

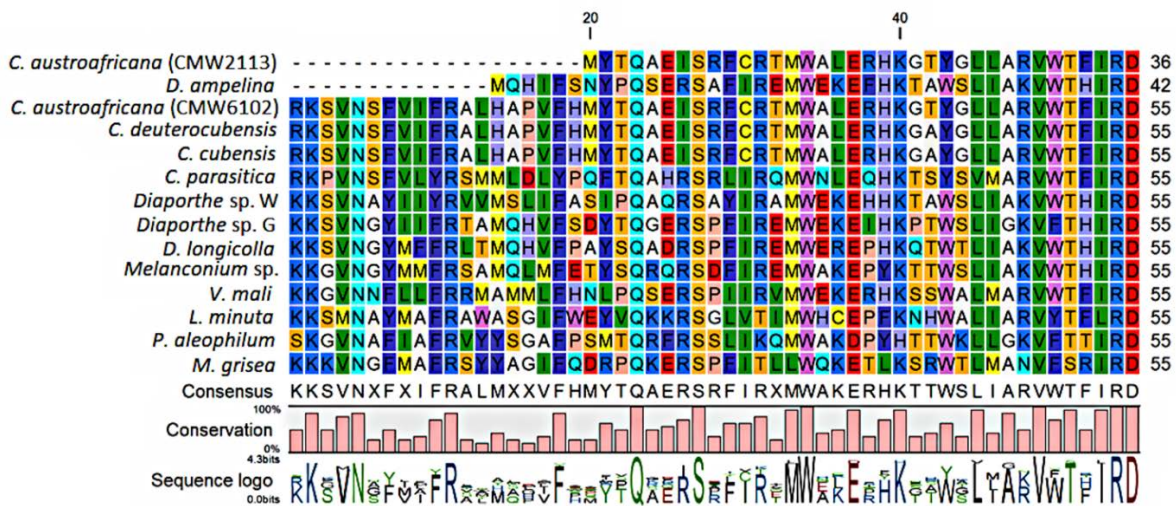
The mating system of the *Eucalyptus* canker pathogen *Chrysosporthe austroafricana* and closely related species

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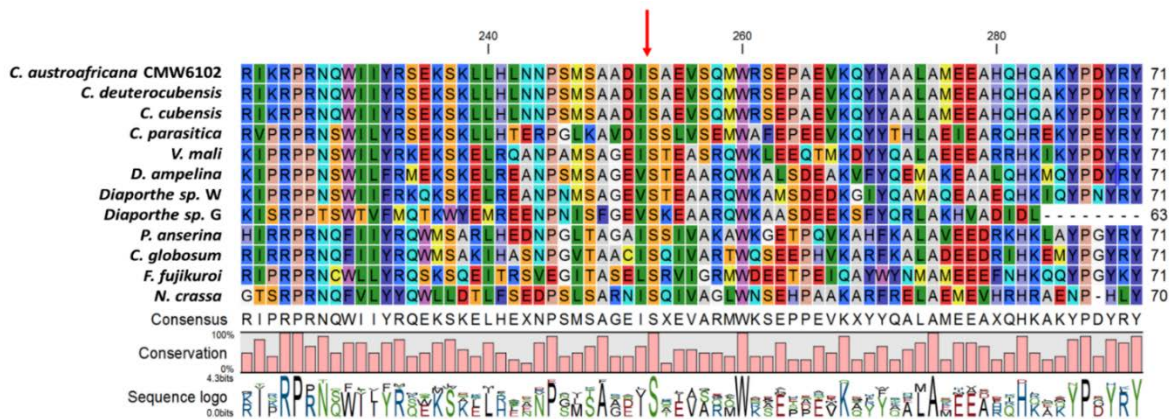
Supplementary material



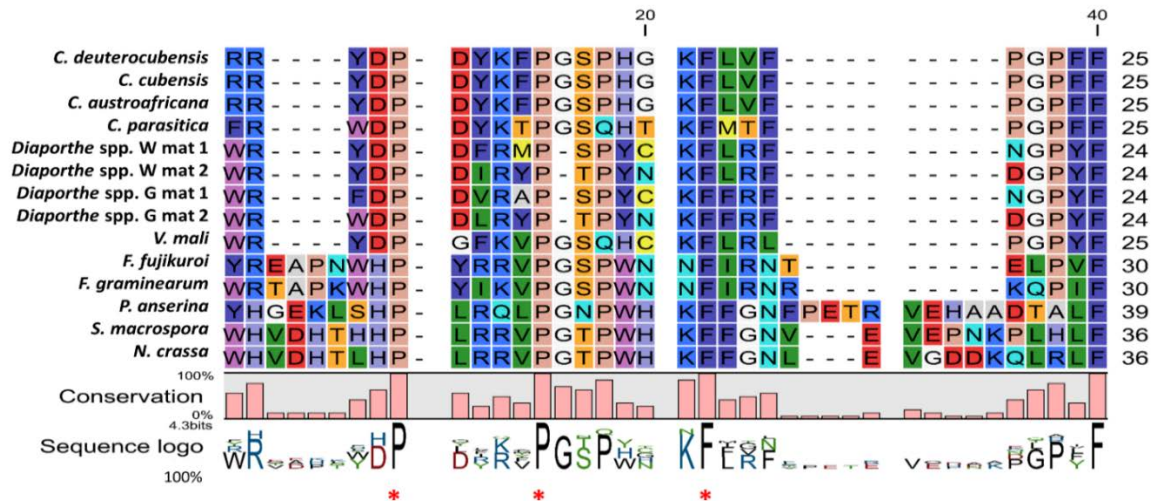
Supplementary figure 1: Amino acid sequence alignment of the α -1 domain deduced from putative MAT1-1-1 proteins. Accession numbers for sequences in the MAT1-1-1 alignment are for *C. parasitica* (AAK83346), *Diaporthe* spp. W (BAE93750), *Diaporthe* spp. G (AB939756), *Valsa mali* (KUI72760.1), and *Magnoportha grisea* (Q86Z74). The MAT1-1-1 genes of *D. longicolla*, *Melanconium* sp, *P. aleophilum* and *L. minuta* were identified from their respective genome sequences (Blanco-Ulate et al., 2013; Inderbitzin and Berbee, 2001; Lamprecht et al., 2011; Li et al., 2015). The bar graph and sequence logo show amino acid conservation along the alignment.



