	cluster_1 -	-0.21 (0.4)	-0.99 (0.01)	0.31 (0.34)	-0.58 (0.21)	0.41 (0.3)	
	cluster_2 -	0.86 (0.07)	-0.12 (0.44)	0.72 (0.14)	0.53 (0.24)	-0.24 (0.38)	
	cluster_3 -	0.32 (0.34)	-0.16 (0.42)	-0.5 (0.25)	-0.57 (0.22)	-0.72 (0.14)	
	cluster_4 -	-0.85 (0.07)	-0.54 (0.23)	0.21 (0.39)	-0.28 (0.36)	0.96 (0.02)	correlation
Cluster	cluster_5 -	-0.48 (0.26)	0.67 (0.17)	-0.59 (0.2)	0.06 (0.47)	0.01 (0.49)	1.0
Clu	cluster_6 -	-0.61 (0.19)	-0.31 (0.35)	-0.79 (0.1)	-0.95 (0.02)	-0.07 (0.47)	0.0 -0.5
	cluster_7 -	0.2 (0.4)	0.19 (0.41)	0.8 (0.1)	0.85 (0.07)	0.46 (0.27)	1.0
	cluster_8 -	0.44 (0.28)	0.7 (0.15)	-0.68 (0.16)	0.02 (0.49)	-0.94 (0.03)	
	cluster_9 -	0.53 (0.23)	0.93 (0.03)	0.02 (0.49)	0.83 (0.09)	-0.45 (0.27)	
	cluster_10 -	-0.1 (0.45)	-0.58 (0.21)	0.9 (0.05)	0.28 (0.36)	0.79 (0.1)	
		flg22	SynCom33	SynCom35 Trait	bacteria	rootlen	