

Table S4

Running MAGIC while taking Mauve’s backbone results as anchors. Size: genome size. RF(#/cov.): #: number of RF segments. cov.: coverage of RF segments. PO: coverage of positional orthologous segments. +IP: adding inparalogs to the previous column. +Transposable: adding transposable elements to the previous column. +Prophages.: adding prophages as well as phagic elements to the previous column. Identity: mean identity of all positional orthologs. Uni.: the result of the Rao uniformity test with 5% as critical value — ✓accepting, - rejecting, and NA not applicable. Compare to Table 2. * indicates that no prophage annotation was available for those species. Pairs in (a) and (b) are as in Table 2. (c) contains the results for the example run.

(a)

Organism	Size	RF(#/cov.)	PO	+IP	+Mobile DNA	+Prophages	Identity	Uni.
<i>B. bronchiseptica</i>	5339179	154/0.77	0.69	0.72	0.73	0.73	0.98	✓
<i>B. pertussis</i>	4086189	154/0.94	0.90	0.91	0.93	0.93	0.98	✓
<i>H. pylori</i>	1667867	38/0.96	0.92	0.92	0.93	0.93	0.93	-
<i>H. pylori</i> j99	1643831	38/0.97	0.93	0.94	0.94	0.94	0.93	-
<i>N. meningitidis</i> a	2184406	43/0.95	0.86	0.89	0.91	0.93	0.96	-
<i>N. meningitidis</i> b	2272351	43/0.90	0.83	0.86	0.87	0.89	0.96	-
<i>S. typhi</i> ty2	4791961	16/0.96	0.87	0.88	0.89	0.92	0.98	✓
<i>S. typhimurium</i>	4857432	16/1	0.86	0.86	0.87	0.91	0.98	✓
<i>Y. pestis</i>	4653728	43/0.97	0.90	0.90	0.94	0.97	0.98	✓
<i>Y. pseudotuberculosis</i>	4744671	43/0.98	0.89	0.89	0.90	0.90	0.98	✓

(b)

Organism	Size	RF(#/cov.)	PO	+IP	+Mobile DNA	+Prophages	Identity	Uni.
<i>B. aphidicola</i> aps	640681	1/0.96	0.93	0.93	0.93	0.93	0.75	NA
<i>B. aphidicola</i> sg	641454	1/0.96	0.93	0.93	0.93	0.93	0.75	NA
<i>E. coli</i> mg1655	4639675	37/0.95	0.80	0.80	0.83	0.86	0.97	✓
<i>S. flexneri</i> 2457t	4599354	37/0.93	0.80	0.80	0.88	0.92	0.98	-
<i>L. monocytogenes</i> egd-e	2944528	17/0.99	0.85	0.85	0.85	0.88	0.87	-
<i>L. innocua</i>	3011208	17/0.96	0.83	0.84	0.84	0.91	0.87	-
<i>P. abyssii</i>	1765118	88/0.89	0.74	0.74	0.74	0.74	0.73	-
<i>P. horikoshii</i>	1738505	88/0.88	0.75	0.75	0.75	0.75	0.73	-
<i>S. pyogenes</i> m18	1895017	9/0.96	0.72	0.73	0.73	0.84	0.98	✓
<i>S. pyogenes</i> ssi1	1894275	9/0.94	0.73	0.73	0.73	0.91	0.98	✓

(c)

Organism	Size	RF(#/cov.)	PO	+IP	+Mobile DNA	+Prophages	Identity	Uni.
<i>S. flexneri</i> 2457t	4599354	104/0.85	0.64	0.65	0.75	0.79	0.79	-
<i>S. typhi</i> ty2	4791961	104/0.85	0.62	0.62	0.63	0.68	0.79	-