

1 Article

2 **Microbiota in waterlogged archaeological wood: use**  
3 **of Next-Generation Sequencing to evaluate the risk**  
4 **of biodegradation**5 Federica Antonelli <sup>1,\*</sup>, Alfonso Esposito <sup>2</sup>, Giulia Galotta <sup>3</sup>, Barbara Davidde Petriaggi <sup>4</sup>, Silvano  
6 Piazza <sup>2</sup>, Manuela Romagnoli <sup>1,\*</sup> and Francesca Guerrieri <sup>5,\*</sup>

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## Supplementary materials

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Table S1. Raw data obtained for 16S and ITS with the two extraction protocols.

Sample	16S reads	ITS reads
1N1	2,702	11,200
1N39	44,964	61,156
1N4	21,415	118,330
1N88	30,056	48,538
1N9	43,020	112,721
1PF	26,894	12,191
1PL1	47,586	48,457
1PL2	26,840	4,079
1PO	18,570	3,170
1PQ	27,112	5,613
2N1	36,694	69,632
2N39	16,018	10,812
2N88	48,885	77,865
2N9	53,661	24,623
2PF	10,708	39,232
2PO	55,023	204
2PQ	34,399	109,015

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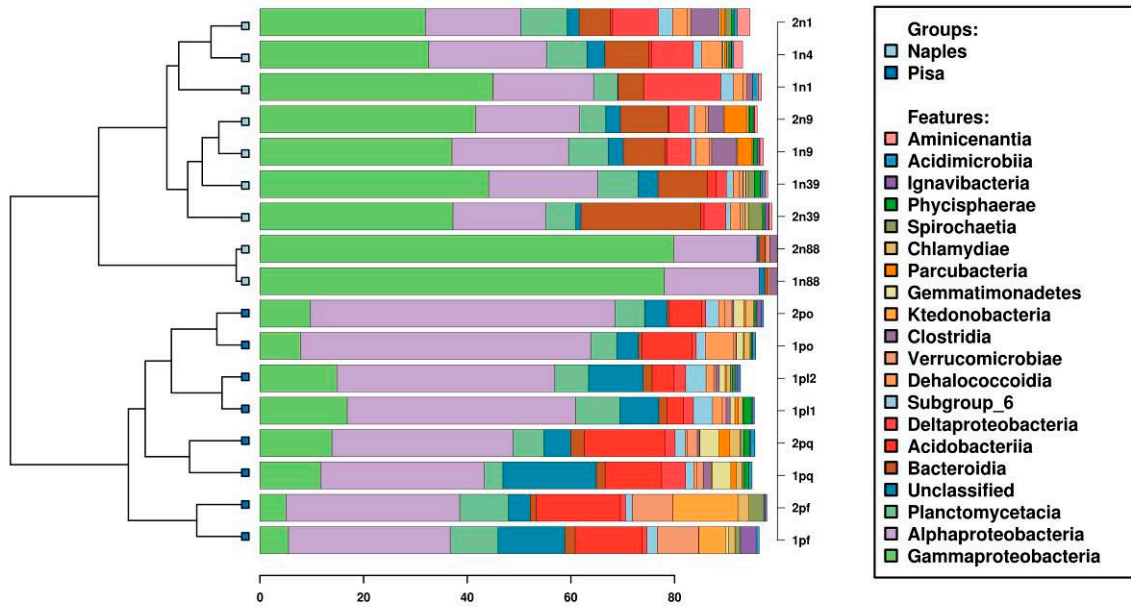
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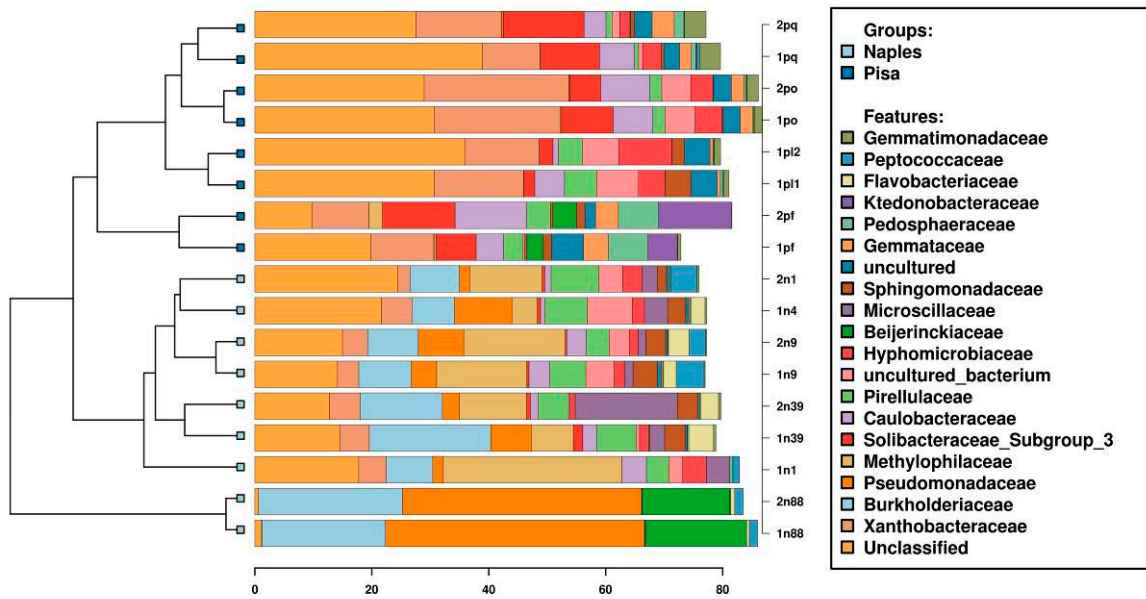
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Figure S1. 16S. Stacked barcharts of the taxonomic profile at class level.



