

Figure S1. [A] A subglacial tunnel was excavated into the basal zone of Taylor Glacier's northern lateral margin. [B] View from inside one of the excavation tunnels. [C] During the 2007 expedition, a vertical shaft was excavated and stratigraphic sequence of multiple basal ice types was sampled. [D] During the 2009 expedition, a large chamber was excavated to sample a horizon of debris-rich banded basal ice.

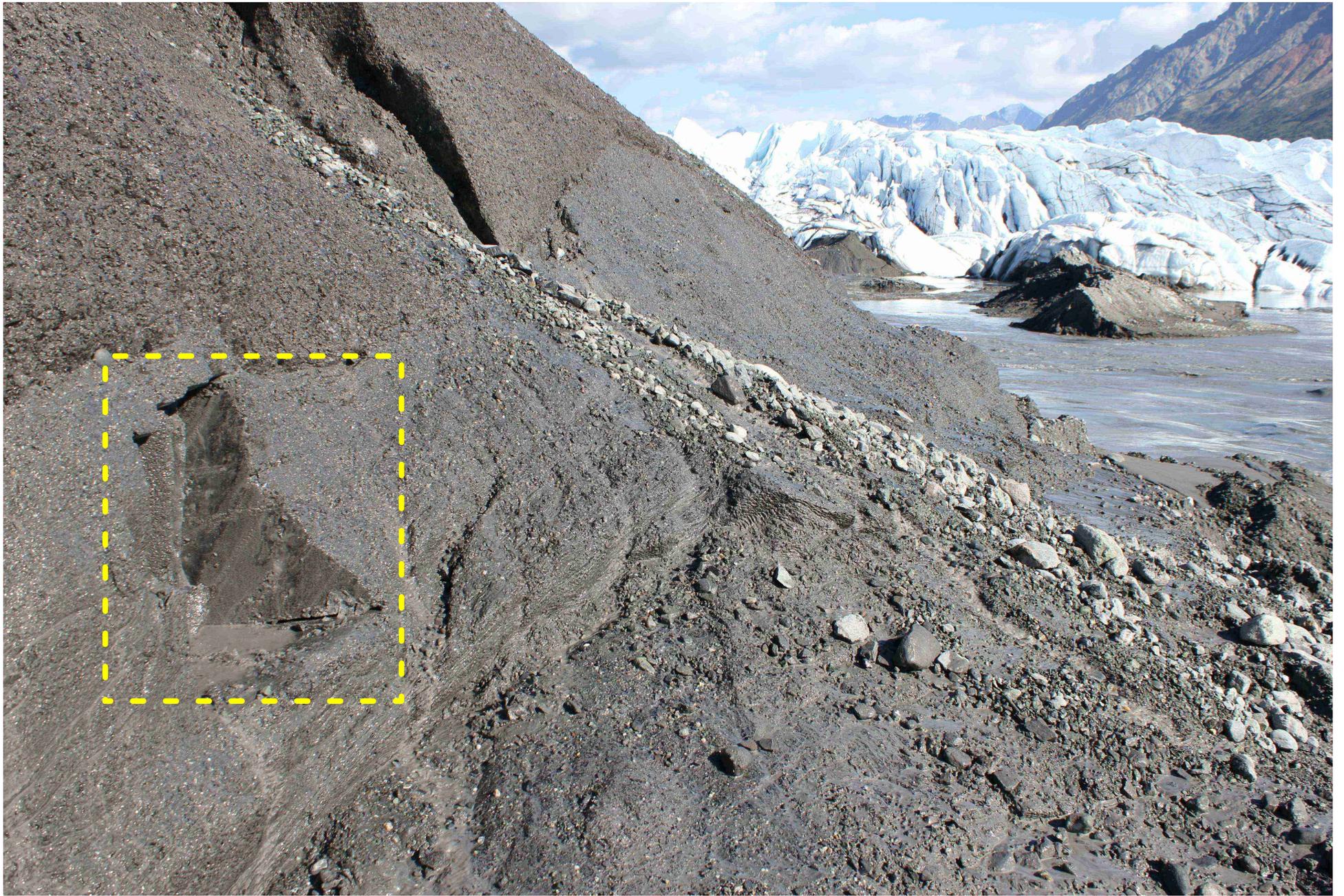
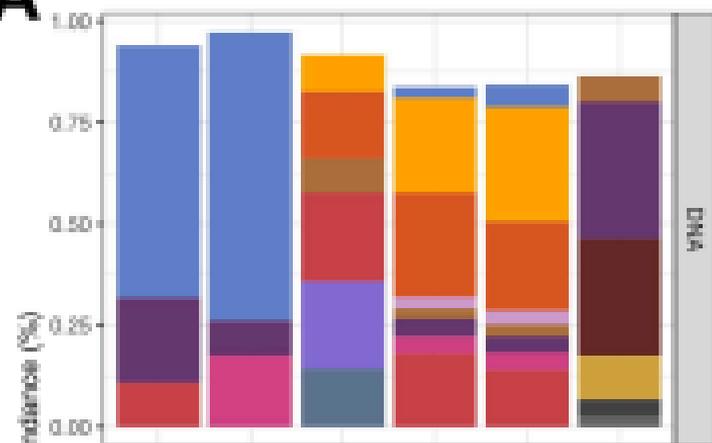
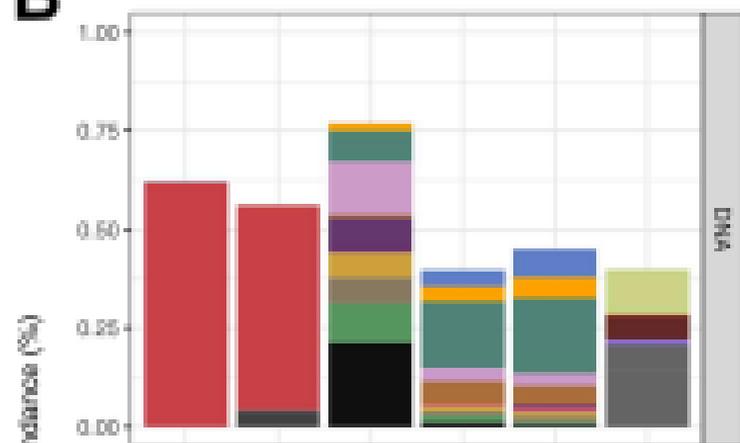


