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SHH designed the study; AA did experimental work; SHH and AA wrote it. All authors read and approved the final manuscript.

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Molecular Diagnosis of *Cladosporium sp.* and *Fusarium equiseti* Fungal Infection for Zoonotic Otitis externa from Formalin-fixed Samples

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Supplementary Files:

Figures and Tables for samples S1 to S7.

Fig. S8. The complete rectangular phylogenetic tree of intergenic spacer sequences is shown in Figure.

Sequences are publicly available at:

<https://www.ncbi.nlm.nih.gov/nuccore/PV650330>

<https://www.ncbi.nlm.nih.gov/nuccore/PV650287>

<https://www.ncbi.nlm.nih.gov/nuccore/PV648457>

<https://www.ncbi.nlm.nih.gov/nuccore/PV661755>

<https://www.ncbi.nlm.nih.gov/nuccore/PV648670>

<https://www.ncbi.nlm.nih.gov/nuccore/PV648672>

<https://www.ncbi.nlm.nih.gov/nuccore/PV648673>



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Supplementary Materials

The following figures and tables are included as supplementary materials in the manuscript.

Sample 1: S1

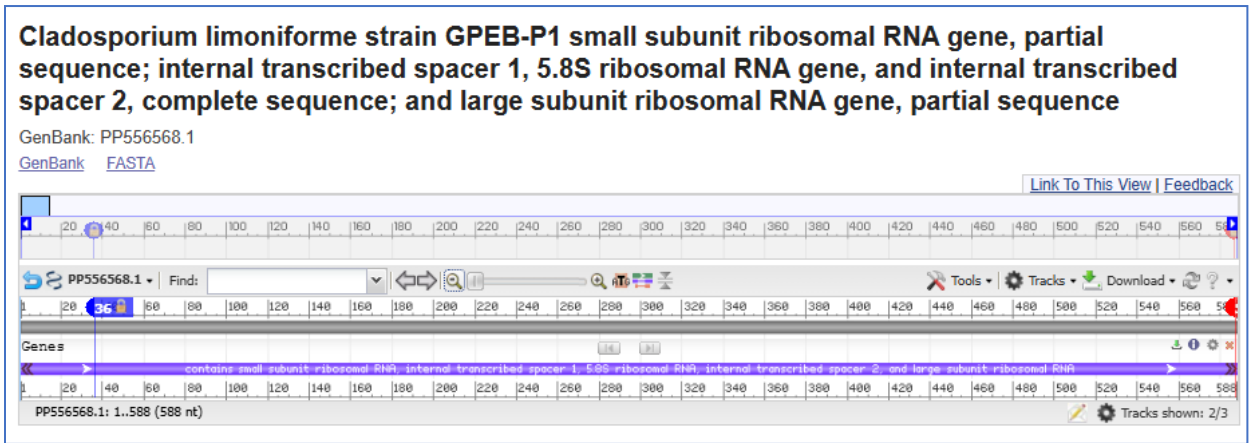


Fig. 1 S1. The exact position of the retrieved PCR amplicon on *Cladosporium limoniforme* (PP556568.1) reference genome.

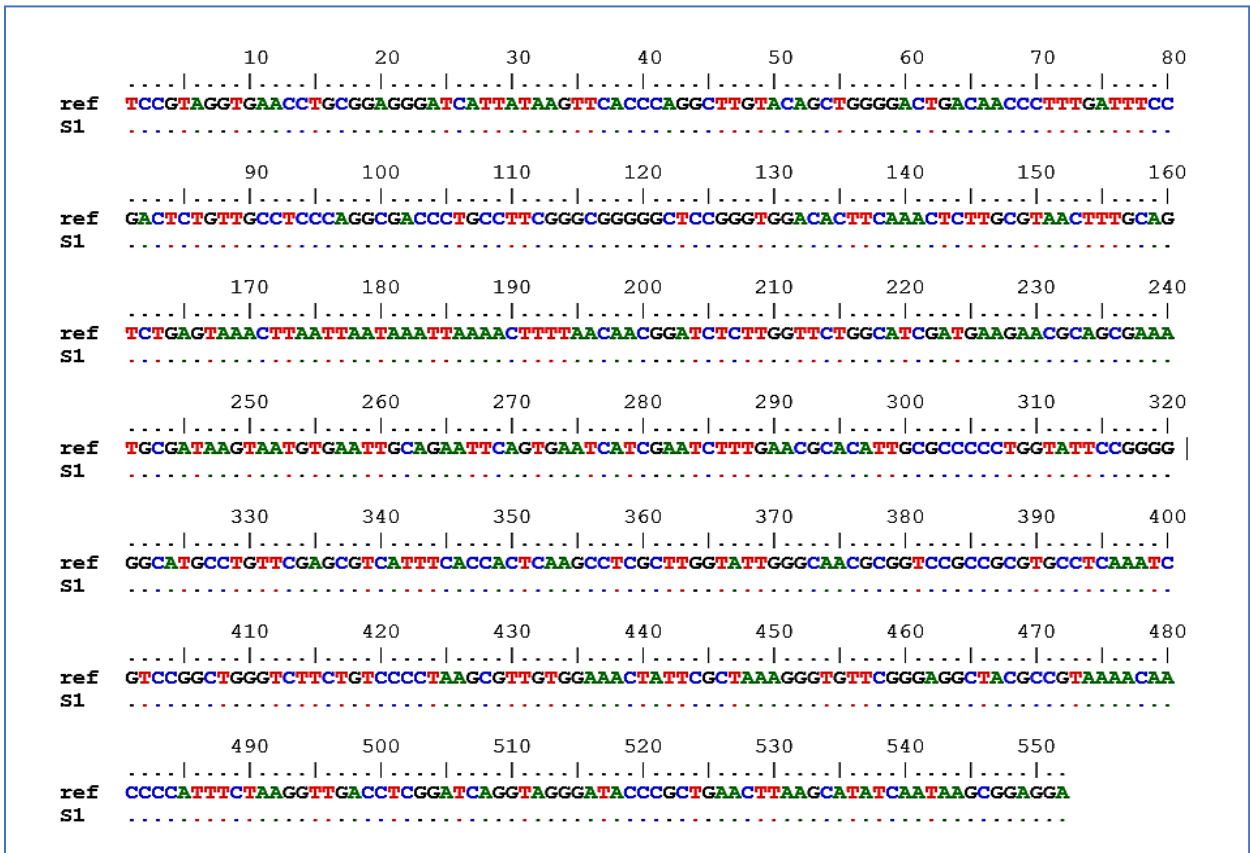


Fig. 2 S1. Nucleic acid sequences alignment of identified S1 *Cladosporium limoniforme* reference genome

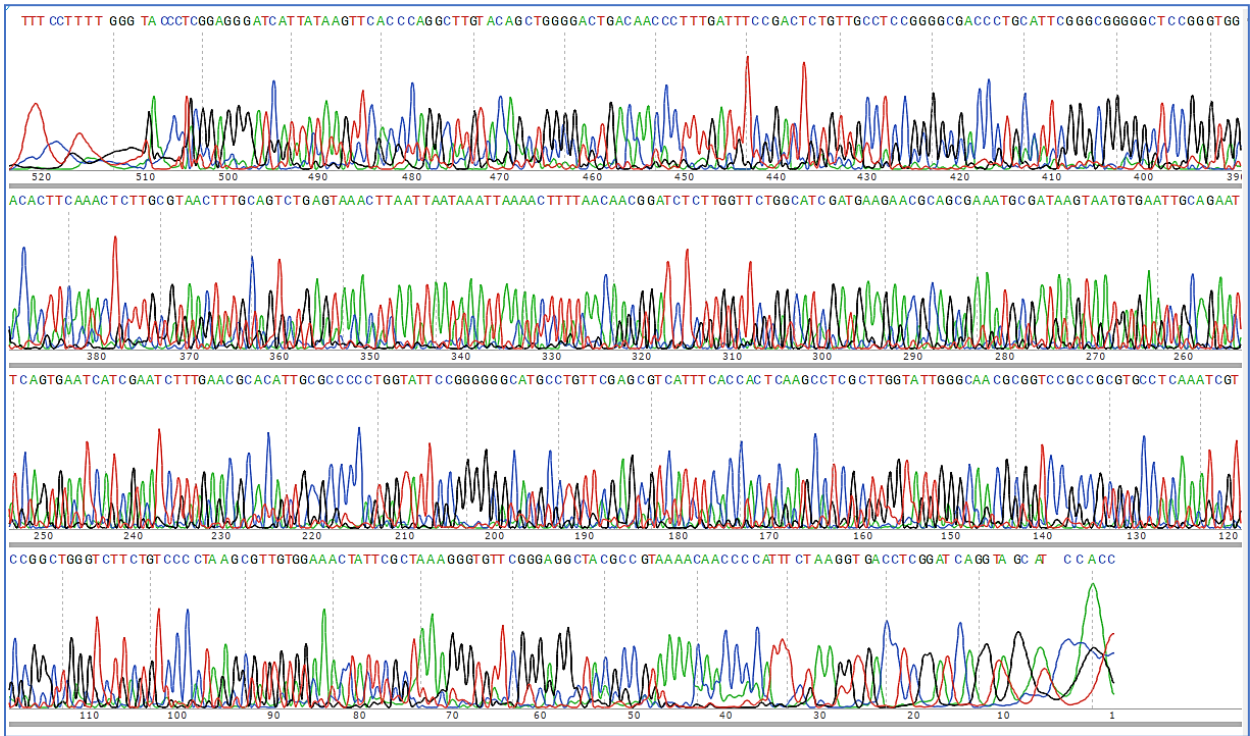


Fig. 3 S1. Sanger sequence chromatogram of S1.

