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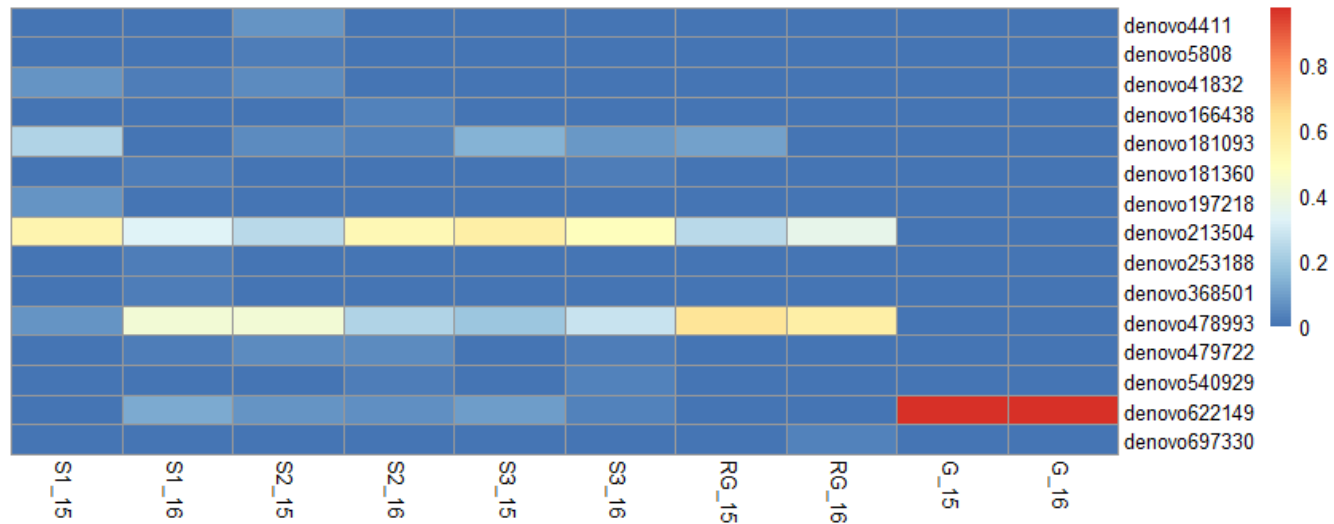
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Soil Crenarchaeotic Group dominant OTUs* (% SCG sequences)

