

**Supplementary Table — Likelihood Ratio Tests (LRTs) and relative rate variation between tunicates and vertebrates using local clocks.**

Gene#	Annotation	Clock type	lnL	rates for branches		KHI2, df = 1 LRT = $2^*(\ln L_1 - \ln L_2)$	p-value	Bonferroni e-value	Rate ratio r1/r2
				r1	r2				
Gene01	<i>CCT5</i>	local 1	-8737.54	1.67					
		local 2	-8727.52	2.24	1.27	20.03	0.0000	0.0003	1.763*
Gene02	<i>RPL10L</i>	local 1	-3221.48	1.25					
		local 2	-3219.93	1.46	1.01	3.10	0.0781	2.7319	1.442
Gene03	<i>HSP90AB1</i>	local 1	-9778.94	1.03					
		local 2	-9777.15	1.15	0.90	3.57	0.0588	2.0587	1.273
Gene04	<i>RPL7A</i>	local 1	-5193.42	1.43					
		local 2	-5173.22	2.21	0.65	40.40	0.0000	0.0000	3.380*
Gene05	<i>PSMA6</i>	local 1	-5252.07	1.75					
		local 2	-5222.50	2.53	0.71	59.13	0.0000	0.0000	3.559*
Gene06	<i>PSMB1</i>	local 1	-5029.45	1.75					
		local 2	-5021.86	2.24	1.24	15.19	0.0001	0.0034	1.807*
Gene07	<i>PDHB</i>	local 1	-6921.46	1.35					
		local 2	-6918.76	1.56	1.11	5.39	0.0202	0.7071	1.410
Gene08	<i>RPLP2</i>	local 1	-1985.45	1.10					
		local 2	-1985.18	0.99	1.17	0.54	0.4605	16.1186	0.841
Gene09	<i>RPL12</i>	local 1	-3206.48	1.33					
		local 2	-3206.29	1.26	1.44	0.37	0.5428	18.9990	0.875
Gene10	<i>RPL13</i>	local 1	-5357.89	1.43					
		local 2	-5348.21	1.76	0.84	19.37	0.0000	0.0004	2.090*
Gene11	<i>RPL15</i>	local 1	-3796.50	1.19					
		local 2	-3786.85	1.52	0.56	19.31	0.0000	0.0004	2.712*
Gene12	<i>RPL13A</i>	local 1	-4266.44	1.22					
		local 2	-4262.36	1.41	0.75	8.17	0.0043	0.1492	1.896
Gene13	<i>RPL18</i>	local 1	-4271.81	1.27					
		local 2	-4269.85	1.46	1.07	3.91	0.0480	1.6802	1.370
Gene14	<i>RPL19</i>	local 1	-3206.84	1.73					
		local 2	-3201.61	2.63	1.23	10.46	0.0012	0.0428	2.135*
Gene15	<i>RPL27A</i>	local 1	-2531.77	1.45					
		local 2	-2526.40	1.94	0.87	10.74	0.0010	0.0367	2.228*
Gene16	<i>RPL8</i>	local 1	-4049.00	1.61					

Gene17	<i>RPL35A</i>	local 2	-4041.84	2.27	1.01	14.33	0.0002	0.0054	2.240*
		local 1	-2378.40	1.80					
Gene18	<i>RPL39L</i>	local 2	-2377.28	2.62	1.77	2.24	0.1346	4.7113	1.480
		local 1	-807.21	1.38					
Gene19	<i>RPL3</i>	local 2	-807.21	1.68	1.72	0.00	0.9659	33.8070	0.979
		local 1	-6541.42	1.42					
Gene20	<i>RPL4</i>	local 2	-6536.77	1.78	1.17	9.31	0.0023	0.0799	1.525
		local 1	-6888.12	1.31					
Gene21	<i>RPL5</i>	local 2	-6873.80	1.80	0.74	28.64	0.0000	0.0000	2.447*
		local 1	-5970.45	0.97					
Gene22	<i>RPL6</i>	local 2	-5969.40	1.05	0.83	2.10	0.1469	5.1421	1.258
		local 1	-5566.16	0.95					
Gene23	<i>RPL7</i>	local 2	-5560.66	1.18	0.65	11.01	0.0009	0.0317	1.83*
		local 1	-5851.74	1.34					
Gene24	<i>RPLP0</i>	local 2	-5850.90	1.47	1.18	1.68	0.1944	6.8033	1.242
		local 1	-6074.22	1.70					
Gene25	<i>RPS10</i>	local 2	-6068.45	2.26	1.32	11.55	0.0007	0.0237	1.715*
		local 1	-2730.65	2.74					
Gene26	<i>RPS13</i>	local 2	-2716.76	5.09	1.22	27.76	0.0000	0.0000	4.186*
		local 1	-1969.95	1.78					
Gene27	<i>RPS16</i>	local 2	-1958.99	3.04	0.40	21.93	0.0000	0.0001	7.531*
		local 1	-2109.81	1.19					
Gene28	<i>RPS18</i>	local 2	-2099.77	1.63	0.43	20.08	0.0000	0.0003	3.791*
		local 1	-2145.71	1.85					
Gene29	<i>RPS3A</i>	local 2	-2141.21	2.38	1.05	9.00	0.0027	0.0943	2.275
		local 1	-4504.35	1.56					
Gene30	<i>RPS27</i>	local 2	-4492.17	2.21	0.83	24.36	0.0000	0.0000	2.665*
		local 1	-992.82	1.66					
Gene31	<i>AHCY</i>	local 2	-984.86	2.52	0.44	15.92	0.0001	0.0023	5.787*
		local 1	-7858.77	1.52					
Gene32	<i>RPSA</i>	local 2	-7848.73	1.96	1.07	20.07	0.0000	0.0003	1.838*
		local 1	-4057.69	1.40					
Gene33	<i>SARS</i>	local 2	-4042.97	1.92	0.61	29.44	0.0000	0.0000	3.133*
		local 1	-9841.59	1.12					
Gene34	<i>SUCLG1</i>	local 2	-9828.36	1.43	0.78	26.46	0.0000	0.0000	1.845*
		local 1	-5627.56	1.00					

Gene35	<i>U2AF1</i>	local 2	-5624.46	1.14	0.75	6.20	0.0128	0.4473	1.524
		local 1	-1968.05	2.30					
		local 2	-1963.46	2.74	0.97	9.17	0.0025	0.0860	2.833

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*E*-values correspond to the *p*-values after being multiplied by 35, the total number of genes tested (Bonferroni correction).

Asterisks indicate genes for which differences in rates between tunicates and vertebrates were found significant at the 5% level (<0.05).