

Antiplasmodial and Cytotoxic Cytochalasins from an Endophytic Fungus, *Nemania* sp. UM10M, Isolated from a Diseased *Torreya taxifolia* Leaf

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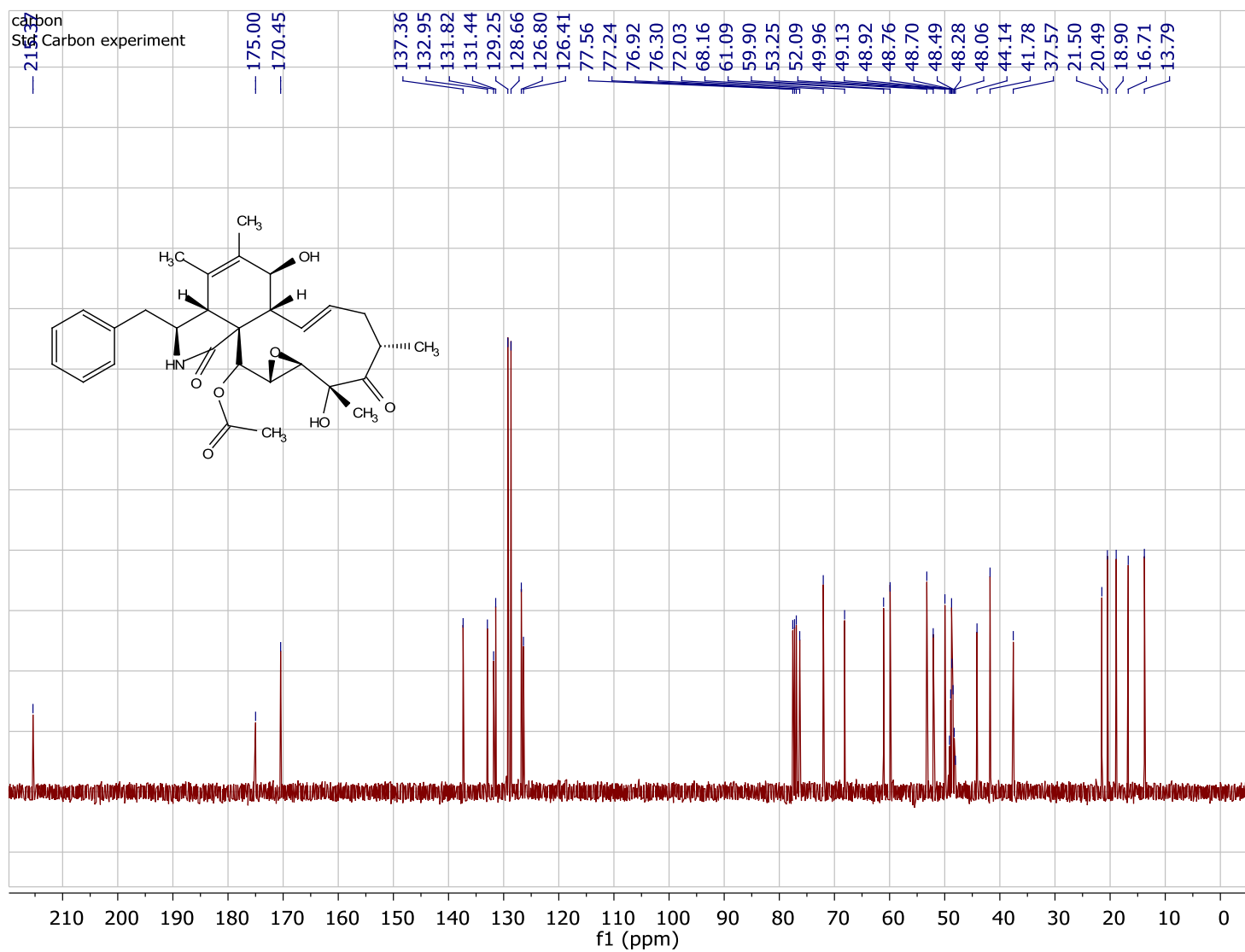