Table S1. Identified nucleotide sequences of S1 *Cladosporium limoniforme* (PP556568.1) reference genome.

>ref_Cladosporium_limoniforme(PP556568.1)	TCCGTAGGTGAACCTGCGGAGGGATCATTATAAGTTACCCAGGCTTGTA CAGCTGGGGACTGACAACCCTTTGATTTCCGACTCTGTTGCCTCCCAGGC GACCTGCCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTTTGCG TAACCTTGCAGTCTGAGTAACTTAATTAATAAATTAACCTTTTAACAACG GATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTA ATGTGAATTGCAGAAATCAGTGAATCATCGAATCTTTGAACGCACATTGCG CCCCCTGGTATTCCGGGGGGGCATGCCTGTTTCGAGCGTCATTTCAACCA CT CAAGCCTCGCTTGGTATTGGGCAACGCGGTCCGCCGCGTGCCTCAAATC GTCCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAACTATTCGCTAAA GGGTGTTTCGGGAGGCTACGCCGTAAAACAACCCATTCTAAGGTTGACC TCGGATCAGGTAGGGATACCCGCTGAACCTAAGCATATCAATAAGCGGAG GA	552bp
>S1	TCCGTAGGTGAACCTGCGGAGGGATCATTATAAGTTACCCAGGCTTGTA CAGCTGGGGACTGACAACCCTTTGATTTCCGACTCTGTTGCCTCCCAGGC GACCTGCCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTTTGCG TAACCTTGCAGTCTGAGTAACTTAATTAATAAATTAACCTTTTAACAACG GATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTA ATGTGAATTGCAGAAATCAGTGAATCATCGAATCTTTGAACGCACATTGCG CCCCCTGGTATTCCGGGGGGGCATGCCTGTTTCGAGCGTCATTTCAACCA CT CAAGCCTCGCTTGGTATTGGGCAACGCGGTCCGCCGCGTGCCTCAAATC GTCCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAACTATTCGCTAAA GGGTGTTTCGGGAGGCTACGCCGTAAAACAACCCATTCTAAGGTTGACC TCGGATCAGGTAGGGATACCCGCTGAACCTAAGCATATCAATAAGCGGAG GA	552bp

Sample 2: S2

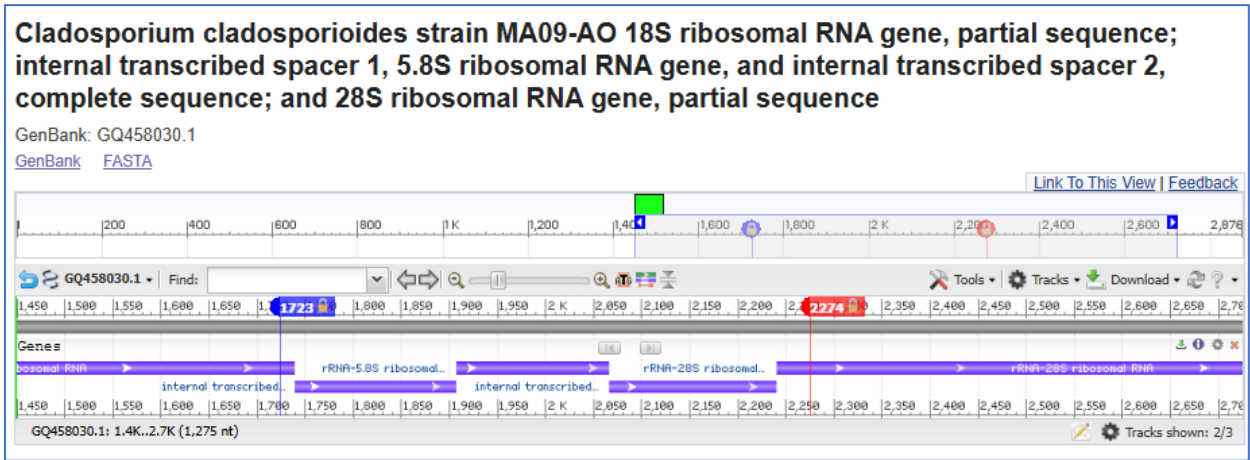


Fig. 1 S2. The exact position of the retrieved PCR amplicon on *Cladosporium cladosporioides* (GQ458030.1) reference genome.

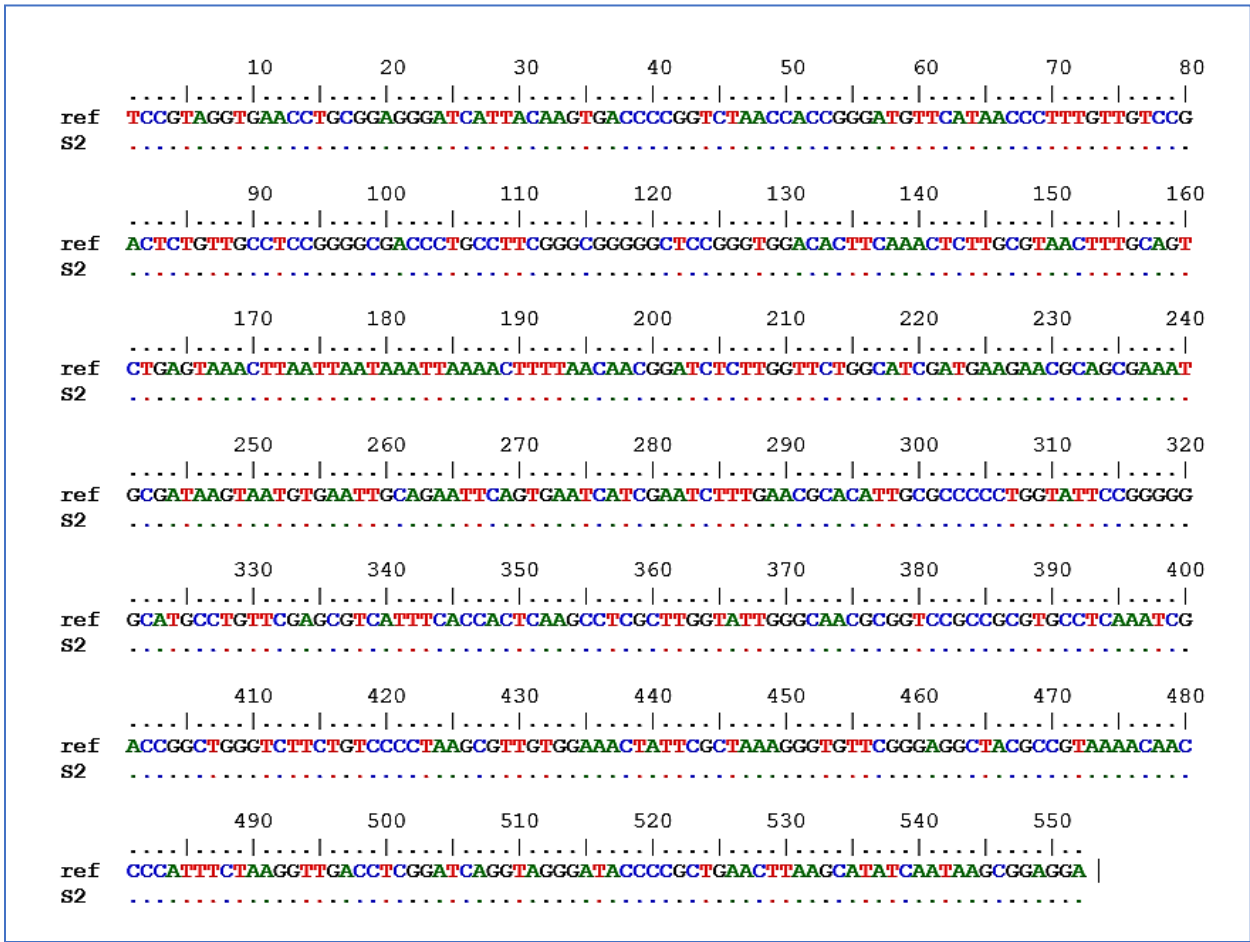


Fig. 2 S2. Nucleic acid sequences alignment of identified S2 *Cladosporium cladosporioides* reference genome.

