Table S3. Results of tree topology tests for the dataset in Figure S1.

Data	Tree	logL	deltaL	bp-RELL*	p-KH*	p-SH*	c-ELW*
16S rRNA	16S rRNA	-3130.05	0.00	1.0000 +	1.0000 +	1.0000 +	1.0000 +
	trpB	-4812.52	1682.48	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	gyrB	-4679.99	1549.94	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	rpoB	-4657.95	1527.90	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	atpD	-4789.51	1659.46	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	recA	-4512.03	1381.98	0.0000 -	0.0000 -	0.0000 -	0.0000 -
trpB	16S rRNA	-14061.37	3526.89	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	trpB	-10534.48	0.00	1.0000 +	1.0000 +	1.0000 +	1.0000 +
	gyrB	-12072.06	1537.59	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	rpoB	-12307.05	1772.57	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	atpD	-12521.32	1986.85	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	recA	-12107.64	1573.17	0.0000 -	0.0000 -	0.0000 -	0.0000 -
gyrB	16S rRNA	-13469.01	4066.09	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	trpB	-10645.80	1242.89	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	gyrB	-9402.92	0.00	1.0000 +	1.0000 +	1.0000 +	1.0000 +
	rpoB	-10862.54	1459.62	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	atpD	-11393.12	1990.20	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	recA	-11077.20	1674.28	0.0000 -	0.0000 -	0.0000 -	0.0000 -
rpoB	16S rRNA	-11908.15	4134.72	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	trpB	-9471.34	1697.91	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	gyrB	-9582.95	1809.52	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	rpoB	-7773.43	0.00	1.0000 +	1.0000 +	1.0000 +	1.0000 +
	atpD	-10203.17	2429.74	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	recA	-9817.47	2044.04	0.0000 -	0.0000 -	0.0000 -	0.0000 -
atpD	16S rRNA	-9036.27	3806.01	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	trpB	-7319.46	2089.20	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	gyrB	-7176.25	1945.99	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	rpoB	-7370.29	2140.03	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	atpD	-5230.26	0.00	1.0000 +	1.0000 +	1.0000 +	1.0000 +
	recA	-7504.43	2274.17	0.0000 -	0.0000 -	0.0000 -	0.0000 -
recA	16S rRNA	-10671.71	3047.17	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	trpB	-8841.54	1217.00	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	gyrB	-8622.65	998.11	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	rpoB	-8873.51	1248.97	0.0000 -	0.0000 -	0.0000 -	0.0000 -
	atpD	-9356.50	1731.97	0.0000 -	0.0000 -	0.0000 -	0.0000 -

	recA	-7624.54	0.00	1.0000 +	1.0000 +	1.0000 +	1.0000 +

deltaL: logL difference from the maximal logL in the set
bp-RELL: bootstrap proportion using RELL method (Kishino *et al.*, 1990)
p-KH: p-value of one sided Kishino-Hasegawa test (Kishino and Hasegawa, 1989)
p-SH: p-value of Shimodaira-Hasegawa test (Shimodaira and Hasegawa, 2000)
c-ELW: Expected Likelihood Weight (Strimmer and Rambaut, 2002)
* Plus signs denote the 95% confidence sets. Minus signs denote significant exclusion.
All tests performed 1000 re-samplings using the RELL method.