Figure S2: ^{13}C NMR Spectrum of compound 1

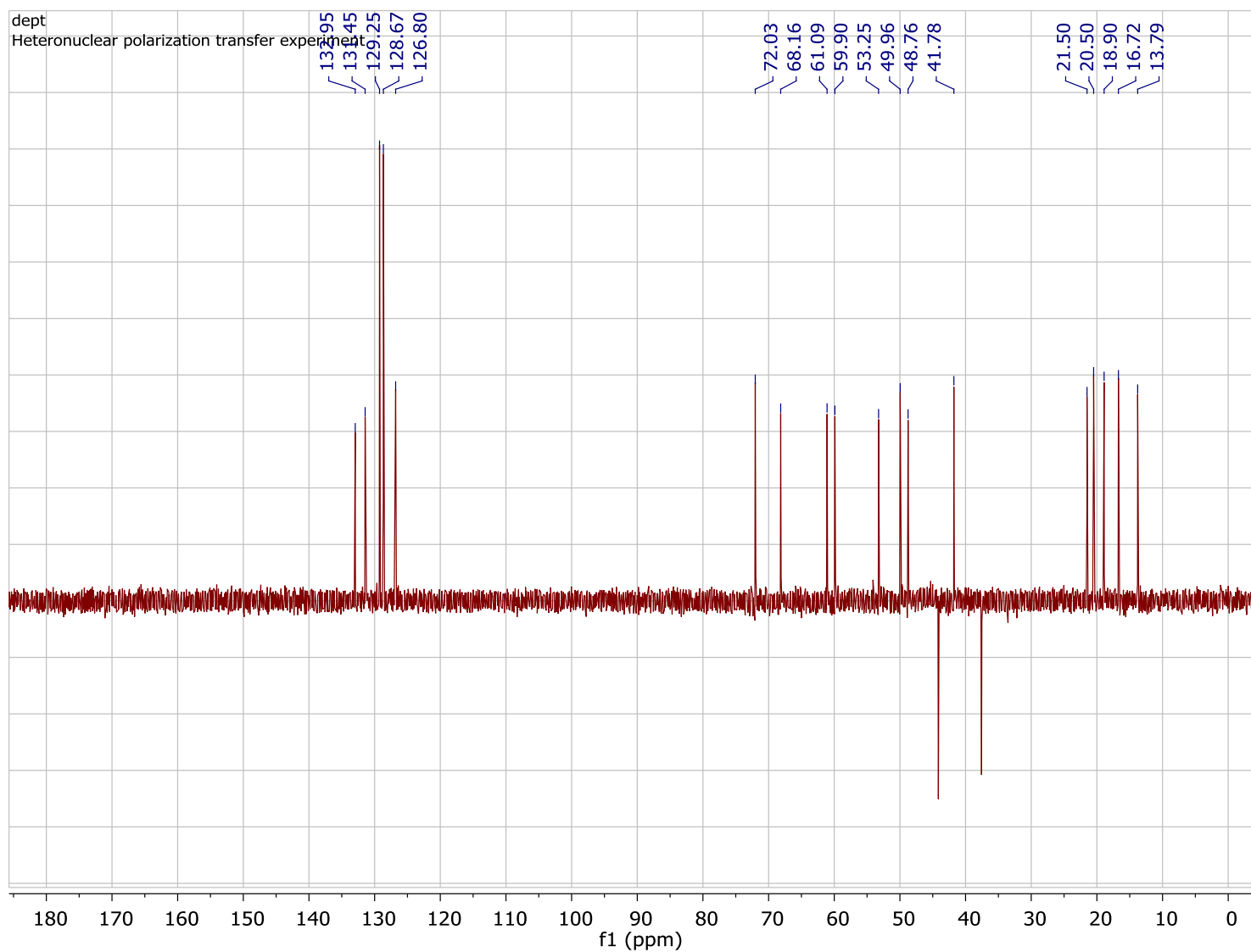


Figure S3: DEPT Spectrum of compound 1

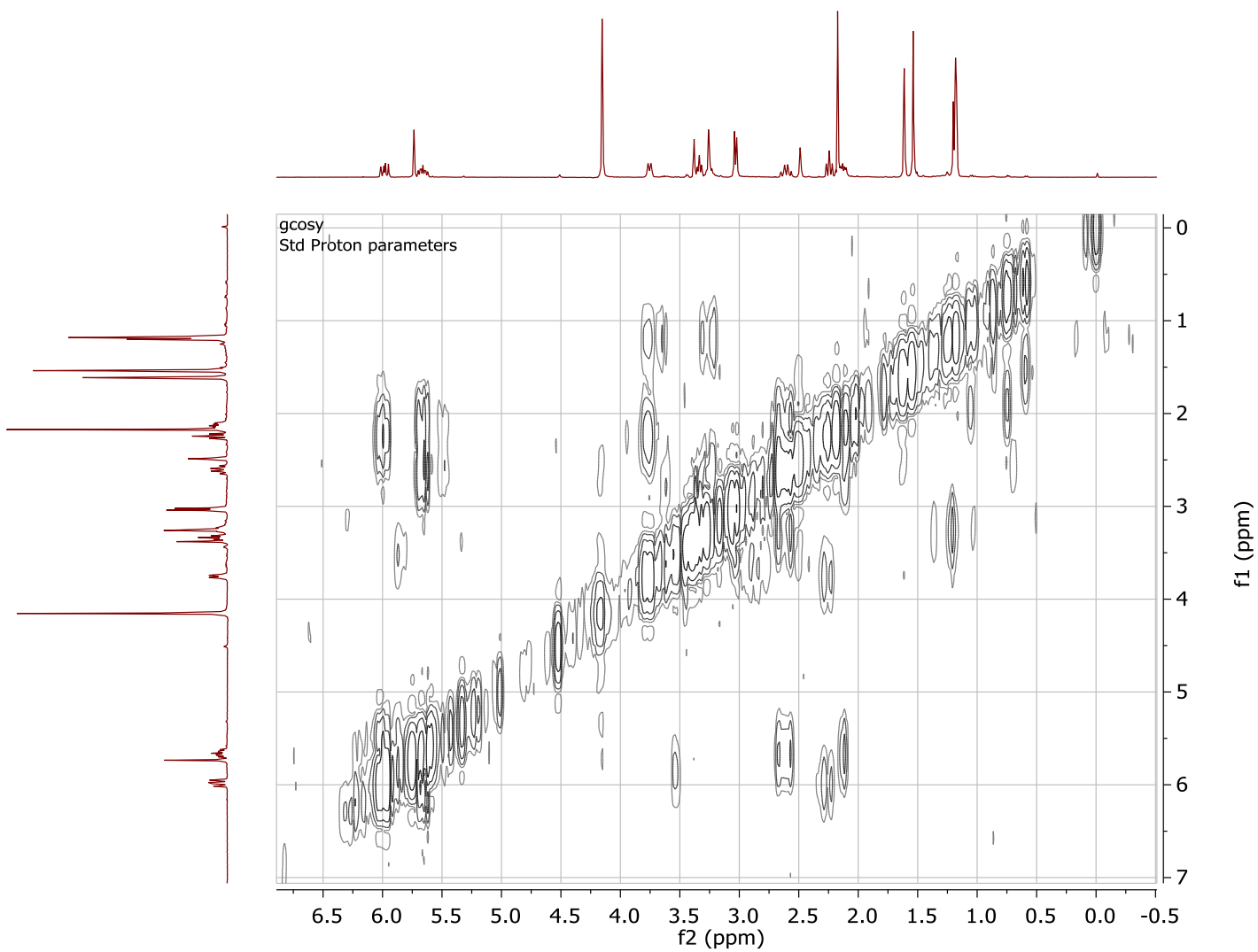


Figure S4: COSY Spectrum of compound **1**

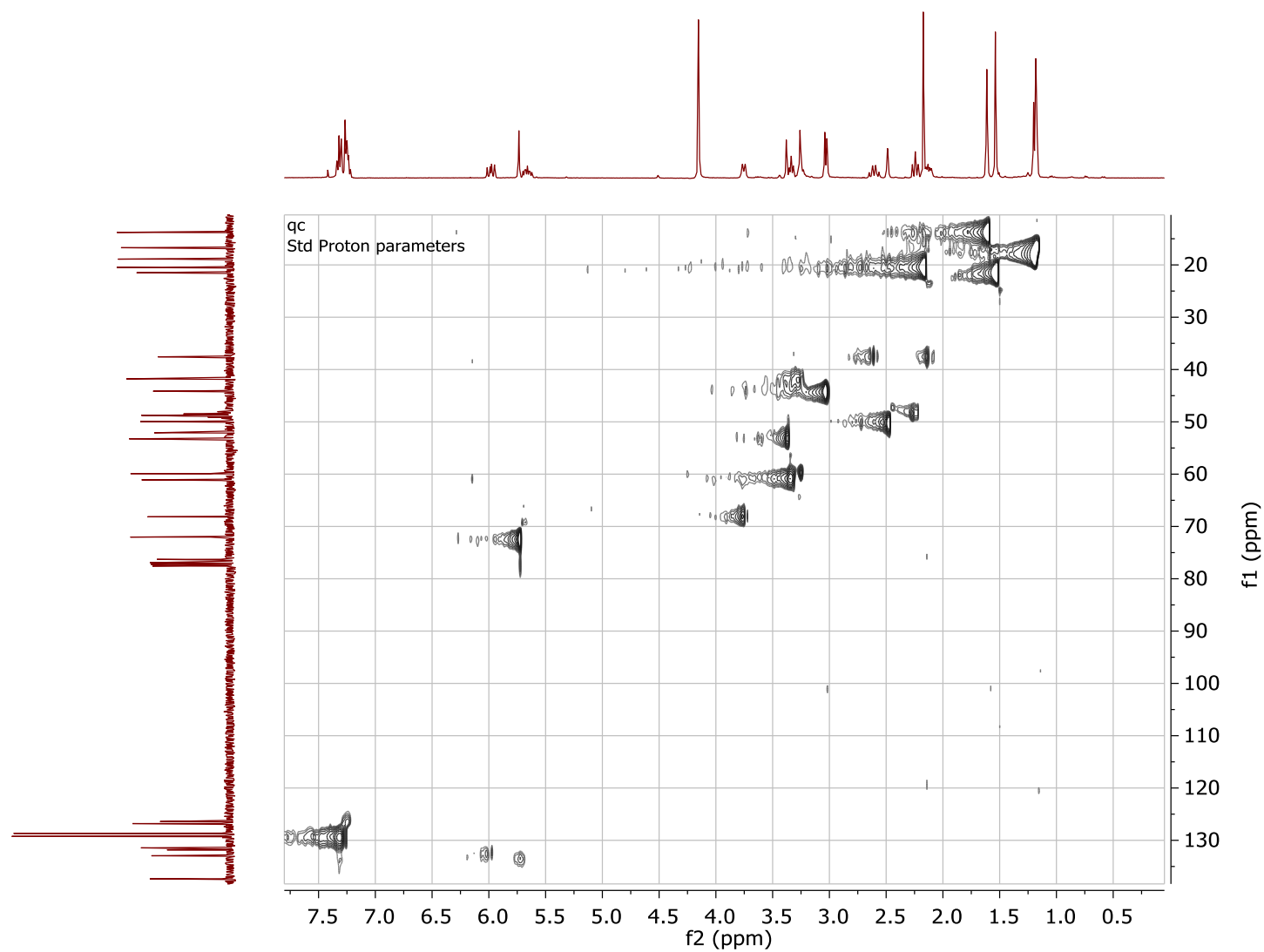


Figure S5: HMQC Spectrum of compound 1

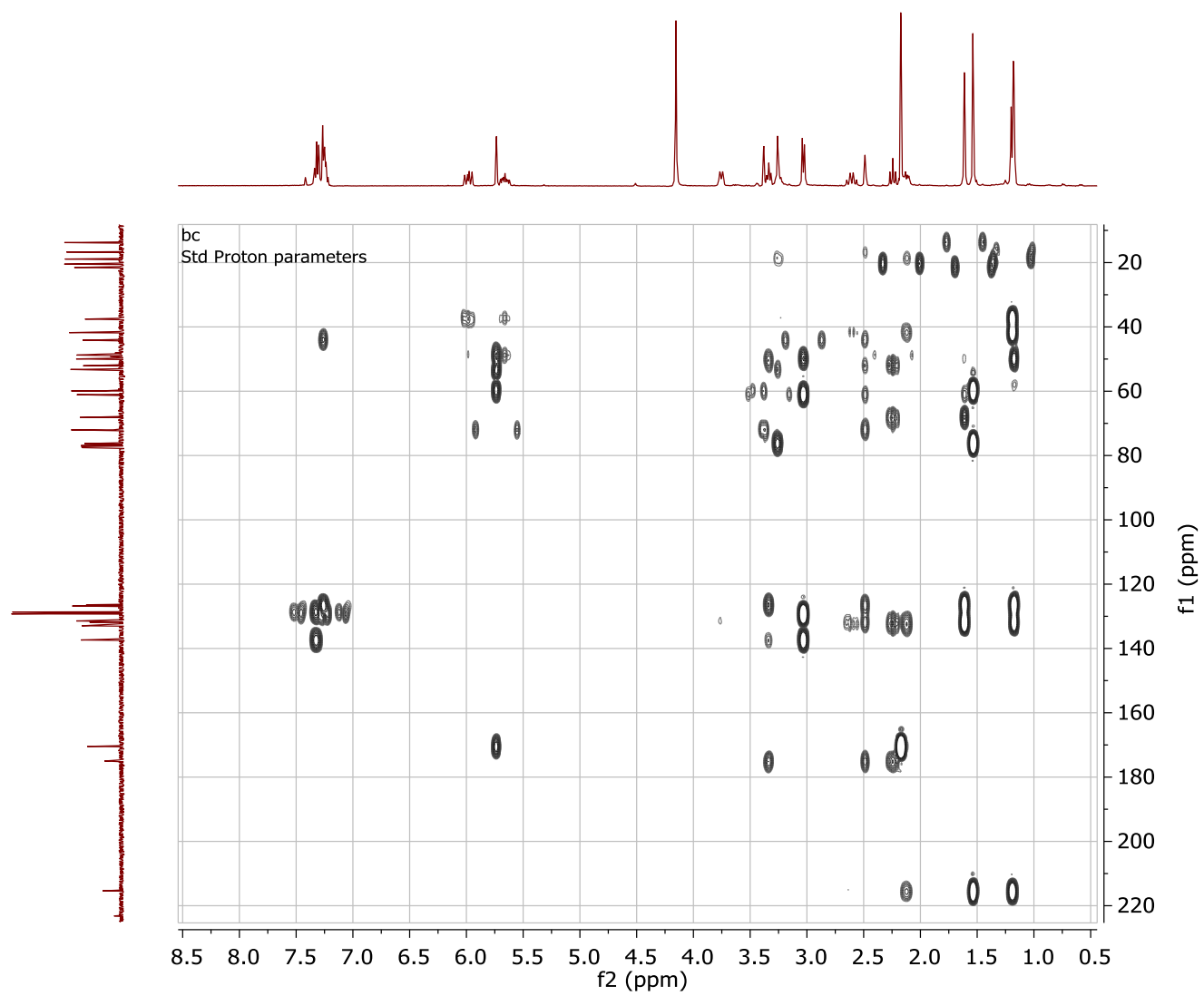


Figure S6: HMBC Spectrum of compound 1

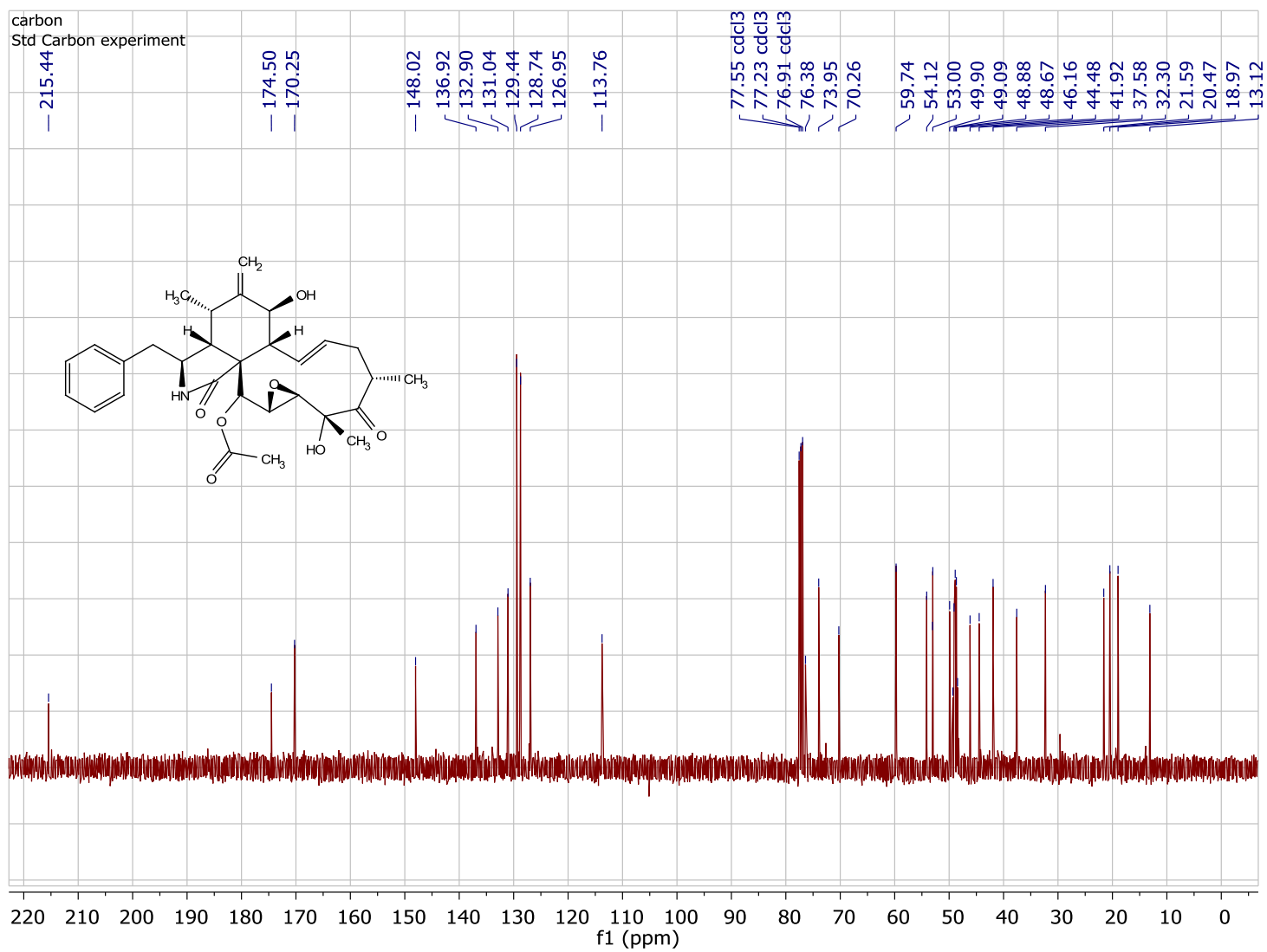


Figure S8: ^{13}C NMR Spectrum of compound 2

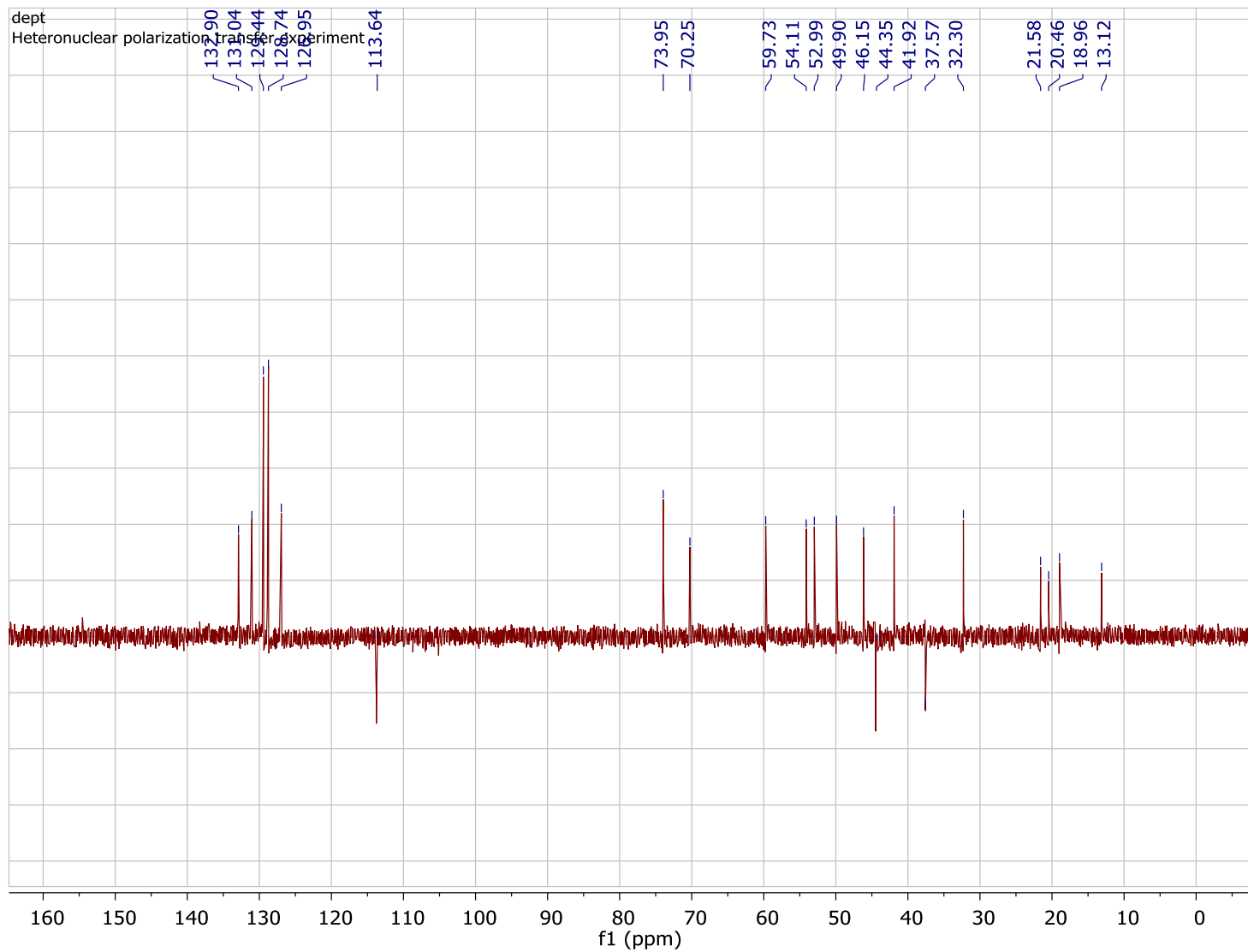


Figure S9: DEPT Spectrum of compound 2

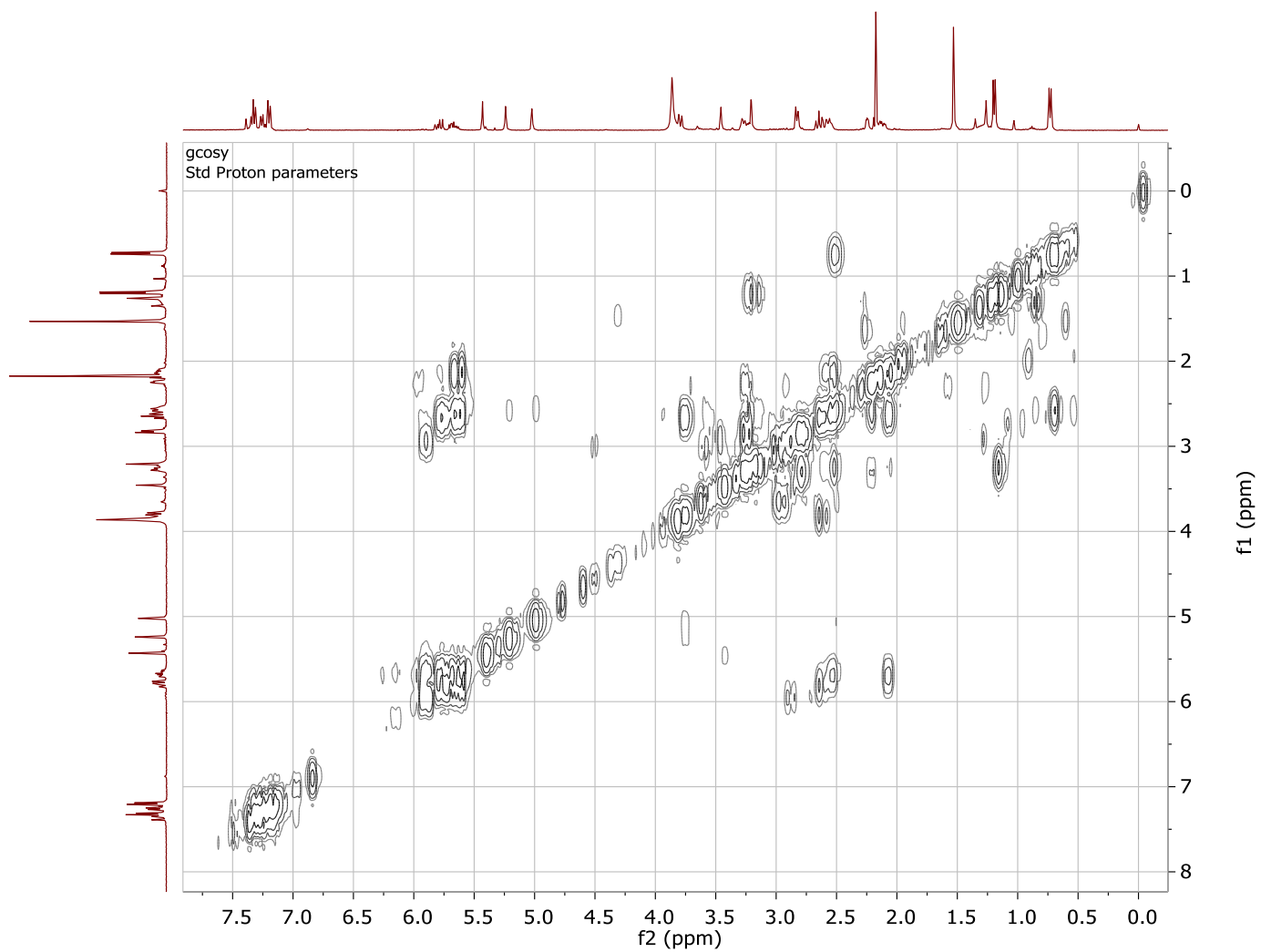


Figure S10: COSY Spectrum of compound 2

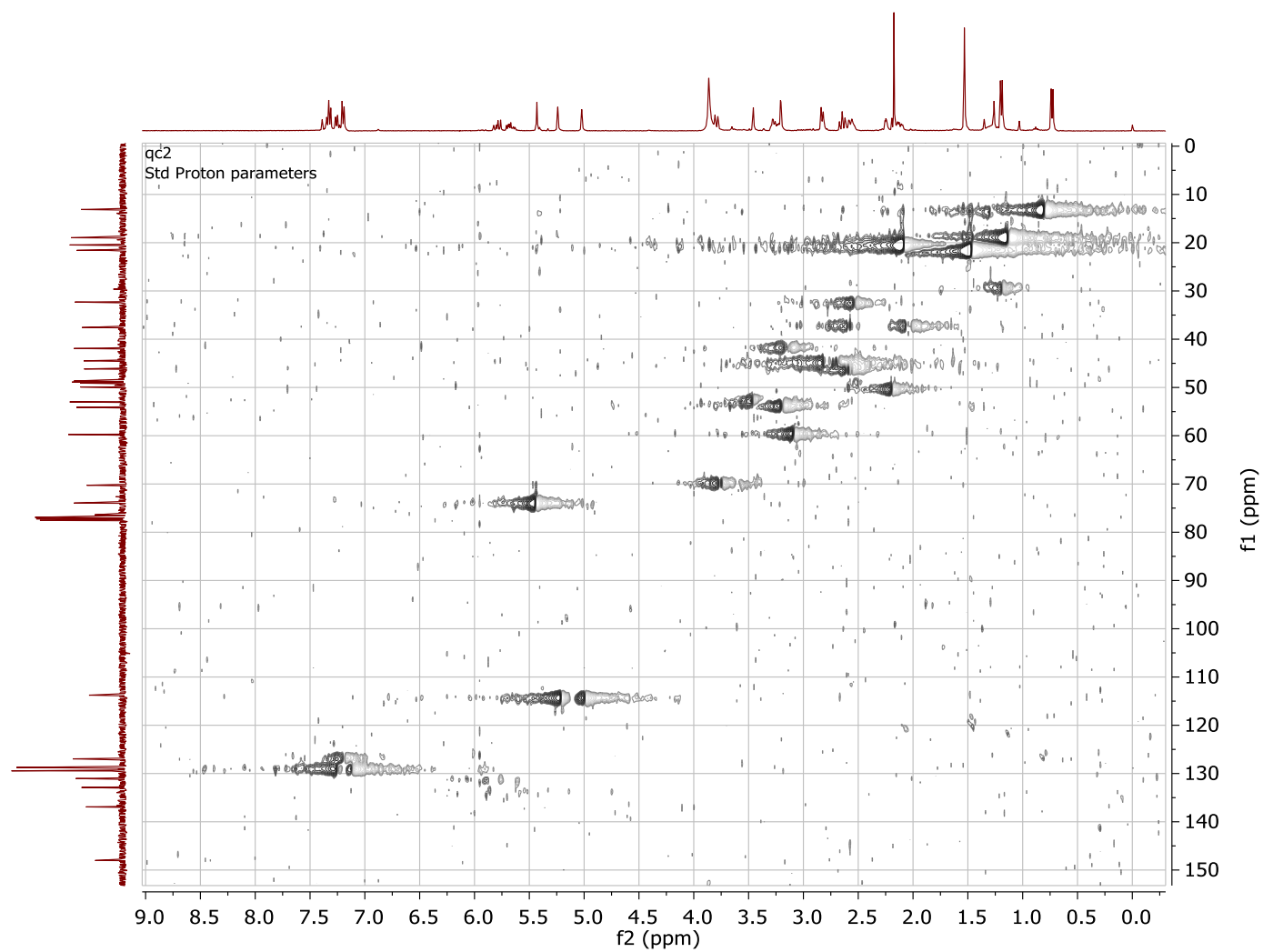


Figure S11: HMQC Spectrum of compound 2

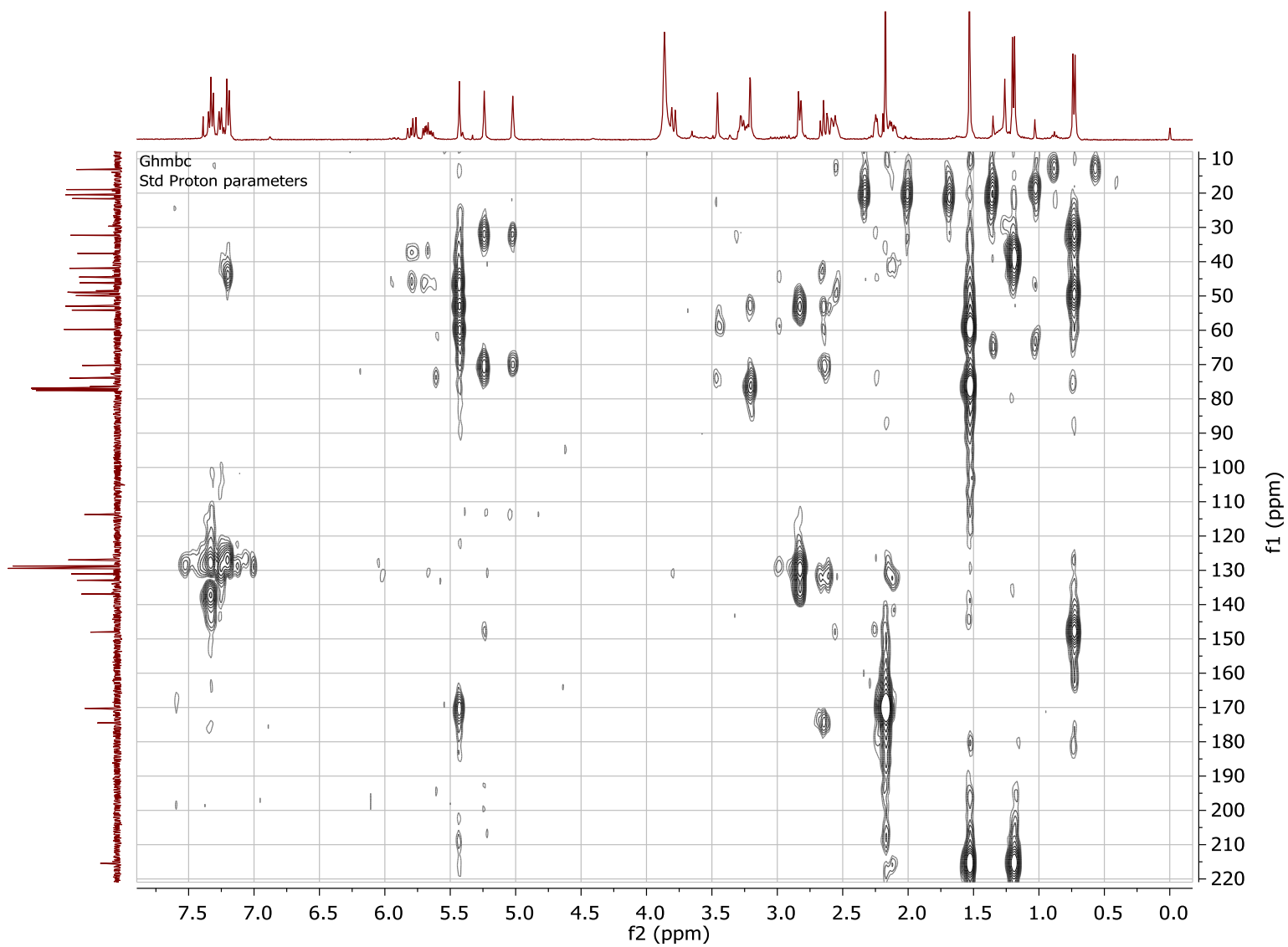


Figure S12: HMBC Spectrum of compound 2

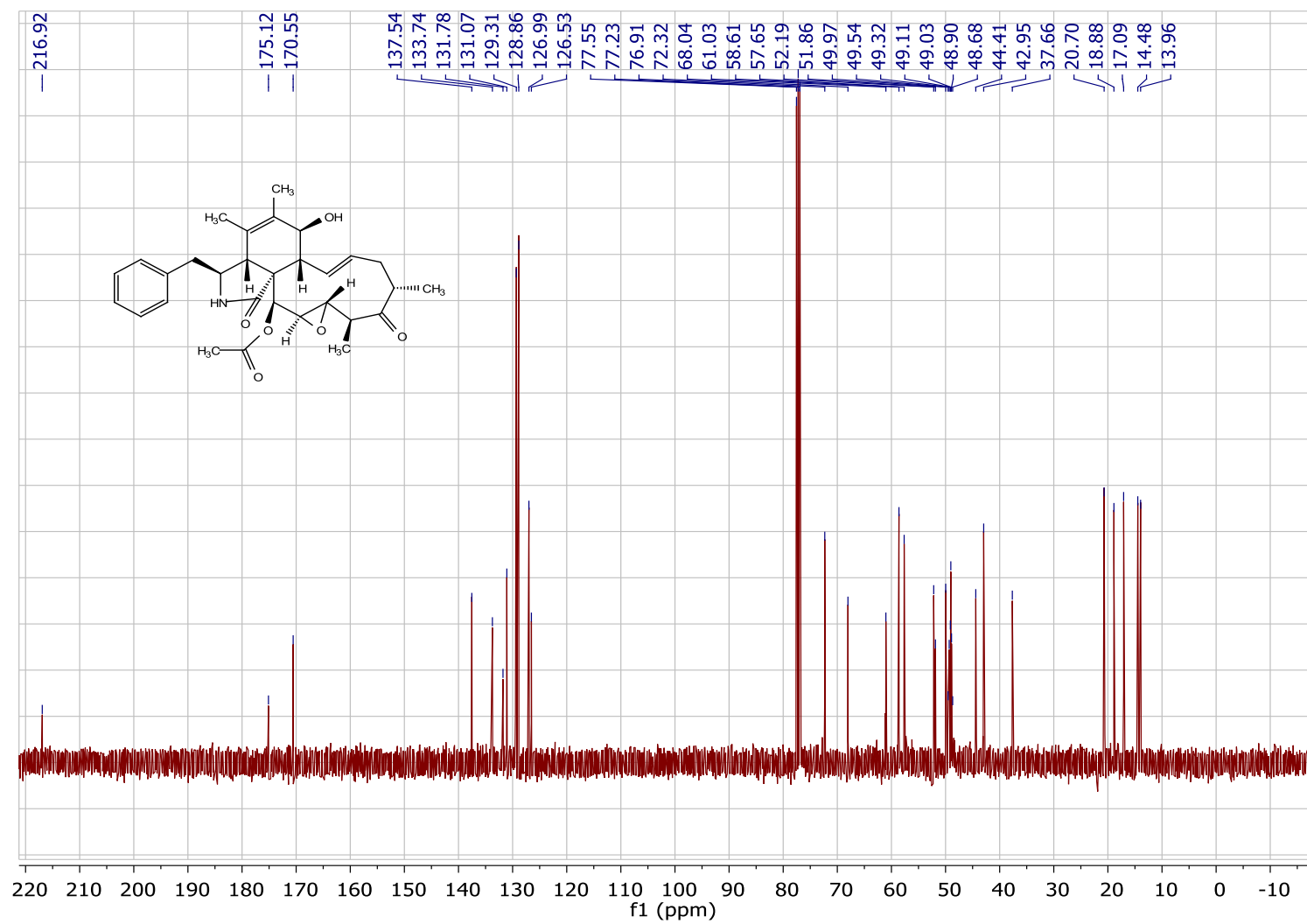


Figure S14: ^{13}C NMR Spectrum of compound 3

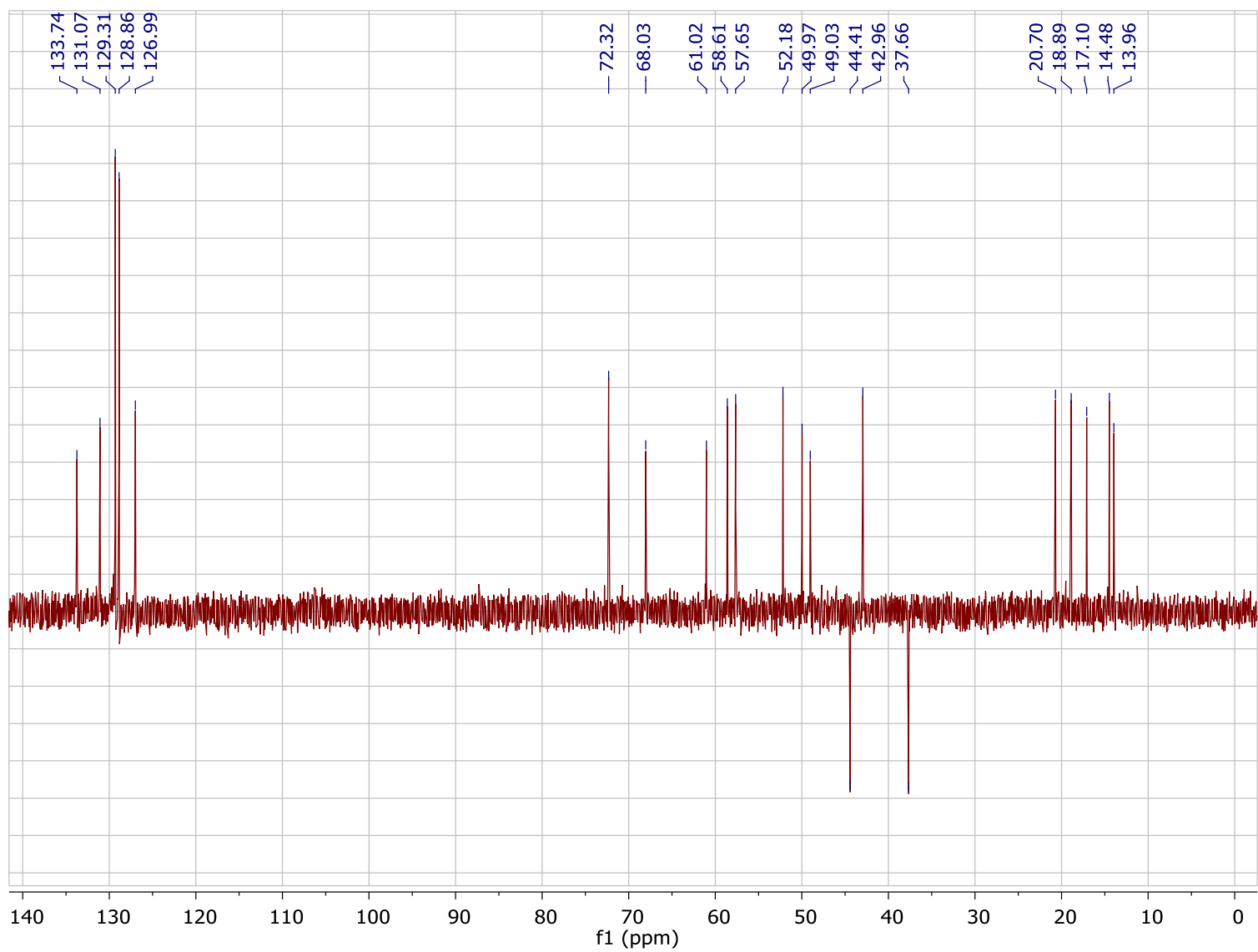


Figure S15: DEPT Spectrum of compound 3

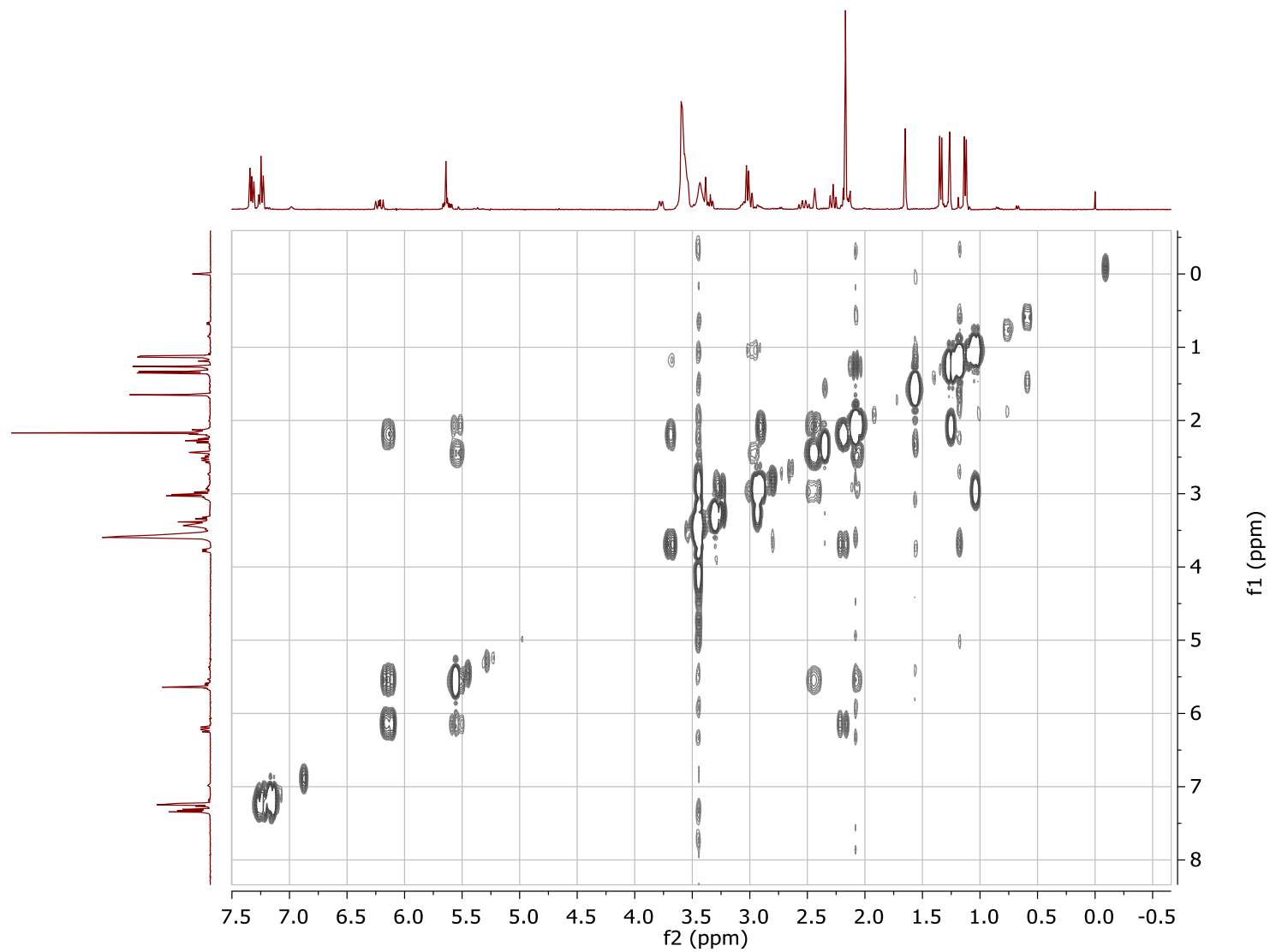


Figure S16: COSY Spectrum of compound 3

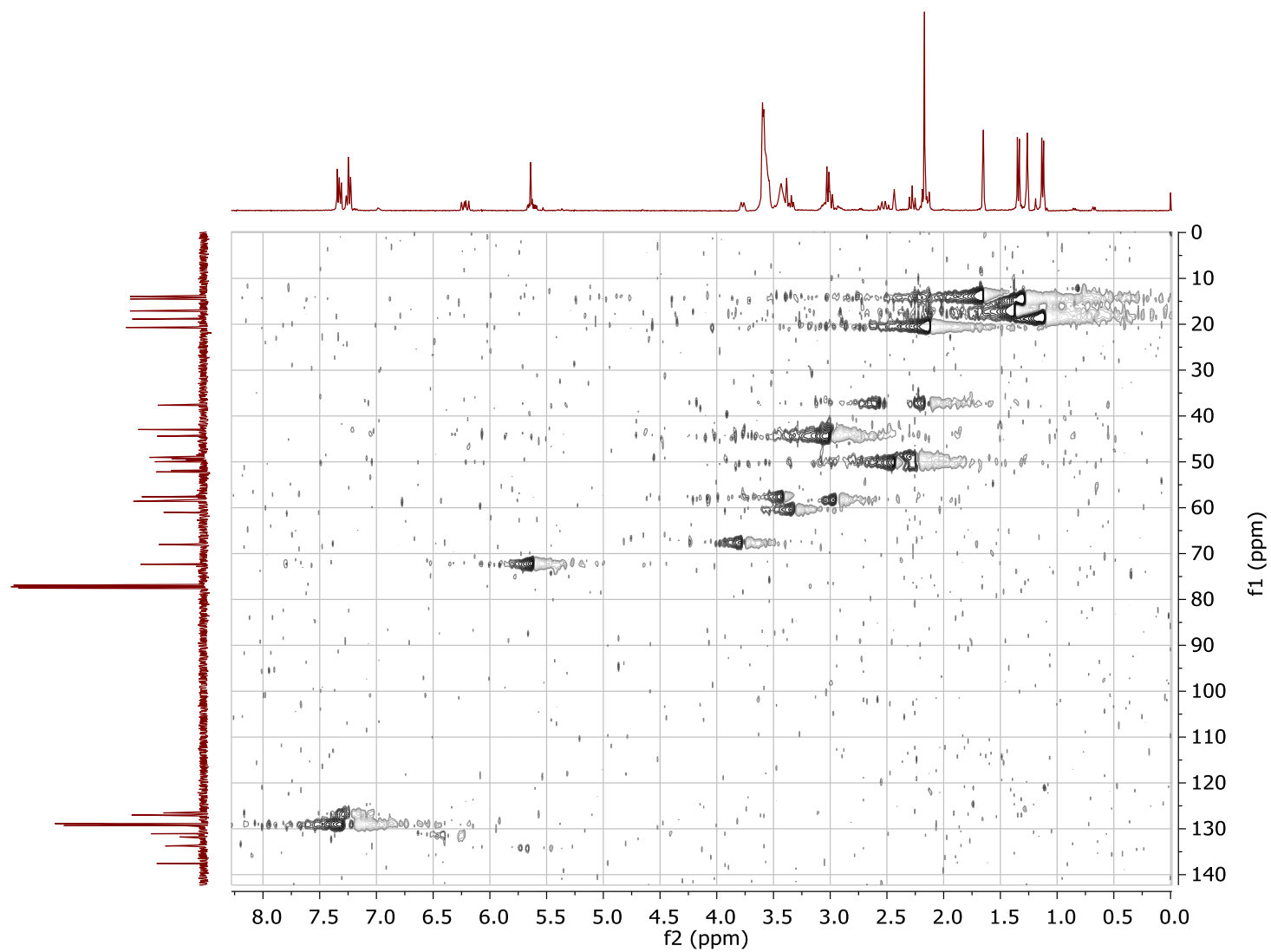


Figure S17: HMQC Spectrum of compound 3

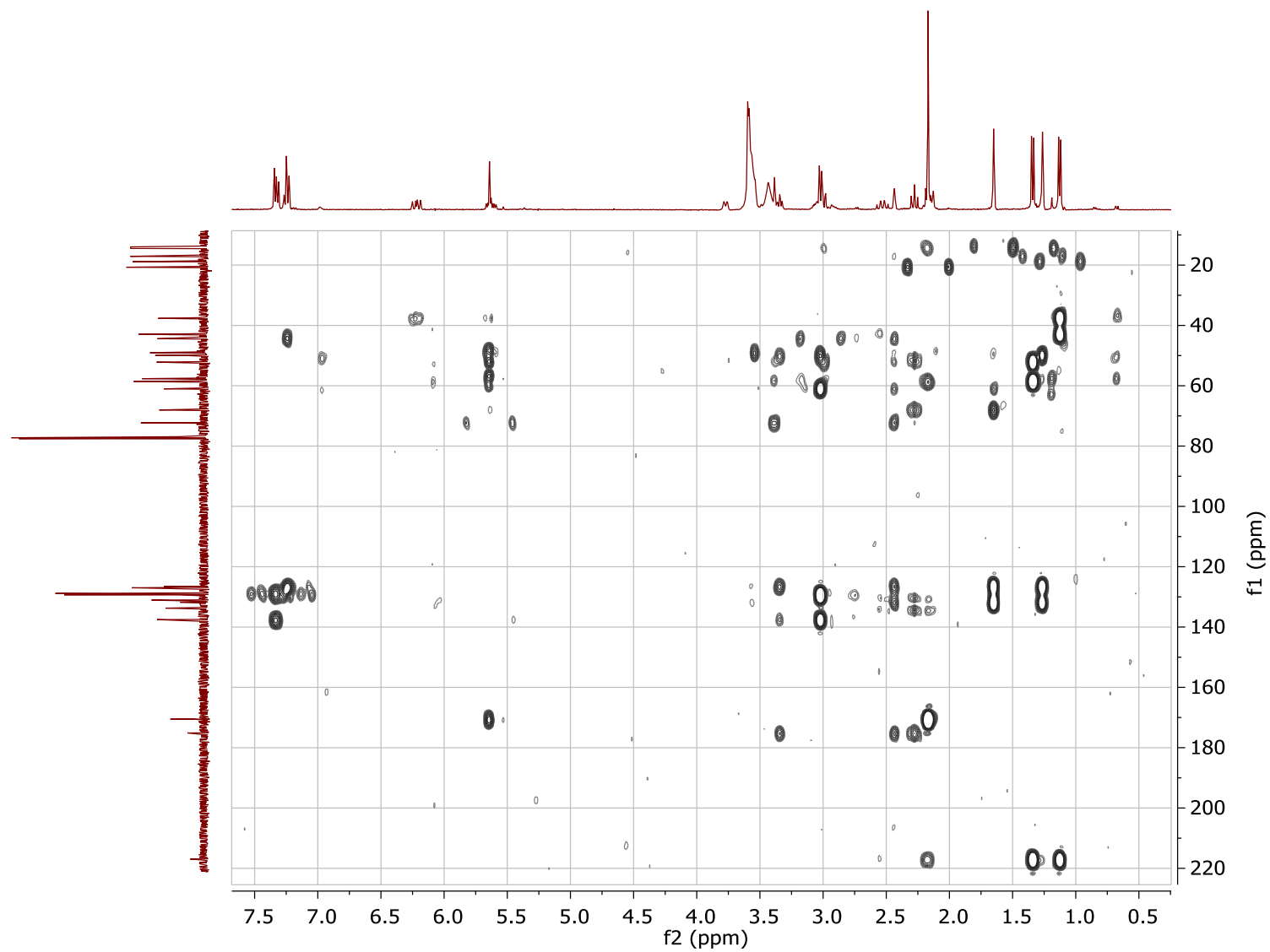


Figure S18: HMBC Spectrum of compound 3

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

		*	20	*	40	*	60	*	80	*	
UM10M	:	TCCGTAGGTGAACCTGCGGAGGGATCATTACCGAGTTGTCCTCCGTG-AC	ACTCCCTTC	ATACCCCT	TGTGAAC	-ATACCATC-	-GTTGCCTC	:	89		
