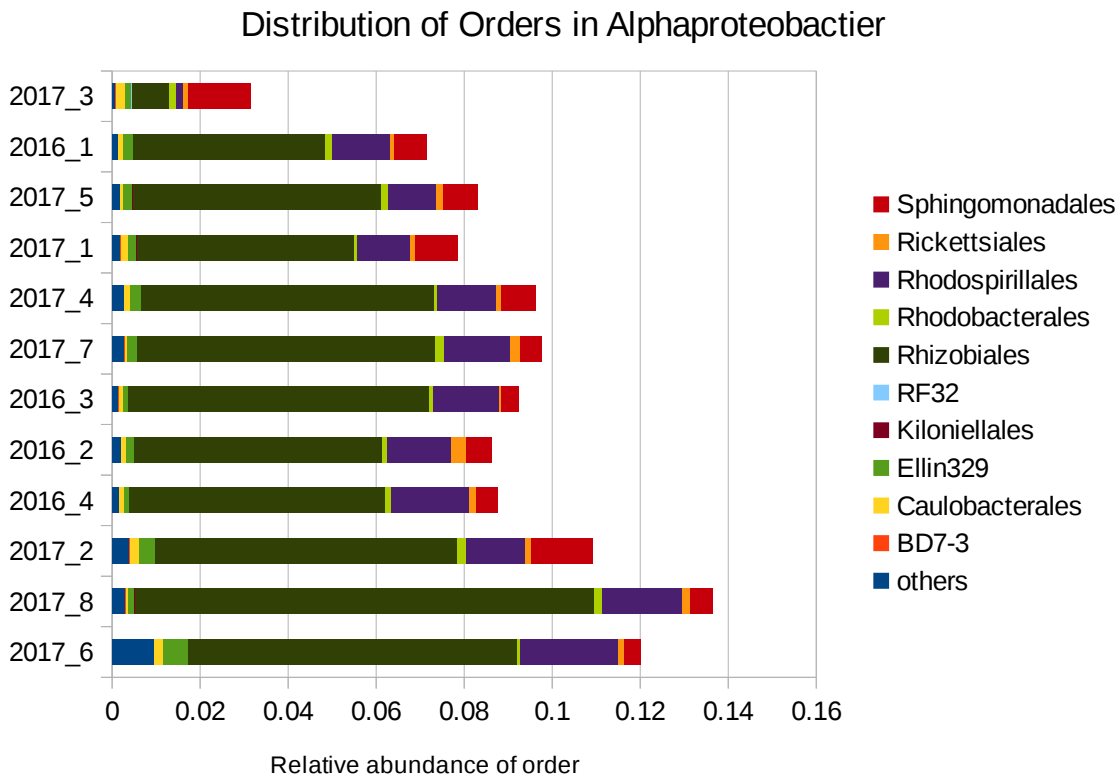
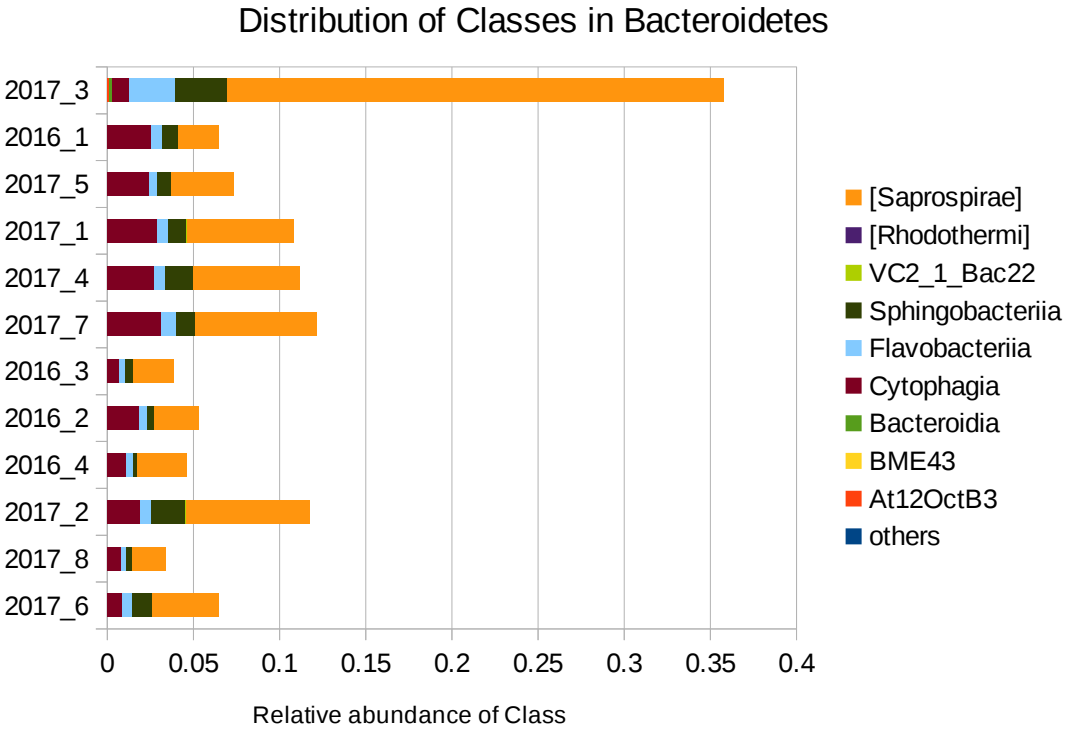
