Table 4: Results from AMOVA for *Pocillopora damicornis*. Four genetic structures are tested. "All samples" indicates that there was no hierarchical structure imposed. '3 regions' tests the significance of a priori geographic structure among Teluk Cenderawasih, Raja Ampat, and Fakfak/Kaimana. Finally, the structures inferred by BAPS and Genetical Bandwidth Mapping (GBM) are tested. Estimators are calculated based on both the infinite alleles model (*F* statistics) and stepwise mutation model (*R* statistics) of microsatellite evolution. Negative values are presented, but are effectively equal to zero.

	F statistic		p	% var	R statistic		p	% var
All samples								
Among localities	F_{ST}	0.139	<0.00001	13.940	R_{ST}	0.130	<0.00001	13.000
Within localities				86.060				87.000
3 regions								
Among groups	F_{CT}	-0.028	0.874	-2.830	R_{CT}	0.017	0.382	1.660
Among localities within regions	F_{SC}	0.156	<0.00001	15.990	R_{SC}	0.120	<0.00001	11.810
Within localities	F_{ST}	0.132	<0.00001	86.840	R_{ST}	0.135	<0.00001	86.540
Structure inferred by BAPS								
Among clusters	F_{CT}	0.140	0.003	14.000	R_{CT}	0.060	0.240	6.020
Among localities within clusters	F_{SC}	0.030	0.007	2.610	R_{SC}	0.079	0.013	7.460
Within localities	F_{ST}	0.166	<0.00001	83.400	R_{ST}	0.135	<0.00001	86.520
Structure inferred by GBM								
Among clusters	F_{CT}	-0.011	0.555	-1.070	R_{CT}	0.063	0.178	5.930
Among localities within clusters	F_{SC}	0.148	<0.00001	14.940	R_{SC}	0.076	0.007	7.160
Within localities	F_{ST}	0.139	<0.00001	86.130	R_{ST}	0.136	<0.00001	86.530