Supplementary material

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Title: Storage of environmental samples for guaranteeing nucleic acid yields for molecular microbiological studies

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Supplementary figures:
Fig. S1: 16S rRNA gene based LH-PCR profiles

No buffer, -20°C, 30d

Ethanol, -20°C, 1d

RNAlater®, -20°C, 30d

PCIAA, -20°C, 30d

amplicon length (bases)
16S rRNA - based LH-PCR profiles

No buffer, -20°C, 1d

Ethanol, +4°C, 30d

RNAlater®, -20°C, 1d

PCIAA, +4°C, 30d
**Fig. S1** Electropherograms of 16S rRNA gene and 16S rRNA based LH-PCR profiles of fresh control samples (black lines) and samples stored under different preservative/temperature conditions (grey lines) for Lake Jyväsjärvi sediment (n=3). Storage conditions and taxonomic bacterial groups affiliated to major LH-PCR peak sizes are indicated in the figure.
**Fig. S2**: 16S rRNA gene based LH-PCR profiles with template dilutions and concentrations

- **Ethanol, -20°C, 1d, concentrated (9:1)**
- **Ethanol, -20°C, 1d, normal**
- **No buffer, -20°C, 30d, diluted (1:10)**
- **No buffer, -20°C, 30d, normal**

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**Graphs**

- [Graph 1](#)
- [Graph 2](#)
- [Graph 3](#)
- [Graph 4](#)

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*Some annotations and labels for the graphs have been omitted for brevity.*

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**Legend**

- Alphaproteobacteria
- Actinobacteria
- Chloroflexi
- Bacteroidetes
- Beta- and Gammaproteobacteria
- Delta proteobacteria
- Verrucomicrobia

**Ethanol, -20ºC, 1d, concentrated (9:1)**

- **AmpliCon length (bases)**

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**Ethanol, -20ºC, 1d, normal**

- **AmpliCon length (bases)**

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**No buffer, -20ºC, 30d, diluted (1:10)**

- **AmpliCon length (bases)**

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**No buffer, -20ºC, 30d, normal**

- **AmpliCon length (bases)**
**Fig. S2** Electropherograms of 16S rRNA gene and 16S rRNA based LH-PCR profiles of fresh control samples (black lines) and samples stored under different preservative/temperature conditions with different concentrations of template in PCR-reactions (grey lines) for Lake Jyväsjärvi sediment. Storage conditions, PCR-template concentrations and taxonomic bacterial groups affiliated to major LH-PCR peak sizes are indicated in the figure.
Fig. S3 Graphical representation of principal coordinate analysis (first two axes shown) of the correlation-based comparison of the 16S rRNA gene based LH-PCR profiles for Lake Jyväsjärvi sediment samples stored under different preservative/temperature conditions with different concentrations of template in PCR-reactions (see text)
Fig. S4 DNA and RNA yields of nucleic acid extractions from samples of bacteria (3 mg of dry *Escherichia coli* mass per sample) and fungae (7 mg of dry *Saccharomyces cerevisiae* mass per sample) cultured overnight after storage with or without soil additions (0.1 g of tundra soil per sample; water content 62%, organic content 66% of dry mass) in two different preservatives at +4°C for 24 h. Yields are shown as percentages (±SD) relative to those of freshly treated control samples. Statistically significant (p < 0.05) deviations from control values are marked with stars (grey stars and white stars denote statistically significantly higher and lower nucleic acid yields than those of control, respectively). N=3 in each treatment.