

Supplementary Table 4. ANOVA and *post hoc* pairwise comparisons (Tukeys HSD) for the treatment effects of microbial taxa at the class level. Treatment groups are ambient T°C and pH (AmbNorm), ambient T°C and low pH (AmbLow), elevated T°C and normal pH (HiNorm), and elevated T°C and low pH (HiLow) for each color morph.

[1] "*Bacteria_Acidobacteria_Acidobacteriia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	54745	7821	1.14	0.38
Residuals	21	144041	6859		

[2] "*Bacteria_Acidobacteria_Blastocatellia_(Subgroup_4)*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	4761	680	1.44	0.24
Residuals	21	9918	472		

[3] "*Bacteria_Acidobacteria_Thermoanaerobaculia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	1786	255	1.84	0.13
Residuals	21	2909	138		

[4] "*Bacteria_Actinobacteria_Acidimicrobiia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	150210	21459	1.96	0.11
Residuals	21	229890	10947		

[5] "*Bacteria_Actinobacteria_Actinobacteria* "

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	45489	6498	2.31	0.065
Residuals	21	59163	2817		

[6] "*Bacteria_Bacteroidetes_Bacteroidia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	15508	2215	0.51	0.82
Residuals	21	91216	4344		

[7] "*Bacteria_Bacteroidetes_Ignavibacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	1.95	0.278	0.78	0.61
Residuals	21	7.50	0.357		

[8] "*Bacteria_Bacteroidetes_Rhodothermia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
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Treatment	7	3387	484	1.69	0.17
Residuals	21	6010	286		

[9] "*Bacteria_Chloroflexi_Anaerolineae*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	83624	11946	2.16	0.081
Residuals	21	115910	5520		

[10] "*Bacteria_Chloroflexi_Chloroflexia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	749	107	0.74	0.64
Residuals	21	3042	145		

[11] "*Bacteria_Chloroflexi_Dehalococcoidia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	296516	42359	2.13	0.085
Residuals	21	417313	19872		

[12] "*Bacteria_Cyanobacteria_Melainbacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	140	20.0	0.77	0.62
Residuals	21	544	25.9		

[13] "*Bacteria_Cyanobacteria_Oxyphotobacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	193913	27702	1.23	0.33
Residuals	21	472551	22502		

[14] "*Bacteria_Dadabacteria_Dadabacteriia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	38996	5571	1.62	0.19
Residuals	21	72341	3445		

[15] "*Bacteria_Entotheonellaeota_Entotheonella*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	1170	167	1.59	0.19
Residuals	21	2210	105		

[16] "*Bacteria_Epsilonbacteria_Camyplobacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	3902	557	0.8	0.59
Residuals	21	14575	694		

[17] "*Bacteria_Firmucutes_Bacilli*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	10997	1571	1.42	0.25

Residuals	21	23154	1103		
[18] "Bacteria_Firmucutes_Clostridia"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	3834	548	7.15	0.0002
Residuals	21	1608	77		

Tukey multiple comparisons of means 95% family-wise confidence level

Comparison	p adj
AmbNorm-HiLow	0.999
AmbNorm-AmbLow	0.599
AmbNorm-HiNorm	0.003
HiNorm-HighLow	0.567
AmbLow-HiLow	0.632
HiNorm-AmbLow	0.083

[19] "Bacteria_Firmucutes_Negativicutes"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	91	13.0	0.76	0.63
Residuals	21	361	17.2		

[20] "Bacteria_Lentisphaerae_Oligosphaeria"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	7.46	1.06	0.98	0.47
Residuals	21	22.75	1.08		

[21] "Bacteria_Nitrospirae_Nitrospira"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	12611	1802	2.39	0.058
Residuals	21	15825	754		

[22] "Bacteria_Patescibacteria_Gracilibacteria"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	69	9.86	1.38	0.26
Residuals	21	150	7.13		

[23] "Bacteria_Planctomycetes_Phycisphaerae"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	13	1.86	0.89	0.53
Residuals	21	44	2.10		

[24] "Bacteria_Planctomycetes_Planctomycetia"					
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	73	10.4	0.46	0.85
Residuals	21	474	22.6		

[25] "*Bacteria_Proteobacteria_Alphaproteobacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	316017	45145	0.77	0.62
Residuals	21	1230549	585980		

[26] "*Bacteria_Proteobacteria_Deltaproteobacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	47808	6830	2.9	0.028
Residuals	21	49469	23565		

Tukey multiple comparisons of means 95% family-wise confidence level

Comparison	p adj
AmbNorm-HiLow	0.565
AmbNorm-AmbLow	0.236
AmbNorm-HiNorm	0.901
HiNorm-HighLow	0.767
AmbLow-HiLow	0.632
HiNorm-AmbLow	0.046

[27] "*Bacteria_Proteobacteria_Gammaproteobacteria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	6672389	953198	1.85	0.13
Residuals	21	10839612	516172		

[28] "*Bacteria_Spirochaetes_Spirochaetia*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	3866	552	1.4	0.26
Residuals	21	8314	396		

[29] "*Archaea_Thaumarchaeota_Nitrososphaeria*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	358845	51264	0.53	0.8
Residuals	21	2014333	95921		

[30] "*Bacteria_Verrucomicrobia_Verrucomicrobiae*"

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	7	48.5	6.93	0.86	0.55
Residuals	21	168.8	8.04		