHC1)

Table S6. Primers used in the study with sequences and sources

Gene	Primer	Sequence (5'-3')
ITS	ITS4	TCCTCCGCTTATTGATATGC
	ITS5	GGAAGTAAAAGTCGTAACAAGG
ACT	ACT-512F	ATGTGCAAGGCCGTTTCGC
	ACT-783R	TACGAGTCCTTCTGGCCCAT
CHS-1	CHS-79F	TGGGGCAAGGATGCTTGGAAGAAG
	CHS-345R	TGGAAGAACCATCTGTGAGAGTTG
TUB2	Bt2a	GGTAACCAAATCGGTGCTGCTTTC
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC
GADPH	GDF1	GCCGTCAACGACCCCTTCATTGA
	GDR1	GGGTGGAGTCGTACTTGAGCATGT
CAL	CL1C	GAATTCAAGGAGGCCTTCTC
	CL2C	CTTCTGCATCTGAGCTGGAC

