

Supplemental Table 3 - Pearson's *r* coefficients* for correlations between the indicated 24 parameters (mean values across either all species per clade, i.e. 'All species', or five randomly selected species per clade, i.e. '5 species - run 1-10') and clade stem ages for CPEB2 orthologs

Paralogs	% A	% C	% D	% E	% F	% G	% H	% I	% K	% L	% M	% N	% P	% Q	% R	% S	% T	% V	% W	% Y	SIM	REP	LLPS	PRD
5 species - run 1	-0.37	0.233	0.909	0.928	0.49	-0.41	0.38	0.98	0.588	-0.88	0.862	0.781	-0.94	-0.33	0.309	0.136	0.08	0.939	0.734	0.842	-0.82	-0.77	-0.79	-0.78
5 species - run 2	-0.36	0.274	0.909	0.942	0.522	-0.45	0.253	0.976	0.571	-0.85	0.883	0.79	-0.94	-0.42	0.309	0.281	0.134	0.942	0.748	0.833	-0.81	-0.76	-0.79	-0.8
5 species - run 3	-0.43	0.271	0.928	0.951	0.476	-0.38	0.361	0.959	0.613	-0.83	0.838	0.804	-0.96	-0.33	0.371	0.175	-0.01	0.961	0.649	0.846	-0.79	-0.74	-0.74	-0.74
5 species - run 4	-0.43	0.266	0.941	0.939	0.599	-0.42	0.432	0.966	0.645	-0.83	0.855	0.779	-0.95	-0.37	0.356	0.104	-0.05	0.942	0.773	0.795	-0.79	-0.75	-0.74	-0.7
5 species - run 5	-0.32	0.17	0.934	0.95	0.6	-0.26	0.287	0.988	0.578	-0.8	0.916	0.822	-0.97	-0.33	0.233	0.111	6E-05	0.968	0.689	0.847	-0.82	-0.79	-0.78	-0.8
5 species - run 6	-0.44	0.303	0.93	0.957	0.536	-0.4	0.294	0.985	0.625	-0.88	0.838	0.796	-0.95	-0.33	0.346	0.092	0.087	0.952	0.686	0.817	-0.82	-0.76	-0.77	-0.77
5 species - run 7	-0.41	0.396	0.927	0.93	0.487	-0.33	0.346	0.994	0.643	-0.82	0.845	0.818	-0.96	-0.35	0.359	0.211	-0.15	0.95	0.777	0.766	-0.77	-0.75	-0.74	-0.69
5 species - run 8	-0.44	0.237	0.937	0.955	0.529	-0.37	0.286	0.989	0.605	-0.83	0.879	0.814	-0.97	-0.29	0.237	0.205	0.165	0.955	0.727	0.863	-0.84	-0.8	-0.78	-0.8
5 species - run 9	-0.39	0.269	0.92	0.951	0.557	-0.41	0.316	0.994	0.635	-0.87	0.846	0.809	-0.95	-0.28	0.318	0.195	-0.1	0.961	0.806	0.84	-0.83	-0.78	-0.8	-0.81
5 species - run 10	-0.46	0.352	0.935	0.942	0.618	-0.42	0.464	0.985	0.635	-0.81	0.862	0.802	-0.95	-0.41	0.247	0.206	0.097	0.965	0.731	0.761	-0.83	-0.79	-0.74	-0.81
All species	-0.43	0.293	0.929	0.947	0.554	-0.4	0.344	0.983	0.634	-0.85	0.868	0.8	-0.96	-0.34	0.294	0.149	0.052	0.957	0.785	0.815	-0.81	-0.77	-0.78	-0.77

*the *r* value for statistically significant changes is in *green* (increase from older to younger clades) or in *red* (decrease from older to younger clades).

Legend

%X = mean percent amino acid frequency across ortholog primary sequences for each clade (where X is any amino acid)

SIM = SIM score

REP = REP score

LLPS = Σ classifier distance P (ParSE)

PRD = PRD score (PLAAC)