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Figure S2. 16S. Stacked barcharts of the taxonomic profile at family level.

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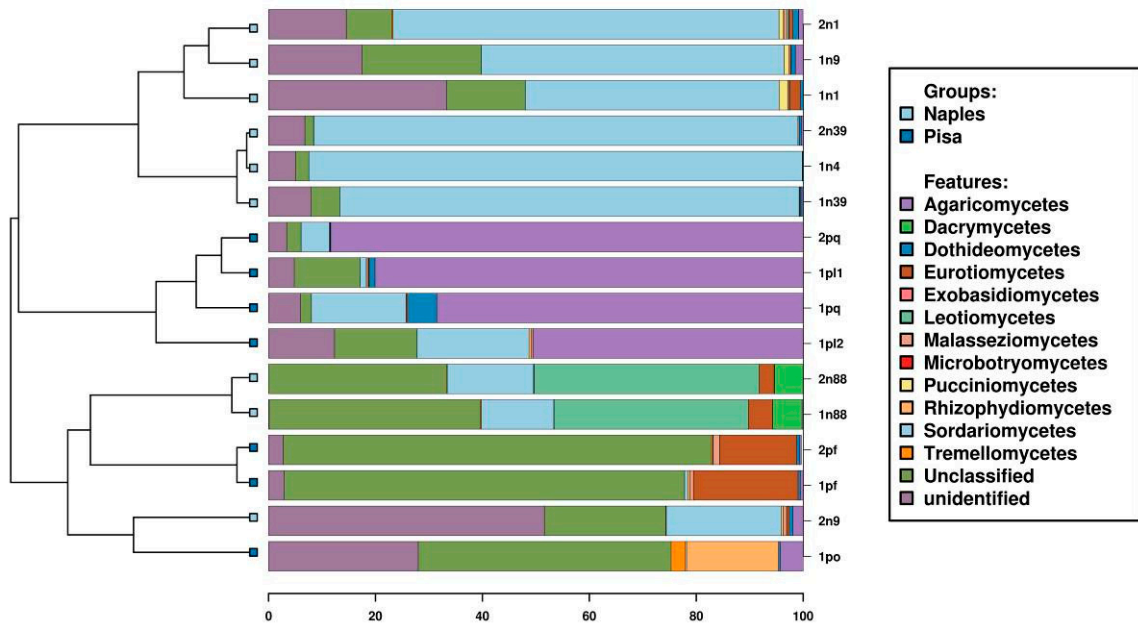


Figure S3. ITS2. Stacked barcharts of the taxonomic profile at class level.

