<table>
<thead>
<tr>
<th>Gene</th>
<th>ENC</th>
<th>CBI</th>
<th>SCh$^2$</th>
<th>GC3</th>
<th>GC</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>P. syringae pv phaseolicola</strong> GC=58.76%, GC3=70.05%*</td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Hrc1 T3SS</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>hrcV</td>
<td>42.023</td>
<td>0.479</td>
<td>0.384</td>
<td>0.746</td>
<td>0.591</td>
</tr>
<tr>
<td>hrcC</td>
<td>46.292</td>
<td>0.393</td>
<td>0.285</td>
<td>0.680</td>
<td>0.580</td>
</tr>
<tr>
<td>hrcN</td>
<td>41.804</td>
<td>0.507</td>
<td>0.365</td>
<td>0.733</td>
<td>0.639</td>
</tr>
<tr>
<td>hrcQ$_A$</td>
<td>41.407</td>
<td>0.500</td>
<td>0.454</td>
<td>0.734</td>
<td>0.658</td>
</tr>
<tr>
<td>hrcQ$_B$</td>
<td>43.626</td>
<td>0.492</td>
<td>0.490</td>
<td>0.688</td>
<td>0.623</td>
</tr>
<tr>
<td>hrpK</td>
<td>46.163</td>
<td>0.369</td>
<td>0.212</td>
<td>0.687</td>
<td>0.591</td>
</tr>
<tr>
<td>hrpQ</td>
<td>42.712</td>
<td>0.446</td>
<td>0.462</td>
<td>0.692</td>
<td>0.604</td>
</tr>
<tr>
<td><strong>2nd T3SS</strong></td>
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</tr>
<tr>
<td>hrc$_{II}$V</td>
<td>44.812</td>
<td>0.437</td>
<td>0.427</td>
<td>0.678</td>
<td>0.599</td>
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<tr>
<td>hrc$_{II}$C$_1$</td>
<td>48.114</td>
<td>0.440</td>
<td>0.338</td>
<td>0.689</td>
<td>0.609</td>
</tr>
<tr>
<td>hrc$_{II}$C$_2$</td>
<td>42.594</td>
<td>0.480</td>
<td>0.377</td>
<td>0.721</td>
<td>0.608</td>
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<tr>
<td>hrc$_{II}$N</td>
<td>48.278</td>
<td>0.413</td>
<td>0.262</td>
<td>0.684</td>
<td>0.628</td>
</tr>
<tr>
<td>hrc$_{II}$Q</td>
<td>48.700</td>
<td>0.422</td>
<td>0.315</td>
<td>0.693</td>
<td>0.617</td>
</tr>
<tr>
<td>hrp$_{II}$K</td>
<td>46.326</td>
<td>0.391</td>
<td>0.251</td>
<td>0.691</td>
<td>0.566</td>
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<tr>
<td>hrp$_{II}$Q</td>
<td>53.515</td>
<td>0.357</td>
<td>0.257</td>
<td>0.611</td>
<td>0.591</td>
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<tr>
<td><strong>P. syringae pv tabaci</strong> GC=57.80%, GC3=68.61%*</td>
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</tr>
<tr>
<td>2nd T3SS</td>
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<tr>
<td>hrc$_{II}$V$_N$</td>
<td>44.798</td>
<td>0.462</td>
<td>0.400</td>
<td>0.699</td>
<td>0.601</td>
</tr>
<tr>
<td>hrc$_{II}$V$_C$</td>
<td>46.157</td>
<td>0.441</td>
<td>0.506</td>
<td>0.611</td>
<td>0.595</td>
</tr>
<tr>
<td>hrc$_{II}$C$_1$</td>
<td>53.571</td>
<td>0.410</td>
<td>0.297</td>
<td>0.653</td>
<td>0.599</td>
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<tr>
<td>hrc$_{II}$C$_2$$_N$</td>
<td>50.221</td>
<td>0.402</td>
<td>0.270</td>
<td>0.700</td>
<td>0.611</td>
</tr>
<tr>
<td>hrc$_{II}$C$_2$$_C$</td>
<td>36.481</td>
<td>0.613</td>
<td>0.851</td>
<td>0.722</td>
<td>0.601</td>
</tr>
<tr>
<td>hrc$_{II}$N$_N$</td>
<td>48.976</td>
<td>0.456</td>
<td>0.303</td>
<td>0.727</td>
<td>0.632</td>
</tr>
<tr>
<td>hrc$_{II}$N$_C$</td>
<td>45.027</td>
<td>0.497</td>
<td>0.515</td>
<td>0.665</td>
<td>0.625</td>
</tr>
<tr>
<td>hrc$_{II}$Q</td>
<td>50.607</td>
<td>0.403</td>
<td>0.292</td>
<td>0.674</td>
<td>0.608</td>
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<tr>
<td>hrp$_{II}$Q</td>
<td>54.875</td>
<td>0.328</td>
<td>0.240</td>
<td>0.599</td>
<td>0.588</td>
</tr>
<tr>
<td>hrp$_{II}$K</td>
<td>46.469</td>
<td>0.379</td>
<td>0.251</td>
<td>0.684</td>
<td>0.566</td>
</tr>
<tr>
<td><strong>Rhizobium sp. NGR234</strong> GC=62.35%, GC3=76.55%*</td>
<td></td>
<td></td>
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<tr>
<td><strong>Rhc1T3SS</strong></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>rhcV</td>
<td>54.210</td>
<td>0.280</td>
<td>0.144</td>
<td>(0.119)</td>
<td>0.631</td>
</tr>
<tr>
<td>rhcC$_1$</td>
<td>54.856</td>
<td>0.367</td>
<td>0.239</td>
<td>(0.148)</td>
<td>0.634</td>
</tr>
<tr>
<td>rhcC$_2$</td>
<td>56.318</td>
<td>0.286</td>
<td>0.183</td>
<td>(0.143)</td>
<td>0.610</td>
</tr>
<tr>
<td>rhcN</td>
<td>54.479</td>
<td>0.321</td>
<td>0.154</td>
<td>(1.113)</td>
<td>0.631</td>
</tr>
<tr>
<td>rhcQ</td>
<td>58.482</td>
<td>0.281</td>
<td>0.169</td>
<td>(0.122)</td>
<td>0.605</td>
</tr>
<tr>
<td>hrpQ-like</td>
<td>54.985</td>
<td>0.314</td>
<td>0.219</td>
<td>(0.145)</td>
<td>0.569</td>
</tr>
<tr>
<td><strong>Rhc$_{II}$T3SS</strong></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rhc$_{II}$V</td>
<td>39.213</td>
<td>0.558</td>
<td>0.318</td>
<td>(0.277)</td>
<td>0.819</td>
</tr>
<tr>
<td>rhc$_{II}$C$_1$</td>
<td>45.007</td>
<td>0.486</td>
<td>0.316</td>
<td>(0.208)</td>
<td>0.771</td>
</tr>
</tbody>
</table>
**B. japonicum** GC=65.59%, GC3=86.46%*