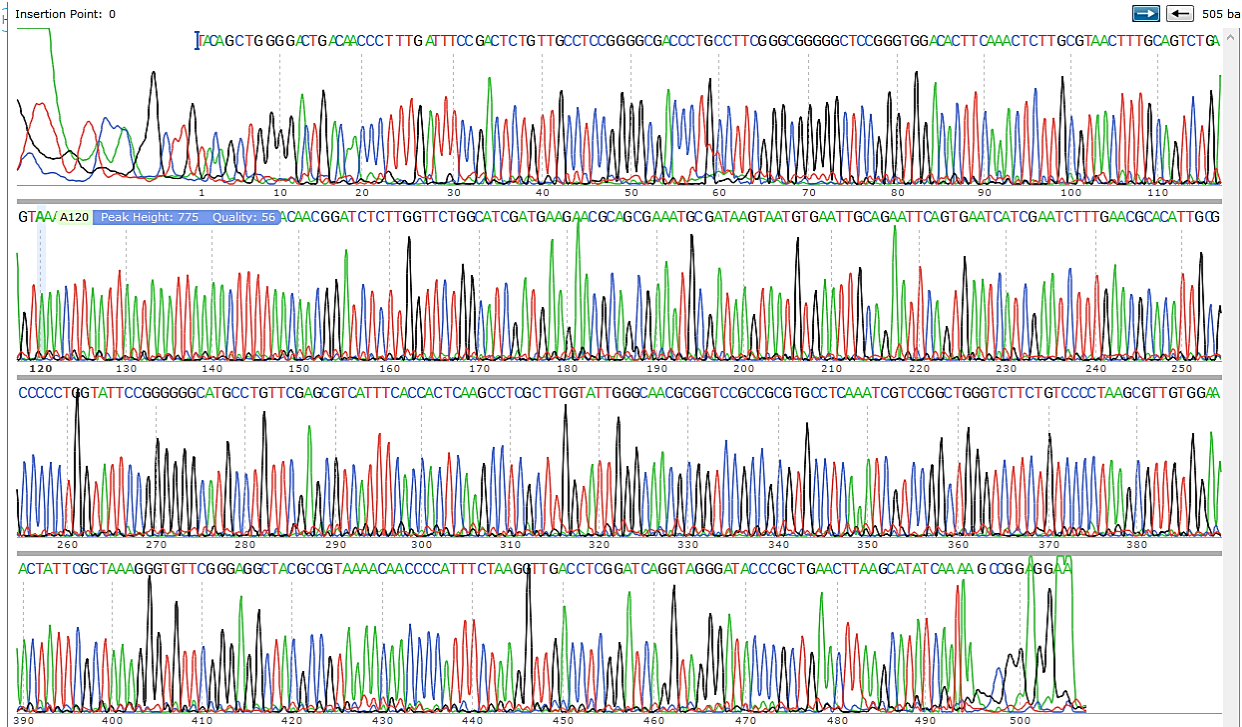


Fig.3 S2. Sanger sequence chromatogram of S2

Table 1 S2. Identified nucleotide sequences of S2 *Cladosporium cladosporioides* (GQ458030.1) reference genome.

>ref_Cladosporium _cladosporioides(G Q458030.1)	TCCGTAGGTGAACCTGCGGAGGGATCATTACAAGTGACCCCGGTCTAACCACC GGGATGTTTCATAACCCTTTGTTGTCCGACTCTGTTGCCTCCGGGGGCGACCTG CCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTTTGCGTAACCTTTGCAG TCTGAGTAAACTTAATTAATAAATTAATAACTTTTAAACGATCTCTTGGTTCT GGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATT CAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGG GCATGCCTGTTTCGAGCGTCATTTACCACTCAAGCCTCGTTGGTATTGGGCA ACGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAA GCGTTGTGGAAACTATTGCTAAAGGGTGTTCGGGAGGCTACGCCGTAAACA ACCCCATTTCTAAGGTTGACCTCGGATCAGGTAGGGATACCCCGCTGAACCTTA AGCATATCAATAAGCGGAGGA	552bp
>S2	TCCGTAGGTGAACCTGCGGAGGGATCATTACAAGTGACCCCGGTCTAACCACC GGGATGTTTCATAACCCTTTGTTGTCCGACTCTGTTGCCTCCGGGGGCGACCTG CCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTTTGCGTAACCTTTGCAG TCTGAGTAAACTTAATTAATAAATTAATAACTTTTAAACGATCTCTTGGTTCT GGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATT CAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGG GCATGCCTGTTTCGAGCGTCATTTACCACTCAAGCCTCGTTGGTATTGGGCA ACGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAA GCGTTGTGGAAACTATTGCTAAAGGGTGTTCGGGAGGCTACGCCGTAAACA ACCCCATTTCTAAGGTTGACCTCGGATCAGGTAGGGATACCCCGCTGAACCTTA AGCATATCAATAAGCGGAGGA	552bp

Sample 3: S3

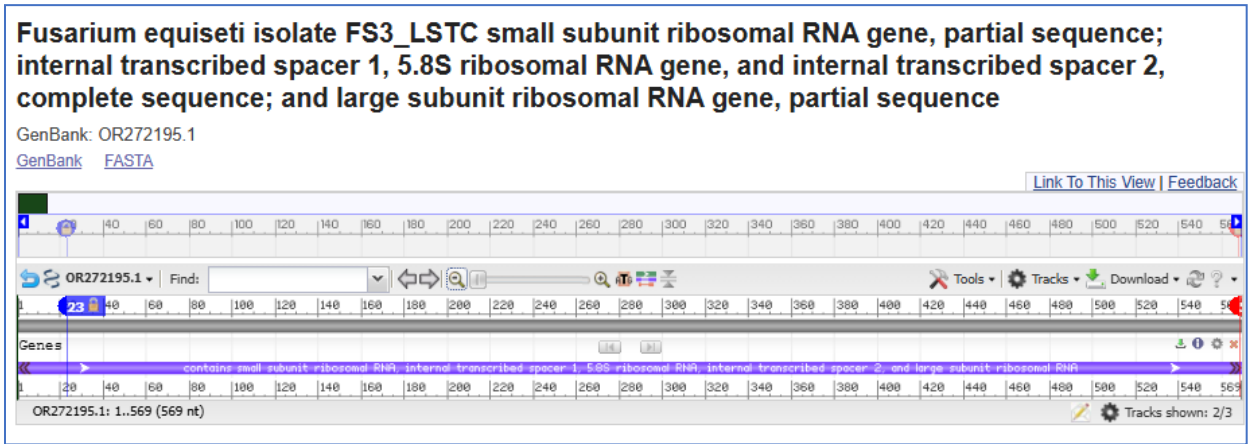


Fig. 1 S3. The exact position of the retrieved PCR amplicon on *Fusarium_equiseti* (OR272195.1) reference genome.