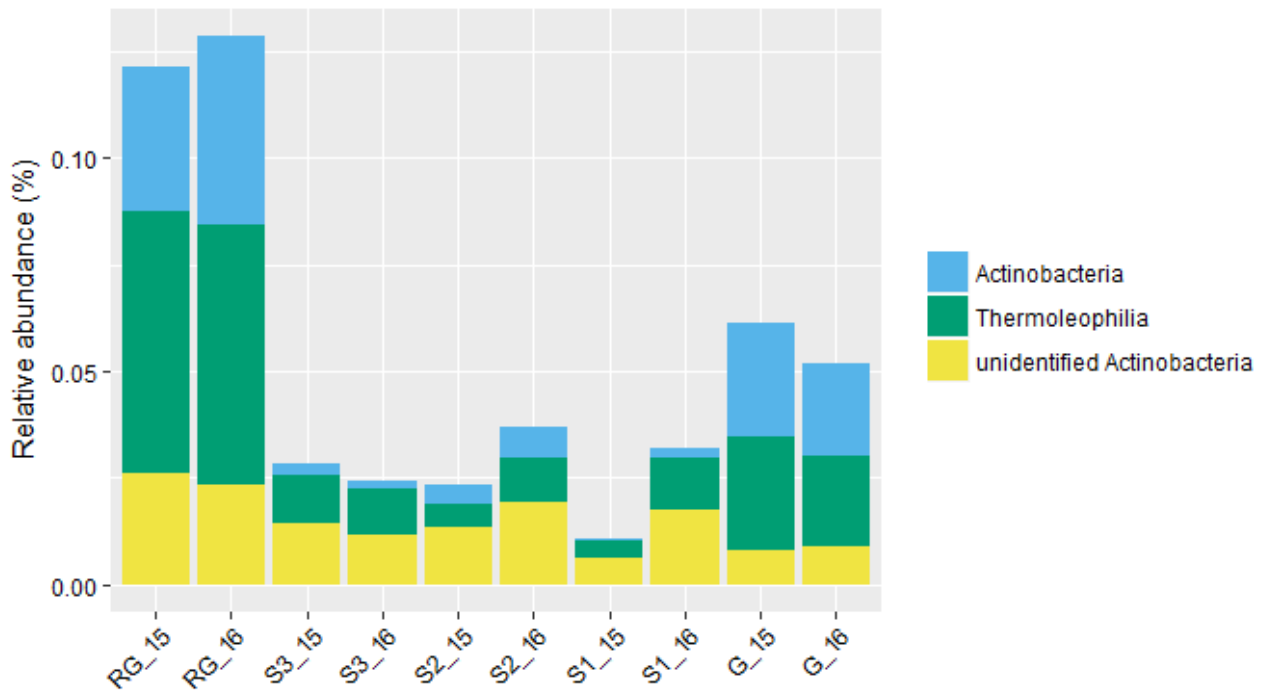


*Only OTUs with relative abundance higher than 1% are shown.

Taxonomic affiliation (97% similarity cutoff) of dominant SCG OTUs

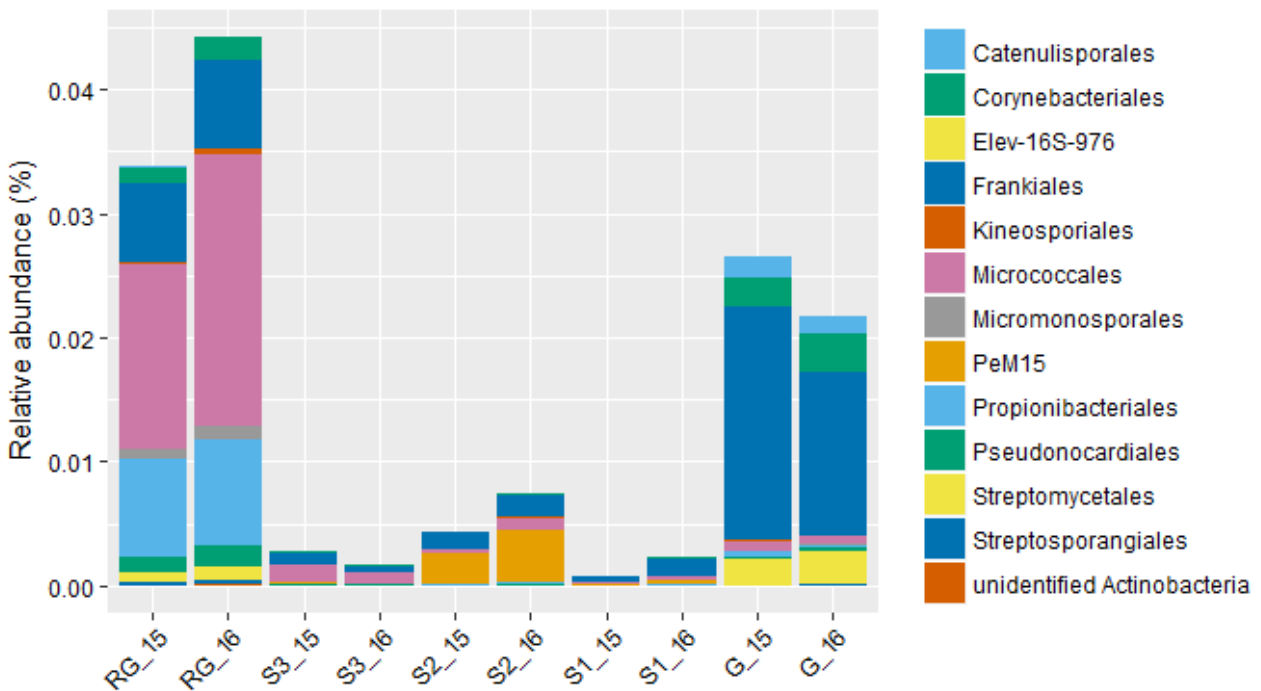
	Order	Family	Genera	Specie
denovo4411	D_3__unculturedbacterium	D_4__unculturedbacterium	D_5__unculturedbacterium	D_6__unculturedbacterium
denovo5808				
denovo41832				
denovo166438	D_3__unculturedcrenarchaeote	D_4__unculturedcrenarchaeote	D_5__unculturedcrenarchaeote	D_6__unculturedcrenarchaeote
denovo181093	D_3__UnknownOrder	D_4__UnknownFamily	D_5__CandidatusNitrososphaera	Ambiguous_taxa
denovo181360	D_3__uncultureddeuryarchaeote	D_4__uncultureddeuryarchaeote	D_5__uncultureddeuryarchaeote	D_6__uncultureddeuryarchaeote
denovo197218	D_3__uncultureddeuryarchaeote	D_4__uncultureddeuryarchaeote	D_5__uncultureddeuryarchaeote	D_6__uncultureddeuryarchaeote
denovo213504				
denovo253188	D_3__unculturedarchaeon	D_4__unculturedarchaeon	D_5__unculturedarchaeon	D_6__unculturedarchaeon
denovo368501	Ambiguous_taxa	Ambiguous_taxa	Ambiguous_taxa	Ambiguous_taxa
denovo478993				
denovo479722				
denovo540929	D_3__unculturedarchaeon	D_4__unculturedarchaeon	D_5__unculturedarchaeon	D_6__unculturedarchaeon
denovo622149	Ambiguous_taxa	Ambiguous_taxa	Ambiguous_taxa	Ambiguous_taxa
denovo697330	D_3__UnknownOrder	D_4__UnknownFamily	D_5__CandidatusNitrososphaera	D_6__unculturedarchaeon