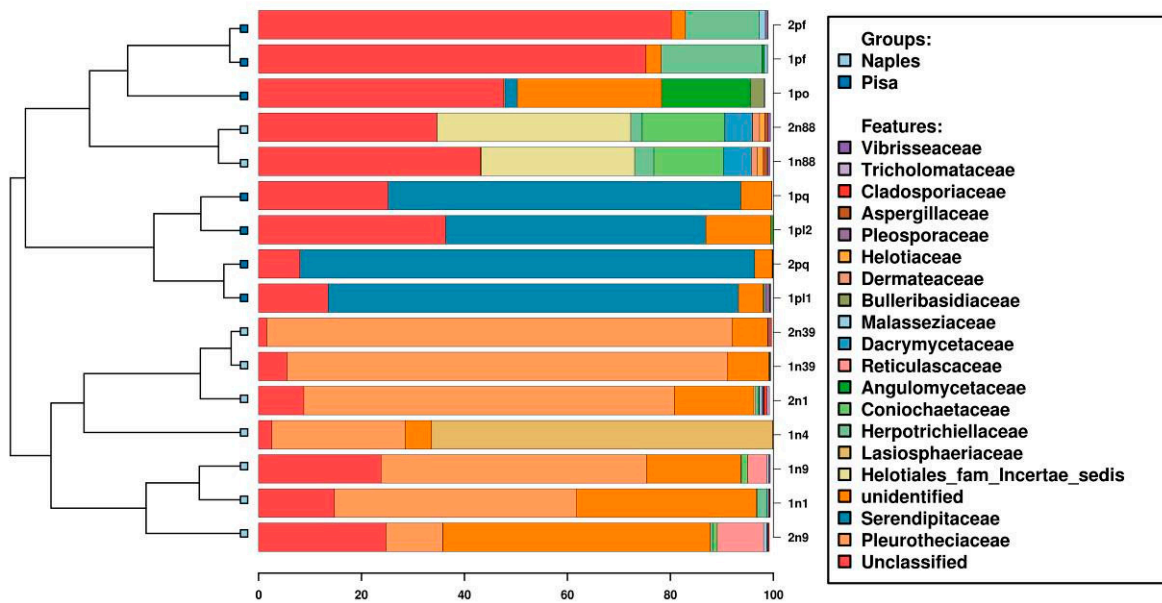
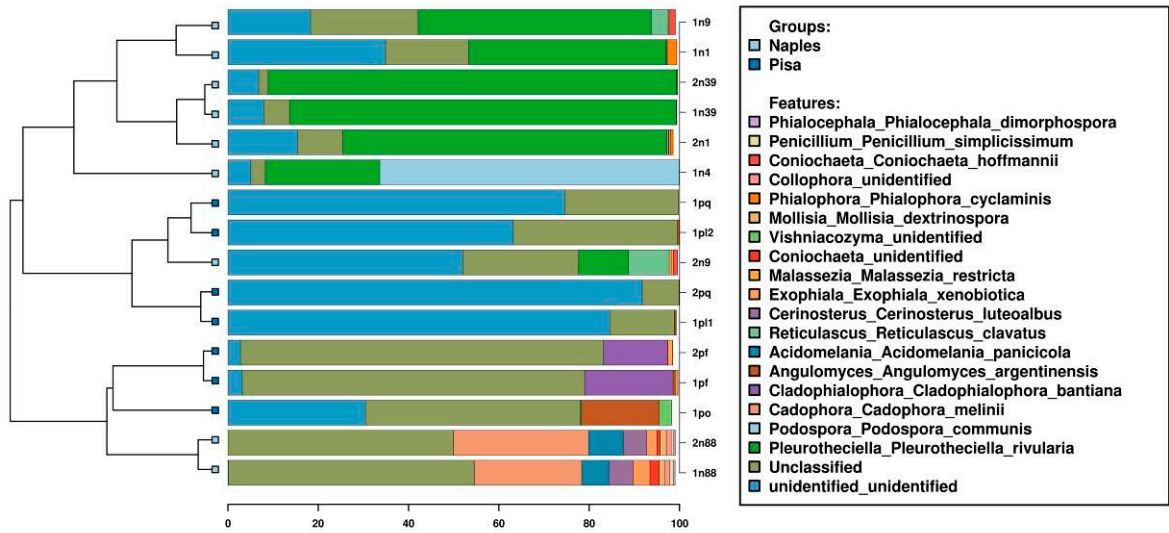


Figure S4. ITS2. Stacked barcharts of the taxonomic profile at family level.



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Figure S5. ITS2. Stacked bar charts of the taxonomic profile at species level.

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