

Table S16. Comparison of metagenomic/metatranscriptomic sequence results with previous cultivation and sequencing results [refs. 14 and 15].

Ice Core Section	Taxon (metagenomic study) ^a	Taxon (cultivation study) ^a
3563 m (V5)	<i>Phoma</i> sp.	<i>Phoma</i> sp.
3582 m	Antarctic alphaproteobacteria	Antarctic alphaproteobacterium
	<i>Carnobacterium</i> sp.	<i>Carnobacterium</i> sp.
	<i>Davidiellaceae</i> sp.	<i>Cladosporium</i> sp.
	<i>Cryptococcus</i> sp.	<i>Cryptococcus</i> sp.
	<i>Dothiodiomyces</i> sp.	<i>Dothioraceae</i> sp.
	<i>Acinitobacter</i> sp., <i>Psychrobacter</i> sp.	<i>Frigoribacterium</i> sp.
	<i>Rhodotorula</i> sp.	<i>Rhodotorula</i> sp.
3585 m (V5)	<i>Carnobacterium</i> sp.	<i>Carnobacterium</i> sp.
	<i>Kocuria</i> sp.	<i>Kocuria</i> sp.
	<i>Penicillium</i> sp.	<i>Penicillium</i> sp.
3606 m (V6)	<i>Agaricomycotina</i> sp.	<i>Cystofilobasidium</i> sp.
	<i>Micrococcus</i> sp.	<i>Micrococcus</i> sp.
	uncultured basidiomycete	<i>Rhodotorula</i> sp.
3610 m	<i>Cladosporium</i> sp.	<i>Cladosporium</i> sp.

3613 m	uncultured ascomycete	<i>Aspergillus</i> sp.
	<i>Cladosporium</i> sp.	<i>Cladosporium</i> sp.
3619 m	Tremellomycete sp.	<i>Cryptococcus</i> sp.
3621 m (V6)	uncultured basidiomycete	<i>Pseudozyma</i> sp.

^aBold font indicates fungi