<table>
<thead>
<tr>
<th>Gene</th>
<th>Schi²</th>
<th>ENC</th>
<th>CBI</th>
</tr>
</thead>
<tbody>
<tr>
<td>rhcV</td>
<td>36.204</td>
<td>0.652</td>
<td>0.450 (0.374)</td>
</tr>
<tr>
<td>rhcN</td>
<td>36.611</td>
<td>0.594</td>
<td>0.382 (0.314)</td>
</tr>
<tr>
<td>hrpQ</td>
<td>40.613</td>
<td>0.555</td>
<td>0.284 (0.195)</td>
</tr>
<tr>
<td>rhC</td>
<td>42.736</td>
<td>0.509</td>
<td>0.274 (0.198)</td>
</tr>
</tbody>
</table>

**R. etli CNF 42** GC=61.96%, GC3=76.72%*

<table>
<thead>
<tr>
<th>Gene</th>
<th>Schi²</th>
<th>ENC</th>
<th>CBI</th>
</tr>
</thead>
<tbody>
<tr>
<td>rhcV</td>
<td>48.594</td>
<td>0.329</td>
<td>0.209</td>
</tr>
<tr>
<td>rhcC</td>
<td>55.937</td>
<td>0.303</td>
<td>0.192</td>
</tr>
<tr>
<td>rhC</td>
<td>47.759</td>
<td>0.370</td>
<td>0.316</td>
</tr>
<tr>
<td>rhn</td>
<td>45.896</td>
<td>0.415</td>
<td>0.244</td>
</tr>
<tr>
<td>rhQ</td>
<td>50.065</td>
<td>0.364</td>
<td>0.221</td>
</tr>
<tr>
<td>y4yQ</td>
<td>47.525</td>
<td>0.383</td>
<td>0.313</td>
</tr>
</tbody>
</table>

**Additional file 7. Table S2**: Codon Usage Bias Table.

**Schi²**: Scaled Chi-square, (Scaled Chi-square computed without Yates' correction)

**ENC**: Effective number of codons,

**CBI**: Codon Bias Index,

**GC3**: G+C content at (synonymous) third codon positions,

*source: www.kazusa.or.jp

**Schi², Scaled Chi Square** (Shields et al. 1988)

The "scaled" 2 (chi square) is a measure based on the chi square statistics; i.e., based on the difference between the observed number of codons and those expected from equal usage of codons. The sum of the chi square values is divided by the total number of codons in the gene excluding those codons coding for a unique amino acid;
i.e. all codons excluding the Trp and Met codons (nuclear universal genetic code).

DnaSP can compute the "scaled" chi square with Yates' correction, and also assuming a given G+C content (by default the G+C content is 50%).

**CBI, Codon Bias Index** (Morton 1993)

CBI is a measure of the deviation from the equal use of synonymous codons. CBI values range from 0 (uniform use of synonymous codons) to 1 (maximum codon bias).

**ENC, Effective Number of Codons** (Wright 1990)

That measure quantifies the "effective" number of codons that are used in a gene. For the nuclear universal genetic code, the value of ENC ranges from 20 (only one codon is used for each amino acid; i.e., the codon bias is maximum) to 61 (all synonymous codons for each amino acid are equally used; i.e., no codon bias).