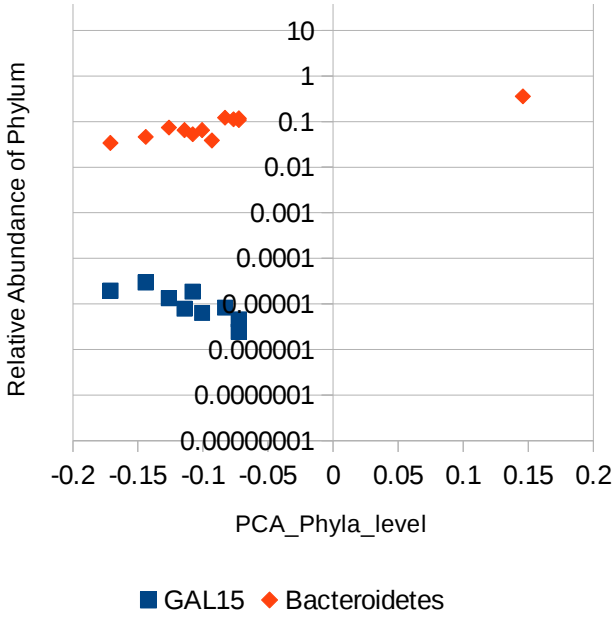
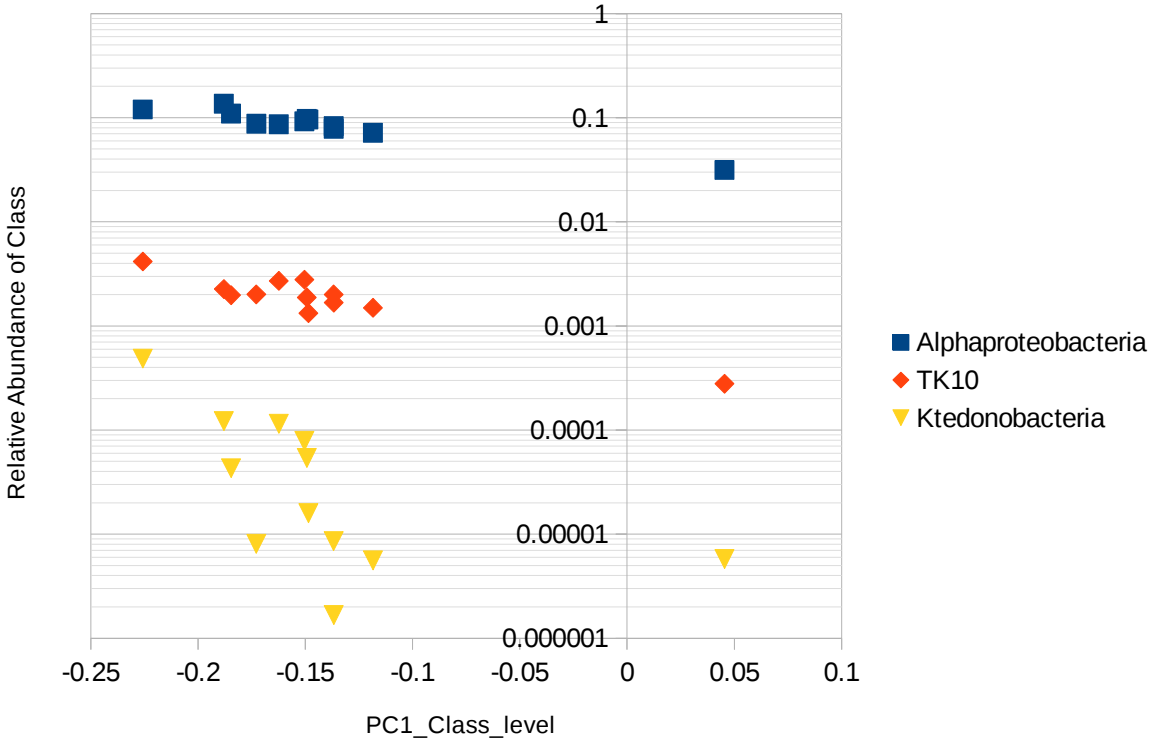
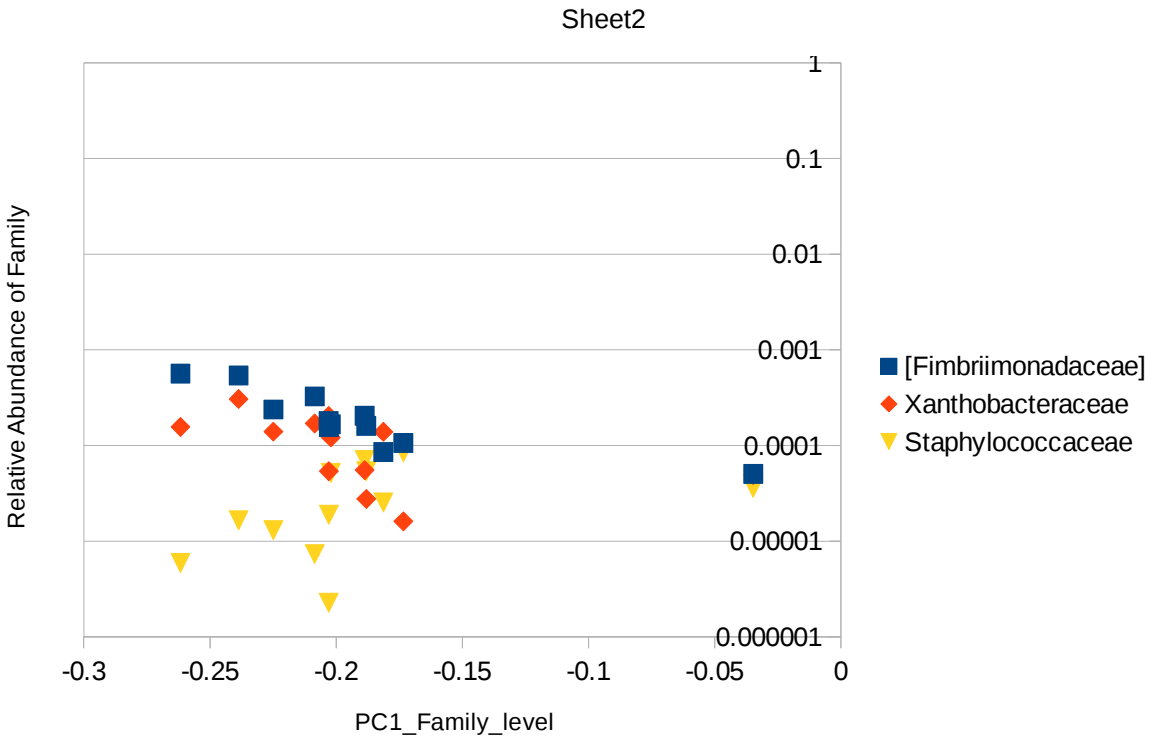

