Gene	ENC	CBI	SChi^2	GC3	GC
***P. syringae* pv phaseolicola** GC=58.76%, GC3=70.05%*					
Hrc1 T3SS					
hrcV	42.023	0.479	0.384	0.746	0.591
hrcC	46.292	0.393	0.285	0.680	0.580
hrcN	41.804	0.507	0.365	0.733	0.639
hrcQ$_A$	41.407	0.500	0.454	0.734	0.658
hrcQ$_B$	43.626	0.492	0.490	0.688	0.623
hrpK	46.163	0.369	0.212	0.687	0.591
hrpQ	42.712	0.446	0.462	0.692	0.604
2nd T3SS					
hrc$_{II}$V	44.812	0.437	0.427	0.678	0.599
hrc$_{II}$C$_1$	48.114	0.440	0.338	0.689	0.609
hrc$_{II}$C$_2$	42.594	0.480	0.377	0.721	0.608
hrc$_{II}$N	48.278	0.413	0.262	0.684	0.628
hrc$_{II}$Q	48.700	0.422	0.315	0.693	0.617
hrp$_{II}$K	46.326	0.391	0.251	0.691	0.566
hrp$_{II}$Q	53.515	0.357	0.257	0.611	0.591
***P. syringae* pv tabaci** GC=57.80%, GC3=68.61%*					
2nd T3SS					
hrc$_{II}$V_N	44.798	0.462	0.400	0.699	0.601
hrc$_{II}$V_C	46.157	0.441	0.506	0.611	0.595
hrc$_{II}$C$_1$	53.571	0.410	0.297	0.653	0.599
hrc$_{II}$C$_2$_N	50.221	0.402	0.270	0.700	0.611
hrc$_{II}$C$_2$_C	36.481	0.613	0.851	0.722	0.601
hrc$_{II}$N_N	48.976	0.456	0.303	0.727	0.632
hrc$_{II}$N_C	45.027	0.497	0.515	0.665	0.625
hrc$_{II}$Q	50.607	0.403	0.292	0.674	0.608
hrp$_{II}$Q	54.875	0.328	0.240	0.599	0.588
hrp$_{II}$K	46.469	0.379	0.251	0.684	0.566
***Rhizobium* sp. NGR234** GC=62.35%, GC3=76.55%*					
Rhc$_1$ T3SS					
rhcV	54.210	0.280	0.144 (0,119)	0.631	0.751
rhcC$_1$	54.856	0.367	0.239 (0.148)	0.634	0.559
rhcC$_2$	56.318	0.286	0.183 (0.143)	0.610	0.561
rhcN	54.479	0.321	0.154 (1.113)	0.631	0.608
rhcQ	58.482	0.281	0.169 (0.122)	0.605	0.582
hrpQ-like	54.985	0.314	0.219 (0.145)	0.569	0.552
Rhc$_{II}$T3SS					
rhc$_{II}$V	39.213	0.558	0.318 (0.277)	0.819	0.655
rhc$_{II}$C$_1$	45.007	0.486	0.316 (0.208)	0.771	0.624

$rhc_{II}C_2$	36.204	0.652	0.450 (0.374)	0.859	0.646
$rhc_{II}N$	36.611	0.594	0.382 (0.314)	0.680	0.679
$hrp_{II}Q$	40.613	0.555	0.284 (0.195)	0.831	0.671
$rhc_{II}Q$	42.736	0.509	0.274 (0.198)	0.784	0.652
B. japonicum GC=65.59%, GC3=86.46%*					
$rhcV$	48.594	0.329	0.209	0.646	0.570
$rhcC_1$	55.937	0.303	0.192	0.642	0.590
$rhcC_2$	47.759	0.370	0.316	0.614	0.603
$rhcN$	45.896	0.415	0.244	0.671	0.619
$rhcQ$	50.065	0.364	0.221	0.666	0.620
$y4yQ$	47.525	0.383	0.313	0.622	0.582
R. etli CNF 42 GC=61.96%, GC3=76.72%*					
$rhcV$	39.671	0.562	0.379	0.818	0.647
$rhcC_1$	37.070	0.637	0.663	0.819	0.645
$rhcN$	37.576	0.575	0.376	0.817	0.667
$rhcQ$	42.110	0.533	0.359	0.773	0.633
$hrpK_1$	38.348	0.541	0.402	0.794	0.619
$hrpK_2$	38.047	0.527	0.397	0.808	0.608

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).

Yates, F. (1934). "Contingency table involving small numbers and the χ^2 test". *Supplement to the Journal of the Royal Statistical Society* **1**(2): 217–235.

Shields, D.C. et al. (1988). "Silent" sites in Drosophila genes are not neutral: Evidence of selection among synonymous codons. *Mol.Bio. Evol.* 5: 704-716.

Morton, B.R. (1993). Chloroplast DNA codon use: Evidence for selection at the psb A locus based on tRNA availability. J. Mol. Evol. 37: 273-280.

Wright, F. (1990). The "effective number of codons" used in a gene. *Gene* 87: 23-29