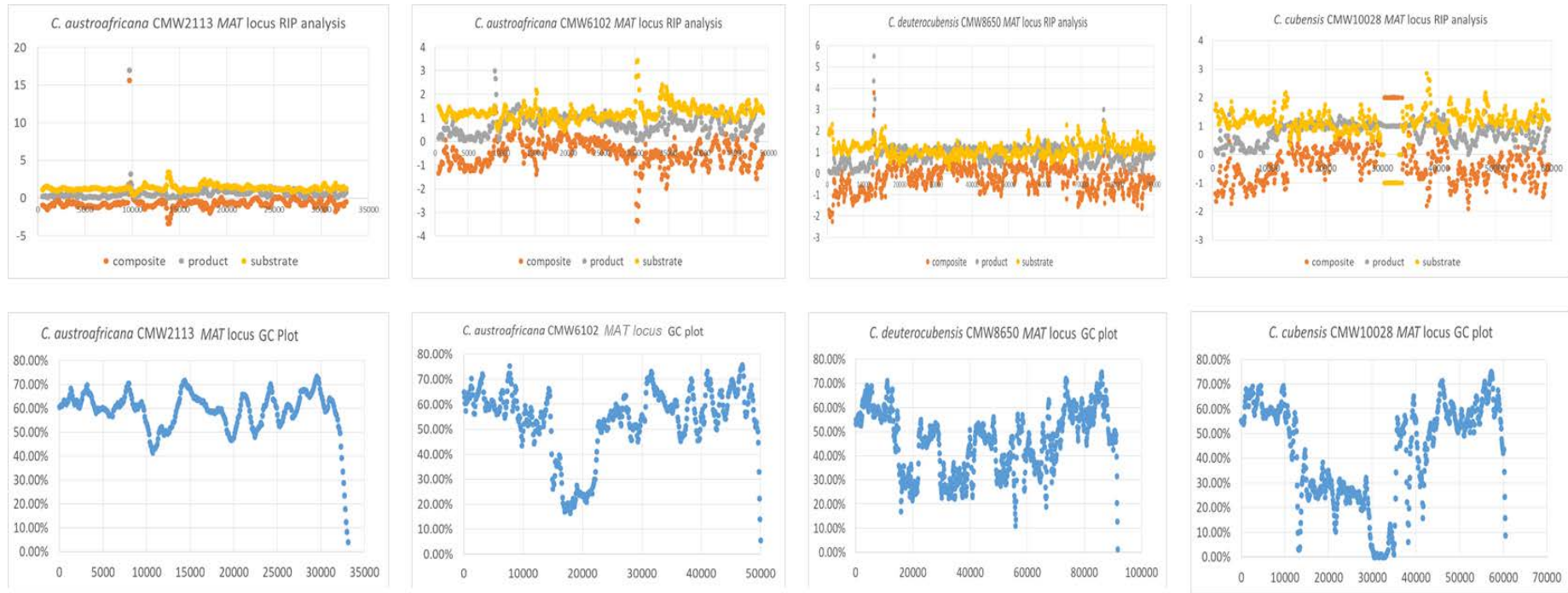
Supplementary figure 2: Amino acid sequence alignment of HMG domain of putative MAT1-2-1 proteins of *Chrysosporthe* species. Accession numbers for sequences in MAT1-2-1 alignment are for *C. parasitica* (AAK83343), *Diaporthe* spp. W (BAE93753), *Diaporthe* spp. G (BAE93759), *Valsa mali* (AQT26490), *Neurospora crassa* (AAA33598), *Sordaria macrospora* (CAA71624), *Podospora anserina* (CAA45520), *Fusarium fujikuroi* (AAC71056), and *Aspergillus fumigatus* (EAL92951). The red arrow in the MAT1-2-1 alignment shows the position of a conserved intron observed in the MAT1-2-1 genes of ascomycetes. The bar graph and sequence logo show amino acid conservation in the alignment.



