Supporting information for Kapitonov and Jurka (2003) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.0732024100

Table 4. Cross-similarities of the *Transib1–4* consensus sequences and proteins encoded by them

Family	Transib1	Transib2	Transib3	Transib4
Transib1	461 aa	64 (2-446)	59 (1-443)	57 (3-357)
	2167 bp	62 (21-2167)	60 (21-2147)	62 (103-2109)
Transib2	46 (2-460)	690 aa	62 (2-688)	50 (1-649)
	62 (20-2844)	2844 bp	62 (1-2844)	61 (1-2844)
Transib3	41 (1-452)	43 (2-688)	685 aa	48 (3-649)
	60 (20-2864)	62 (1-2883)	2883 bp	60 (1-2883)
Transib4	43 (3-367)	34 (1-536)	32 (3-535)	533 aa
	62 (100-1893)	61 (1-2656)	60 (1-2656)	2656 bp

Lengths of transposases and transposons are shown in diagonal cells. Each underdiagonal cell ij shows an identity between the i and j transposases (the first line) and nucleotide identity between the i and j transposons (the second line). Numbers in parentheses are positions of the matching regions in the i transposase and transposon. Each above-diagonal cell ji shows a similarity between the j and i transposases (the first line) and nucleotide identity between the j and i transposans (the second line). Numbers in parentheses are positions of the matching regions in the j transposase and transposon.