JQ761479.1	:	-----GGATCATTACCGAGTTGTCCTCCGTG-AC	ACTCCCTTC	ATACCCCT	TGTGAAC	-ATACCATC-	-GTTGCCTC	:	68		
KC477228.1	:	-----TCATTACCGAGTTGTCCT-CTGTGAC	ACTCCCTTC	ATACCCCT	TGTGAAC	-ATACCATC-	-GTTGCCTC	:	65		
KX037428.1	:	-----GGATCATTACTGAGTTGTCCTCCGAGGAC	ACTCCCTTC	ACACCCCT	TGTGAAC	-ATACCGTC-	-GTTGCCTC	:	69		
KU683913.1	:	-----GGATCATTACTGAGTTGTCCTCCGAGGAC	ACTCCCTTC	ACACCCCT	TGTGAAC	-ATACCGTC-	-GTTGCCTC	:	69		
AF201704.1	:	TCGGTTGGTGAACCAAGCGGAGGGATCATTACAGAGTTAC----	CAAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	80		
DQ641634.1	:	-----GGGATCATTACTGAGTTTT--GAAAAAAG-	ACTCCC--	AAACCC--	TGTGAAC	-CTACC-TATCGTTGCCTC	:	63			
EF026121.1	:	TCCGTAGGTGAACCTGCGGAGGGATCATTAAAGAGTTTT--C-TACA-	ACTCCC--	AAACCC--	TGTGAAC	-ATACCTTC-TGTTGCCTC	:	81			
EF026122.1	:	TCCGTAGGTGAACCTGCGGAGGGATCATTAAAGAGTT-T---	AAAACA-	ACTCCT--	AAACCCA-	TGTGAAC	-ATACCTTC-TGTTGCCTC	:	81		
GU292818.1	:	TCCGTAGGTGAACCTGCGGAGGGATCATTAAAGAGAGCC---	TAAAAA-	ACTCCGCA	AAACCCA-	TGTGAAC	-ATACCAT-ACGTTGCCTC	:	85		
GU292822.2	:	TCCGTAGGTGAACCTGCGGAGGGATCATTAAAGAGTTCT-----	ATA-	ACTCCC--	AAACCCA-	TGTGAAC	-ATACCTTC-ACGTTGCCTC	:	79		
JQ759872.1	:	-----GGATCATTACAGAGTTAT---CTAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	59			
JQ760608.1	:	-----GGATCATTACAGAGTTGT---CCTA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACCGTC-TGTTGCCTC	:	59			