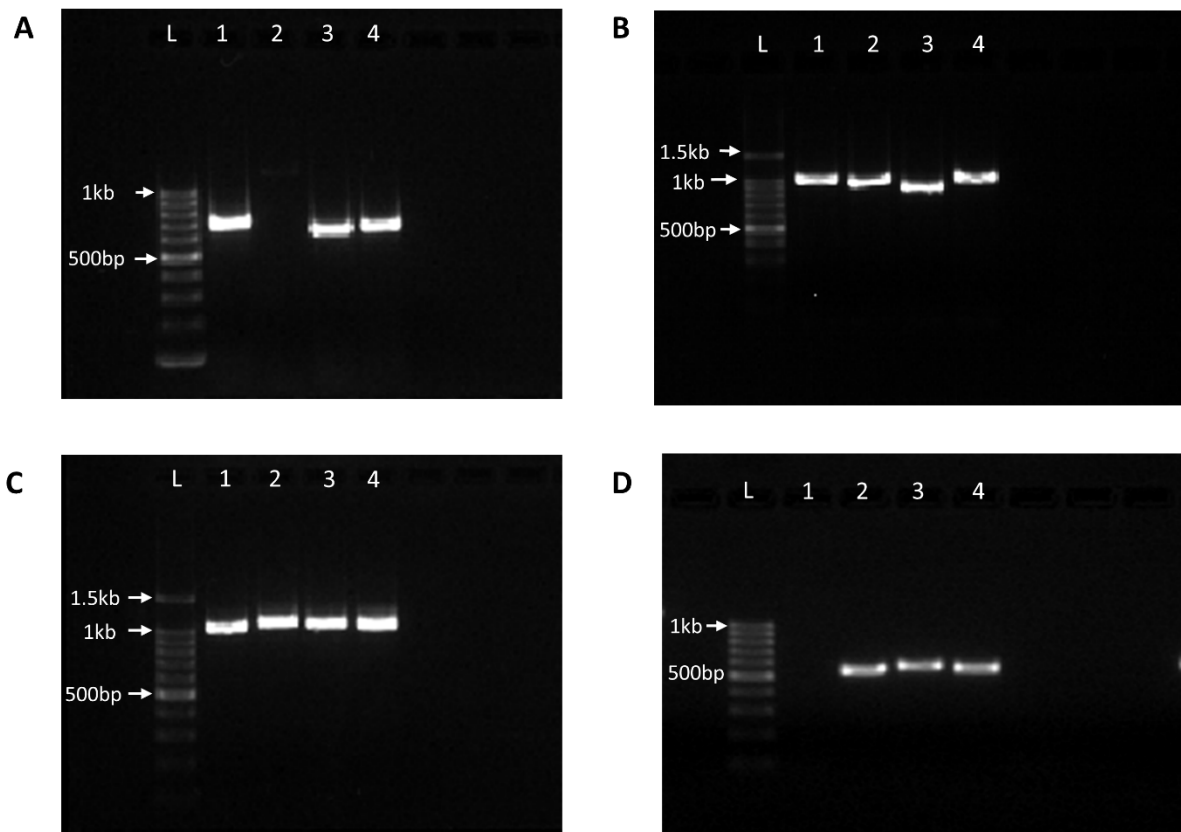
Supplementary figure 3: Species and accession numbers for MAT1-1-3 protein sequences include *C. parasitica* (AAK83344), *Diaporthe ampelina* (KKY31413), *Diaporthe* sp. W (BAE93751), *Diaporthe* sp. G (BAE93754), *P. anserina* (CAA52051), *Chaetomium globosum* (EAQ89965), *F. fujikuroi* (AAC71053), and *N. crassa* (AAC27476). The red arrow in the MAT1-1-3 HMG domain alignment indicates the position of a conserved intron across most ascomycete MAT1-1-3 genes.



Supplementary figure 4: Multiple sequence alignment showing conserved PPF residues of MAT1-1-2 protein sequences of *Chrysosporthe* species and selected ascomycetes. Sequences used in this alignment include *Cryphonectria parasitica* (AAK83345), *Diaporthe* sp. W MAT1-1 (BAE93749), *Diaporthe* sp. W MAT1-2 (BAE93752), *Diaporthe* sp. G MAT1-1 (BAE93755), *Diaporthe* sp. G MAT1-2 (BAE93758), *Valsa mali* (KUI72759), *Fusarium graminearum* (XP_011319816), *Fusarium fujikuroi* (AAC71054), *Podosporea anserina* (CAA52052), *Sordaria macrospora* (CAA71626), and *Neurospora crassa* (AAC37477). Red stars at the bottom of the alignment indicate the conserved PPF residues.



Supplementary figure 5: RIP analysis and GC plots for the *MAT* loci of *C. austroafricana* CMW2113 (*MAT*1-2), *C. austroafricana* CMW6102 (*MAT*1-1), *C. cubensis* CMW10028 and *C. deuterocubensis* CMW8650.



Supplementary figure 6: Agarose gels showing PCR amplification of A) *MAT1-2-1* B) *MAT1-1-1*, C) *MAT1-1-2* and D) *MAT1-1-3* gene fragments amplified in *Chrysosporthe austroafricana* CMW2113 (lane 1), *C. austroafricana* CMW6102 (lane 2), *C. cubensis* (lane 3), and *C. deuterocubensis* (lane 4).

Supplementary Table 1: Predicted transposable elements in the *MAT* loci of *C. deuterocubensis*, *C. cubensis* and *C. austroafricana* using CENSOR.