Actinobacteria - Classes* (% total sequences Bacteria)

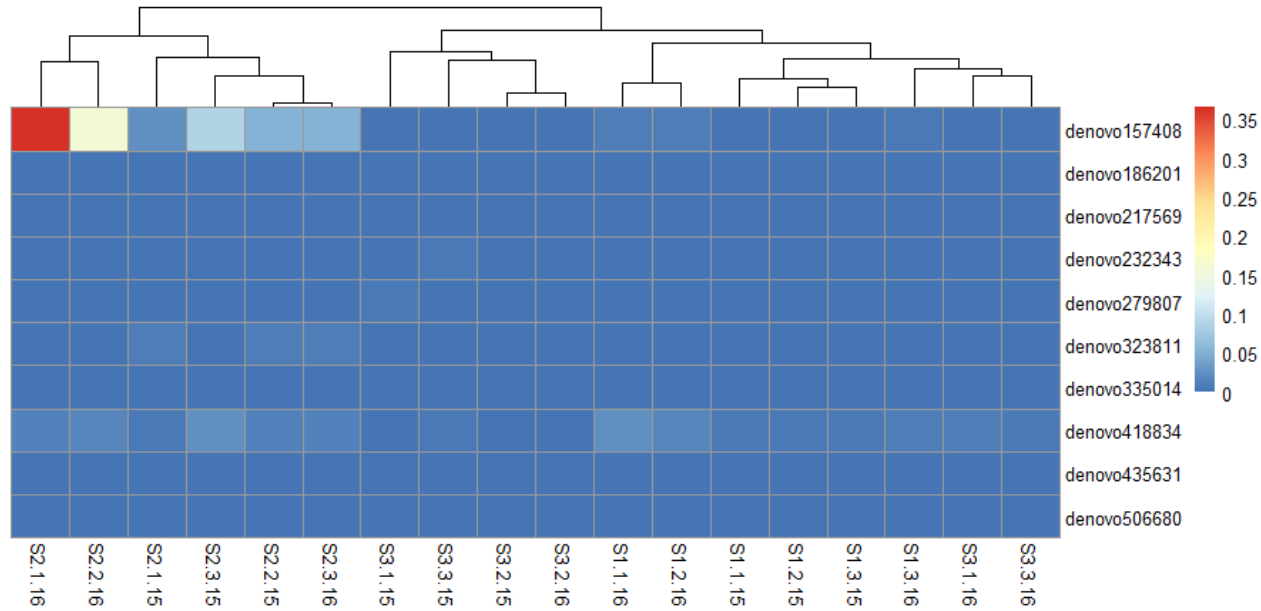


*Only Classes with relative abundance higher than 1% are shown.

