

Additional file 7 – Branch length correlations among data types for each vertebrate clade.

For each clade, all branches shared between a pair of trees (combined + mtDNA, combined + nucDNA, mtDNA + nucDNA) were tested for correlation. Nearly all comparisons show significant positive correlations in all possible combinations between the lengths of shared branches among trees. The two clades that do not show significant correlations in all combinations (Dicaeid birds and Cervid mammals) have very small sample sizes of shared branches, making detection of significant patterns difficult.

Clade	Combined vs. mtDNA	Combined vs. nucDNA	mtDNA vs. nucDNA
Balistid fish	$r_s=0.909, P < 0.0001$	$r_s=0.885, P < 0.0001$	$r_s=0.833, P < 0.05$
Scarine fish	$r_s=0.825, P << 0.0001$	$r_s=0.922, P << 0.0001$	$r_s=0.792, P << 0.0001$
Hemiphractid frogs	$r_s=0.838, P << 0.0001$	$r_s=0.680, P < 0.0005$	$r_s=0.620, P < 0.01$
Hylid frogs	$r_s=0.867, P << 0.0001$	$r_s=0.805, P << 0.0001$	$r_s=0.435, P < 0.005$
<i>Plethodon</i> salamanders	$r_s=0.960, P < 0.0001$	$r_s=0.728, P < 0.0001$	$r_s=0.526, P < 0.03$
Phrynosomatid lizards	$r_s=0.938, P << 0.0001$	$r_s=0.894, P << 0.0001$	$r_s=0.738, P < 0.0005$
Alcid birds	$r_s=0.9925, P << 0.0001$	$r_s=0.870, P < 0.0001$	$r_s=0.802, P < 0.001$
Caprimulgid birds	$r_s=0.842, P << 0.0001$	$r_s=0.820, P << 0.0001$	$r_s=0.555, P < 0.005$
Cotingid birds	$r_s=0.907, P << 0.0001$	$r_s=0.928, P << 0.0001$	$r_s=0.811, P < 0.0001$
Dicaeid birds	$r_s=0.905, P << 0.0001$	$r_s=0.209, P = 0.473$	$r_s=-0.0545, P = 0.884$

		(small sample size)	(small sample size)
Emydid turtles	$r_s=0.946, P << 0.0001$	$r_s=0.465, P < 0.05$	$r_s=0.685, P < 0.05$
Cervid mammals	$r_s=0.896, P << 0.0001$	$r_s=0.433, \text{ns (small sample size)}$	$r_s=-0.143, \text{ns (small sample size)}$
Murid rodents (Philippines)	$r_s=0.789, P << 0.0001$	$r_s=0.820, P << 0.0001$	$r_s=0.675, P < 0.0001$
Murid rodents (Sahul)	$r_s=0.867, P << 0.0001$	$r_s=0.958, P << 0.0001$	$r_s=0.776, P << 0.0001$
