

Figure. S1 The UPGMA tree of coral samples is based on the Unweighted Unifrac distance matrix. A, B, and C represent *Montipora sp.*, *Platygyra sp.*, and *Pocillopora sp.*, respectively. 1,2 and 3 represented HH, HA and AA samples, respectively.

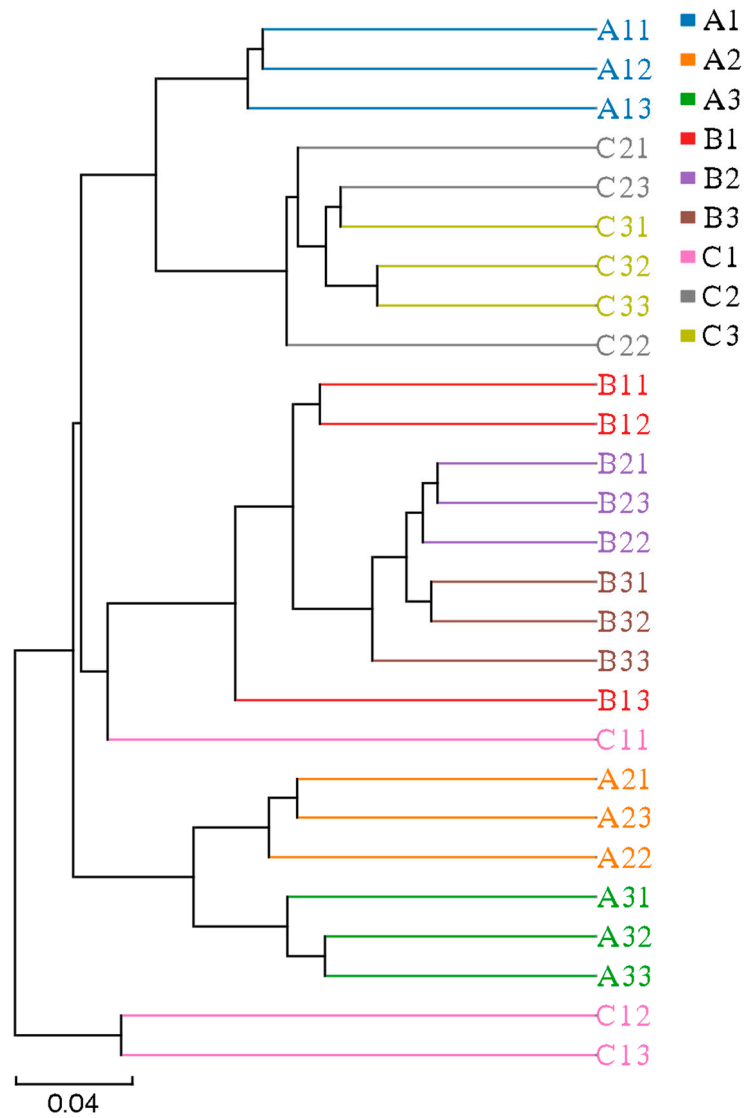


Figure. S2 Relative abundance (%) of major bacterial communities at the class level.

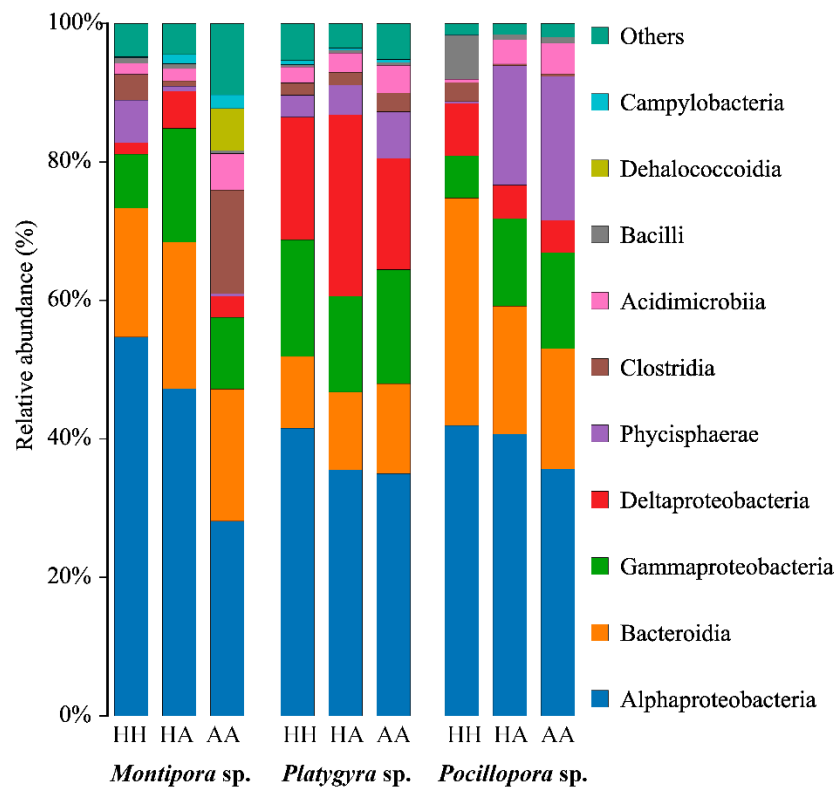


Table S1 Number of bacteria obtained at all taxonomic levels in 3 coral genera

Coral genus	Condition	Phylum	Class	Order	Family	Genus
<i>Pocillopora</i> sp.	HH	23	54	122	221	389
	HD	22	48	115	215	391
	DD	24	53	121	221	397
<i>Montipora</i> sp.	HH	23	49	121	218	382
	HD	23	48	117	212	384
	DD	22	50	118	215	380
<i>Platygyra</i> sp.	HH	23	50	117	213	358
	HD	21	47	116	212	375
	DD	23	50	120	221	396

Table S2 Relative abundance (%) of some important bacterial communities at the genus level.

Coral genus	Condition	Relative abundance (%)		
		<i>Vibrio</i>	<i>Arcobacter</i>	<i>Desulfovibrio</i>
<i>Montipora</i> sp.	HH	0.123	0.119	0.009
	HA	2.606	1.329	0.003
	AA	0.358	1.984	0.003
<i>Platygyra</i> sp.	HH	0.292	0.230	0.211
	HA	0.401	0.041	0.072
	AA	0.594	0.004	0.101
<i>Pocillopora</i> sp.	HH	0.216	0.018	0.084
	HA	0.127	0.002	0.005
	AA	0.311	0.009	0.004