Supplementary Materials

Weng et al., --Plastid-nuclear interaction and accelerated coevolution in plastid ribosomal genes in Geraniaceae

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Supplementary Data

Data file S1. Sequence alignments included in the study (zip file).

Data file S2. Coevolution analysis results (excel file).

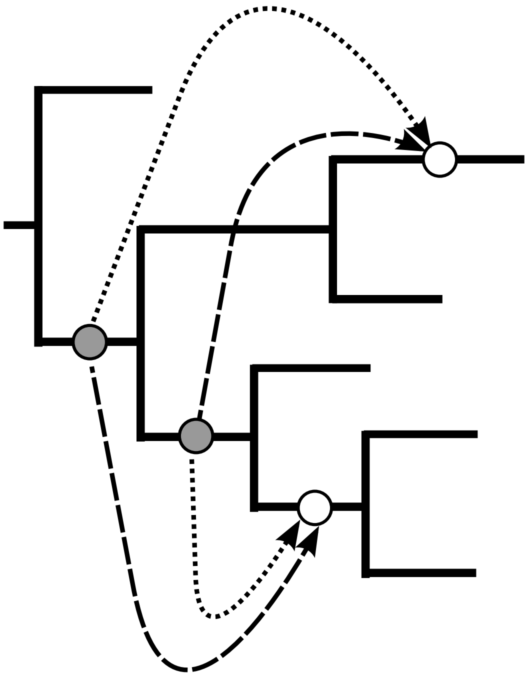

Figure S1. Schematic representation of consecutive substitutions.

Grey dots denote a nonsynonymous substitution at site *i* in leading protein. Open dots denote nonsynonymous substitution at site *j* in trailing protein. Dotted lines indicate consecutive nonsynonymous substitutions between site *i* of leading protein and site *j* in trailing protein because they occur in the same lineage and are not separated by additional substitutions. Dashed lines are nonconsecutive nonsynonymous substitutions because they are not in the same lineage or there are additional substitutions between them.

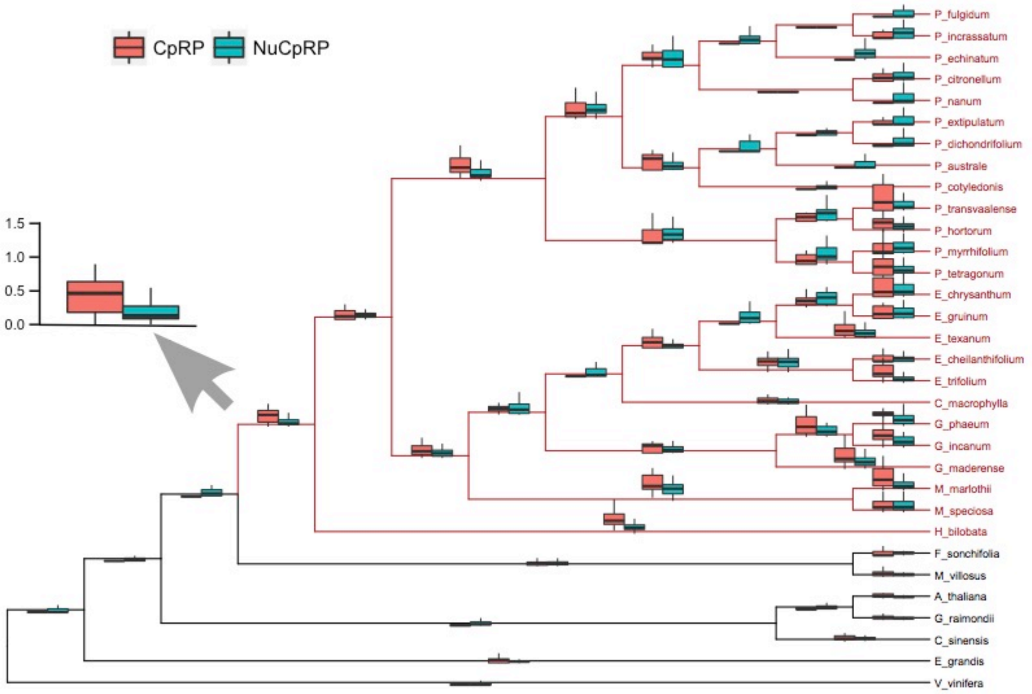

Figure S2. Distribution of ω for CpRP and NuCpRP on the Geraniaceae phylogeny. Geraniaceae and ourgroups branches are indicated in red and black, respectively. Boxplots of branch-specific ω between CpRP and NuCpRP are shown on each branch. The y-axes of all boxplots (see inset example) are in the same scale. The figure was generated using ggtree package (Yu et al. submitted)

