

# Table S1

Running Mauve with default parameters on the 10 prokaryotic pairs as in Table 2 — (a) and (b) — and on the example run — (c). Size: genome size. LCB(#/cov.): #: number of locally-collinear blocks. cov.: coverage of LCB blocks (Mauve’s LCBs are comparable with MAGIC’s RFs). Backbone: coverage of backbone segments (Mauve’s Backbones are comparable with MAGIC’s positional orthologs). Identity: mean identity of all backbone segments Uni.: the result of the Rao uniformity test with 5% as critical value — ✓ accepting, - rejecting, and NA not applicable. The default value of some of the parameters are: The seed for calculating multi-MUMS equals  $seed\_size = \log_2(\frac{g_1+g_2}{2})/1.5$  (for the given genomes the  $seed\_size$  ranges between 12.8 and 15). The threshold for the gaps that are extracted from the alignments of collinear blocks for defining the “backbones” equals  $maxBackboneGapSize = 50$ , and the threshold for the length of backbone segments equals  $minBackboneSize = 50$ .

(a)

Organism	Size	LCB(#/cov.)	Backbone	Identity	Uni.
<i>B. bronchiseptica</i>	5339179	210/0.75	0.69	0.99	-
<i>B. pertussis</i>	4086189	210/0.95	0.91	0.99	-
<i>H. pylori</i>	1667867	100/0.84	0.79	0.94	-
<i>H. pylori</i> j99	1643831	100/0.85	0.80	0.94	-
<i>N. meningitidis</i> a	2184406	248/0.92	0.89	0.97	-
<i>N. meningitidis</i> b	2272351	248/0.90	0.85	0.97	-
<i>S. typhi</i> ty2	4791961	104/0.93	0.90	0.98	-
<i>S. typhimurium</i>	4857432	104/0.94	0.89	0.98	-
<i>Y. pestis</i>	4653728	124/0.97	0.94	0.99	-
<i>Y. pseudotuberculosis</i>	4744671	124/0.96	0.92	0.99	-

(b)

Organism	Size	LCB(#/cov.)	Backbone	Identity	Uni.
<i>B. aphidicola</i> aps	640681	10/0.99	0.95	0.77	✓
<i>B. aphidicola</i> sg	641454	10/0.99	0.95	0.77	✓
<i>E. coli</i> mg1655	4639675	151/0.91	0.84	0.98	-
<i>S. flexneri</i> 2457t	4599354	151/0.92	0.84	0.98	-
<i>L. monocytogenes</i> egd-e	2944528	82/0.98	0.89	0.88	-
<i>L. innocua</i>	3011208	82/0.92	0.87	0.88	-
<i>P. abyssi</i>	1765118	80/0.37	0.26	0.75	-
<i>P. horikoshii</i>	1738505	80/0.30	0.26	0.75	-
<i>S. pyogenes</i> m18	1895017	128/0.43	0.39	0.98	-
<i>S. pyogenes</i> ssi1	1894275	128/0.43	0.39	0.98	-

(c)

Organism	Size	LCB(#/cov.)	Backbone	Identity	Uni.
<i>S. flexneri</i> 2457t	4599354	283/0.84	0.68	0.80	-
<i>S. typhi</i> ty2	4791961	283/0.81	0.65	0.80	-