Figure S2. An exposed horizon debris-rich basal ice near the terminus of Matanuska Glacier, Alaska. The sampled area, collected using an electric chainsaw, is highlighted inside the yellow-box.

A**Class**

- Bacilli
- Clostridia
- Actinobacteria
- Thermoleophilia
- Acidimicrobia
- Deltaproteobacteria
- Gammaproteobacteria
- Alphaproteobacteria
- Thermodesulfobacteria
- Bacteroidia
- JS1
- Mollicutes
- 37010
- Anaerolineae
- ND4-46
- Holophagae
- Parabacteriia

B**taxonomy**

- Candidatus_Nitrospira
- Clostridium_sensu_stricto_13
- Cryobacterium
- Desulfocopea
- Fusibacter
- Lutibacter
- Marisediminicola
- Oryzihumus
- Paenispinosarina
- Rhodoflex
- Timobacillus
- unassigned_Actinobacteria
- unassigned_Bacillaceae
- unassigned_Bacteroidales
- unassigned_Desulfotulnacaceae
- unassigned_Trimastixaceae
- unassigned_JS1
- unassigned_Planococcaceae
- unassigned_Thermodesulfobacteria

Clean Ice



Banded Ice



Solid Ice



Dispersed Ice



Figure S3. Examples of each type of basal ice analyzed in this study. Clean ice, banded ice, and solid ice were collected from Taylor Glacier, Antarctica. Dispersed ice was collected from Matanuska Glacier, Alaska.