Class Actinobacteria - Orders (% total sequences Bacteria)



Cyanobacteria - dominant OTUs

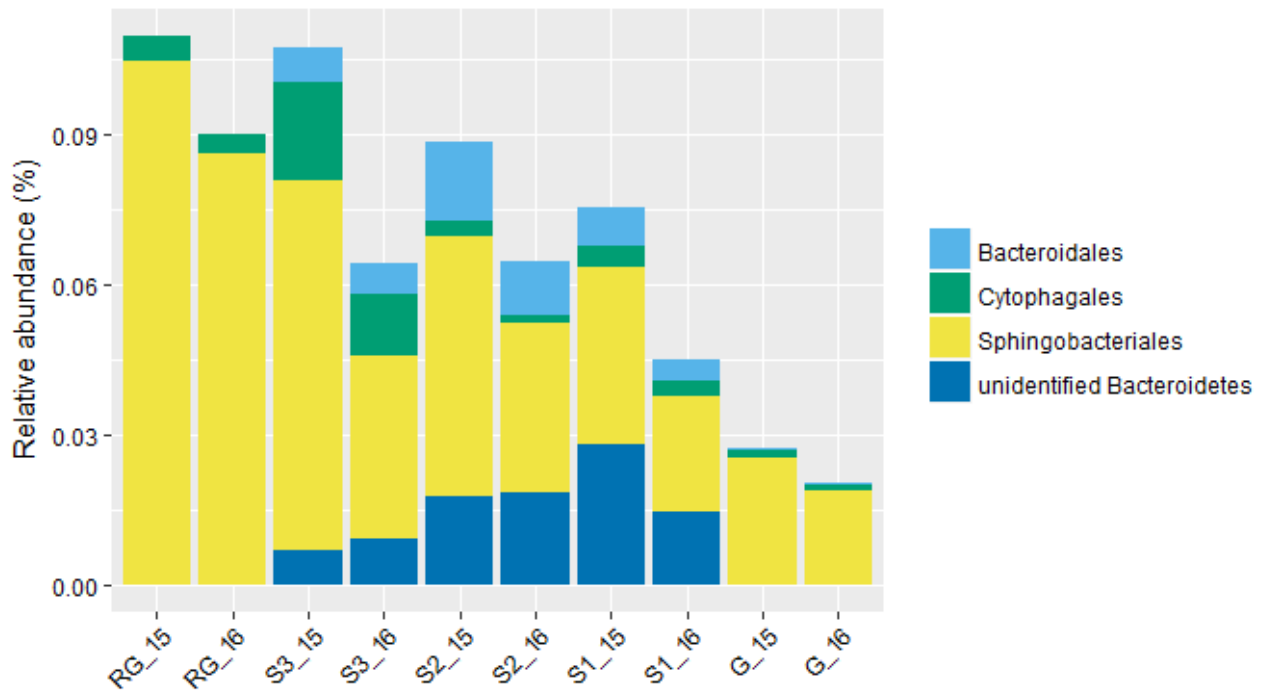


Distribution of cyanobacterial OTUs showing relative abundance on total bacterial sequences higher than 0.1%. Samples clustering was performed on Bray-Curtis distance matrix calculated from total cyanobacterial OTUs, using the UPGMA method

Taxonomic affiliation (97% similarity cutoff) of dominant SCG OTUs

	Order	Family	Genera	Specie
denovo157408	D_3__SubsectionI	D_4__FamilyI	Ambiguous_taxa	Ambiguous_taxa
denovo186201	D_3__SubsectionI	D_4__FamilyI	D_5__Synechococcus	Ambiguous_taxa
denovo217569	D_3__Obscuribacterales	D_4__unculturedbacterium	D_5__unculturedbacterium	D_6__unculturedbacterium
denovo232343	D_3__SubsectionIII	D_4__FamilyI	D_5__uncultured	D_6__unculturedAntarcticcyanobacterium
denovo279807	D_3__SubsectionIII	D_4__FamilyI	D_5__unculturedAntarcticcyanobacterium	D_6__unculturedAntarcticcyanobacterium
denovo323811	D_3__Obscuribacterales	Ambiguous_taxa	Ambiguous_taxa	Ambiguous_taxa
denovo335014	D_3__SubsectionI	D_4__FamilyI	D_5__Snowella	Ambiguous_taxa
denovo418834	D_3__SubsectionI	D_4__FamilyI	Ambiguous_taxa	Ambiguous_taxa
denovo435631	D_3__Obscuribacterales	D_4__unculturedbacterium	D_5__unculturedbacterium	D_6__unculturedbacterium
denovo506680	D_3__SubsectionI	D_4__FamilyI	D_5__Cyanobacterium	Ambiguous_taxa

Bacteroidetes - Orders* (% total sequences Bacteria)



*Only Orders with relative abundance higher than 1% are shown.