TABLE S1

Power of GENECONV to detect simulated gene conversion events of various sizes between two sequences (1500 bp each) at varying levels of divergence in 1000 simulations

<table>
<thead>
<tr>
<th>Length of conversion tract (bp)</th>
<th>Divergence</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.01</td>
</tr>
<tr>
<td>501</td>
<td>37.1%</td>
</tr>
<tr>
<td>402</td>
<td>27.0%</td>
</tr>
<tr>
<td>252</td>
<td>15.2%</td>
</tr>
<tr>
<td>150</td>
<td>9.6%</td>
</tr>
<tr>
<td>90</td>
<td>6.7%</td>
</tr>
<tr>
<td>45</td>
<td>5.3%</td>
</tr>
</tbody>
</table>