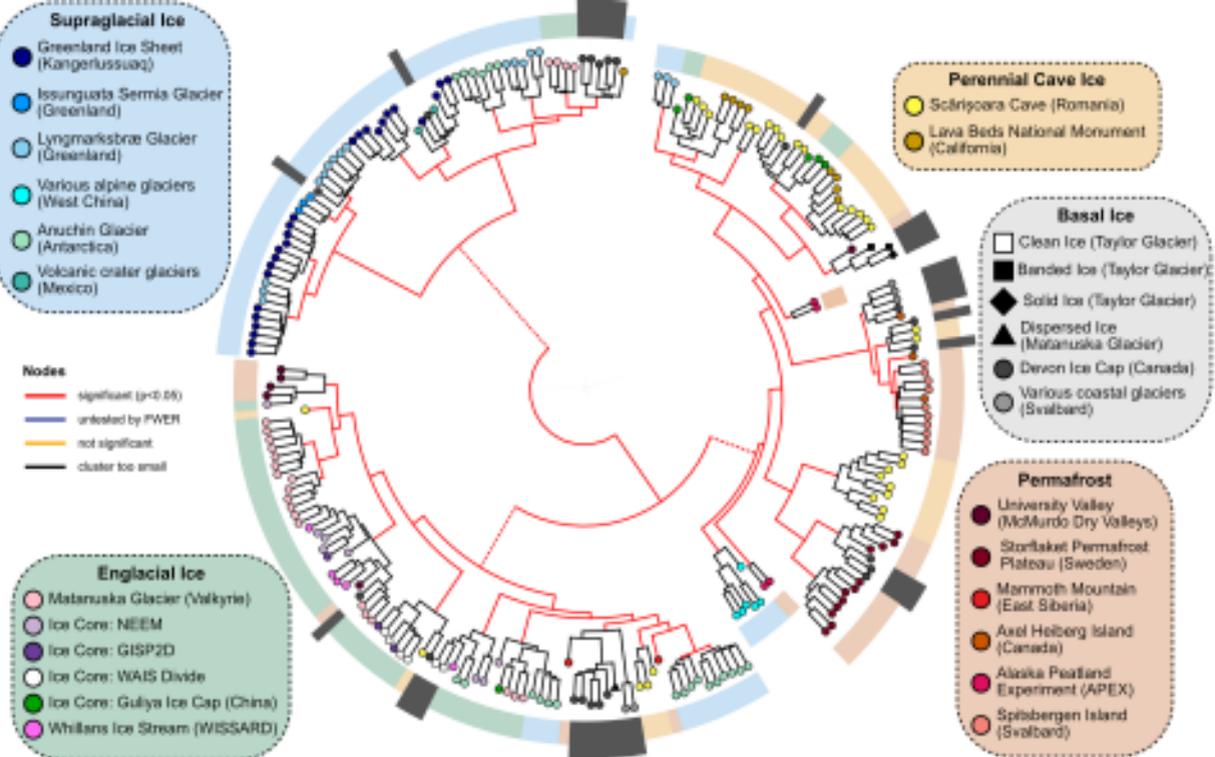


Figure S4. Hierarchical cluster analysis of wUF distances between samples using Ward's minimum variance method. The significance of each node was calculated with a Monte Carlo simulation using the 'sigclust2' R package. Family-wise error rate (FWER) was controlled across the dendrogram using a sequential testing procedure starting at the central node. The three dashed branches in the dendrogram were lengthened slightly to improve legibility and are thus not to scale.