<i>C. cubensis</i>	Repeat Class	Fragments	Length (bp)
	Transposable Element	14	6488
	DNA transposon	3	989
	Mariner/Tc1	2	830
	Zisupton	1	159
	LTR Retrotransposon	11	5499
	Copia	2	332
	Gypsy	9	5167
	Total	14	6488
<i>C. deuterocubensis</i>	Repeat Class	Fragments	Length (bp)
	Transposable Element	39	16672
	DNA transposon	2	229
	EnSpm/CACTA	1	71
	MuDR	1	158
	LTR Retrotransposon	37	16443
	Copia	2	209
	Gypsy	34	16067
	Total	40	16790
<i>C. austroafricana</i> (CMW2113)	Repeat Class	Fragments	Length (bp)
	Interspersed Repeat	1	139
	LTR Retrotransposon	3	153
	Copia	2	113
	Gypsy	1	40
	Transposable Element	3	153
	Total	4	292

Supplementary Table 2: BLAST comparison of *MAT1-2-1*, *MAT1-1-1*, *MAT1-1-2* and *MAT1-1-3* of *Chrysosporthe* species and other species in the *Diaporthales*.

Protein sequence	Species	Accession no.	Amino acid identity (%)	Protein length
MAT1-1-1	<i>C. austroafricana</i> (CMW6102)	-		409
	<i>C. austroafricana</i> (CMW2113)	-	99.16	357
	<i>C. deuterocubensis</i> (CMW8650)	-	74.39	355
	<i>C. cubensis</i> (CMW10028)	-	74.26	352
	<i>C. parasitica</i>	AAK83346.1	35.70	327
	<i>V. mali</i>	KUI72760.1	29.53	362
	<i>P. aleophilum</i>	XP_007913910.1		
	<i>Melanconium</i> sp.	-	27.13	349
	<i>D. ampelina</i>	KKY31411.1	26.48	288
	<i>Diaporthe</i> sp. p-pt-19	BAE93750.1	26.18	358
	<i>D. longicolla</i>	-	33.01	350
	<i>L. minuta</i>	-	27.51	403
MAT1-2-1	<i>C. austroafricana</i> (CMW2113)	-	-	292
	<i>C. cubensis</i> (CMW10028)	-	97.26	292
	<i>C. deuterocubensis</i> (CMW8650)	-	97.13	292
	<i>C. parasitica</i>	AAK83343.1	58.20	311
	<i>L. minuta</i>	-	38.82	271
	<i>Diaporthe</i> sp. p-pt-16	BAE93753.1	62.77	225
MAT1-1-3	<i>C. austroafricana</i> CMW6102	-	-	201
	<i>C. deuterocubensis</i>	-	98.01	201
	<i>C. cubensis</i>	-	95.24	201
	<i>C. parasitica</i>	AAK83344	48.12	140
	<i>V. mali</i>	KUI72756	35.27	202
	<i>Diaporthe</i> sp. p-pt-16	BAE93751	36.21	246
	<i>Diaporthe</i> sp. p-pt-19	BAE93748	30.59	232
	<i>D. ampelina</i>	KKY31413	32.27	223
	<i>D. longicolla</i>	-	31.25	213
	<i>L. minuta</i>	-	32.50	189
	<i>P. aleophilum</i>	XP_007913914	50.00	278
	<i>Melanconium</i> sp.	-	30.93	240
MAT1-1-2	<i>C. austroafricana</i> (CMW6102)	-	-	372
	<i>C. austroafricana</i> (CMW2113)	-	100.00	372
	<i>C. deuterocubensis</i>	-	95.98	373
	<i>C. cubensis</i>	-	97.58	372
	<i>C. parasitica</i>	AAK83345.1	49.49	406
	<i>V. mali</i>	KUI72759.1	30.21	411

	<i>Diaporthe</i> sp. p-pt-16	BAE93752.1	29.28	398
	<i>Diaporthe</i> sp. p-pt-19	BAE93749.1	29.54	398
	<i>D. ampelina</i>	KKY31412.1	27.75	379
	<i>D. longicolla</i>	-	27.15	399
	<i>L. minuta</i>	-	25.44	423
	<i>P. aleophilum</i>	XP_007913911.1	45.45	385
	<i>Melanconium</i> sp.	-	28.65	396

Supplementary Table 3: List of *Chrysoporthe austroafricana* isolates used to screen for the frequency of *MAT1-2* and *MAT1-1* in natural populations. All isolates were obtained from the Forestry and Agricultural Biotechnology Institute (FABI) Culture Collection, University of Pretoria, South Africa. *MAT1-1-1** Denotes that the primer pair used detects the truncated *MAT1-1-1* observed in the *MAT1-2* locus of *C. austroafricana* 2113 and the full gene in the *MAT1-1* locus of *C. austroafricana* CMW6102. “+” Indicates positive PCR amplification of the named *MAT* gene. Grey shaded and non-shaded boxes represent *MAT1-1* and *MAT1-2* isolates respectively.

