

**Table S1.** Statistics of phylogenetically reconstructed trees of tRNA structures derived from 17 data matrices. Number of taxa analyzed is shown in parentheses. CI = consistency index (with/without uninformative characters), RI = retention index, RC = rescaled consistency index.

Taxa	No. of trees	Tree length	CI	RI	RC	$g_1$
<i>Bacillus subtilis</i> (19)	1	131	0.626/0.566	0.739	0.463	-0.691
<i>Bos taurus</i> (33)	23	355	0.369	0.656	0.242	-0.545
<i>Drosophila melanogaster</i> (13)	3	166	0.633/0.585	0.653	0.413	-0.827
<i>Escherichia coli</i> (45)	502	216	0.454/0.413	0.761	0.345	-0.589
<i>Halobacterium cutirubrum</i> (12)	2	116	0.672/0.604	0.568	0.382	-0.537
<i>Haloferax volcanii</i> (41)	40	209	0.450/0.419	0.739	0.332	-0.467
<i>Homo sapiens</i> (22)	1	287	0.453/0.416	0.588	0.266	-0.422
<i>Lupinus</i> spp. (13)	5	161	0.615/0.566	0.523	0.322	-0.450
<i>Mus musculus</i> (17)	9	186	0.618/0.580	0.689	0.426	-0.731
<i>Mycoplasma capricolum</i> (29)	12	168	0.548/0.500	0.675	0.370	-0.704
<i>Neurospora crassa</i> (10)	2	158	0.658/0.609	0.518	0.341	-0.728
<i>Nicotiana</i> (11)	2	126	0.659/0.606	0.682	0.449	-0.309
Phage (13)	2	145	0.662/0.602	0.608	0.403	-0.828
<i>Phaseolus vulgaris</i> (21)	74	170	0.606/0.573	0.796	0.483	-0.411
<i>Rattus norvegicus</i> (27)	10	229	0.480/0.466	0.749	0.36	-0.617
<i>Saccharomyces cerevisiae</i> (51)	1521	383	0.339/0.336	0.689	0.234	-0.288
<i>Spinacia oleracea</i> (11)	6	129	0.682/0.637	0.568	0.388	-0.722