Supplemental Table 1. Proteins used in Maximum Likelihood Analyses and their Levels of Support for the Monophyly of Chara and Land Plants

	Sites[a]			
Protein	Total	Variable	Rate of Evolution[b]	Support[c]
Atp1	465	172	1.00	_
Atp6	238	108	1.06	0.64*
Atp8	75	70	3.78	0.31
Atp9	73	29	0.40	_
Cob	370	123	0.76	0.25
Cox1	506	95	0.37	0.70*
Cox2	238	103	0.87	0.48
Cox3	260	110	1.18	_
MttB	193	175	4.97	0.84*
Nad1	319	116	0.94	_
Nad2	438	232	1.68	0.66*
Nad3	114	66	1.18	0.25
Nad4	466	195	1.20	0.88*
Nad4L	100	57	1.06	_
Nad5	636	274	1.35	0.93*
Nad6	152	91	1.40	0.65*
Nad9	163	105	1.89	0.58
Rpl5	65	63	4.83	0.23*
Rps3	154	131	3.74	
Rps4	125	117	5.16	0.53*
Rps7	101	77	2.81	0.44*
Rps12	115	69	1.49	0.54
Ymf39	104	97	5.06	-

[a] Number of sites corresponding to each protein in the concatenated amino acid data set.

[b] Specific rates of evolution were estimated from the concatenated data set using CODEML (option Mgene = 0) and a gamma-distributed rate of substitutions across sites ($\alpha = 1.0$).

[c] For each protein, a RELL bootstrap value is provided for the best tree only if the topology of this tree supports the monophyly of Chara and land plants. The presence of an asterisk indicates that the topology of the best tree is identical to that shown in Figure 3. Bootstrap values were obtained by analyzing the concatenated data set using CODEML (option Mgene = 1) and a gamma-distributed rate of substitutions across sites ($\alpha = 0.93$).