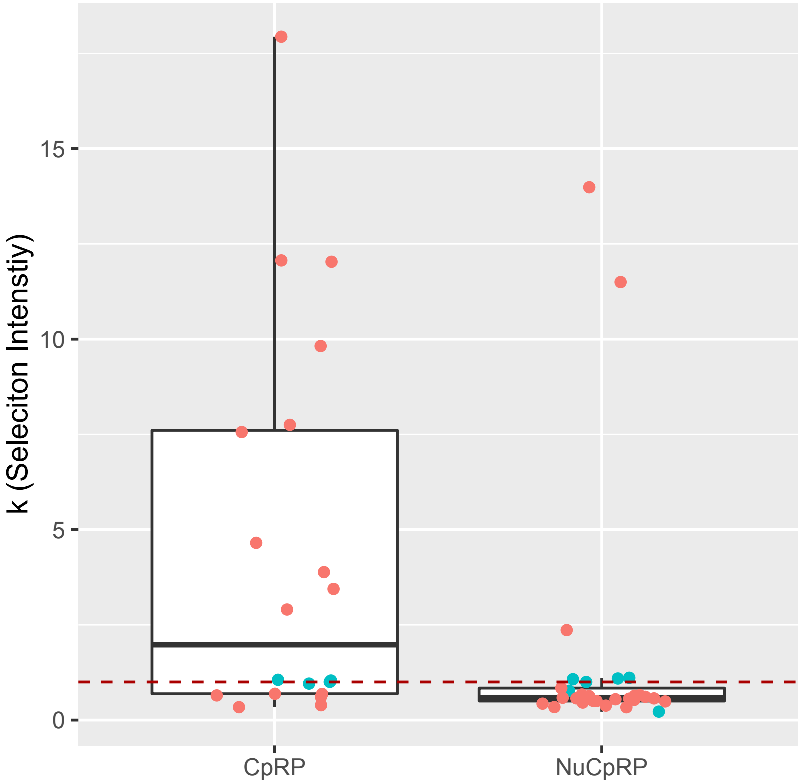

Figure S3. Comparison of the selection intensity parameter (k) for CpRP and NuCpRP. The selection intensity parameter was estimated using RELAX (Wertheim et al. 2015). The significant and non-significant results are indicated by red and green dots, respectively.