Distribution of Orders in Alphaproteobactier
2017_3
2016_1
2017_5
2017_1
2017_4
2017_7
2016_3
2016_2
2016_4
2017_2
2017_8
2017_6
0
0.02
0.04
0.06
0.08
0.1
0.12
0.14
0.16
Relative abundance of order
Sphingomonadales
Rickettsiales
Rhodospirillales
Rhodobacterales
Rhizobiales
RF32
Kiloniellales
Ellin329
Caulobacterales
BD7-3
others

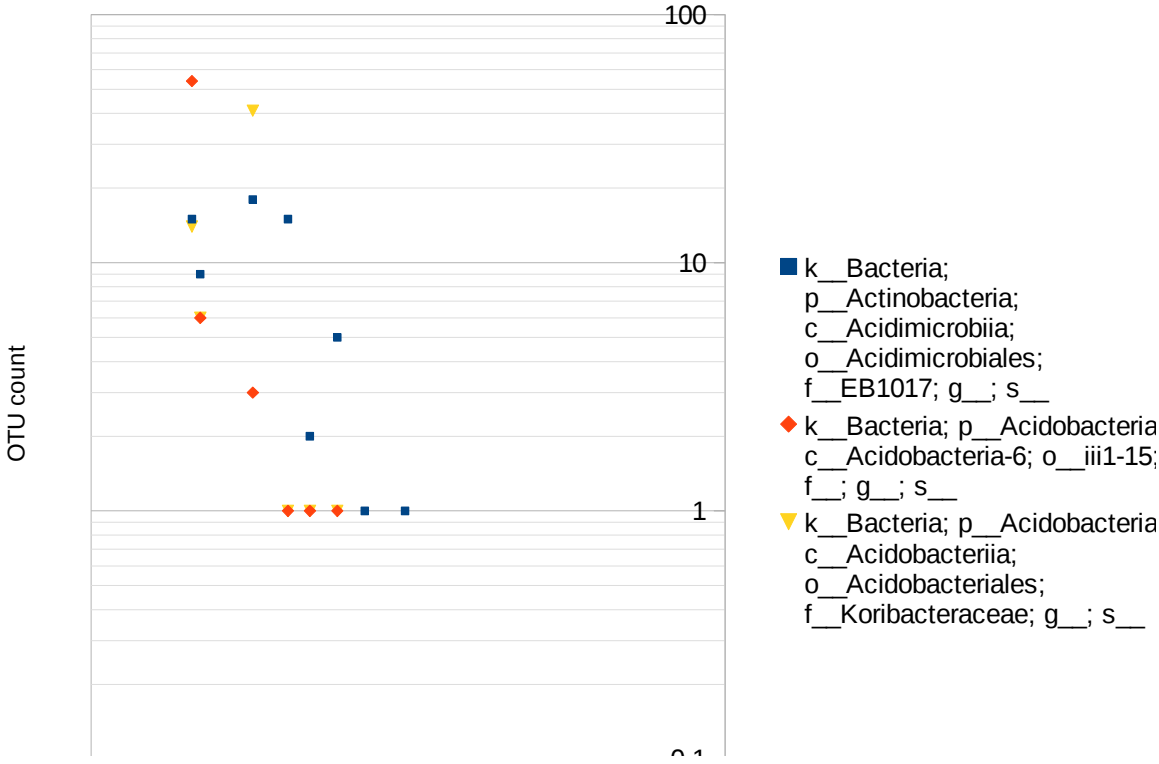

Distribution of Classes in Bacteroidetes
2017_3
2016_1
2017_5
2017_1
2017_4
2017_7
2016_3
2016_2
2016_4
2017_2
2017_8
2017_6
0
0.05
0.1
0.15
0.2
0.25
0.3
0.35
0.4
Relative abundance of Class
[Saprospirae]
[Rhodothermi]
VC2_1_Bac22
Sphingobacteriia
Flavobacteriia
Cytophagia
Bacteroidia
BME43
At12OctB3
others

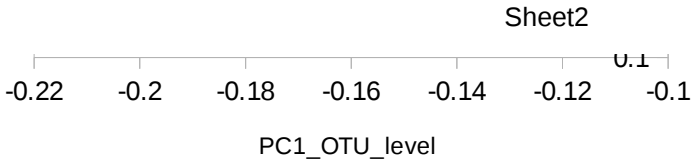
100


Relative Abundance of Phylum
10
1
0.1
0.01
0.001
0.0001
0.00001
0.000001
0.0000001
0.00000001
-0.2 -0.15 -0.1 -0.05 0 0.05 0.1 0.15 0.2
PCA_Phyla_level
GAL15
Bacteroidetes


Relative Abundance of Class
1
0.1
0.01
0.001
0.0001
0.00001
0.000001
-0.25 -0.2 -0.15 -0.1 -0.05 0 0.05 0.1
PC1_Class_level
Alphaproteobacteria
TK10
Ktedonobacteria


Sheet2
Relative Abundance of Family
1
0.1
0.01
0.001
0.0001
0.00001
0.000001
-0.3
-0.25
-0.2
-0.15
-0.1
-0.05
0
PC1_Family_level
[Fimbriimonadaceae]
Xanthobacteraceae
Staphylococcaceae


OTU count
100
10
1
k__Bacteria; p__Actinobacteria; c__Acidimicrobiia; o__Acidimicrobiales; f__EB1017; g__; s__
k__Bacteria; p__Acidobacteria c__Acidobacteria-6; o__iii1-15; f__; g__; s__
k__Bacteria; p__Acidobacteria c__Acidobacteriia; o__Acidobacteriales; f__Koribacteraceae; g__; s__


Sheet2
-0.22
-0.2
-0.18
-0.16
-0.14
-0.12
-0.1
PC1_OTU_level

ų;
'

ų;

#SampleID	compare	Sample Name	Sample Descr	Sample ID	Run ID
2016_1	2016_1	16S_Gordon_Square		2016_1	2016_1
2016_3	2016_3	16S_Gordon_Square		2016_3	2016_3
2016_2	2016_2	16S_Gordon_Square		2016_2	2016_2
2016_4	2016_4	16S_Gordon_Square		2016_4	2016_4
2017_2	2017_2	16S_Gordon_Square		2017_2	2017_2
2017_1	2017_1	16S_Gordon_Square		2017_1	2017_1
2017_3	2017_3	16S_Gordon_Square		2017_3	2017_3
2017_4	2017_4	16S_Gordon_Square		2017_4	2017_4
2017_5	2017_5	16S_Gordon_Square		2017_5	2017_5
2017_6	2017_6	16S_Gordon_Square		2017_6	2017_6
2017_7	2017_7	16S_Gordon_Square		2017_7	2017_7
2017_8	2017_8	16S_Gordon_Square		2017_8	2017_8