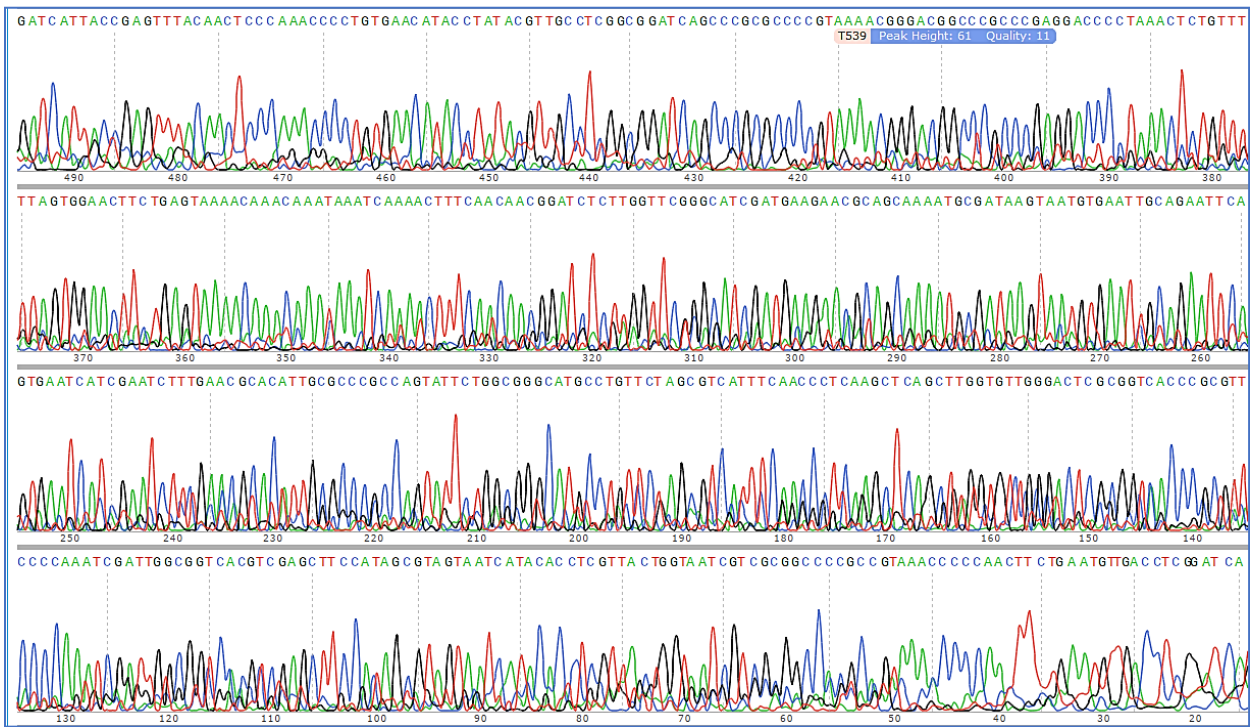
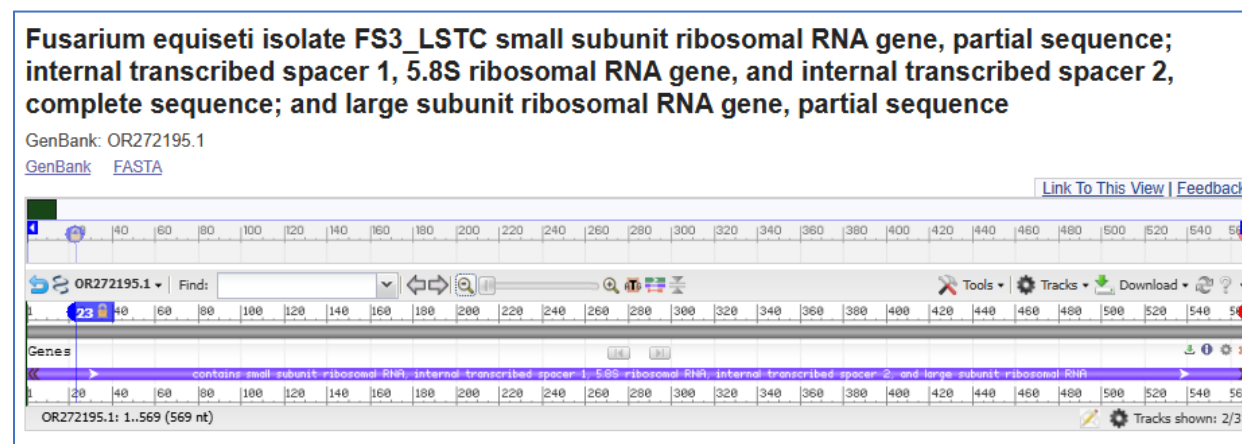


Fig. 2 S3. Sanger sequence chromatogram of S3.

Table 1 S3. Identified nucleotide sequences of S3 and *Fusarium equiseti* (OR272195.1) reference genome.

>Ref_ <i>Fusarium equiseti</i> (OR272195.1)	TCCGTAGGTGAACCTGCGGAGGGATCATTACCGAGTTTACAACCTCCCAAACCCCT GTGAACATACCTATACGTTGCCTCGGCGGATCAGCCCGCGCCCCGTAAAACGGGA CGGCCCCGCCGAGGACCCCTAAACTCTGTTTTAGTGGAACCTTCTGAGTAAACAA ACAAATAAATCAAACTTTCAACAACGGATCTCTTGTTCTGGCATCGATGAAGAAC GCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTT GAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATT TCAACCCTCAAGCTCAGCTTGGTGTGGGACTCGCGGTAACCCGCGTTCCCCAAA TCGATTGGCGGTCACGTCGAGCTTCCATAGCGTAGTAATCATACACCTCGTTACTG GTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCA GGTAGGAATACCCGCTGAACCTTAAGCATATCAATAAGCGGAGGA	546bp
S3	TCCGTAGGTGAACCTGCGGAGGGATCATTACCGAGTTTACAACCTCCCAAACCCCT GTGAACATACCTATACGTTGCCTCGGCGGATCAGCCCGCGCCCCGTAAAACGGGA CGGCCCCGCCGAGGACCCCTAAACTCTGTTTTAGTGGAACCTTCTGAGTAAACAA ACAAATAAATCAAACTTTCAACAACGGATCTCTTGTTCTGGCATCGATGAAGAAC GCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTT GAACGCACATTGCGCCCCGCCAGTATTCTGGCGGGCATGCCTGTTTCGAGCGTCATT TCAACCCTCAAGCTCAGCTTGGTGTGGGACTCGCGGTAACCCGCGTTCCCCAAA TCGATTGGCGGTCACGTCGAGCTTCCATAGCGTAGTAATCATACACCTCGTTACTG GTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCA GGTAGGAATACCCGCTGAACCTTAAGCATATCAATAAGCGGAGGA	546bp

Sample 4: S4**Fig. 1 S4.** The exact position of the retrieved PCR amplicon on *Fusarium equiseti* (OR272195.1) reference genome.

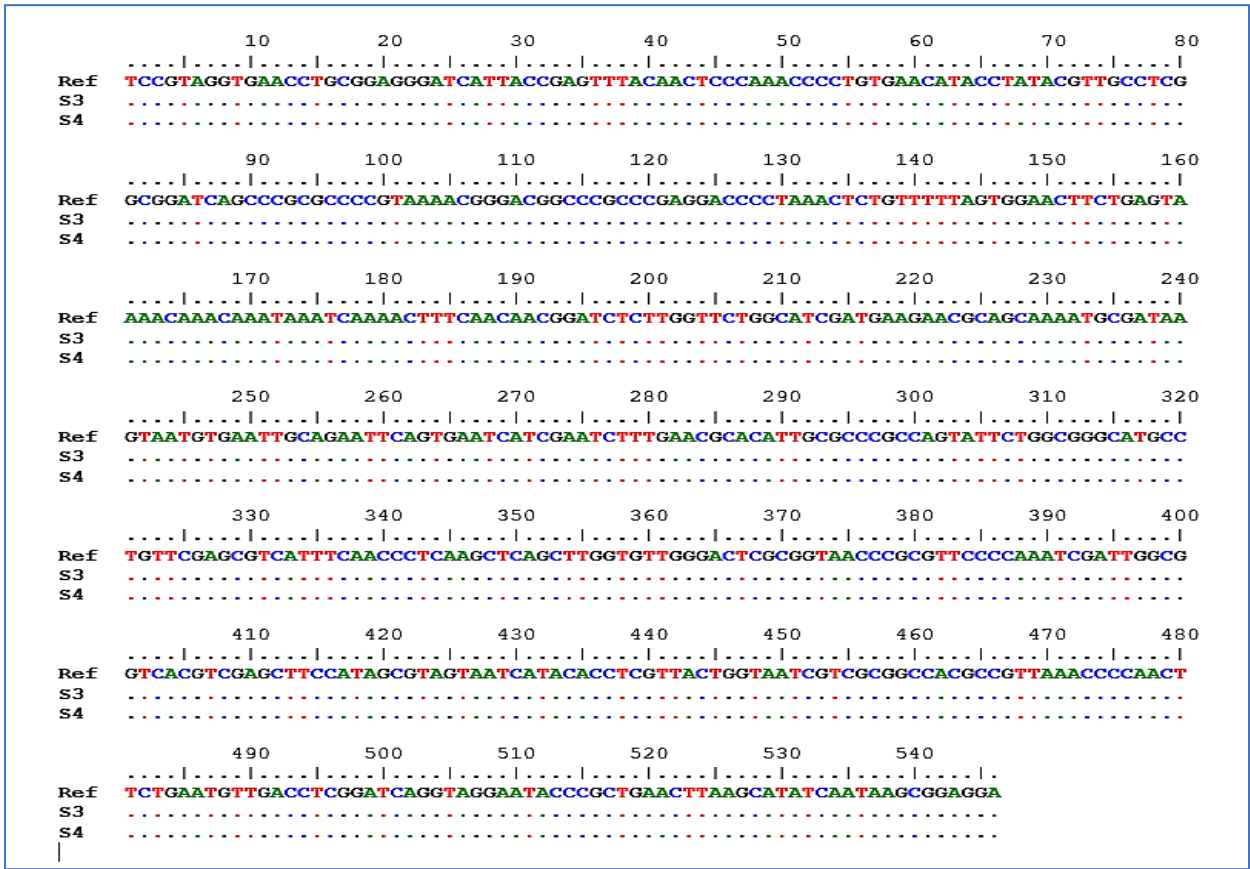


Fig. 2 S4. Nucleic acid sequences alignment of identified S4 *Fusarium equiseti* reference genome.

