

Supplementary Table S3 (Ahn et al.)

Codon substitution rates in segments B and C.

	sites		π_s	π_a
	synonymous	nonsynonymous		
Segment B (39 sites)				
TFL1 (18 sequences)	9.74	29.26	0.71036	0.27318
FT (10 sequences)	10.68	28.32	0.68639	0.02117
Segment C (81 sites)				
TFL1 (18 sequences)	18.51	62.49	0.73415	0.14216
FT (10 sequences)	18.68	62.32	0.70656	0.07644

Only complete sequences were considered.

Synonymous sites: Average number of sites at which mutations can cause changes that do not affect the encoded amino acid.

Nonsynonymous sites: Average number of sites at which mutations can cause changes that change the encoded amino acid.

π_s : Average pairwise fraction of changes at synonymous sites.

π_a : Average pairwise fraction of changes at nonsynonymous sites.