L2					
taxonomy					
k__Bacteria;p__GAL15	6.30632E-06	0	1.86262E-05	2.96025E-05	4.57029E-06
k__Bacteria;p__Bacteroidetes	0.064798828	0.038463251	0.052829006	0.045994241	0.117121045
L3					
taxonomy					
k__Bacteria;p__Proteobacteria;c__	0.071478622	0.092491478	0.08638199	0.087569633	0.109373486
k__Bacteria;p__Chloroflexi;c__TK1	0.001493897	0.002786731	0.002714248	0.00201028	0.00197528
k__Bacteria;p__Chloroflexi;c__Kte	5.60562E-06	7.88938E-05	0.000114861	8.07341E-06	4.29607E-05
L4					
taxonomy					
k__Bacteria;p__Proteobacteria;c__	0.001369172	0.001342466	0.002038531	0.00158508	0.003965185
k__Bacteria;p__Actinobacteria;c__	0.013776504	0.00885646	0.013129384	0.031602035	0.027386104
k__Bacteria;p__Actinobacteria;c__	0.0112778	0.005826686	0.009817029	0.020904761	0.026372413
k__Bacteria;p__Armatimonadetes;c	0.000153454	8.52562E-05	0.000187297	0.000156086	0.000578599
L5					
taxonomy					
k__Bacteria;p__Armatimonadetes;c	0.000105806	8.52562E-05	0.000166601	0.000156086	0.000541123
k__Bacteria;p__Proteobacteria;c__	0.001369172	0.001342466	0.002038531	0.00158508	0.003965185
k__Bacteria;p__Proteobacteria;c__	1.61161E-05	0.0001387	0.00012107	5.38228E-05	0.00030621
k__Bacteria;p__Actinobacteria;c__	0	1.27248E-06	1.03479E-05	5.38228E-06	0.000226686
k__Bacteria;p__Firmicutes;c__Baci	0.000084785	2.54496E-05	5.17394E-05	0.000018838	1.64531E-05
k__Bacteria;p__Armatimonadetes;c	0	0	0	0	4.57029E-06
k__Bacteria;p__Acidobacteria;c__T	0.000018919	4.83542E-05	0.000028974	5.38228E-05	6.12419E-05
OTU					
taxonomy					
k__Bacteria; p__Actinobacteria; c_	0	5	2	1	9
k__Bacteria; p__Acidobacteria; c__	0	1	1	0	6
k__Bacteria; p__Acidobacteria; c__	0	1	1	0	6

pca1_unweighted_unifrac	PD_whole_tre	PD_whole_tree_norm	
-0.1588944987	53.420071	-37.7530931	-37.7530931
-0.1734083502	46.111076	-34.24767	-34.24767
-0.178612254	54.32961	-37.7084701	-37.7084701
-0.1682163966	51.441517	-33.5140845	-33.5140845
-0.1993571503	62.101873	-42.2899438	-42.2899438
-0.189409743	52.738632	-38.2475474	-38.2475474
-0.1062547935	43.751128	-33.5696251	-33.5696251
-0.1827526326	56.027202	-40.4132663	-40.4132663
-0.1629941146	54.398441	-36.6539732	-36.6539732
-0.2009299066	47.634752	-31.3145985	-31.3145985
-0.152856657	55.668784	-35.8745998	-35.8745998
-0.1606037523	53.597421	-36.8905834	-36.8905834

pca1_L3	PD_whole_tre	PD_whole_tree_norm
-0.1184902648	53.420071	-37.7530931
-0.150447765	46.111076	-34.24767
-0.1623632855	54.32961	-37.7084701
-0.1728538859	51.441517	-33.5140845
-0.1846149128	62.101873	-42.2899438
-0.1368112076	52.738632	-38.2475474
0.0453873483	43.751128	-33.5696251
-0.1485541602	56.027202	-40.4132663
-0.1367810965	54.398441	-36.6539732
-0.2257962679	47.634752	-31.3145985
-0.1492770975	55.668784	-35.8745998
-0.1880055969	53.597421	-36.8905834

Biome	Experiment typ	Instrument mo	Release versi	pca1_L2	pca1_L3	pca1_L4
sample	amplicon	Illumina MiSeq		-0.10066544	-0.11849026	-0.15615945
sample	amplicon	Illumina MiSeq		-0.09318462	-0.15044777	-0.1662395
sample	amplicon	Illumina MiSeq		-0.10792866	-0.16236329	-0.18339065
sample	amplicon	Illumina MiSeq		-0.1440242	-0.17285389	-0.19278608
sample	amplicon	Illumina MiSeq		-0.0724556	-0.18461491	-0.22141733
sample	amplicon	Illumina MiSeq		-0.07248727	-0.13681121	-0.1845634
sample	amplicon	Illumina MiSeq		0.14584106	0.045387348	-0.06089523
sample	amplicon	Illumina MiSeq		-0.07660038	-0.14855416	-0.19099272
sample	amplicon	Illumina MiSeq		-0.12620985	-0.1367811	-0.17613504
sample	amplicon	Illumina MiSeq		-0.11413677	-0.22579627	-0.24123565
sample	amplicon	Illumina MiSeq		-0.08310558	-0.1492771	-0.1793073
sample	amplicon	Illumina MiSeq		-0.17109995	-0.1880056	-0.23499936