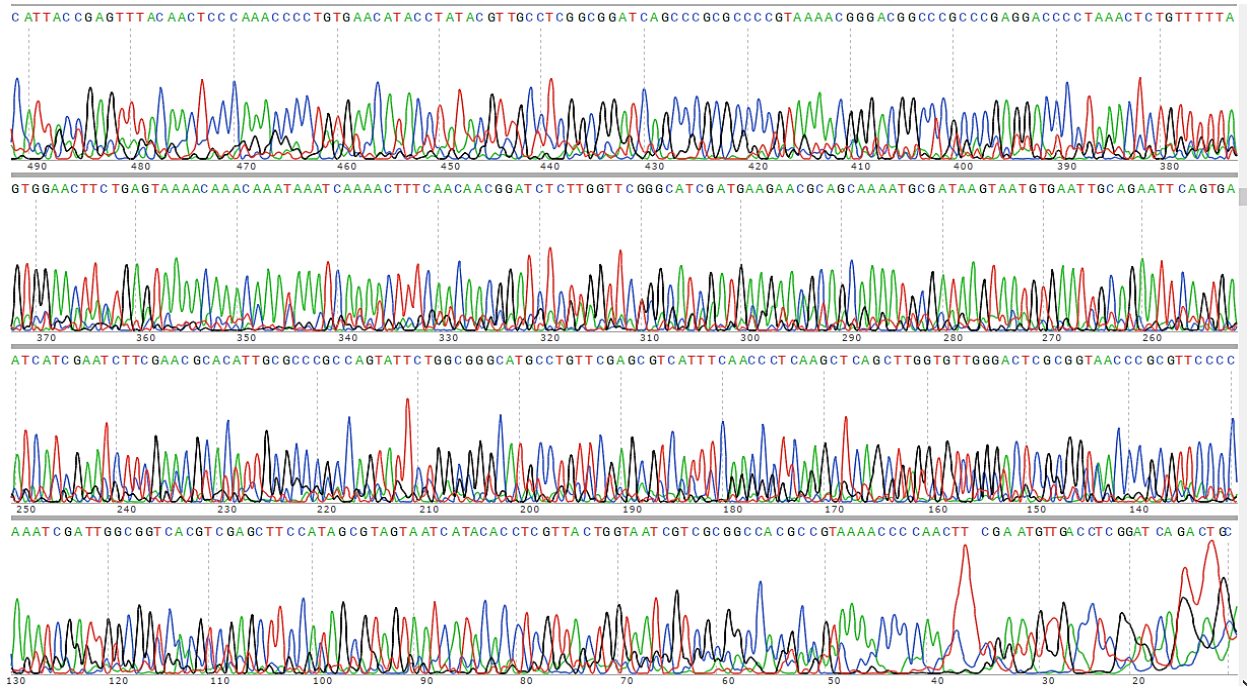
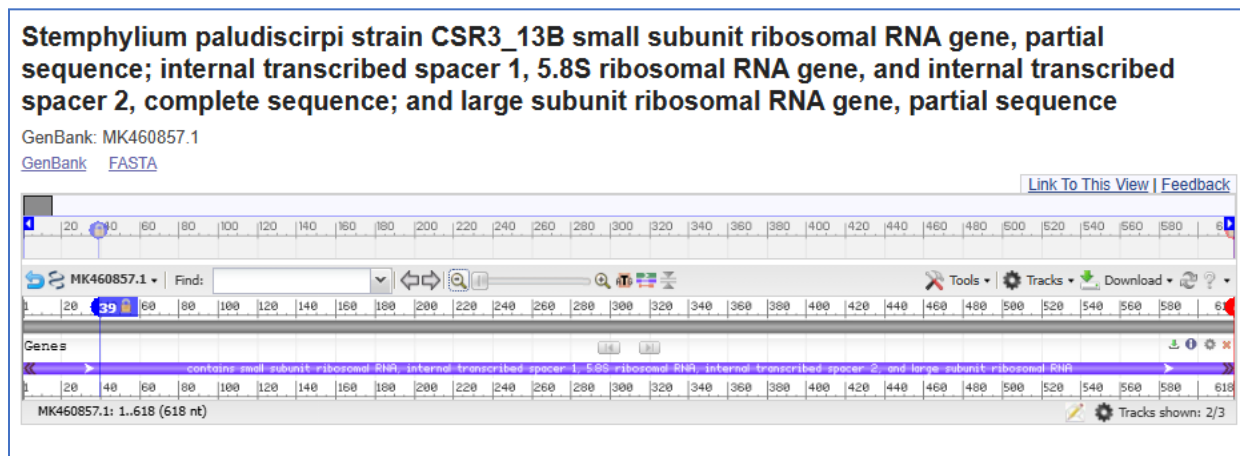


Fig. 3 S4. Sanger sequence chromatogram of S4.

Table 1 S4. Identified nucleotide sequences of S4 *Fusarium equiseti* (OR272195.1) reference genome.

>Fusarium_equiseti (OR272195.1)	TCCGTAGGTGAACCTGCGGAGGGATCATTACCGAGTTTACAACCTCCCAAACCCCTGTG AACATACCTATACGTTGCCTCGGCGGATCAGCCCCGCGCCCCGTAAAACGGGACGGCC CGCCCCGAGGACCCCTAAACTCTGTTTTAGTGGAACCTCTGAGTAAAACAAACAAATAA ATCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAAT GCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTG CGCCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCT CAGCTTGGTGTGGGACTCGCGGTAACCCGCGTTCCCAAATCGATTGGCGGGTCACG TCGAGCTTCCATAGCGTAGTAATCATACACCTCGTTACTGGTAATCGTCGCGGCCACG CCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAAC TTAAGCATATCAATAAGCGGAGGA	546bp
S4	TCCGTAGGTGAACCTGCGGAGGGATCATTACCGAGTTTACAACCTCCCAAACCCCTGTG AACATACCTATACGTTGCCTCGGCGGATCAGCCCCGCGCCCCGTAAAACGGGACGGCC CGCCCCGAGGACCCCTAAACTCTGTTTTAGTGGAACCTCTGAGTAAAACAAACAAATAA ATCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCAAAAT GCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTG CGCCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGTCATTTCAACCCTCAAGCT CAGCTTGGTGTGGGACTCGCGGTAACCCGCGTTCCCAAATCGATTGGCGGGTCACG TCGAGCTTCCATAGCGTAGTAATCATACACCTCGTTACTGGTAATCGTCGCGGCCACG CCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCAGGTAGGAATACCCGCTGAAC TTAAGCATATCAATAAGCGGAGGA	546bp

Sample 5: S5**Fig. 1 S5.** The exact position of the retrieved PCR amplicon on *Stemphylium paludiscirpi* ([MK460857.1](#)) reference genome.