Species	Isolate (CMW)	Country	Source host	<i>MAT1-2-1</i>	<i>MAT1-1-1*</i>	<i>MAT1-1-2</i>	<i>MAT1-1-3</i>
<i>Chrysoporthe austroafricana</i>	CMW2113	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW2562	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW2563	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW2853	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6098	South Africa	<i>Eucalyptus</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW6102	South Africa	<i>Eucalyptus</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW7094	South Africa	<i>Eucalyptus</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW9342	South Africa	<i>Eucalyptus</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW11335	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11339	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11341	South Africa	<i>Eucalyptus</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW21595	South Africa	<i>Eucalyptus</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW10080	South Africa	<i>Syzygium</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10088	South Africa	<i>Syzygium</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW22554	South Africa	<i>Syzygium</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9327	South Africa	<i>Tibouchina</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9328	South Africa	<i>Tibouchina</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW9343	South Africa	<i>Tibouchina</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW21593	South Africa	<i>Tibouchina</i> spp.	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6100	South Africa	<i>Eucalyptus</i> spp.		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW6115	South Africa	<i>Eucalyptus</i> spp.		+	+	+

<i>Chrysoporthe austroafricana</i>	CMW10067	South Africa	<i>Syzygium spp.</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW11324	South Africa	<i>Syzygium spp.</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW2611	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW2793	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW2857	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6092	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6099	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11318	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11321	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11330	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11337	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11342	South Africa	<i>Eucalyptus spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9369	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10038	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10039	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10043	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10046	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10058	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10063	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10069	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10083	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10086	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10191	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11323	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW17642	South Africa	<i>Syzygium spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9345	South Africa	<i>Tibouchina spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9349	South Africa	<i>Tibouchina spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9370	South Africa	<i>Tibouchina spp.</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6114	South Africa	<i>Eucalyptus grandis</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW9978	South Africa	<i>Syzygium cordatum</i>	+	+	+	

<i>Chrysoporthe austroafricana</i>	CMW9977	South Africa	<i>Syzygium cordatum</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10194	South Africa	<i>Syzygium cordatum</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6088	South Africa	<i>Eucalyptus grandis</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6103	South Africa	<i>Eucalyptus grandis</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11331	South Africa	<i>Eucalyptus grandis</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW10052	South Africa	<i>Syzygium cordatum</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW10061	South Africa	<i>Syzygium cordatum</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW10055	South Africa	<i>Syzygium cordatum</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW9934	South Africa	<i>Syzygium cordatum</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW11329	South Africa	<i>Eucalyptus grandis</i>		+	+	+
<i>Chrysoporthe austroafricana</i>	CMW9368	South Africa	<i>Syzygium cordatum</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW17641	South Africa	<i>Syzygium paniculatum</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW6087	South Africa	<i>Eucalyptus grandis</i>	+	+	+	
<i>Chrysoporthe austroafricana</i>	CMW11320	South Africa	<i>Syzygium cordatum</i>		+		+

Supplementary table 3: KOG annotation of BUSCO genes used to generate reference tree of species in *Diaporthales* analysed in this study.

BUSCO gene	Hit	E-value	Identity	Class	Class description
BUSCOfEOG7P2Z35	KOG3031	6,00E-85	47	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7J9W0C	KOG0978	2,00E-16	19	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7JT755	KOG2407	9,00E-65	43	MO	Multiple classes
BUSCOfEOG7KM623	KOG1837	1,00E-95	19	S	Function unknown
BUSCOfEOG780RWX	KOG2580	2,00E-77	34	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG761C34	KOG1107	1,00E-111	54	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG7WQ83Z	KOG0820	2,00E-93	56	A	RNA processing and modification
BUSCOfEOG783N5X	KOG2881	3,00E-66	37	S	Function unknown
BUSCOfEOG7XH6ZR	KOG3818	2,00E-62	27	L	Replication, recombination and repair
BUSCOfEOG7J9W0X	KOG2971	3,00E-87	52	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG70GMQZ	KOG2153	3,00E-87	35	JU	Multiple classes
BUSCOfEOG7QG4GH	KOG3445	3,00E-34	40	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG72RN6K	KOG4592	2,00E-53	20	S	Function unknown
BUSCOfEOG7SN8N7	KOG1424	1,00E-140	44	R	General function prediction only
BUSCOfEOG71K6BB	KOG2274	1,00E-114	26	UY	Multiple classes
BUSCOfEOG7RFITM	KOG2560	3,00E-84	38	A	RNA processing and modification
BUSCOfEOG741ZBG	KOG0068	1,00E-122	47	E	Amino acid transport and metabolism
BUSCOfEOG7VQJQC	KOG2047	0	50	A	RNA processing and modification
BUSCOfEOG718KRM	KOG3498	1,00E-19	56	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG7RBZNO	KOG1472	7,00E-22	35	BK	Multiple classes
BUSCOfEOG75XGVN	KOG1250	1,00E-121	40	E	Amino acid transport and metabolism
BUSCOfEOG7WHHNP	KOG2839	2,00E-23	40	T	Signal transduction mechanisms
BUSCOfEOG70W3NS	KOG2968	0	41	R	General function prediction only
BUSCOfEOG7QRR35	KOG2011	9,00E-63	27	D	Cell cycle control, cell division, chromosome partitioning
BUSCOfEOG757D5M	KOG0920	0	38	A	RNA processing and modification
BUSCOfEOG7WDNBS	KOG0370	1,00E-146	56	R	General function prediction only
BUSCOfEOG7KQ29H	KOG0263	1,00E-121	29	K	Transcription

