Table S3. AMOVA results for geographic populations of *P. ramorum*. A significant genetic differentiation was detected among the three geographical populations, namely Monterey, Santa Cruz and Sonoma.

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>Sum of squares</th>
<th>Variance components</th>
<th>% of variation</th>
<th>$\Phi_{ST}$</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Among all populations</td>
<td>2</td>
<td>13.726</td>
<td>0.187</td>
<td>11.4</td>
<td>0.11425</td>
<td>0.0000</td>
</tr>
<tr>
<td>Within populations</td>
<td>89</td>
<td>123.306</td>
<td>1.385</td>
<td>88.6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

AMOVA was conducted on microsatellite multilocus genotypes to measure the genetic differentiation among populations using the program ARLEQUIN (Excoffier and Schneider, 2005). The AMOVA calculates $\Phi_{ST}$, an index of population subdivision. The significance of $F_{ST}$ was tested by 10,000 permutations. All isolates in Table 1, set1 except for Pr-52, a total of 46 isolates were used. Pr-102 from Malin County was included in the Sonoma County population.