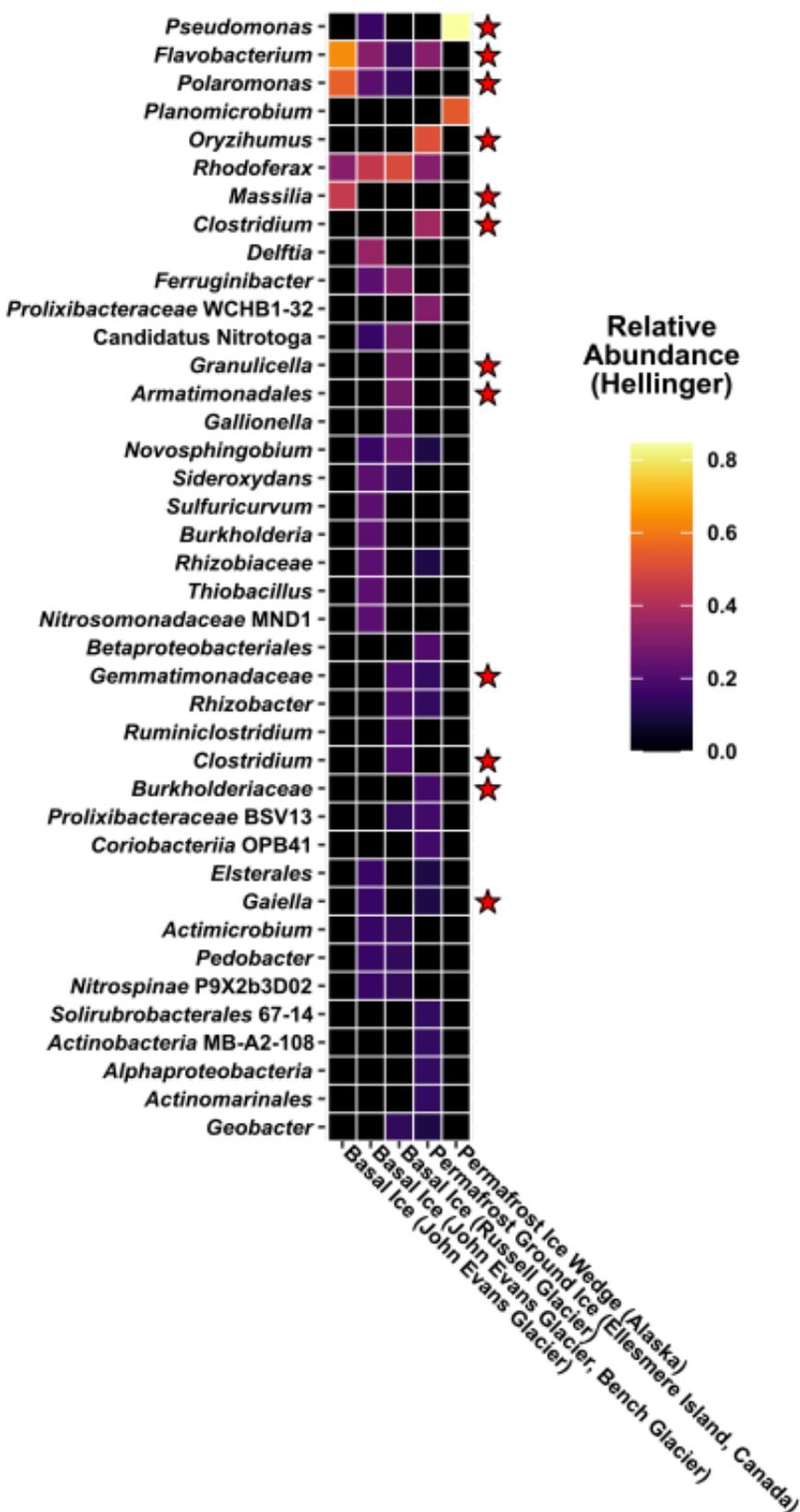


Figure S5. Heatmap of the 40 taxa identified in five early 16S rRNA clone library studies of icy environments. Red stars denote 'indicator' microbial taxa which were identified in the overall meta-analysis (Fig. 4). Taxa abundances were transformed with a Hellinger transformation to facilitate a clearer visual comparison between abundant and sparse taxa.