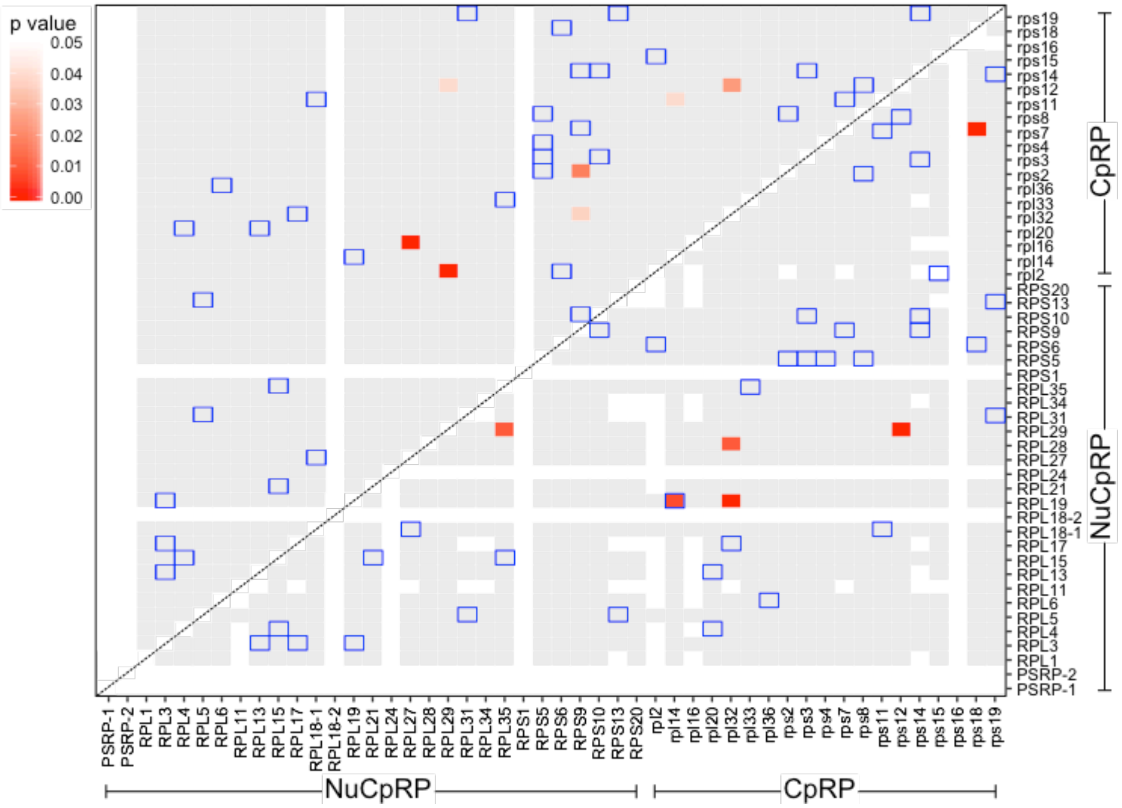

Figure S4. Matrix of p-values for the type I coevolution statistics based on alignments that only include contact residues. The type I coevolution statistic for a protein pair is defined as the number of codons that share nonsynonymous substitutions on three branches. False discovery rate adjusted p-values smaller than 5% are highlighted in red gradient. The nonsignificant p-values are shown in grey squares. The blue open squares indicate the protein pairs that have residues within 10Å. The protein pairs that did not have valid type I coevolution statistics are in white squares. Above and below the diagonal are results from protein and rRNA contact residues, and results from protein contact residues, respectively.

Supplementary Table S1. Sources for plastid- and nuclear-encoded genes included in the study.

	Plastid-encoded genes	Nuclear-encoded genes[1]
Vitis vinifera	NC_007957	Phytozome v9.1
Eucalyptus grandis	NC_014570	Phytozome v9.1
Citrus sinensis	NC_008334	Phytozome v9.1
Gossypium raimondii	NC_016668	Phytozome v9.1
Arabidopsis thaliana	NC_000932	TAIR
Melianthus villosus	NC_023256	SRX910270
Francoa sonchifolia	NC_021101	SRX910417
Hypseocharis bilobata	NC_023260	SRX910270
Pelargonium tetragonum	KM527899	SRX911056
Pelargonium myrrhifolium	KM527895	SRX908171
Pelargonium hortorum	NC_008454	SRX148706
Pelargonium transvaalense	KM527900	SRX910975
Pelargonium cotyledonis	KM459516	SRX910267
Pelargonium australe	KM459517	SRX910974
Pelargonium dichondrifolium	KM459515	SRX910883
Pelargonium extipulatum	KM527892	SRX908169
Pelargonium nanum	KM527896	SRX910973
Pelargonium citronellum	KM527888	SRX910186
Pelargonium echinatum	KM527891	SRX908170
Pelargonium incrassatum	KM527894	SRX910811
Pelargonium fulgidum	KM527893	SRX910878
Monsonia emarginata	KT692738	SRX910269
Monsonia marlothii	KT692739	SRX911055
Geranium maderense	KT760576	SRX190475
Geranium incanum	KT760575	SRX910268
Geranium phaem	KT760577	SRX911054
California macrophylla	JQ031013	SRX910976
Erodium texanum	NC_014569	SRX907966
Erodium gruinum	KF804069	SRX908000
Erodium chrysanthum	KJ701602	SRX907975
Erodium trifolium	KF441758	SRX900105
Erodium foetidum ssp. *cheilanthifolium*	JQ014209	SRX907801

[1] Accession numbers of nuclear-encoded genes obtained from Phytozome and TAIR are listed in Supplementary Table S2. SRX numbers are accession number for the Short Read Archive at GenBank reported in Ruhlman et al. 2015.

Supplementary Table S2. Accession numbers for nuclear-encoded genes from *Arabidopsis thaliana*, *Vitis vinifera*, *Gossypium raimondii*, *Eucalyptus grandis* and *Citrus sinensis*.