BUSCOfEOG7MSMX7	KOG1879	0	36	G	Carbohydrate transport and metabolism
BUSCOfEOG7C8GV0	KOG0877	2,00E-83	69	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7GJ6QS	KOG2309	2,00E-93	70	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7966R8	KOG0555	0	52	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG76MKJK	KOG2762	1,00E-101	41	G	Carbohydrate transport and metabolism
BUSCOfEOG7WX0KP	KOG3045	6,00E-48	32	A	RNA processing and modification
BUSCOfEOG7DFXNZ	KOG2423	1,00E-172	49	R	General function prediction only
BUSCOfEOG722JJW	KOG2911	9,00E-30	23	S	Function unknown
BUSCOfEOG7RJQ36	KOG0816	4,00E-55	39	A	RNA processing and modification
BUSCOfEOG75TMNV	KOG3928	3,00E-23	21	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7WHHK2	KOG0906	0	42	TU	Multiple classes
BUSCOfEOG73545F	KOG1707	1,00E-177	46	V	Defense mechanisms
BUSCOfEOG7TN012	KOG0399	0	64	E	Amino acid transport and metabolism
BUSCOfEOG7M98RW	KOG4438	3,00E-26	17	D	Cell cycle control, cell division, chromosome partitioning
BUSCOfEOG7M0P2N	KOG3052	1,00E-106	55	C	Energy production and conversion
BUSCOfEOG75XGVQ	KOG0442	0	40	L	Replication, recombination and repair
BUSCOfEOG7WMCVV	KOG3800	6,00E-40	30	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7B05P0	KOG3655	4,00E-19	25	Z	Cytoskeleton
BUSCOfEOG7B05P0	KOG4226	8,00E-16	28	T	Signal transduction mechanisms
BUSCOfEOG751NRJ	KOG1861	2,00E-82	36	K	Transcription
BUSCOfEOG7WDN9V	KOG1248	0	28	S	Function unknown
BUSCOfEOG7C5MHX	KOG0274	1,00E-50	26	R	General function prediction only
BUSCOfEOG7327X6	KOG2004	0	49	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7327X6	KOG3109	6,00E-28	28	R	General function prediction only
BUSCOfEOG7TJ3T6	KOG0678	1,00E-173	62	Z	Cytoskeleton
BUSCOfEOG790G80	KOG1798	0	47	L	Replication, recombination and repair
BUSCOfEOG7ZGXCZ	KOG0633	1,00E-105	42	E	Amino acid transport and metabolism
BUSCOfEOG78D7VT	KOG1253	1,00E-107	35	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7Z0K75	KOG2902	3,00E-98	43	F	Nucleotide transport and metabolism
BUSCOfEOG75XGWD	KOG2872	1,00E-122	54	H	Coenzyme transport and metabolism

BUSCOfEOG7WMCW5	KOG2703	1,00E-133	46	R	General function prediction only
BUSCOfEOG73V6VV	KOG0927	8,00E-35	20	R	General function prediction only
BUSCOfEOG7VHT6T	KOG1498	1,00E-121	46	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7DVVK9	KOG0560	0	51	P	Inorganic ion transport and metabolism
BUSCOfEOG7JX3GH	KOG2629	4,00E-27	25	MOU	Multiple classes
BUSCOfEOG706113	KOG1416	1,00E-23	33	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7QG4CT	KOG2314	0	41	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG74FF9N	KOG1087	3,00E-23	19	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG7W9S43	KOG2291	1,00E-88	33	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG79GTJ1	KOG0711	1,00E-108	56	H	Coenzyme transport and metabolism
BUSCOfEOG776T0T	KOG2160	1,00E-26	32	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7X6M8Z	KOG2866	1,00E-15	26	S	Function unknown
BUSCOfEOG747PT4	KOG3855	1,00E-113	40	HC	Multiple classes
BUSCOfEOG7W6WVP	KOG2834	1,00E-133	44	YU	Multiple classes
BUSCOfEOG73BVMX	KOG4121	4,00E-38	18	YU	Multiple classes
BUSCOfEOG7V4B6X	KOG2208	2,00E-11	22	I	Lipid transport and metabolism
BUSCOfEOG70PC6X	KOG0788	4,00E-55	40	T	Signal transduction mechanisms
BUSCOfEOG7QNVVW	KOG2529	1,00E-129	64	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7MPRR4	KOG0162	1,00E-09	25	Z	Cytoskeleton
BUSCOfEOG76QFST	KOG1468	1,00E-108	49	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7X0VRZ	KOG2154	8,00E-84	31	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG789CMF	KOG1872	1,00E-102	32	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7XSTQ5	KOG1523	1,00E-104	47	Z	Cytoskeleton
BUSCOfEOG7CG77P	KOG2346	1,00E-05	20	S	Function unknown
BUSCOfEOG7HMS8K	KOG0681	1,00E-137	37	Z	Cytoskeleton
BUSCOfEOG7FBRS5	KOG3758	5,00E-86	29	S	Function unknown
BUSCOfEOG7FJH7Z	KOG1241	0	43	YU	Multiple classes
BUSCOfEOG7ZPNX4	KOG3329	5,00E-13	28	T	Signal transduction mechanisms
BUSCOfEOG7NPG2M	KOG0169	1,00E-124	29	T	Signal transduction mechanisms
BUSCOfEOG7NPG2M	KOG0566	4,00E-06	23	U	Intracellular trafficking, secretion, and vesicular transport