JQ846087.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTACTGAGTTTT--GAAAAAAG-	ACTCCC--	AAACCC--	TGTGAAC	-CTACC-TATCGTTGCCTC	:	83			
KC708575.1	:	-----			TGTGAAC	-ATACCTTC-TGTTGCCTC	:	24			
KC845930.1	:	-----			TGAAC	-ATACCTTC-TGTTGCCTC	:	22			
KP133215.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTAGAGAGTTCT---	CATACA-	ACTCCG--	AAACCCA-	TGTGAAC	-ATACCTTC-TGTTGCCTC	:	82		
KP133218.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTAAAGAGAGCC---	TAAAAA-	ACTCCCGTA	AAACCCA-	TGTGAAC	-ATACCAT-ACGTTGCCTC	:	85		
KU683765.1	:	-----GGATCATTATAGAGTTAT---CTAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	59			
KU683999.1	:	-----		ATA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TCATGTTGCCTC	:	40	
KU747773.1	:	-----TACAGAGTTGT---C-AA--	ACTCCC--	AA-CCCA-	TGTGAAC	-CTACC-TGCGGTTGCCTC	:	50			
KU747908.1	:	-----		AAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGTCGTTGCCTC	:	40	
KX774096.1	:	-----			TGTGAAC	-ATACC-TCATGTTGCCTC	:	23			
KX778681.1	:	-----			C--	AA-CCCT-TTTTAA--TTACTTCATGTTGCCTC	:	30			
KY250390.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTAAAGAGTTTT----	TACA-	ACTCCC--	AAACCC--	TGTGAAC	-ATACCTTC-TGTTGCCTC	:	80		
KY250391.1	:	TC-GT-GGTGA--CAGCGGAGGGATCATTAAAGAGTTTT----	TACA-	ACTCCC--	AAACCC--	TGTGAAC	-ATACCTTC-TGTTGCCTC	:	76		
LN714575.1	:	-----ATCATTAAAGAGT-GT---AATA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TCATGTTGCCTC	:	56			