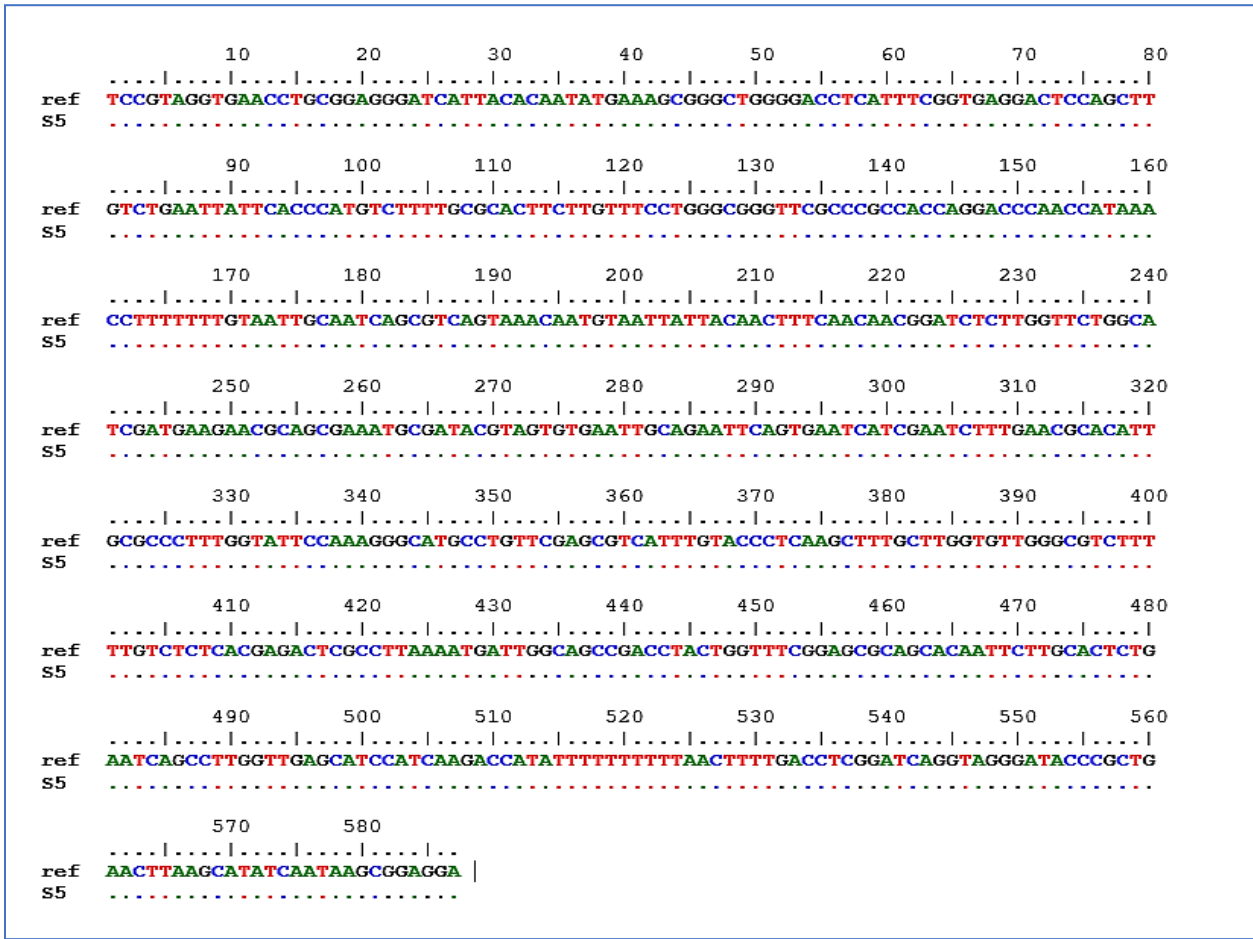


Fig. 2 S5. Nucleic acid sequences alignment of identified S5 *Stenphylium paludiscirpi* reference genome.

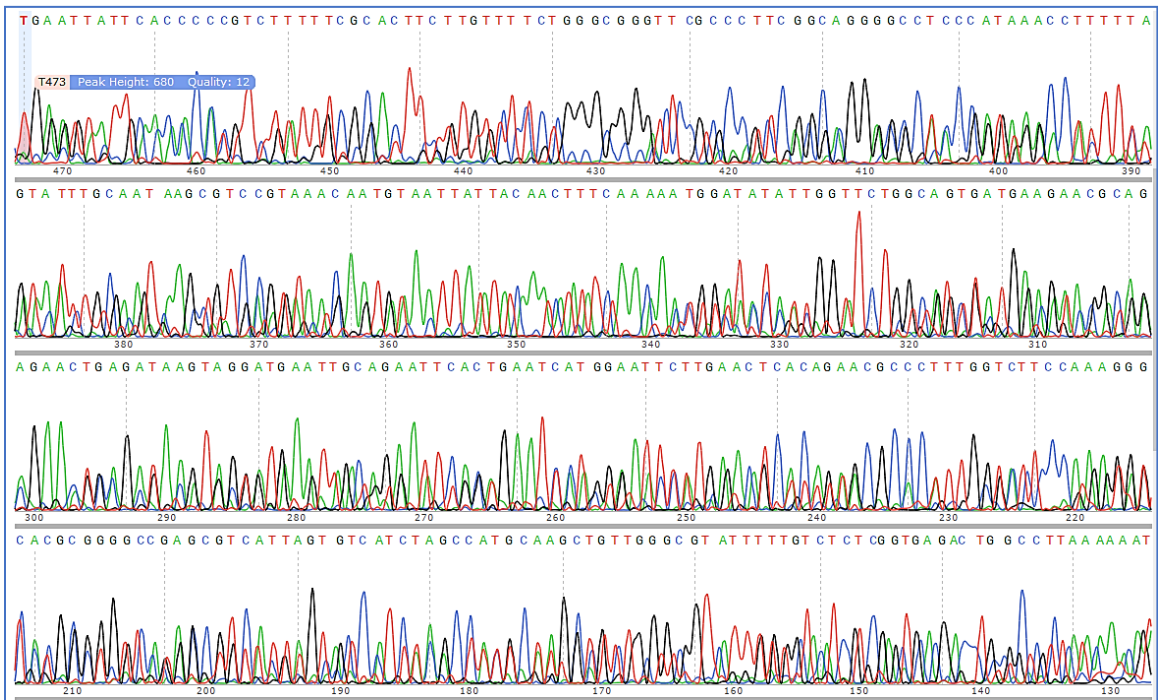
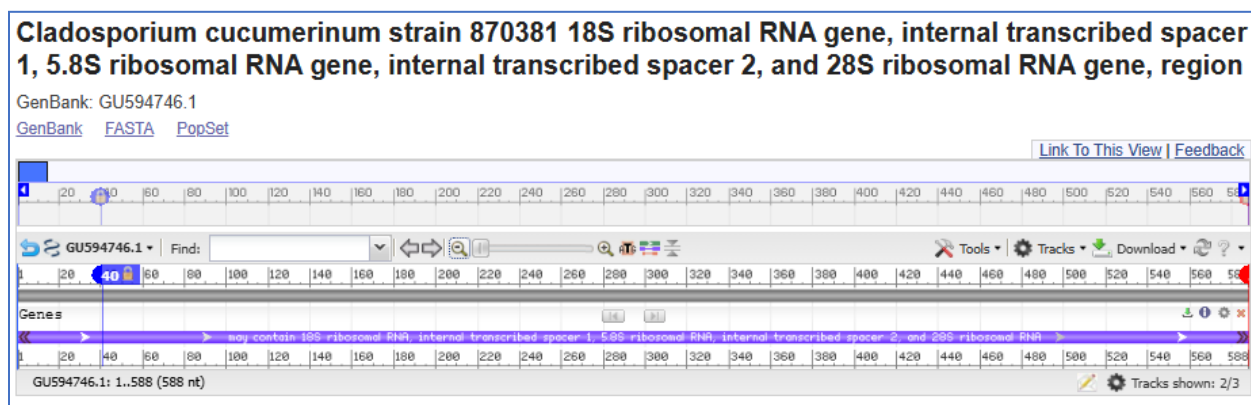


Fig. 3 S5. Sanger sequence chromatogram of S5.

Table 1 S5. Identified nucleotide sequences of S5 *Stemphylium paludiscirpi* (MK460857.1) reference genome.

>Stemphylium_ paludiscirpi(MK 460857.1)	TCCGTAGGTGAACCTGCGGAGGGATCATTACACAATATGAAAGCGGGCTGGGGAC CTCATTTTCGGTGAGGACTCCAGCTTGTCTGAATTATTCACCCATGTCTTTTTCGCA CTTCTTGTTCCTGGGCGGGTTCGCCCCGCCACCAGGACCCAACCATAAACCTTTTT TTGTAATTGCAATCAGCGTCAGTAAACAATGTAATTATTACAACCTTTCAACAACGGA TCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAGTGTGAAT TGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTC CAAAGGGCATGCCTGTTTCGAGCGTCATTTGTACCCTCAAGCTTTGCTTGGTGTGG GCGTCTTTTTGTCTCTCACGAGACTCGCCTTAAATGATTGGCAGCCGACCTACTG GTTTCGGAGCGCAGCACAATTCTTGCACTCTGAATCAGCCTTGGTTGAGCATCCAT CAAGACCATATTTTTTTTTTAACCTTTGACCTCGGATCAGGTAGGGATACCCGCTGA ACTTAAGCATATCAATAAGCGGAGGA	587bp
S5	TCCGTAGGTGAACCTGCGGAGGGATCATTACACAATATGAAAGCGGGCTGGGGAC CTCATTTTCGGTGAGGACTCCAGCTTGTCTGAATTATTCACCCATGTCTTTTTCGCA CTTCTTGTTCCTGGGCGGGTTCGCCCCGCCACCAGGACCCAACCATAAACCTTTTT TTGTAATTGCAATCAGCGTCAGTAAACAATGTAATTATTACAACCTTTCAACAACGGA TCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAGTGTGAAT TGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTC CAAAGGGCATGCCTGTTTCGAGCGTCATTTGTACCCTCAAGCTTTGCTTGGTGTGG GCGTCTTTTTGTCTCTCACGAGACTCGCCTTAAATGATTGGCAGCCGACCTACTG GTTTCGGAGCGCAGCACAATTCTTGCACTCTGAATCAGCCTTGGTTGAGCATCCAT CAAGACCATATTTTTTTTTTAACCTTTGACCTCGGATCAGGTAGGGATACCCGCTGA ACTTAAGCATATCAATAAGCGGAGGA	587bp

Sample 6: S6**Fig. 1 S6.** The exact position of the retrieved PCR amplicon on *Cladosporium cucumerinum* (GU594746.1) reference genome.