	Gene symbol	Gene description	Uniprot ID[1]	*Arabidopsis thaliana*[2]	*Vitis vinifera*[3]	*Gossypium raimondii*[3]	*Eucalyptus grandis*[3]	*Citrus sinensis*[3]
NuCyRP	RPL10AA	60S ribosomal protein L10a-1	Q8VZB9	AT1G08360.1	GSVIVT01033841001|PACid:17839478	Gorai.006G112000.5|PACid:26831055	Eucgr.J00492.2|PACid:23598268	orange1.1g027876m|PACid:18111118
NuCyRP	RPL12A	60S ribosomal protein L12-1	P50883	AT2G37190.1	GSVIVT01016274001|PACid:17826737	Gorai.013G266700.1|PACid:26787487	Eucgr.K03247.1|PACid:23604953	orange1.1g031095m|PACid:18097625
NuCyRP	RPL17A	60S ribosomal protein L17-1	Q93VI3	AT1G27400.1	GSVIVT01010449001|PACid:17822617	Gorai.004G276000.1|PACid:26773005	Eucgr.K02735.2|PACid:23604358	orange1.1g030676m|PACid:18102320
NuCyRP	RPL23AA	60S ribosomal protein L23a-1	Q8LD46	AT2G39460.1	GSVIVT01025041001|PACid:17833112	Gorai.011G249300.1|PACid:26811627	Eucgr.L03160.4|PACid:23607662	orange1.1g031794m|PACid:18095316
NuCyRP	RPL26B	60S ribosomal protein L26-2	Q9FJX2	AT5G67510.1	GSVIVT01000121001|PACid:17816726	Gorai.004G263100.1|PACid:26775957	Eucgr.I00709.1|PACid:23595242	orange1.1g032182m|PACid:18124616
NuCyRP	RPL3A	60S ribosomal protein L3-1	P17094	AT1G43170.1	GSVIVT01034555001|PACid:17839987	Gorai.009G255300.4|PACid:26769932	Eucgr.F02696.2|PACid:23583563	orange1.1g038172m|PACid:18091957
NuCyRP	RPL3B	60S ribosomal protein L3-2	P22738	AT1G61580.1	GSVIVT01023241001|PACid:17831785	Gorai.012G169700.1|PACid:26827058	Eucgr.I02767.1|PACid:23597566	orange1.1g016469m|PACid:18113395
NuCyRP	RPL4A	60S ribosomal protein L4-1	Q9SF40	AT3G09630.1	GSVIVT01025547001|PACid:17833516	Gorai.007G374700.1|PACid:26784992	Eucgr.K03205.1|PACid:23604901	orange1.1g048058m|PACid:18132026
NuCyRP	RPL7A	60S ribosomal protein L7-1	Q9SAI5	AT1G80750.1	GSVIVT01034230001|PACid:17839780	Gorai.012G017500.3|PACid:26826918	Eucgr.J03165.1|PACid:23601333	orange1.1g025547m|PACid:18122310
NuCyRP	RPL8B	60S ribosomal protein L8-2	Q4PSL7	AT3G51190.1	GSVIVT01014552001|PACid:17825516	Gorai.003G010500.1|PACid:26800318	Eucgr.I02360.1|PACid:23597109	orange1.1g024947m|PACid:18128096
NuCyRP	RPP0C	60S acidic ribosomal protein P0-3	P57691	AT3G11250.1	GSVIVT01032857001|PACid:17838724	Gorai.012G076000.1|PACid:26825309	Eucgr.G03042.1|PACid:23588826	orange1.1g020952m|PACid:18138282