2.44312E-06	0	0	1.33873E-05	7.86008E-06	8.28563E-06	1.95065E-05
0.107822263	0.3574890859	0.111911131	0.073748751	0.064885965	0.121156674	0.033940357
0.078418079	0.0314621192	0.096229533	0.083081346	0.120162979	0.097624095	0.136502673
0.002007024	0.00027826	0.001325541	0.001673408	0.004160931	0.001879458	0.002259966
8.55092E-06	0.000005767	0.000015902	1.67341E-06	0.000486343	5.38566E-05	0.000121683
0.001847	0.0007598083	0.00275331	0.001808954	0.009476312	0.002701116	0.002922257
0.024279737	0.002726371	0.021016703	0.029425201	0.042403181	0.030274324	0.038521594
0.016204001	0.0069550574	0.017920365	0.015363556	0.015574754	0.016144557	0.032181057
0.000338372	5.046165E-05	0.000187416	0.000232604	0.000566908	0.000182284	0.000261944
0.000326157	5.046165E-05	0.000179465	0.000204156	0.000565926	0.000160189	0.000237793
0.001847	0.0007598083	0.00275331	0.001808954	0.009476312	0.002701116	0.002922257
0.000169797	4.901989E-05	0.000203318	5.52225E-05	0.000156219	2.76188E-05	0.000139332
0.000317606	1.585938E-05	0.000180601	4.85288E-05	0.000383179	6.62851E-05	0.000155123
7.32936E-06	0.000036044	2.27171E-06	7.02831E-05	5.89506E-06	5.38566E-05	1.30043E-05
2.44312E-06	0	2.27171E-06	0	6.87757E-06	0	0
0.000153917	0	5.33851E-05	2.51011E-05	0.000348791	9.52848E-05	6.87371E-05
18	0	15	0	15	0	1
3	0	1	0	54	0	0
41	0	1	0	14	0	0

PD_whole_tree	Alphaproteobacteria
-37.75309313	0.071478622
-34.24766995	0.092491478
-37.7084701	0.08638199
-33.51408455	0.087569633
-42.28994385	0.109373486
-38.2475474	0.078418079
-33.56962513	0.031462119
-40.41326629	0.096229533
-36.65397325	0.083081346
-31.31459851	0.120162979
-35.87459985	0.097624095
-36.89058336	0.136502673

PD_whole_tree	Bacteroidetes
-37.75309313	0.064798828
-34.24766995	0.038463251
-37.7084701	0.052829006
-33.51408455	0.045994241
-42.28994385	0.117121045
-38.2475474	0.107822263
-33.56962513	0.357489086
-40.41326629	0.111911131
-36.65397325	0.073748751
-31.31459851	0.064885965
-35.87459985	0.121156674
-36.89058336	0.033940357

pca1_L5	pca1_unweigh	random	constant	PD_whole_tre	PD_whole_tre	Latitude
-0.1733718	-0.1588945	0.312865064	34	53.420071	282.7590678	51.524735
-0.18130261	-0.17340835	0.819153231	35	46.111076	250.9450889	51.524392
-0.20212931	-0.17861225	0.175414018	36	54.32961	282.1168817	51.523861
-0.20291905	-0.1682164	0.884593389	37	51.441517	245.3158544	51.524309
-0.23865182	-0.19935715	0.085465797	38	62.101873	321.2143745	51.524531
-0.20847987	-0.18940974	0.925062344	39	52.738632	285.1937688	51.524102
-0.03471949	-0.10625479	0.830912146	40	43.751128	242.1665683	51.524341
-0.20293203	-0.18275263	0.106222422	41	56.027202	305.4715348	51.524586
-0.18868732	-0.16299411	0.223491957	42	54.398441	270.8291736	51.524074
-0.26170908	-0.20092991	0.637291947	43	47.634752	226.1467301	51.524073
-0.18804141	-0.15285666	0.195245233	44	55.668784	265.9234894	51.524371
-0.2249034	-0.16060375	0.681228137	45	53.597421	273.8214234	51.524185

Longitude	Humidity	pH	Temperature	L2	GAL15	Bacteroidetes
-0.13108	0	0	0		6.30632E-06	0.064798828
-0.13112	0	0	0		0	0.038463251
-0.1306	0	0	0		1.86262E-05	0.052829006
-0.130543	0	0	0		2.96025E-05	0.045994241
-0.1309062	0	0	0		4.57029E-06	0.117121045
-0.130661	0	7.5	5		2.44312E-06	0.107822263
-0.130825	0	0	0		0	0.357489086
-0.131266	0	8	6		0	0.111911131
-0.130824	85	5.5	8		1.33873E-05	0.073748751
-0.130863	0	0	0		7.86008E-06	0.064885965
-0.130757	0	0	0		8.28563E-06	0.121156674
-0.130664	0	0	0		1.95065E-05	0.033940357
				Test stat.	-0.81692167	0.783216783

L3	Alphaproteoba	TK10	Ktedonobacte	L4	k__Bacteria;p	k__Bacteria;p
	0.071478622	0.001493897	5.60562E-06		0.001369172	0.013776504
	0.092491478	0.002786731	7.88938E-05		0.001342466	0.00885646
	0.08638199	0.002714248	0.000114861		0.002038531	0.013129384
	0.087569633	0.00201028	8.07341E-06		0.00158508	0.031602035
	0.109373486	0.00197528	4.29607E-05		0.003965185	0.027386104
	0.078418079	0.002007024	8.55092E-06		0.001847	0.024279737
	0.031462119	0.00027826	0.000005767		0.000759808	0.002726371
	0.096229533	0.001325541	0.000015902		0.00275331	0.021016703
	0.083081346	0.001673408	1.67341E-06		0.001808954	0.029425201
	0.120162979	0.004160931	0.000486343		0.009476312	0.042403181
	0.097624095	0.001879458	5.38566E-05		0.002701116	0.030274324
	0.136502673	0.002259966	0.000121683		0.002922257	0.038521594
Test stat.	-0.86013986	-0.78321678	-0.8041958	Test stat.	-0.85314685	-0.76923077