MF153390.1	:	-----AAGAGTTTT--C-TACA-	ACTCCC--	AAACCC--	TGTGA-C	GTACCTTC-TGTTGCCTC	:	50			
MF663581.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTAGAGAGTCT-----	AAACA-	ACTCCC--	AAACCCAC	TGTGAAC	-ATACC-CCACGTTGCCTC	:	81		
MG543928.1	:	-----		AAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	40	
MG543932.1	:	-----		AAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	40	
MG543935.1	:	-----		AAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	40	
MG543943.1	:	-----		AAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	40	
MG543947.1	:	-----		AAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	40	
MG832444.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTAAAGAGTGT-----	AATA-	ACTCCG--	AAACCCA-	TGTGAAC	-ATACC-TCATGTTGCCTC	:	79		
MH178723.1	:	-----TTACAGAGTTAT---CAAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	53			
MH305505.1	:	-----					ATACCAT-ACGTTGCCTC	:	17		
MH931277.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTACAGAGTTAT---	CTAA--	ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	80		
MK192915.1	:	-----			ACTCCC--	AAACCCA-	TGTGAAC	-ATACC-TGTCGTTGCCTC	:	37	
MK367486.1	:	-----GGGAATAGG---TGTATA-	ACTCCC--	AA-CCCA-	TGTGAAC	-ATACC-TCATGTTGCCTC	:	51			
MK367543.1	:	-----GGGGC-TTA-AGAG---CTTCAA-	ACTCCC--	AA-CCCA-	TGTGAAC	-ATACC-TGCGGTTGCCTC	:	55			
NR_160210.1	:	TCCGTTGGTGAACCAAGCGGAGGGATCATTACAGAGTTCT---	CGCA--	ACTCCG--	ACACCT-	TGTGAAC	-CATACC-ACATGTTGCCTC	:	81		