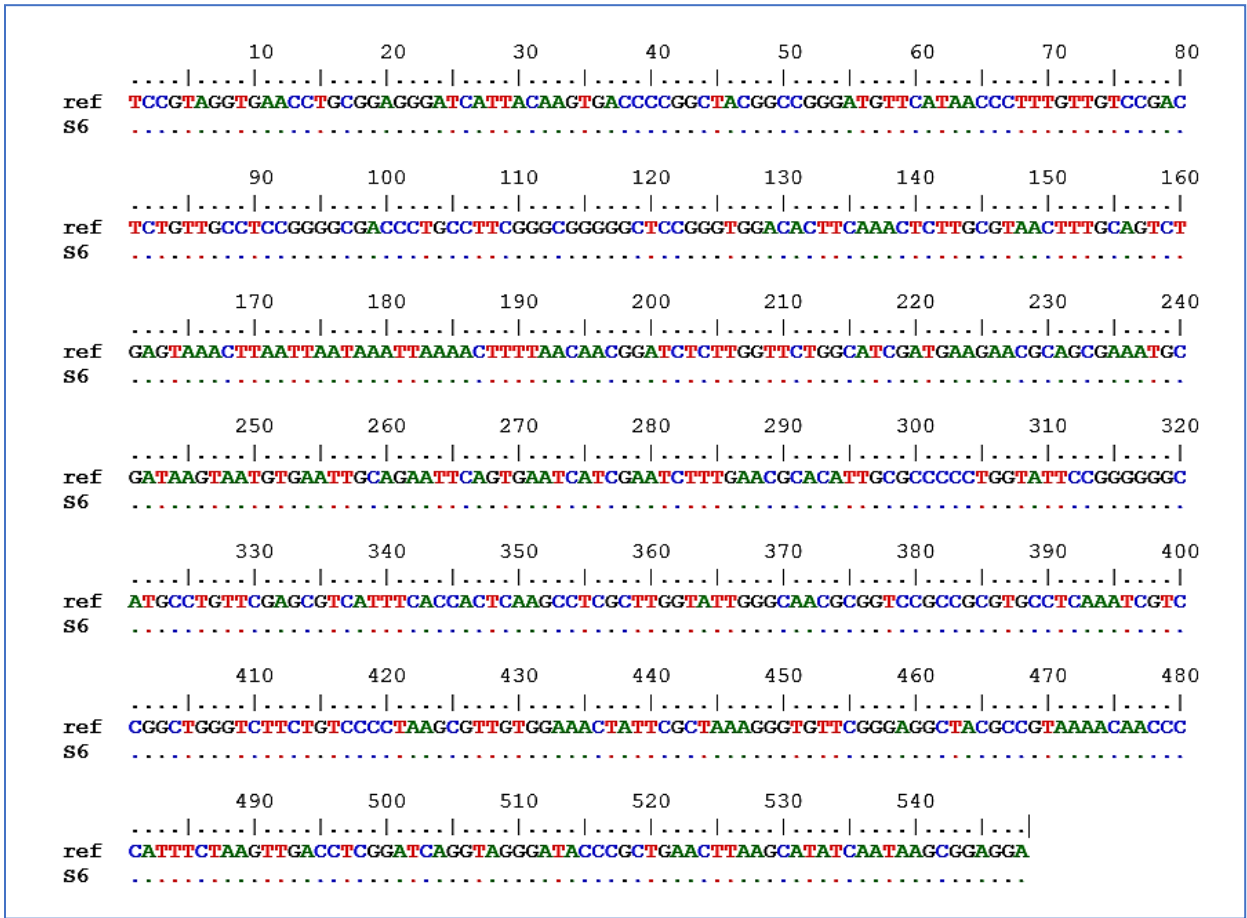


Fig. 2 S6. Nucleic acid sequences alignment of identified S6 *Cladosporium limoniforme* reference genome.

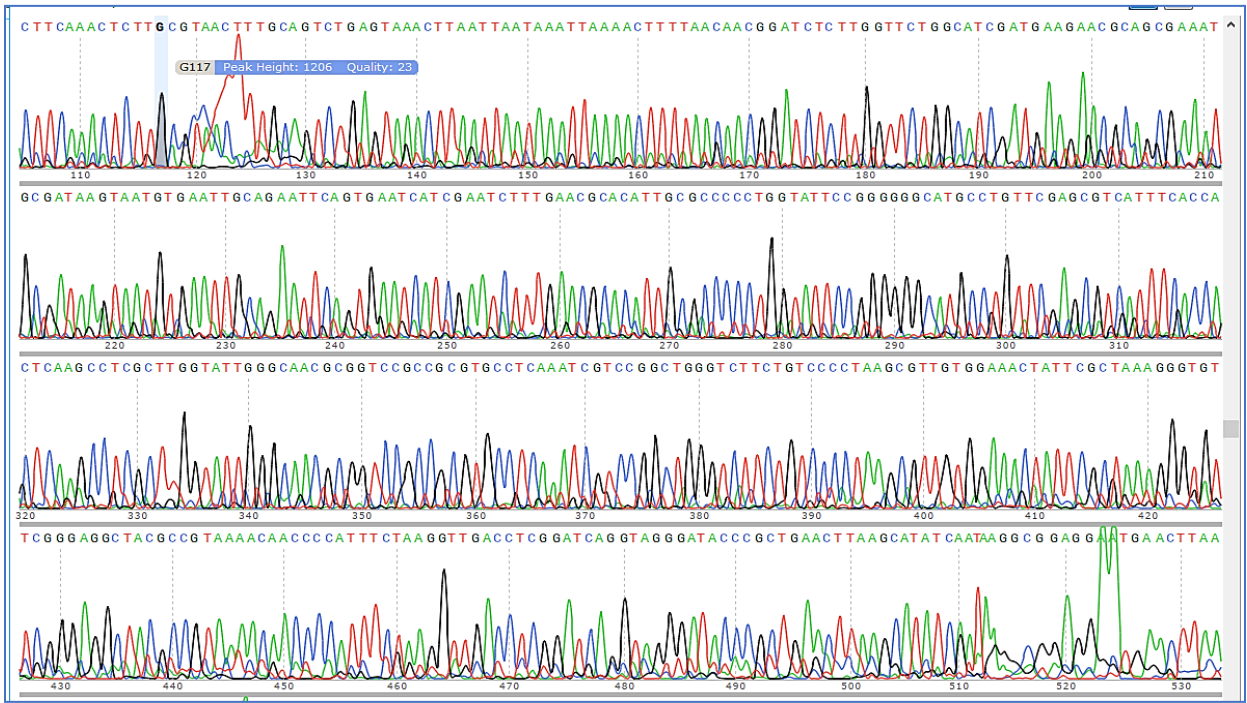


Fig. 3 S6. Sanger sequence chromatogram of S6.

Table 1 S6. Identified nucleotide sequences of S6 *Cladosporium cucumerinum* (GU594746.1) reference genome

>ref_Cladosporium_cucumerinum(GU594746.1)	TCCGTAGGTGAACCTGCGGAGGGATCATTACAAGTGACCCCGGCTACGGCCGGGATGTTCA	5
	TAACCCTTTGTTGTCCGACTCTGTTGCCTCCGGGGCGACCTGCCTTCGGGCGGGGGCTCC	4
	GGGTGGACACTTCAAACCTCTTGCGTAACCTTGCAGTCTGAGTAACTTAATTAATAAATTA	8
	CTTTTAACAACGGATCTCTTGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA	b
	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTC	p
>S6	CGGGGGGCATGCCTGTTGAGCGTCATTTACCACTCAAGCCTCGCTTGGTATTGGGCAAC	
	GCGGTCCGCCGCGTGCCTCAAATCGTCCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAA	
	ACTATTCGCTAAAGGGTGTTCTGGGAGGCTACGCCGTAAACAACCCCATTTCTAAGTTGACCT	
	CGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA	
	TCCGTAGGTGAACCTGCGGAGGGATCATTACAAGTGACCCCGGCTACGGCCGGGATGTTCA	5
	TAACCCTTTGTTGTCCGACTCTGTTGCCTCCGGGGCGACCTGCCTTCGGGCGGGGGCTCC	4
	GGGTGGACACTTCAAACCTCTTGCGTAACCTTGCAGTCTGAGTAACTTAATTAATAAATTA	8
	CTTTTAACAACGGATCTCTTGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA	b
	TGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTC	p
	CGGGGGGCATGCCTGTTGAGCGTCATTTACCACTCAAGCCTCGCTTGGTATTGGGCAAC	
	GCGGTCCGCCGCGTGCCTCAAATCGTCCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAA	
	ACTATTCGCTAAAGGGTGTTCTGGGAGGCTACGCCGTAAACAACCCCATTTCTAAGTTGACCT	
	CGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA	

