

Additional file 1 – Statistical analyses of congruence

Results of statistical analyses comparing how congruence between mtDNA and nucDNA (and the resolution of discordance between them in the combined analyses) is related to the length and depth of branches in the combined-data tree. Significant *P*-values are boldfaced, indicating that the mean branch lengths being compared are significantly different from each other.

	Clade Comparison	Balistid fish		Scarine fish		Hemiphractid frogs		Hylid frogs		<i>Plethodon</i> salamanders	
		<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>
Branch Lengths	<i>Concordant mtD NA wins</i> vs. <i>Discordant mtD NA wins</i>	58	0.03595	231	0.01134	35.5	8.80E-06	743	0.0005	131.5	0.0055
	<i>Unique mtD NA wins</i> vs. <i>Discordant mtD NA wins</i>	5	0.5714	29	0.2218	46	0.5789	37	0.0475	75	0.5
	<i>Unique mtD NA wins</i> vs. <i>Discordant mtD NA wins</i>	43	0.06194	78.5	0.0099	54	0.0015	435	2.94E-08	67	0.0007
	<i>Unique mtD NA wins</i> vs. <i>Discordant mtD NA wins</i>	13	0.1702	41.5	0.166	43	0.1909	215	0.002392	104	0.015
Node Depth	<i>mtD NA wins</i> vs. <i>nucD NA wins</i>	6.5	0.875	27.5	0.3097	69	0.0055	91.5	0.2554	80	0.3454
		Phrynosomatid lizards		Alcid birds		Caprimulgid birds		Cotingid birds		Dicaeid birds	

Branch Lengths	<i>Concordant</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>
	<i>mtD</i>	212	7.78	76	0.046	507	7.24	244	9.29	34	0.009
	<i>NA wins</i>		E-05		1		E-05		E-06		34
	<i>vs. nucD</i>										
Node Depth	<i>NA wins</i>	13	0.923	5	0.571	91	0.001	13	0.502	26	1
	<i>Unique vs. Concordant</i>	68	0.000	-	-	124	3.82	21	0.173	10	0.181
	<i>Unique vs. Discordant</i>	42.5	0.131	-	-	68	0.029	11	0.307	14	0.444
		4					17		7		4
	<i>mtD</i>	12	1	4.5	0.714	65	0.266	17	0.969	29.5	0.676
	<i>NA wins</i>				3		4		7		5
	<i>vs. nucD</i>										
	<i>NA wins</i>										
		Emydid turtles		Cervid Mammals		Murid Rodents (Philippines)		Murid Rodents (Sahul)			
Branch Lengths	<i>Concordant</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>	<i>W</i>	<i>P</i>		
	<i>mtD</i>	32	0.000	12	0.002	515	0.000	570	0.000		
	<i>NA wins</i>		5				1415		2		
	<i>vs. nucD</i>										
	<i>NA wins</i>	47.5	0.665	25	0.1	49	0.816	36.5	0.249		
	<i>Unique vs. Concordant</i>		2				8		6		
	<i>Unique vs. Discordant</i>										

	<i>Unique vs. Concordant</i>	60	0.0003	-	-	87	0.0162	39.5	0.1628
	<i>Unique vs. Discordant</i>	87	0.002541	-	-	41	0.3546	12	0.6667
Node	<i>mtD</i>	39	0.815	14	1	41.5	0.7693	9	0.0584
Dept	<i>NA</i>								
h	<i>wins vs. nucD</i>								
	<i>NA</i>								
	<i>wins</i>								