k__Bacteria;p	k__Bacteria;p L5	taxonomy	[Fimbriimonad	k__Bacteria;p	Xanthobacter
0.0112778	0.000153454		0.000105806	0.001369172	1.61161E-05
0.005826686	8.52562E-05		8.52562E-05	0.001342466	0.0001387
0.009817029	0.000187297		0.000166601	0.002038531	0.00012107
0.020904761	0.000156086		0.000156086	0.00158508	5.38228E-05
0.026372413	0.000578599		0.000541123	0.003965185	0.00030621
0.016204001	0.000338372		0.000326157	0.001847	0.000169797
0.006955057	5.04617E-05		5.04617E-05	0.000759808	4.90199E-05
0.017920365	0.000187416		0.000179465	0.00275331	0.000203318
0.015363556	0.000232604		0.000204156	0.001808954	5.52225E-05
0.015574754	0.000566908		0.000565926	0.009476312	0.000156219
0.016144557	0.000182284		0.000160189	0.002701116	2.76188E-05
0.032181057	0.000261944		0.000237793	0.002922257	0.000139332
-0.77622378	-0.78321678	Test stat.	-0.91608392	-0.86713287	-0.7972028

k__Bacteria;p	Staphylococc	k__Bacteria;p	k__Bacteria;p OTU	taxonomy	k__Bacteria; p
0	0.000084785	0	0.000018919		0
1.27248E-06	2.54496E-05	0	4.83542E-05		5
1.03479E-05	5.17394E-05	0	0.000028974		2
5.38228E-06	0.000018838	0	5.38228E-05		1
0.000226686	1.64531E-05	4.57029E-06	6.12419E-05		9
0.000317606	7.32936E-06	2.44312E-06	0.000153917		18
1.58594E-05	0.000036044	0	0		0
0.000180601	2.27171E-06	2.27171E-06	5.33851E-05		15
4.85288E-05	7.02831E-05	0	2.51011E-05		0
0.000383179	5.89506E-06	6.87757E-06	0.000348791		15
6.62851E-05	5.38566E-05	0	9.52848E-05		0
0.000155123	1.30043E-05	0	6.87371E-05		1
-0.7972028	0.762237762	-0.75720363	-0.76923077		-0.92932038

k__Bacteria; p	k__Bacteria; pa	pc1		others	BD7-3
0	0	-0.22579627	2017_6	0.009476312	0.000148359
1	1	-0.1880056	2017_8	0.002922257	0.000185776
1	1	-0.18461491	2017_2	0.003965185	0.000192866
0	0	-0.17285389	2016_4	0.00158508	0.000126483
6	6	-0.16236329	2016_2	0.002038531	0.000183157
3	41	-0.15044777	2016_3	0.001342466	0.000165422
0	0	-0.1492771	2017_7	0.002701116	0.000215426
1	1	-0.14855416	2017_4	0.00275331	9.76834E-05
0	0	-0.13681121	2017_1	0.001847	0.000247977
54	14	-0.1367811	2017_5	0.001808954	0.000143913
0	0	-0.11849026	2016_1	0.001369172	5.74576E-05
0	0	0.045387348	2017_3	0.000759808	0.000162919
-0.9073512	-0.90674579				

Caulobacteral	Ellin329	Kiloniellales	RF32	Rhizobiales	Rhodobactera	Rhodospirillale
0.001897227	0.005794846	0.000001965	0	0.074765106	0.000641579	0.022253859
0.000566617	0.001472275	2.78664E-06	0	0.10444237	0.001834539	0.018063006
0.002047491	0.003520953	0	0	0.068658583	0.002016413	0.013474135
0.000880002	0.001359025	0	0	0.058142038	0.001264835	0.017807261
0.000915787	0.0019216	6.20872E-06	0	0.056436275	0.000984083	0.014616373
0.001026891	0.001182134	0	0	0.068380527	0.000843654	0.014937642
0.00061728	0.00227993	8.28563E-06	0	0.067541722	0.002012028	0.01500252
0.001180152	0.002538633	0	0	0.06649856	0.000853026	0.013354233
0.001553825	0.00201191	1.22156E-06	0	0.04933883	0.00079035	0.011876012
0.000714545	0.002081719	0.000008367	0	0.056459103	0.00149268	0.010810214
0.001143546	0.002228233	1.75176E-05	0	0.043667054	0.001622826	0.013028154
0.002064602	0.001528267	1.44176E-06	1.44176E-06	0.008388168	0.001665235	0.001621982