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

```

UM10M      : 100      *      120      *      140      *      160      *      180
JQ761479.1 : ---GG-----CGTG-----GGGCGCCGCGGTG : 108
KC477228.1 : GGTGGG-----CGTG-----GCGCCGCGCGGTG : 87
KX037428.1 : GGTGGG-----GCGGTCACAACGCGCCGCGGTG : 93
KU683913.1 : GGTGGG-----GCGGTTACCAAGCGCCGCGCGG : 97
AF201704.1 : GGCAGGTGG---CGT---CCTACCC---CGTGAGAC---TACCTGTAGG-A---CCTACCCGG---TAG-GC---G---AC---CCTGCCGACG : 147
DQ641634.1 : GGTAGGTGGCCTCAT---TGAC---CGTGGGATATCTCCTATGG-----TATAGTG---GGTGC-----AC---CCTGCCGAAG : 128
EF026121.1 : GGCAGGCCT---CG---CCTACCT---CGTAGCCCC-TACACCGTAGG-G---CCTACGCCGGG-TGGTGCGCG---AC---CCTGCCGCG : 155
EF026122.1 : GGCAGGTCG---CG---CTTACCC---TGTAGCGCT-TACCTGTAGG-G---CCTACCCGA---AGGCGGG---TAAACCTGCCGCG : 155
GU292818.1 : GGCAGGCCT---CAT-ACGTGCCCC---C-TCATGGCG-TGCCGGCGCGAGCCCCGCAAGGGGGGGGGCGCGGGTGAGACCTGCCGGTG : 169
GU292822.2 : GGCAGGT---CGT-GCCTACCC---CGTAGCGCC-TACCTGTAGG-A---CCTACCCGGT---AGACGGG---TAAGCCTGCCGCG : 152
JQ759872.1 : GGCAGGTGG---CGT---CCTACCC---CGTGATAC---TACCTGTAGG-A---CCTACCCGG---TAG-GC---G---AC---CCTGCCGACG : 126
JQ760608.1 : GGCAGGTCA---AGG---CCCGGT---AGCGTG-C---AGAC---CCTGCCGCG : 101
JQ846087.1 : GGTAGGTGGCCTCAT---TGAC---CGTGGGATATCTCCTATGG-----TATAGTG---GGTGC-----AC---CCTGCCGAAG : 148
KC708575.1 : GGCAGGCCT---CG---CCTACCT---CGTAGCCCC-TACACCGTAGG-G---CCTACGCCGGG-TGGTGCGCG---AC---CCTGCCGCG : 98
KC845930.1 : GGCAGGCCT---CG---CCTACCT---CGTAGCCCC-TACACCGTAGG-G---CCTACGCCGGG-TGGTGCGCG---AC---CCTGCCGCG : 96
KP133215.1 : GGCAGGTCGCGCGGCGCCTACCG---CGTAGCACCT-TACCCGTAGG-G---CCTACCC---GGGACGCGTGCGGGTCCCTGCCGCG : 165
KP133218.1 : GGCAGGCCT---CAT-ACGTGCCCC---CCTCATG-CG-TGCCGGCGCGCAACCCGCAAGGGGGGGGGACGCGGGTGGAACCTGCCGGTG : 169
KU683765.1 : GGCAGGTGG---CGT---CCTACCC---CGTGATAC---TACCTGTAGG-A---CCTACCCGG---TAG-GC---G---AC---CCTGCCGACG : 126
KU683999.1 : GGCAGGTCG---CG---CCTCCT---CGTAGGCC-TACCCGTAGG-CT-CCTACCCGG---AAG-GC---GCGGGTACCTGCCGGTG : 113
KU747773.1 : GGCAGGCGG---CGT---CCCAACC---TGGAAGAC---TACCCGTAGG-AGGCCTATCCGGGGCGG-GC---G---AC---CCTGCCGAAG : 122
KU747908.1 : GGCAGGCGC---CGT---CCTACCC---ACC---A---CCGGT-GG-A---GG---G---G---AAACCCGCCGACG : 89
KX774096.1 : GGCAGGT---CGT-GCCT-CCCT---CGTAGGTC---TACCTGTAGGCT---CCTACCCGA---AGGCAAGG---TACCCCTGCCGGTG : 96
KX778681.1 : GGCAGGT---CGT-GCCT-CCCT---CGTAGGTC---TACCTGTAGG-CT-CCTACCCGA---AGGCGGG---TACCCCTGCCGGTG : 103
KY250390.1 : GGCAGG-C---CTG-GCCTACCC---TGTAGCGCCCTACCTGTAGG-G---CCTGCTTTAGGGGGGCGGTGGGGGAAC---TGCCGGCG : 158
KY250391.1 : GGCAGG-C---CTG-GCCTACCC---TGTAGCGCCCTACCTGTAGG-G---CTTGCTTGAGGGGGGCGGTGGGGGAAC---TGCCGGCG : 154
LN714575.1 : GGCAGGTCG---CG---CCTCCT---CGTAGGCC-TACCCGTAGG-CT-CCTACCGG---AAG-GC---GCGGGTACCTGCCGGTG : 129
MF153390.1 : GGCAGGCCT---CG---CCTACCT---CGTAGCCCC-TACACCGTAGG-G---CCTACGC---GGG-GGGTGCGGGG---AC---CCTGCCGCG : 123
MF663581.1 : GGCAGG---CGC---CCGGTCT---CGGACCCCTCGGGGCTGCGGGGTGGC-----CCTGCCGCG : 134
MG543928.1 : GGCAGGTGG---CGT---TCGCCC---CGTAAGAAC-TACCTGTAGGAA---CGTACCCGG---TAG-AG---AC---CCTGCCGACG : 108
MG543932.1 : GGCAGGTGG---CGT---CTCGCC---CGTAAGAAC-TACCTGTAGGAC---CTTACCCGG---TAG-AG---AC---CCTGCCGACG : 109
MG543935.1 : GGCAGGTGG---CGT---CCTACCC---CGTGAGACC-TACCTGTAGG-A---CCTACCCGG---TAG-GC---G---AC---CCTGCCGACG : 107
MG543943.1 : GGCAGGTGG---CGT---CTCGCC---CGTAAGAAC-TACCTGTAGGGT---CTTACCCGG---TAG-AG---AC---CCTGCCGACG : 109
MG543947.1 : GGCAGGTGG---CGT---CTCGCC---CGTAAGAAC-TACCTGTAGGAT---CTTACCCGG---TAG-AG---AC---CCTGCCGACG : 109
MG832444.1 : GGCAGGTCG---CG---CCT-CTCT---CGTAGGTC---TACCGGGAAG---CGCGGG---TACCCCTGCCGCG : 137
MH178723.1 : GGCAGGTGG---CGC---CCCGCCT---GTAGGGCC-TACCTGTAGGAG---CTCACCCGG---TGGTG---CCCTGCCGACG : 122
MH305505.1 : GGCAGGCCT---CAT-ACGTGCCCC---C-TCATGGCG-TGCCGGCGCGAGCCCCGCAAGGGGGGGGGCGCGGGTGAGACCTGCCGGTG : 101
MH931277.1 : GGCAGGTGG---CGT---CCTACCC---CGTGATAC---TACCTGTAGG-A---CCTACCCGG---TAG-GC---G---AC---CCTGCCGACG : 147
MK192915.1 : GGCAGGCGC---CGT---CCTACCCCTCGCGGGTGGTGAAACCC-----GCCGAAG : 83
MK367486.1 : GGCAGGT---CGT-GCCT-CCCT---CGTAGGTC---TACCTGTAGG-CT-CCTACCCGA---AGGCGGG---TACCCCTGCCGGTG : 124
MK367543.1 : GGCAGGTGG---CGT---CTCGCC---CGTAAGGTGC-TACCTGTAGGGT---CTTACCCGG---TAG-AG---AC---CCTGCCGACG : 124
NR_160210.1 : GGCAGGCGC---CGA---CC-ACC---TGTGGCAACC-TACCTGTAGGCG---CTACCTGTG---GACCGGC---TCACCC---GCCGCG : 154

```

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

	*	200	*	220	*	240	*	260	*	28	
UM10M	:	GCCCATTACTACC-AAATTCGTACACTTTGAAAACCTTGATCTGA	----	ACTT	----	ATAACAAATATGTTAAAA	----	CTTTCAACAACGG	:	189	
JQ761479.1	:	GCCCATTACTACC-AAATTCGTACATTTGAAAAATTGACCTGA	----	ACTT	----	ATAACAAATCATGTTAAAA	----	CTTTCAACAACGG	:	168	
KC477228.1	:	GCCCATTATAC-CAAATTCGTTTACTTTGAAAATTTACTCTGA	----	ATAT	----	ATAACAAATCATGTTAAAA	----	CTTTCAACAACGG	:	174	
KX037428.1	:	GCCCCTT--TACCTAAATTCGTTAATCTT-CTACTT	----	CTGA	----	ATAACAAATCATGTTAAAA	----	CTTTCAACAACGG	:	172	
KU683913.1	:	GCCCCTT--TACCTAAATTCGTTAATCTT-CTACTT	----	CTGA	----	ATAACAAATCATGTTAAAA	----	CTTTCAACAACGG	:	172	
AF201704.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTGGA-CTTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	221	
DQ641634.1	:	GCCCCCTATAAACTCT-TTGTATTTTG-AACT-ATTGGATCTCTGA	----	GTGG	----	AAAAAAAATTAAGTTAAAA	----	CTTTCAACAACGG	:	207	
EF026121.1	:	GCCCCGCG-AAACTCT-GTTTT-----AGC-CTGAA-TCCTGA	----	ACAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	225	
EF026122.1	:	GCCCAAG-AAACTCT-GTTTT-----AGC-ATTGAA--TCTGA	----	ATAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	224	
GU292818.1	:	GCCCAAGCAAAACCT-GTT-----ATC-CTGAA--TCTGAGCCC	----	GCAT	----	GTAGGAAATTAAGTCAAAA	----	CTTTCAACAACGG	:	242	
GU292822.2	:	GCCCAAG-AAACTCT-GTTTT-----AGT-ATTGAA--TCTGA	----	ACCT	----	GTAACAAATAAGTTAAAA	----	CTTTCAACAACGG	:	221	
JQ759872.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTGGA-CTTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	200	
JQ760608.1	:	GCCCAAG-AAATCT-GTTTT-----CTTC--TTGAA--TCTGA	----	AACTGAAAC	----	AAAAAAAATAAGTTAAAA	----	CTTTCAACAACGG	:	176	
JQ846087.1	:	GCCCCCTATAAACTCT-TTGTATTTTG-AACT-ATTGGATCTCTGA	----	GTGG	----	AAAAAAAATTAAGTTAAAA	----	CTTTCAACAACGG	:	227	
KC708575.1	:	GCCCCGCG-AAACTCT-GTTTT-----AGC-CTGAA-TCCTGA	----	ACAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	168	
KC845930.1	:	GCCCCGCG-AAACTCT-GTTTT-----AGC-CTGAA-TCCTGA	----	ACAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	166	
KP133215.1	:	GCCCAAG-AAACTCT-GTTTT-----AGCTTATTGAA--TCTGA	----	ACGT	----	ATAACTAAATTAAGTTAAAA	----	CTTTCAACAACGG	:	236	
KP133218.1	:	GCCCAAGCAAAACCT-GTC-----GTC-CTGAA--TCTGAGCCC	----	GCAT	----	GTAGGAAATTAAGTCAAAA	----	CTTTCAACAACGG	:	242	
KU683765.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTGGA-CTTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	200	
KU683999.1	:	GCCCAAG-AAACTCT-GTCT-----CATC-GTTGAA--TCTGA	----	ACCT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	183	
KU747773.1	:	GCCCCCCC-AAACTCT-GTCT-T-CT-ACAGC-ATTGGA-CCTCTGA	----	AAAG	----	ATGACTAAATCAGTTAAAA	----	CTTTCAACAACGG	:	198	
KU747908.1	:	GCCCCCG-AAACTCT-GTTTTTCT-ATAGC-ATTGGA-CCTCTGAAGC	----	AAAG	----	ATAACTAAATCAGTTAAAA	----	CTTTCAACAACGG	:	168	
KX774096.1	:	GCCCAAG-AAACTCT-GTCT-----CATC-GTTGAA--TCTGA	----	ACCT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	166	
KX778681.1	:	GCCCAAG-AAACTCT-GTCT-----CATC-GTTGAA--TCTGA	----	ACCT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	173	
KY250390.1	:	GCCCCGCA-AAACTCT-GTTTT-----AGC-ATTGAA--TCTGA	----	ACGT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	227	
KY250391.1	:	GCCCCGCA-AAACTCT-GTTTT-----AGC-ATTGAA--TCTGA	----	ACGT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	223	
LN714575.1	:	GCCCAAG-AAACTCT-GTCT-----CATC-GTTGAA--TCTGA	----	ACCT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	199	
MF153390.1	:	GCCCCGCA-AAACTCT-GTTTT-----AGC-CTGAA-TCCTGA	----	ACAT	----	GCAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	193	
MF663581.1	:	GCCCAAG-AAACTCTTGCT-----AGC-CTGAA--TCTGAGCCCC	----	GAGGGATA	----	AAACAAATTAAGTTAAAA	----	CTTTCAACAACGG	:	214	
MG543928.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTAAA-CTTCTGA	----	AAAC	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	181	
MG543932.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTAAA-CTTCTGA	----	AAAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	182	
MG543935.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTGGA-CTTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	181	
MG543943.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTAAA-TTCTGA	----	AAAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	182	
MG543947.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTAAA-CTTCTGA	----	AAAT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	182	
MG832444.1	:	GCCCAAG-AAACTCT-GTCT-----CATC-GTTGAA--TCTGA	----	ACCT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	207	
MH178723.1	:	GCCCAAG-AAACTCT-GTTTTTTTATAGC-ATTAGA-CCTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	199	
MH305505.1	:	GCCCAAGCAAAACCT-GTT-----ATC-CTGAA--TCTGAGCCC	----	GCAT	----	GTAGGAAATTAAGTCAAAA	----	CTTTCAACAACGG	:	174	
MH931277.1	:	GCCCCCG-AAACTCT-GTTTT--T-ATAGC-ATTGGA-CTTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	221	
MK192915.1	:	GCCCCCG-AAACTCT-GTTTTT-T-ATAGC-ATTAGA-CCTCTGAAA	----	AAAG	----	ATAACTAAATCAGTTAAAA	----	CTTTCAACAACGG	:	160	
MK367486.1	:	GCCCAAG-AAACTCT-GTCT-----CATC-GTTGAA--TCTGA	----	ACCT	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	194	
MK367543.1	:	GCCCTCG-AAACTCT-GTTTTT--ATAAC-ATTAGA-CTTCTGA	----	AAAG	----	ATAACTAAATAAGTTAAAA	----	CTTTCAACAACGG	:	198	
NR_160210.1	:	GCCCAAC-CAAACCT-GTTTT-----ACT-TTGAA--TCTGA	----	ACCT	----	ATAACGAAATACGTTAAAA	----	CTTTCAACAACGG	:	223	