BUSCOfEOG7P2Z2N	KOG2929	2,00E-49	33	K	Transcription
BUSCOfEOG799302	KOG0188	0	49	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7PP5JH	KOG4776	2,00E-07	43	S	Function unknown
BUSCOfEOG74J9H5	KOG0368	0	54	I	Lipid transport and metabolism
BUSCOfEOG7W9S4R	KOG2602	5,00E-68	31	R	General function prediction only
BUSCOfEOG7CCC0Z	KOG0595	4,00E-83	35	OUT	Multiple classes
BUSCOfEOG7DRJDW	KOG2330	4,00E-95	41	A	RNA processing and modification
BUSCOfEOG72C57M	KOG0262	0	41	K	Transcription
BUSCOfEOG7S7SR3	KOG3036	1,00E-111	67	R	General function prediction only
BUSCOfEOG7FJH7X	KOG2099	0	52	G	Carbohydrate transport and metabolism
BUSCOfEOG7FJH7X	KOG0082	2,00E-35	49	DT	Multiple classes
BUSCOfEOG7NPG2Q	KOG2328	6,00E-87	26	BD	Multiple classes
BUSCOfEOG793BK3	KOG3151	1,00E-47	32	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7ZWDB2	KOG2380	1,00E-121	35	E	Amino acid transport and metabolism
BUSCOfEOG7F2528	KOG1969	9,00E-71	21	DL	Multiple classes
BUSCOfEOG7HHX1P	KOG1360	0	47	H	Coenzyme transport and metabolism
BUSCOfEOG7K6Q51	KOG0089	1,00E-61	31	H	Coenzyme transport and metabolism
BUSCOfEOG7N37PR	KOG1302	1,00E-129	35	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG7008K9	KOG1462	3,00E-39	24	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7PZS7V	KOG3980	8,00E-61	34	A	RNA processing and modification
BUSCOfEOG72NS06	KOG2613	1,00E-172	49	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG7SN8MQ	KOG1822	1,00E-154	21	S	Function unknown
BUSCOfEOG70ZZXC	KOG2656	1,00E-47	28	BK	Multiple classes
BUSCOfEOG7R5729	KOG2732	3,00E-97	36	L	Replication, recombination and repair
BUSCOfEOG7PCJSB	KOG0008	2,00E-92	26	K	Transcription
BUSCOfEOG7BGHVG	KOG1968	1,00E-115	28	L	Replication, recombination and repair
BUSCOfEOG712V4J	KOG1809	1,00E-138	23	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG712V4J	KOG1796	5,00E-09	17	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG712V4J	KOG2993	9,00E-05	22	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG7RBZKK	KOG3062	6,00E-53	35	R	General function prediction only

BUSCOfEOG70PC63	KOG0212	1,00E-100	47	S	Function unknown
BUSCOfEOG7QNVVM	KOG0462	0	49	J	Translation, ribosomal structure and biogenesis
BUSCOfEOG706108	KOG1070	0	33	A	RNA processing and modification
BUSCOfEOG7Q8CX4	KOG4224	0	61	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfEOG7NPG2S	KOG1626	1,00E-103	65	C	Energy production and conversion
BUSCOfEOG7NPG2S	KOG1030	1,00E-13	26	R	General function prediction only
BUSCOfEOG7NPG2S	KOG1011	1,00E-04	26	TU	Multiple classes
BUSCOfEOG78SQSW	KOG2779	1,00E-137	50	I	Lipid transport and metabolism
BUSCOfEOG7Z95XD	KOG3964	1,00E-110	41	I	Lipid transport and metabolism
BUSCOfEOG79W9F2	KOG0405	1,00E-179	57	Q	Secondary metabolites biosynthesis, transport and catabolism
BUSCOfEOG7PCJR4	KOG0889	0	36	TBLD	Multiple classes
BUSCOfEOG7PCJR4	KOG1175	1,00E-90	25	I	Lipid transport and metabolism
BUSCOfEOG7HXD0B	KOG0350	1,00E-44	25	A	RNA processing and modification
BUSCOfEOG7HXD0B	KOG0331	1,00E-21	36	A	RNA processing and modification
BUSCOfEOG7HXD0B	KOG3671	3,00E-05	31	TZ	Multiple classes
BUSCOfEOG74FFB1	KOG4174	4,00E-37	28	S	Function unknown
BUSCOfEOG7W9S45	KOG1463	1,00E-125	51	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG780RVR	KOG2250	2,00E-88	26	E	Amino acid transport and metabolism
BUSCOfEOG7XDBSV	KOG0174	2,00E-83	56	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG78H45S	KOG3174	7,00E-88	52	Z	Cytoskeleton
BUSCOfEOG7Z95X9	KOG0643	1,00E-126	57	JT	Multiple classes
BUSCOfEOG7380D8	KOG0970	0	39	L	Replication, recombination and repair
BUSCOfEOG7TQVCM	KOG1088	5,00E-28	38	S	Function unknown
BUSCOfEOG73V6WQ	KOG3034	3,00E-33	26	R	General function prediction only
BUSCOfEOG7VQJNP	KOG3823	1,00E-112	37	S	Function unknown
BUSCOfEOG7B5X74	KOG3094	2,00E-61	38	S	Function unknown
BUSCOfEOG7MKWG6	KOG3574	1,00E-129	40	P	Inorganic ion transport and metabolism
BUSCOfEOG78SQWR	KOG0050	1,00E-104	34	AD	Multiple classes
BUSCOfEOG7ZD23R	KOG0446	1,00E-68	26	UR	Multiple classes
BUSCOfEOG7FJHC7	KOG1004	5,00E-43	37	J	Translation, ribosomal structure and biogenesis

