SUPPLEMENTARY MATERIAL

Table S1: Five most relatively abundant genes related to C and N cycles detected in soils sampled at Falkland Island, Signy Island, Anchorage Island, Fossil Bluff and Coal Nunatak

					C cycle						**N cycle**		
			gene	organism	taxa	ARA[1]	geneID		gene	organism	taxa	ARA	gene ID/clone #
FI	Veg	1	chitinase	*Burkholderia gladioli*	β-proteo	0.59	7209516	1	*nasA*	uncultured env.	Bacteria	0.85	16506200
		2	chitinase	*Streptomyces coelicolor*	Actinobact.	0.44	21224347	2	*gdh*	*Peptostreptococcus anaerobius*	Firmicutes	0.84	13625820
		3	chitinase	*Vibrio mimicus*	γ-proteo	0.26	7158972	3	*amoA*	lab clone	Bacteria	0.65	C12197-11568
		4	*rbcL*	uncultured	Proteo	0.21	37791351	4	*narG*	*Pseudomonas* sp.	γ-proteo	0.64	17385458
		5	cellulase	*Pectobacterium carotovorum*	γ-proteo	0.19	662361	5	*nirK*	uncultured env.	Bacteria	0.59	27125563
	Bare	1	cellulase	*Thermotoga maritima*	Thermotagae	1.38	15643808	1	urease	*Helicobacter hepaticus*	ε-proteo	0.66	32261959
		2	FTHFS	*Thermotoga maritima*	Thermotagae	1.24	15644511	2	*nasA*	uncultured env.	Bacteria	0.65	16506200
		3	cellulase	*Agrobacterium tumefaciens*	α-proteo	1.17	17937015	3	*narG*	*Pseudomonas* sp.	γ-proteo	0.54	17385458
		4	cellulase	*Xanthomonas campestris*	γ-proteo	1.15	21229505	4	*nifH*	unidentified env.	Bacteria	0.45	780723
		5	cellulase	*Clostridium acetobutylicum*	Firmicutes	1.13	15894198	5	*nifH*	uncultured	Bacteria	0.38	13936681
SI	Veg	1	cellulase	*Clostridium acetobutylicum*	Firmicutes	0.77	15894198	1	*nirK*	Uncultured	Bacteria	0.87	27125563
		2	cellulase	*Agrobacterium tumefaciens*	α-proteo	0.54	17937015	2	*narG*	Uncultured	Bacteria	0.69	29652566
		3	chitinase	*Burkholderia gladioli*	β -proteo	0.53	7209516	3	*narG*	*Pseudomonas* sp.	γ-proteo	0.64	17385458
		4	cellulase	*Xanthomonas campestris*	γ-proteo	0.40	21229505	4	urease	*Nitrosospira multiformis*	β-Proteo	0.55	32966209
		5	cellulase	*Thermotoga maritima*	Thermotagae	0.36	15643808	5	*nasA*	uncultured	Bacteria	0.48	30269537
	Bare	1	laccase	*Gaeumannomyces graminis*	Ascomycota	0.66	19309738	1	*narG*	*Pseudomonas* sp.	γ-proteo	0.72	17385458
		2	cellulase	*Thermotoga maritima*	Thermotagae	0.63	15643808	2	*narG*	uncultured env.	Bacteria	0.69	26278746

				C cycle							**N cycle**		
			gene	organism	taxa	ARA[1]	geneID		gene	organism	taxa	ARA	gene ID/clone #
		3	mannase	*Thermotoga neapolitana*	Thermotagae	0.59	18642982	3	urease	*Bradyrhizobium japonicum*	α-proteo	0.51	27376564
		4	cellulase	*Agrobacterium tumefaciens*	α-proteo	0.44	17937015	4	*amoA*	lab clone	Bacteria	0.44	C1087-650
		5	chitinase	*Burkholderia gladioli*	β -proteo	0.38	7209516	5	*nasA*	Uncultured marine	Bacteria	0.43	16506200
AI	Veg	1	chitinase	uncultured *Neotyphodium*	Ascomycota	1.33	31540489	1	*narG*	uncultured	Bacteria	0.92	38427058
		2	laccase	*Phaeosphaeria spartinicola*	Ascomycota	0.99	23305785	2	*nasA*	Uncultured marine	Bacteria	0.82	16506200
		3	chitinase	*Burkholderia fungorum*	β-proteo	0.44	22983227	3	*narG*	Pseudomonas sp.	γ-proteo	0.81	17385458
		4	chitinase	*Vibrio* sp.	γ -proteo	0.39	17863089	4	*gdh*	*Peptostreptococcus anaerobius*	Firmicutes	0.60	13625820
		5	chitinase	*Burkholderia gladioli*	β-proteo	0.35	7209516	5	*narG*	uncultured	Bacteria	0.56	29652408
	Bare	1	*rbcL*	uncultured cyan	Cyanobacteria	0.45	28932488	1	*nifH*	unidentified marine	Bacteria	1.16	780713
		2	laccase	*Lentinula edodes*	Basidiomycota	0.44	18461106	2	*narG*	*Paenibacillus* sp.	Firmicutes	0.75	17385484
		3	laccase	*Pleurotus sajor-caju*	Basidiomycota	0.43	11036956	3	*narG*	uncultured	Bacteria	0.66	32307941
		4	chitinase	*Shewanella oneidensis*	γ-proteo	0.40	24375572	4	*nifH*	uncultured	Bacteria	0.65	22449987
		5	chitinase	*Burkholderia gladioli*	β-proteo	0.37	7209516	5	*gdh*	*Peptostreptococcus anaerobius*	Firmicutes	0.57	13625820
FB	Bare	1	chitinase	*Escherichia coli*	γ -proteo	1.33	26249933	1	urease	*Synechococcus* sp.	Cyanobact.	0.78	33866975
		2	cellulase	*Clostridium thermocellum*	Firmicutes	1.15	23021597	2	*gdh*	*Pyrococcus abyssi*	Euryarch.	0.64	6685385
		3	mannase	*Bacillus* sp	Firmicutes	0.48	3327375	3	*nifH*	*Acetobacterium woodii*	Firmicutes	0.62	7339869
		4	chitinase	*Mycobacterium tuberculosis*	Actinobacteria	0.45	1403468	4	*gdh*	*Peptostreptococcus anaerobius*	Firmicutes	0.62	13625820
		5	cellulase	*Dictyostelium discoideum*	Mycetozoa	0.44	28829566	5	*narG*	*Paenibacillus* sp.	Firmicutes	0.59	17385484
CN	Bare	1	chitinase	uncultured	Bacteria	1.10	18182574	1	*nirK*	lab clone	Bacteria	1.79	gene1956
		2	cellulase	*Filobasidiella neoformans*	Basidiomycota	0.99	20975611	2	*norB*	uncultured	Bacteria	1.00	29466000
		3	polygalacturonase	*Pseudomonas syringae*	γ-proteo	0.61	28871107	3	*amoA*	lab clone	Bacteria	0.90	C334508-333801
		4	mannase	*Thermobifida fusca*	Actinobacteria	0.60	3970820	4	*nasA*	*Bacillus subtilis*	Firmicutes	0.78	2632619

		C cycle							N cycle			
		gene	organism	taxa	ARA[1]	geneID		gene	organism	taxa	ARA	gene ID/clone #
	5	*pgl*	*Neisseria meningitidis*	β-proteo	0.33	15794502	5	*narG*	uncultured	bacteria	0.78	29652566

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[1] ARA: Average Relative Abundance: Relative abundance of the gene, averaged over the replicates, for each type of plots.