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.

<table>
<thead>
<tr>
<th></th>
<th>F-statistic</th>
<th>p</th>
<th>% var</th>
<th>R-statistic</th>
<th>p</th>
<th>% var</th>
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</thead>
<tbody>
<tr>
<td><strong>All samples</strong></td>
<td></td>
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<tr>
<td>Among localities</td>
<td><em>F</em>&lt;sub&gt;ST&lt;/sub&gt; 0.357 &lt;0.00001 35.710</td>
<td><em>R</em>&lt;sub&gt;ST&lt;/sub&gt; 0.246 &lt;0.00001 24.560</td>
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<tr>
<td>Within localities</td>
<td>64.290</td>
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<td></td>
<td></td>
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<td>75.440</td>
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<tr>
<td><strong>3 regions</strong></td>
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<tr>
<td>Among groups</td>
<td><em>F</em>&lt;sub&gt;CT&lt;/sub&gt; 0.068 0.034 6.840</td>
<td><em>R</em>&lt;sub&gt;CT&lt;/sub&gt; 0.043 0.177 4.290</td>
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<tr>
<td>Among localities within regions</td>
<td><em>F</em>&lt;sub&gt;SC&lt;/sub&gt; 0.324 &lt;0.00001 30.140</td>
<td><em>R</em>&lt;sub&gt;SC&lt;/sub&gt; 0.222 &lt;0.00001 21.210</td>
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<tr>
<td>Within localities</td>
<td><em>F</em>&lt;sub&gt;ST&lt;/sub&gt; 0.370 &lt;0.00001 63.020</td>
<td><em>R</em>&lt;sub&gt;ST&lt;/sub&gt; 0.255 &lt;0.00001 74.510</td>
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<td><strong>Structure inferred by BAPS</strong></td>
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<tr>
<td>Among clusters</td>
<td><em>F</em>&lt;sub&gt;CT&lt;/sub&gt; 0.325 0.016 32.530</td>
<td><em>R</em>&lt;sub&gt;CT&lt;/sub&gt; 0.286 0.018 28.620</td>
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<tr>
<td>Among localities within clusters</td>
<td><em>F</em>&lt;sub&gt;SC&lt;/sub&gt; 0.050 0.088 3.400</td>
<td><em>R</em>&lt;sub&gt;SC&lt;/sub&gt; -0.054 0.919 -3.830</td>
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<tr>
<td>Within localities</td>
<td><em>F</em>&lt;sub&gt;ST&lt;/sub&gt; 0.359 &lt;0.00001 64.070</td>
<td><em>R</em>&lt;sub&gt;ST&lt;/sub&gt; 0.248 &lt;0.00001 75.220</td>
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<td><strong>Structure inferred by GBM</strong></td>
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<td>Among clusters</td>
<td><em>F</em>&lt;sub&gt;CT&lt;/sub&gt; 0.142 0.006 14.170</td>
<td><em>R</em>&lt;sub&gt;CT&lt;/sub&gt; -0.031 0.566 -3.080</td>
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<td>Among localities within clusters</td>
<td><em>F</em>&lt;sub&gt;SC&lt;/sub&gt; 0.263 &lt;0.00001 22.610</td>
<td><em>R</em>&lt;sub&gt;SC&lt;/sub&gt; 0.270 &lt;0.00001 27.370</td>
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<tr>
<td>Within localities</td>
<td><em>F</em>&lt;sub&gt;ST&lt;/sub&gt; 0.368 &lt;0.00001 63.220</td>
<td><em>R</em>&lt;sub&gt;ST&lt;/sub&gt; 0.243 &lt;0.00001 75.710</td>
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