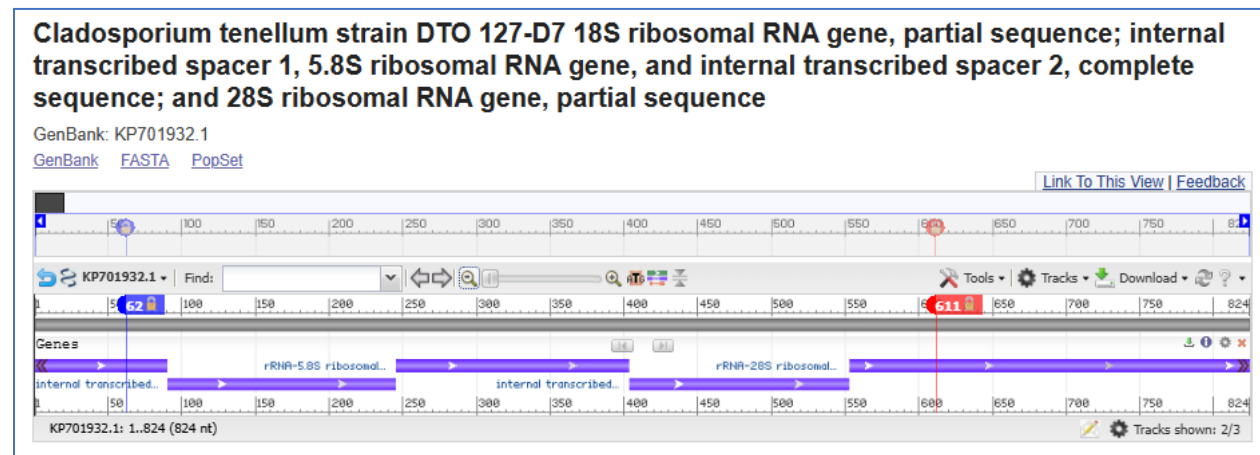
Sample 7: S7**Fig. 1 S7.** The exact position of the retrieved PCR amplicon on *Cladosporium tenellum* ([KP701932.1](#)) reference genome.



Fig. 2 S7. Nucleic acid sequences alignment of identified S7 *Cladosporium tenellum* reference genome.

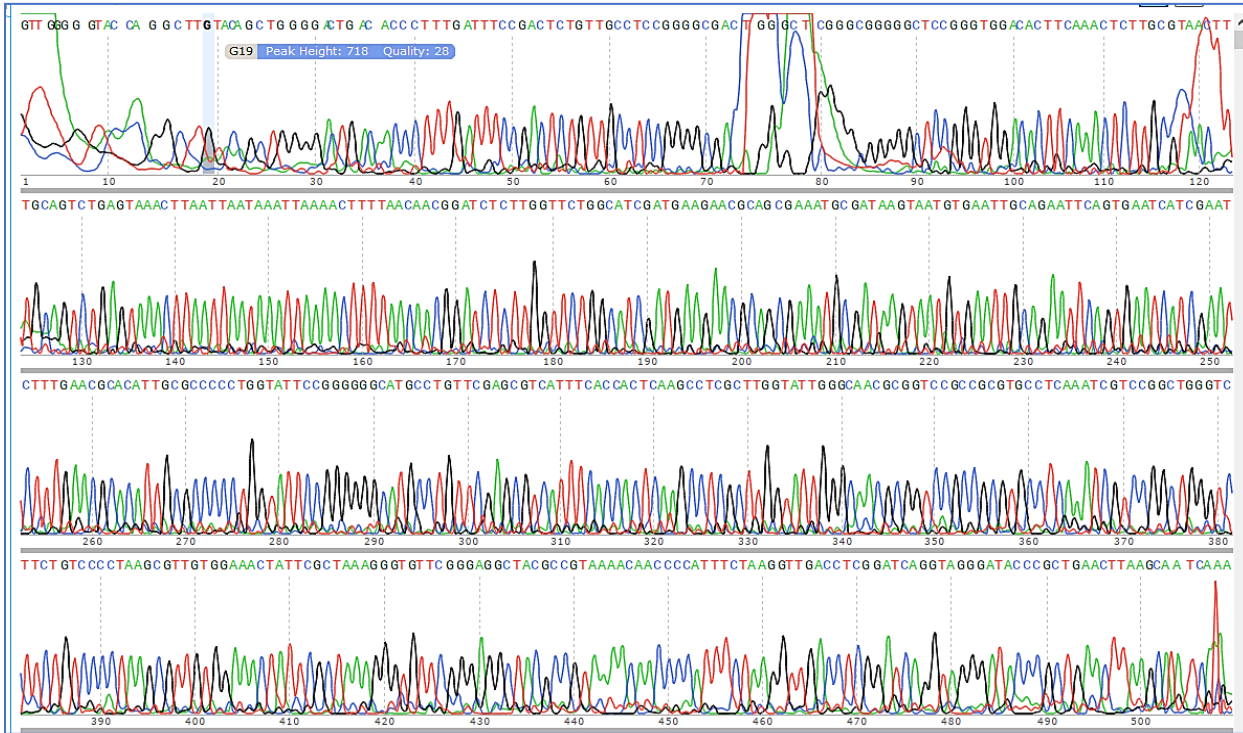
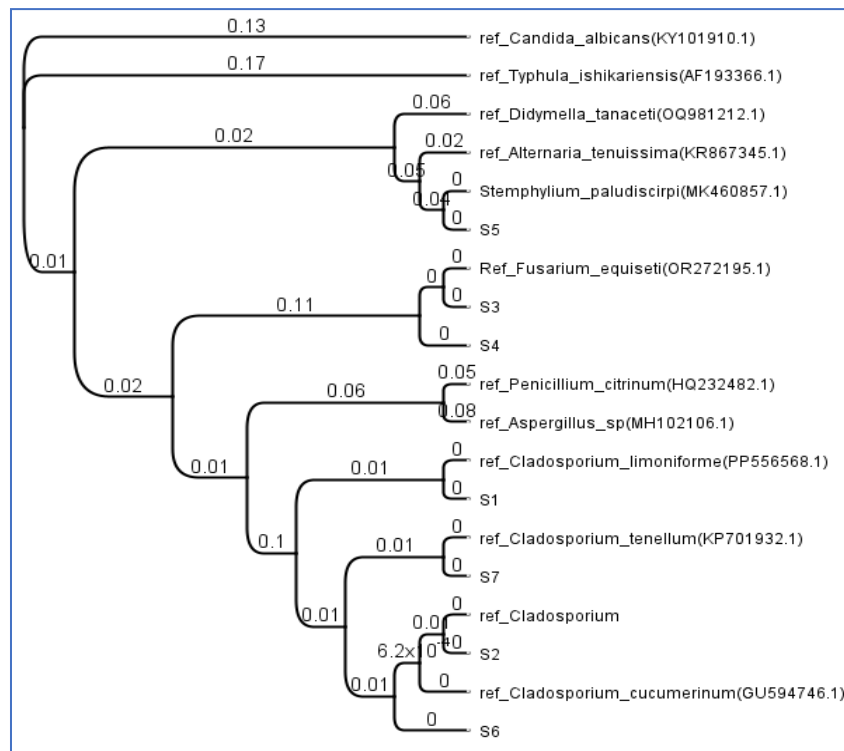


Fig. 3 S7. Sanger sequence chromatogram of S7.

Table 1 S7. Identified nucleotide sequences of S7 *Cladosporium tenellum* (KP701932.1) reference genome

>ref_Cladosporium_tenellum(KP701932.1)	TCTCCGTAGGTGAACCTGCGGAGGGATCATTACAAGAACTTCCGGGCTTCGGCCTGTTATTTCATAACCCCTTTGTTGTCCGACTCTGTTGCCTCCGGGGCGACCCTGCCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTTTCGCGTAACCTTTGCAGTCTGAGTAACTTAATTAATAAATTAATAAATTTTAAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTGAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTTTCGAGCGTCATTTACCACTCAAGCCTCGCTTGGTATTGGGCAACGCGGTCCGCCGCGTGCCTCAAATCGTCCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAACTATTCGCTAAAGGGTGTTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAA GCATATCAATAAGCGGAGGA	552bp
S7	TCTCCGTAGGTGAACCTGCGGAGGGATCATTACAAGAACTTCCGGGCTTCGGCCTGTTATTTCATAACCCCTTTGTTGTCCGACTCTGTTGCCTCCGGGGCGACCCTGCCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTTTCGCGTAACCTTTGCAGTCTGAGTAACTTAATTAATAAATTAATAAATTTTAAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTGAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTTTCGAGCGTCATTTACCACTCAAGCCTCGCTTGGTATTGGGCAACGCGGTCCGCCGCGTGCCTCAAATCGTCCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAACTATTCGCTAAAGGGTGTTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAA GCATATCAATAAGCGGAGGA	552bp

**Fig. S8.** The complete rectangular phylogenetic tree of intergenic spacer sequences is shown in Figure. All of the aforementioned figures corresponded to each relevant species' GenBank accession number. The degree of scale range among the comprehensive tree-categorized organisms is indicated by the number at the base of the tree. The code of the examined samples is denoted by the letter "S#."