BUSCOfeOG74N5S1	KOG2217	9,00E-26	26	A	RNA processing and modification
BUSCOfeOG7WDN9S	KOG0392	0	39	K	Transcription
BUSCOfeOG7J70SV	KOG1331	1,00E-47	32	R	General function prediction only
BUSCOfeOG7FFN2S	KOG2318	2,00E-69	36	S	Function unknown
BUSCOfeOG7FR7QW	KOG0301	1,00E-122	33	I	Lipid transport and metabolism
BUSCOfeOG7673K5	KOG2034	0	34	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfeOG7WT4D5	KOG1653	1,00E-05	23	L	Replication, recombination and repair
BUSCOfeOG7Q8CWW	KOG1956	0	49	L	Replication, recombination and repair
BUSCOfeOG77M90N	KOG3998	9,00E-66	44	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfeOG7X9GGC	KOG2062	0	48	O	Posttranslational modification, protein turnover, chaperones
BUSCOfeOG76TB2T	KOG1284	4,00E-39	41	H	Coenzyme transport and metabolism
BUSCOfeOG7X3R27	KOG1027	1,00E-114	42	T	Signal transduction mechanisms
BUSCOfeOG7PVX16	KOG4131	2,00E-50	41	R	General function prediction only
BUSCOfeOG7GBG5H	KOG0519	4,00E-17	24	T	Signal transduction mechanisms
BUSCOfeOG7GBG5H	KOG0566	4,00E-05	24	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfeOG7HMSC2	KOG3188	3,00E-62	43	S	Function unknown
BUSCOfeOG72NS19	KOG3996	6,00E-49	35	CO	Multiple classes
BUSCOfeOG7SN8MR	KOG1932	1,00E-140	24	K	Transcription
BUSCOfeOG7SN8MR	KOG0162	4,00E-04	18	Z	Cytoskeleton
BUSCOfeOG72890P	KOG1907	0	41	F	Nucleotide transport and metabolism
BUSCOfeOG7S2265	KOG2066	7,00E-63	24	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfeOG7S2265	KOG0943	6,00E-04	45	O	Posttranslational modification, protein turnover, chaperones
BUSCOfeOG7PZS60	KOG2604	9,00E-35	24	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfeOG7DJSVT	KOG1156	1,00E-175	41	B	Chromatin structure and dynamics
BUSCOfeOG7CNZQ6	KOG2081	3,00E-80	29	U	Intracellular trafficking, secretion, and vesicular transport
BUSCOfeOG7JX3DQ	KOG2055	2,00E-85	30	R	General function prediction only
BUSCOfeOG74FF8R	KOG1122	1,00E-138	54	A	RNA processing and modification
BUSCOfeOG7W9S33	KOG1397	3,00E-59	28	P	Inorganic ion transport and metabolism
BUSCOfeOG7W9S33	KOG0670	1,00E-06	17	A	RNA processing and modification
BUSCOfeOG7MSN0V	KOG1581	2,00E-71	35	G	Carbohydrate transport and metabolism

BUSCOfEOG7KQ28X	KOG0692	1,00E-177	42	E	Amino acid transport and metabolism
BUSCOfEOG7BW0V6	KOG2592	1,00E-102	38	S	Function unknown
BUSCOfEOG7KH9T3	KOG1964	5,00E-31	20	YU	Multiple classes
BUSCOfEOG7DJSWM	KOG2799	1,00E-158	60	C	Energy production and conversion
BUSCOfEOG7J1899	KOG2823	6,00E-30	27	R	General function prediction only
BUSCOfEOG7CRTZV	KOG2229	1,00E-137	38	DZ	Multiple classes
BUSCOfEOG74XSH4	KOG2769	2,00E-79	32	A	RNA processing and modification
BUSCOfEOG7WDN9T	KOG3657	0	43	L	Replication, recombination and repair
BUSCOfEOG78WM14	KOG1992	0	37	YU	Multiple classes
BUSCOfEOG7ZGXCR	KOG1111	1,00E-161	53	MOI	Multiple classes
BUSCOfEOG7MWH55	KOG0732	1,00E-158	33	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7MWH55	KOG2393	2,00E-05	21	K	Transcription
BUSCOfEOG7FBRWF	KOG3093	2,00E-38	35	H	Coenzyme transport and metabolism
BUSCOfEOG7GXPM5	KOG0495	0	47	A	RNA processing and modification
BUSCOfEOG7G7M0Q	KOG3763	2,00E-44	25	A	RNA processing and modification
BUSCOfEOG7G7KXG	KOG1066	0	46	GMO	Multiple classes
BUSCOfEOG7DC2CX	KOG0104	1,00E-122	30	O	Posttranslational modification, protein turnover, chaperones
BUSCOfEOG7HXD2Z	KOG3000	8,00E-62	40	DZ	Multiple classes