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

	0	*	300	*	320	*	340	*	360	*	
UM10M	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	282				
JQ761479.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	261				
KC477228.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	267				
KX037428.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	265				
KU683913.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	265				
AF201704.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	314				
DQ641634.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	306				
EF026121.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	318				
EF026122.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	317				
GU292818.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	335				
GU292822.2	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	314				
JQ759872.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	293				
JQ760608.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	269				
JQ846087.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	320				
KC708575.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	261				
KC845930.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	259				
KP133215.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	329				
KP133218.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	335				
KU683765.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	293				
KU683999.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	276				
KU747773.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	291				
KU747908.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	261				
KX774096.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	259				
KX778681.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	266				
KY250390.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	320				
KY250391.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	316				
LN714575.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	292				
MF153390.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	286				
MF663581.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	307				
MG543928.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	274				
MG543932.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	275				
MG543935.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	274				
MG543943.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	275				
MG543947.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	275				
MG832444.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	300				
MH178723.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	292				
MH305505.1	:	ATCTCTTGGTTCTGGCATC	TATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	267				
MH931277.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	314				
MK192915.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	253				
MK367486.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	287				
MK367543.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	291				
NR_160210.1	:	ATCTCTTGGTTCTGGCATC	GATGAAGAACGCAGCGAAATGCGATA	CGTAATGTGAATTGCAGAATT	CAGTGAATCATCGAATCTTTGAACGCA	:	316				

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

	380	*	400	*	420	*	440	*	460	
UM10M	: CATTGCGCCC	GCTGGTATTC	CAGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGTGTTGGGAGA	-CTACCG	C	: 373
JQ761479.1	: CATTGCGCCC	GCTGGTATTC	CAGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGTGTTGGGAGA	-CTACC	-C	: 351
KC477228.1	: CATTGCGCCC	GCTGGTATTC	CAGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGATC	ACCCCG		: 359
KX037428.1	: CATTGCGCCC	GCTGGTATTC	CAGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGTGTTGGGAGC	-CTACC	-C	: 355
KU683913.1	: CATTGCGCCC	GCTGGTATTC	CAGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGTGTTGGGAGA	-CTACC	-G	: 355
AF201704.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACT	CG	: 405
DQ641634.1	: CATTGCGCCC	GCCAGTATTC	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCTGTC	GCTTAGTGTTGGGAGA	-CTGCTAG		: 391
EF026121.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 408
EF026122.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACAG	-	: 406
GU292818.1	: CATTGCGCCC	GCCAGTATTC	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 426
GU292822.2	: CATTGTGCCC	ACTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGTGTTGGGAGC	-CTACG	G-	: 404
JQ759872.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGTGTTGGGAGC	-CTACTG	G	: 384
JQ760608.1	: CATTGCGCCC	ATTAGCATTCT	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCTGTC	GCTTAGTGTTGGGAGC	-CTAC	-GG	: 360
JQ846087.1	: CATTGCGCCC	GCCAGTATTC	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCTGTC	GCTTAGTGTTGGGAGA	-CTGCTAG		: 411
KC708575.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 351
KC845930.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 349
KP133215.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGCGTTGGGAGC	-CTACG	G	: 420
KP133218.1	: CATTGCGCCC	GCCAGTATTC	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 426
KU683765.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGTGTTGGGAGC	-CTACTG	G	: 384
KU683999.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTAC	-GG	: 366
KU747773.1	: CATTGCGCCC	GCCAGCATTCT	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACCG	G	: 381
KU747908.1	: CATTGCGCCC	ACCAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCAGCT	GCTTAGCGTTGGGAGC	-CTACCG	G	: 352
KX774096.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 349
KX778681.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 356
KY250390.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 410
KY250391.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 406
LN714575.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTAC	-GG	: 382
MF153390.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 376
MF663581.1	: CATTGCGCCC	GCCAGTATTC	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCAGCT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 397
MG543928.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTAGGAGC	-CTACCG	G	: 365
MG543932.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTAGGAGC	-CTACCG	G	: 366
MG543935.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACTG	G	: 365
MG543943.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTAAGAGC	-CTACCG	G	: 366
MG543947.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTAGGAGC	-CTACCG	G	: 366
MG832444.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 390
MH178723.1	: CATTGCGCCC	ACCAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACCG	G	: 383
MH305505.1	: CATTGCGCCC	GCCAGTATTC	TGGCGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 358
MH931277.1	: CATTGCGCCC	ACTAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCGTT	GCTTAGTGTTGGGAGC	-CTACTG	G	: 405
MK192915.1	: CATTGCGCCC	ACCAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTCAGTT	GCTTAGCGTTGGGAGC	-CTACCG	G	: 344
MK367486.1	: CATTGCGCCC	ATTAGTATTC	TAGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACG	G-	: 377
MK367543.1	: CATTGCGCCC	ACCAGTATTC	TGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACCC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACTG	G	: 382
NR_160210.1	: CATTGCGCCC	ACTGGTATTC	CGGTGGGCATGCCTGTT	CGAGCGTCATT	CAACAC	-TTAAGCCCTGTT	GCTTAGCGTTGGGAGC	-CTACGA	-	: 405

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

	*	480	*	500	*	520	*	540	*	5			
UM10M	:	CGCCATCCATGG	GGCGGCG	GTAGCTCCCT	AAAGCGAGTGGCG	-GAGCCGGTCC	CGTGCTCTAGG	CGTAGTAGAT	---	TTT-AT	-----	CTCG	: 456
JQ761479.1	:	CGCC----	ATGGGGCGGCG	GTAGCTCCCT	AAAGCGAGTGGCG	-GAGCCGGTCC	CGTGCTCTAGG	CGTAGTAGAT	---	TTT-AT	-----	CTCG	: 430
KC477228.1	:	CACC-----	CCGCGGCG	GTAGCTCCCT	AAAGCGAGTAGCG	-GAGCCGGTCCG	TGCTCTAGG	CGTAGTAGAT	---	TTTCGT	-----	CTCG	: 434
KX037428.1	:	CGCC----	ATGGCGCCGCG	GTAGCTCCCC	AAAGCGAGTGGCG	-GAGCCGG-	CCCGTGCTCTAGG	CGTAGTAGAT	---	TTTCAT	-----	CTCG	: 434
KU683913.1	:	CGCC----	ATGGCGG-GCG	GTAGCTCCCT	AAAGCGAGTGGCG	-GAGCCGA-C	CTGTGCTCTAGG	CGTAGTAGAT	---	TTTCGT	-----	CTCG	: 433
AF201704.1	:	AACT-----	CTCCT	GTAGCTCTC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAT	-----	ATCG	: 478
DQ641634.1	:	GATTT-----	TTCTT	ACAGCTCCCT	AAATTCAGTGGCG	-GAGTAGGTTCA	-TGCCCC	CAGACGTAGTAGCTA	---	TTACA	-----	TCG	: 464
EF026121.1	:	-----	CAGC	GTAGCTCCCC	AAAGTTAGTGGCG	-TGGTCGGTTCA	-CACTCC	CAGACGTAGTAGAT	---	TTTCGT	-----	CTCG	: 475
EF026122.1	:	-----	CT	GTAGCTCCCC	AAAGTTAGTGGCG	-GAGTCGGTTCA	-CACTCT	CAGACGTAGTAAT	---	TTTCAC	-----	CTCG	: 471
GU292818.1	:	--CC-----	CGCC	GTAGCTCCTC	AAAGTTAGTGGCG	-GAGTCGGCCCG	-TACCC	CAGGCGTAGTAGTT	CATT	-CAG	-----	CTCG	: 496
GU292822.2	:	--T-----	CATA	GTAGCTCCTC	AAAGTTAGTGGCG	-GAGCTGGCTCA	-CACTCC	CAGGCGTAGTAGAT	GTATC	-----	TCG	: 471	
JQ759872.1	:	AACT-----	CTCCT	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	ATCG	: 457
JQ760608.1	:	--CG-----	TGCC	GTAGCTCCTT	AAAGTTAGTGGCG	-GAGTCGGTTCA	-CACCTC	CAGACGTAGTAGGTTT	TAAGC	-----	ATCG	: 431	
JQ846087.1	:	GATTT-----	TTCTT	ACAGCTCCCT	AAATTCAGTGGCG	-GAGTAGGTTCA	-TGCCCC	CAGACGTAGTAGCTA	---	TTACA	-----	TCG	: 484
KC708575.1	:	-----	CAGC	GTAGCTCCCC	AAAGTTAGTGGCG	-TGGTCGGTTCA	-CACTCC	CAGACGTAGTAGAT	---	TTTCGT	-----	CTCG	: 418
KC845930.1	:	-----	CAGC	GTAGCTCCCC	AAAGTTAGTGGCG	-TGGTCGGTTCA	-CACTCC	CAGACGTAGTAGAT	---	TTTCGT	-----	CTCG	: 416
KP133215.1	:	GTCA-----	CCC	GTAGCTCCTC	AAAGTTAGTGGCG	-GAGTCGGTTCA	-CACTCT	CAGACGTAGTAGAT	---	TTTCAC	-----	CTCG	: 490
KP133218.1	:	--CC-----	CGCC	GTAGCTCCTC	AAAGTTAGTGGCG	-GAGTCGGCCCG	-TACCC	CAGGCGTAGTAGTT	CATT	-CAG	-----	CTCG	: 496
KU683765.1	:	AACT-----	CTCCT	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	ATCG	: 457
KU683999.1	:	-----	CACC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGCTCA	-CACTCT	CAGACGTAGTAAT	TAAT	-CAC	-----	CTCG	: 433
KU747773.1	:	GAGC-----	CCCCG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CGCCCC	CAGACGTAGTAGCCCC	TTACAC	-----	GTCG	: 455	
KU747908.1	:	AGAC-----	CTCTCCG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTTAA	CACCTC	CAGACGTAGTAGCTC	-ATACAC	-----	ATCG	: 429	
KX774096.1	:	-----	CACC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGCTCA	-CACTCT	CAGACGTAGTAAT	TTCT	-CAC	-----	CTCG	: 416
KX778681.1	:	-----	CACC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGCTCA	-CACTCT	CAGACGTAGTAAT	TTCT	-CAC	-----	CTCG	: 423
KY250390.1	:	--A-----	AGC	GTAGCTCCCT	AAAGTTAGTGGCG	-TGGTCGGTTCA	-CACTCC	CAGACGTAGTAGAT	---	TTTCAC	-----	CTCG	: 477
KY250391.1	:	--A-----	AGC	GTAGCTCCCT	AAAGTTAGTGGCG	-TGGTCGGTTCA	-CACTCC	CAGACGTAGTAGAT	---	TTTCAC	-----	CTCG	: 473
LN714575.1	:	-----	CACC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGCTCA	-CACTCT	CAGACGTAGTAAT	TAAT	-CAC	-----	CTCG	: 449
MF153390.1	:	-----	CAGC	GTAGCTCCCC	AAAGTTAGTGGCG	-TGGTCGGTTCA	-CACTCC	CAGACGTAGTAGAT	---	TTTCGT	-----	CTCG	: 443
MF663581.1	:	-----	CT	GTAGCTCCTC	AAAGTCAGTGGCG	-TGGCTGGCTCG	-CACCC	CAGATGTAGTAGTTA	---	TTTCTC	-----	TCA	: 463
MG543928.1	:	AACT-----	C-TCTG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	GTCG	: 438
MG543932.1	:	AACT-----	C-TCTG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAT	-----	GTCG	: 439
MG543935.1	:	AACT-----	CTCCT	GTAGCTCCTC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAT	-----	ATCG	: 438
MG543943.1	:	AACT-----	C-TCTG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	GTCG	: 439
MG543947.1	:	AACT-----	C-TCTG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	GTCG	: 439
MG832444.1	:	-----	CACC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGTCGGCTCA	-CACTCT	CAGACGTAGTAAT	TTCT	-CAC	-----	CTCG	: 457
MH178723.1	:	AAAC-----	CGTCCG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	GTCG	: 457
MH305505.1	:	--CC-----	CGCC	GTAGCTCCTC	AAAGTTAGTGGCG	-GAGTCGGCCCG	-TACCC	CAGGCGTAGTAGTT	CATT	-CAG	-----	CTCG	: 428
MH931277.1	:	AACT-----	CTCCT	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	ATCG	: 478
MK192915.1	:	ACCC-----	CGTCCC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGCTTGAC	ACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	GTCG	: 419
MK367486.1	:	-----	CACC	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGCTCA	-CACTCT	CAGACGTAGTAAT	TTCT	-CAC	-----	CTCG	: 444
MK367543.1	:	ACCT-----	TGTCCG	GTAGCTCCCC	AAAGTCAGTGGCG	-GAGCCGGTTCG	-CACTCC	CAGACGTAGTAGCTT	---	TTACAC	-----	GTCG	: 456
NR_160210.1	:	--CG-----	TACC	GTAGCTCCTC	AAAGTTAGTGGCG	-GAGCCGGTTCG	-TGCTCT	TAGGCGTAGTAGAT	---	TTTCGT	-----	CTCG	: 474

