

Table 5: Results from AMOVA for *Seriatopora hystrix*. 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} 0.357	<0.00001	35.710	R_{ST} 0.246	<0.00001	24.560
Within localities			64.290			75.440
3 regions						
Among groups	F_{CT} 0.068	0.034	6.840	R_{CT} 0.043	0.177	4.290
Among localities within regions	F_{SC} 0.324	<0.00001	30.140	R_{SC} 0.222	<0.00001	21.210
Within localities	F_{ST} 0.370	<0.00001	63.020	R_{ST} 0.255	<0.00001	74.510
Structure inferred by BAPS						
Among clusters	F_{CT} 0.325	0.016	32.530	R_{CT} 0.286	0.018	28.620
Among localities within clusters	F_{SC} 0.050	0.088	3.400	R_{SC} -0.054	0.919	-3.830
Within localities	F_{ST} 0.359	<0.00001	64.070	R_{ST} 0.248	<0.00001	75.220
Structure inferred by GBM						
Among clusters	F_{CT} 0.142	0.006	14.170	R_{CT} -0.031	0.566	-3.080
Among localities within clusters	F_{SC} 0.263	<0.00001	22.610	R_{SC} 0.270	<0.00001	27.370
Within localities	F_{ST} 0.368	<0.00001	63.220	R_{ST} 0.243	<0.00001	75.710