Rickettsiales	Sphingomona	pca1_L3		others	At12OctB3	BME43
0.001505206	0.003678519	0.045387348	2017_6	0	0.000001965	0
0.001943218	0.005069829	-0.11849026	2017_8	0	2.04354E-05	0
0.001477118	0.014020742	-0.1367811	2017_2	0	0.000124312	2.46796E-05
0.001633521	0.004771388	-0.13681121	2016_4	0	1.61468E-05	1.61468E-05
0.003427216	0.005852758	-0.14855416	2016_2	1.03479E-06	7.24351E-06	3.10436E-06
0.000598066	0.004014674	-0.1492771	2016_3	0	2.03597E-05	7.63488E-06
0.00233931	0.004906476	-0.15044777	2017_7	0	2.07141E-05	2.76188E-06
0.001200597	0.007753338	-0.16236329	2017_4	0	3.40756E-06	0
0.001137273	0.009613681	-0.17285389	2017_1	0	5.49702E-05	1.22156E-06
0.001735324	0.007826528	-0.18461491	2017_5	0	1.17139E-05	5.02022E-06
0.000959261	0.0073854	-0.1880056	2016_1	2.80281E-06	1.47147E-05	2.10211E-06
0.000945796	0.014322459	-0.22579627	2017_3	0	0.001128899	0

Bacteroidia	Cytophagia	Flavobacteriia	Sphingobacteı	VC2_1_Bac22	[Rhodothermi]	[Saprospirae]
1.96502E-05	0.008428956	0.006184903	0.011516004	1.37551E-05	0	0.038720732
6.03772E-05	0.008529908	0.00227297	0.003933808	8.35992E-06	0	0.019114498
1.91952E-05	0.019327765	0.0059167	0.020168699	0.00012157	1.82812E-06	0.071416297
0.000018838	0.011273177	0.003622272	0.002427407	1.07646E-05	0	0.028609489
0.000028974	0.018863141	0.004221933	0.004059471	3.00088E-05	0	0.025614095
4.58093E-05	0.006750506	0.003414064	0.004788342	0	0	0.023436536
0.000229236	0.031113934	0.008600487	0.010943941	2.48569E-05	0	0.070220743
4.08907E-05	0.027161672	0.006188131	0.016742485	2.61246E-05	1.13585E-06	0.061747284
2.32097E-05	0.028732326	0.006666056	0.010611696	9.40602E-05	0	0.061638723
1.17139E-05	0.024609134	0.004365921	0.008199698	0.000036815	1.67341E-06	0.036507063
2.52253E-05	0.025605056	0.006275488	0.009376796	4.13414E-05	0	0.023455302
0.002188594	0.009222948	0.027155578	0.029762282	0.000005767	5.91122E-05	0.287965905

pca1_L2	Sample ID	k__Bacteria;p	k__Bacteria;p	k__Bacteria;p	k__Bacteria;p
-0.17109995	2017_8	0	2.04354E-05	0	6.03772E-05
-0.1440242	2016_4	0	1.61468E-05	1.61468E-05	0.000018838
-0.12620985	2017_5	0	1.17139E-05	5.02022E-06	1.17139E-05
-0.11413677	2017_6	0	0.000001965	0	1.96502E-05
-0.10792866	2016_2	1.03479E-06	7.24351E-06	3.10436E-06	0.000028974
-0.10066544	2016_1	2.80281E-06	1.47147E-05	2.10211E-06	2.52253E-05
-0.09318462	2016_3	0	2.03597E-05	7.63488E-06	4.58093E-05
-0.08310558	2017_7	0	2.07141E-05	2.76188E-06	0.000229236
-0.07660038	2017_4	0	3.40756E-06	0	4.08907E-05
-0.07248727	2017_1	0	5.49702E-05	1.22156E-06	2.32097E-05
-0.0724556	2017_2	0	0.000124312	2.46796E-05	1.91952E-05
0.14584106	2017_3	0	0.001128899	0	0.002188594

k__Bacteria;p	k__Bacteria;p	k__Bacteria;p	k__Bacteria;p	k__Bacteria;p	k__Bacteria;p__Bacteroidete
0.008529908	0.00227297	0.003933808	8.35992E-06	0	0.019114498
0.011273177	0.003622272	0.002427407	1.07646E-05	0	0.028609489
0.024609134	0.004365921	0.008199698	0.000036815	1.67341E-06	0.036507063
0.008428956	0.006184903	0.011516004	1.37551E-05	0	0.038720732
0.018863141	0.004221933	0.004059471	3.00088E-05	0	0.025614095
0.025605056	0.006275488	0.009376796	4.13414E-05	0	0.023455302
0.006750506	0.003414064	0.004788342	0	0	0.023436536
0.031113934	0.008600487	0.010943941	2.48569E-05	0	0.070220743
0.027161672	0.006188131	0.016742485	2.61246E-05	1.13585E-06	0.061747284
0.028732326	0.006666056	0.010611696	9.40602E-05	0	0.061638723
0.019327765	0.0059167	0.020168699	0.00012157	1.82812E-06	0.071416297
0.009222948	0.027155578	0.029762282	0.000005767	5.91122E-05	0.287965905

es;c__[Saprospirae]