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

	60	*	580	*	600	*	620	*	640	*	
UM10M	: CCTCCGTA-GCCGGATCTGGT	TTTTCTGCCATAAAA	-CGAAGATT-TTTCTTCA	---CTT---	CTTTTAAGGTTGACCTCGGATCAGGTA	:	538				
JQ761479.1	: CCTCTGTA-GCCGGATCTGGT	TTTTCTGCCATAAAA	-CGAAGATT-TTTCTTCA	---CTT---	ATTTCAGGTTGACCTCGGATCAGGTA	:	512				
KC477228.1	: CCTCT-GTAGCCGGGTCTGGT	TTTCCAGCCAAAAA	-----	-----	-----	:	469				
KX037428.1	: CCTCTGTAAGCCGGGTCTGGT	TTTTCTGCCGTAAAA	-CGAAGAGA-ACACACCTTGT	-CTT---	CTCTATGGTTGACCTCGGATCAGGTA	:	519				
KU683913.1	: CCTCTGTAAGTCAGGTCTGGT	TTTTCTGCCGTAAAA	-CGAAGAGA-ACACACCTTGT	CTCTTTTACCTCTA	-GGTTGACCTCGGATCAGGTA	:	523				
AF201704.1	: CCTGTAGC-TT-GGACCCGGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAAATCT	-----TCTAGGTTGACCTCGGATCAGGTA	:	547				
DQ641634.1	: CCTGTGGTATA-GGTCT--ATCT	-CTTGCCGTAAAA	-----	-----	-----	:	496				
EF026121.1	: CCTGTAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTC	-----AAAAGGTTGACCTCGGATCAGGTA	:	542				
EF026122.1	: CCTGTAG--TT-GGACC-GGTCT	-CTTGCCGTAAAA	-CA-----	CCCCAATTTT	TTT-----TAAAGGTTGACCTCGGATCAGGTA	:	541				
GU292818.1	: CCGCGCG--TC-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CACC-ATTTT	TT-----AAGGTTGACCTCGGATCAGGTA	:	562				
GU292822.2	: CTTGT-GAGTT-AGGCC-GGTCC	-CCAGCCGTAAAA	-C-----	CCCCTAATTT	T-----TAAAGGTTGACCTCGGATCAGGTA	:	539				
JQ759872.1	: CCTGTAGC-TT-GGACCCGGTCC	-CCTGCCGTAAAA	-C-----	CCCCCAATTT	TA-----T-AGGTTGACCTCGGATCAGGTA	:	527				
JQ760608.1	: CCTATGGT-TT-GGACCCGG-CC	-CCTGCCGTAAAA	-CAAAAAA-ACGAC	ACCTAGTGTCTG	-----TCAAGGTTGACCTCGGATCAGGTA	:	512				
JQ846087.1	: CCTGTGGTATA-GGTCT--ATCT	-CTTGCCGTAAAA	-----	ATGCCTAAAAAAGCAC	-----TATAGGTTGACCTCGGATCAGGTA	:	557				
KC708575.1	: CCTGTAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTC	-----AAAAGGTTGACCTCGGATCAGGTA	:	485				
KC845930.1	: CCTGTAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTC	-----AAAAGGTTGACCTCGGATCAGGTA	:	483				
KP133215.1	: CCTGTAGTGCT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCTATT	CT-----AAAAGGTTGACCTCGGATCAGGTA	:	561				
KP133218.1	: CCGCGCG--TC-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CACC-ATTT	CTC-----GCAAGGTTGACCTCGGATCAGGTA	:	565				
KU683765.1	: CCTGTAGC-TT-GGACCCGGTCC	-CCTGCCGTAAAA	-CA-----	C-----C	CCCCCAATTTA-----T-AGGTTGACCTCGGATCAGGTA	:	527				
KU683999.1	: CCTATAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CG-----	C-----C	CCC--AGTATCT-----AAAAGGTTGACCTCGAATCAGGTA	:	501				
KU747773.1	: CCTGCCGT-GC-GTGCCCGGCC	-CCTGCCGTAAAA	-C-----	C-----C	CCCCCAATTTCT-----TTCAGGTTGACCTCGGATCAGGTA	:	526				
KU747908.1	: CCTGTAGC-CT-AAACCCGGCC	-CCTGCCGTAAAA	-CA-----	C-----C	AACG-AATAITG-----TATAGGTTGACCTCGGATCAGGTA	:	500				
KX774096.1	: CCTATAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CG-----	CCCCAGTAT	T-----AAAAGGTTGACCTCGAATCAGGTA	:	484				
KX778681.1	: CCTATAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CG-----	CCCC-AGTAT	TT-----AAAAGGTTGACCTCGAATCAGGTA	:	491				
KY250390.1	: CCTGTAG--CT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCC--AAT	TT-----TAAAGGTTGACCTCGGATCAGGTA	:	544				
KY250391.1	: CCTGTAG--CT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCC--AAT	TT-----TAAAGGTTGACCTCGGATCAGGTA	:	540				
LN714575.1	: CCTATAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CG-----	C-----C	CCC--AGTATCT-----AAAAGGTTGACCTCGAATCAGGTA	:	517				
MF153390.1	: CCTGTAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTC	-----GAAAGGTTGACCTCGGATCAGGTA	:	510				
MF663581.1	: CCTGTGG--TC-GGGCT-AGTCC	-CCTGCCGTAAAA	-C-----	CCCCCAGAC	TTT-----TAGTCTTTGACCTCGGATCAGGTA	:	532				
MG543928.1	: CCTGTAGC-GC-GGGCC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTT	-----TATAGGTTGACCTCGGATCAGGTA	:	506				
MG543932.1	: CCTGTAGC-GT-GAGCC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTT	-----TATAGGTTGACCTCGGATCAGGTA	:	507				
MG543935.1	: CCTGTAGC-TT-GGACCCGGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAAATC	-----TCTAGGTTGACCTCGGATCAGGTA	:	507				
MG543943.1	: CCTGTAGC-GC-GGGCC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTT	-----TATAGGTTGACCTCGGATCAGGTA	:	507				
MG543947.1	: CCTGTAGC-GC-GGGCC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTT	-----TATAGGTTGACCTCGGATCAGGTA	:	507				
MG832444.1	: CCTACAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CG-----	CCCC-AGTC	TT-----AAAAGGTTGACCTCGGATCAGGTA	:	525				
MH178723.1	: CCTGTAGC-GC-GGGCC-GGTCC	-CCTGCCGTAAAA	-A-----	CCCCAAATTC	-----TATAGGTTGACCTCGGA-----	:	518				
MH305505.1	: CCGCGCG--TC-GGACC-GGTCC	-CCTGCCGTAAAA	-CA-----	CACC-ATTT	TT-----AAGGTTGACCTCGGATCAGGTA	:	494				
MH931277.1	: CCTGTAGC-TT-GGACCCGGTCC	-CCTGCCGTAAAA	-CA-----	C-----C	CCCCCAATTT-----TATAGGTTGACCTCGGATCAGGTA	:	548				
MK192915.1	: CCTGTAGCCCA-AG-CCCGGCG	-CCTGCCGTAAAA	-CAC-----	CCCCCAGTG	-----ATAGGTTGACCTCGGATCAGGTA	:	488				
MK367486.1	: CCTATAG--TT-GGACC-GGTCC	-CCTGCCGTAAAA	-CG-----	CCCC-AGTA	TT-----AAAAGGTTGACCTCGAATCAGGTA	:	512				
MK367543.1	: CCTGTAGC-GC-GGGCC-GGTCC	-CCTGCCGTAAAA	-CA-----	CCCCAATTC	-----TATAGGTTGACCTCGGATCAGGTA	:	524				
NR_160210.1	: CCTGTAGC--C-GGGCCGGTCC	-CCTGCCGTAAAA	-CA-----	CACCTATTT	C-----TCAAGGTTGACCTCGGATCAGGTA	:	543				

Figure S19: ITS sequence alignment of UM10M with sequences published in GenBank

	660	*	680	*	
UM10M	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 578
JQ761479.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 552
KC477228.1	: -----				: -
KX037428.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 559
KU683913.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 563
AF201704.1	: GGAATACCCGCTGAACCTTAA		-----		: 567
DQ641634.1	: -----				: -
EF026121.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 582
EF026122.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 581
GU292818.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 602
GU292822.2	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 579
JQ759872.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 567
JQ760608.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 552
JQ846087.1	: GGAATACCCGCTGAACCTTAA		GCATATCAT	-----	: 586
KC708575.1	: GGAATACCCGCTGAACCTTAA		GCATATCAA	-----	: 514
KC845930.1	: GGAATACCCGCTGAACCTTAA		GCATATCA	-----	: 511
KP133215.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 601
KP133218.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 605
KU683765.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 567
KU683999.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 541
KU747773.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 566
KU747908.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 540
KX774096.1	: GGAATACCCGCTGAACCTTAA		-----		: 504
KX778681.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 531
KY250390.1	: GGAATACCCGCTGAACCTTAA		GCATATCA	-TA-----	: 574
KY250391.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	-----	: 573
LN714575.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 557
MF153390.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 550
MF663581.1	: GGAATACCCGCTGAACCTTAA		-----		: 552
MG543928.1	: GGAATACCCGCTGAACCTTAA		-----		: 526
MG543932.1	: GGAATACCCGCTGAACCTTAA		-----		: 527
MG543935.1	: GGAATACCCGCTGAACCTTAA		-----		: 527
MG543943.1	: GGAATACCCGCTGAACCTTAA		-----		: 527
MG543947.1	: GGAATACCCGCTGAACCTTAA		-----		: 527
MG832444.1	: GGAATACCCGCTGAACCTTAA		GCAT	-----	: 549
MH178723.1	: -----				: -
MH305505.1	: GGAATACCCGCTGAACCTTAA		GCATAT	--ATAAGCCGGAGGA	: 533
MH931277.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 588
MK192915.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	- CGGAGGA	: 528
MK367486.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATAAG	GGCGGAGGA	: 553
MK367543.1	: GGAATACCCGCTGAACCTTAA		-----		: 544
NR_160210.1	: GGAATACCCGCTGAACCTTAA		GCATATCAATA	-----	: 574

Table S1: Sequences used for alignment analysis and to identify close relatives

UM10M	
JQ761479.1*	<i>Nemania</i> sp. genotype 547 isolate NC0453
KU683913.1*	<i>Nemania</i> sp. ARIZ FL1860
KX037428.1*	<i>Nemania</i> sp. strain BCC30850
AF201704.1	<i>Nemania aenea</i> variety <i>aureolatum</i>
DQ641634.1	<i>Nemania plumbea</i>
EF026121.1	<i>Nemania primolutea</i> isolate 91102001
EF026122.1	<i>Nemania illita</i> isolate 236
GU292818.1	<i>Nemania bipapillata</i> isolate 90080610
GU292822.2	<i>Nemania maritima</i> isolate 89120401
JQ759872.1	<i>Nemania serpens</i> isolate AK1587
JQ760608.1	<i>Nemania beaumontii</i> isolate FL0980
JQ846087.1	<i>Nemania plumbea</i> isolate 6540
KC477228.1	<i>Nemania pouzarii</i> strain ATCC 2612
KC708575.1	<i>Nemania primolutea</i> strain NY2
KC845930.1	<i>Nemania primolutea</i> isolate FG9
KP133215.1	<i>Nemania abortiva</i> isolate 18.2
KP133218.1	<i>Nemania bipapillata</i> isolate 64.2
KU683765.1	<i>Nemania serpens</i> isolate CBS 679.86
KU683999.1	<i>Nemania diffusa</i> isolate NC1333
KU747773.1	<i>Nemania</i> sp. strain F1454
KU747908.1	<i>Nemania</i> sp. strain F2130
KX774096.1	<i>Nemania</i> sp. strain 43
KX778681.1	<i>Nemania diffusa</i> isolate CNUZ-L414
KY250390.1	<i>Nemania</i> sp. voucher GAB127
KY250391.1	<i>Nemania</i> sp. voucher GAB137
LN714575.1	<i>Nemania diffusa</i>
MF153390.1	<i>Nemania primolutea</i> isolate ZCL5
MF663581.1	<i>Nemania</i> sp. strain LTL428
MG543928.1	<i>Nemania</i> sp. isolate EP04
MG543932.1	<i>Nemania</i> sp. isolate EP20
MG543935.1	<i>Nemania</i> sp. isolate EP26
MG543943.1	<i>Nemania</i> sp. isolate PA19
MG543947.1	<i>Nemania</i> sp. isolate PA33
MG832444.1	<i>Nemania</i> sp. strain TS-24
MH178723.1	<i>Nemania</i> sp. isolate IUB:B.Whitaker:OTU54
MH305505.1	<i>Nemania bipapillata</i> strain Ct-BC70
MH931277.1	<i>Nemania serpens</i> isolate m22
MK192915.1	<i>Nemania</i> sp. isolate S1.5
MK367486.1	<i>Nemania</i> sp. isolate Z-Y-43
MK367543.1	<i>Nemania</i> sp. isolate Z-G-12
NR_160210.1	<i>Nemania macrocarpa</i> CBS 109567

*) BLAST hit