NuCyRP	RPS13B	40S ribosomal protein S13-2	P59224	AT4G00100.1	GSVIVT01027637001|PACid:17834981	Gorai.001G174200.2|PACid:26823605	Eucgr.D02462.1|PACid:23576371	orange1.1g031857m|PACid:18127912
NuCyRP	RPS15AE	40S ribosomal protein S15a-5	Q9M0E0	AT4G29430.1	GSVIVT01016890001|PACid:17827227	Gorai.009G030100.1|PACid:26768980	Eucgr.G02917.1|PACid:23588686	orange1.1g032980m|PACid:18126775
NuCyRP	RPS20C	40S ribosomal protein S20-1	P49200	AT5G62300.1	GSVIVT01018553001|PACid:17828462	Gorai.006G064700.6|PACid:26834301	Eucgr.K03281.1|PACid:23604997	orange1.1g033482m|PACid:18127830
NuCyRP	RPS5B	40S ribosomal protein S5-2	P51427	AT3G11940.1	GSVIVT01026328001|PACid:17834075	Gorai.002G154300.1|PACid:26792413	Eucgr.A02519.2|PACid:23564451	orange1.1g028585m|PACid:18118282
NuCyRP	RPS9C	40S ribosomal protein S9-2	Q9FLF0	AT5G39850.1	GSVIVT01011384001|PACid:17823254	Gorai.006G020700.1|PACid:26830565	Eucgr.I01938.1|PACid:23596646	orange1.1g046291m|PACid:18135051
NuCyRP	RPSaA	40S ribosomal protein Sa-1	Q08682	AT1G72370.1	GSVIVT01016695001|PACid:17827063	Gorai.011G056700.1|PACid:26810268	Eucgr.J02605.2|PACid:23600765	orange1.1g021262m|PACid:18121035
NuCyRP	CAO	chlorophyll a oxygenase	Q9MBA1	AT1G44446.1	GSVIVT01008862001|PACid:17821388	Gorai.005G089400.2|PACid:26806492	Eucgr.F03791.1|PACid:23584980	orange1.1g009406m|PACid:18107778
NuCpOT	CRTISO	carotenoid isomerase	Q9M9Y8	AT1G06820.1	GSVIVT01022527001|PACid:17831348	Gorai.002G153800.1|PACid:26791956	Eucgr.A02546.1|PACid:23564477	orange1.1g005823m|PACid:18118279
NuCpOT	OEP80	outer envelope protein of 80 kDa;AtOEP80 is paralog to the chloroplastic protein translocation channel Toc75	Q9C5J8	AT5G19620.1	GSVIVT01019114001|PACid:17828871	Gorai.N002100.1|PACid:26777950	Eucgr.K02362.3|PACid:23603943	orange1.1g027843m|PACid:18119637
NuCpOT	PDH-E1 BETA	pyruvate dehydrogenase E1 beta	Q9C6Z3	AT1G30120.1	GSVIVT01026353001|PACid:17834089	Gorai.010G167000.1|PACid:26760281	Eucgr.E01909.1|PACid:23578573	orange1.1g015415m|PACid:18112487
NuCpOT	PSAK	photosystem I subunit K	Q9SUI5	AT1G30380.1	GSVIVT01021584001|PACid:17830659	Gorai.005G266900.1|PACid:26802279	Eucgr.D00234.1|PACid:23573995	orange1.1g033067m|PACid:18114176
NuCpOT	PSAL	photosystem I subunit L	Q9SUI4	AT4G12800.1	GSVIVT01019114001|PACid:17828871	Gorai.N002100.1|PACid:26777950	Eucgr.K02362.3|PACid:23603943	orange1.1g027843m|PACid:18119637
NuCpOT	PSBO2	photosystem II subunit O-2	Q9S841	AT3G50820.1	GSVIVT01009624001|PACid:17821997	Gorai.007G208000.1|PACid:26783248	Eucgr.I01025.1|PACid:23595525	orange1.1g019870m|PACid:18124684

NuCpOT	PSBQ-2	photosystem II subunit Q-2	Q41932	AT4G05180.1	GSVIVT01002809001|PACid:17818205	Gorai.009G175700.1|PACid:26762434	Eucgr.D00854.1|PACid:23574601	orange1.1g026780m|PACid:18114658
NuCpOT	PSBR	photosystem II subunit R	P27202	AT1G79040.1	GSVIVT01020484001|PACid:17829836	Gorai.009G354500.1|PACid:26762670	Eucgr.F03186.5|PACid:23584217	orange1.1g032633m|PACid:18123674
NuCpOT	PSY	phytoene synthase	P37271	AT5G17230.1	GSVIVT01035255001|PACid:17840447	Gorai.001G083700.1|PACid:26819400	Eucgr.F02913.1|PACid:23583838	orange1.1g044623m|PACid:18123242
NuCpOT	SS1	Glycogen/starch synthases	Q9FNF2	AT5G24300.1	GSVIVT01038557001|PACid:17842794	Gorai.012G002300.1|PACid:26825622	Eucgr.K00387.1|PACid:23601847	orange1.1g006091m|PACid:18115573
NuCpOT	TOC33	translocon at the outer envelope membrane of chloroplasts 33	O23680	AT1G02280.1	GSVIVT01011531001|PACid:17823369	Gorai.N022100.2|PACid:26819295	Eucgr.A02951.4|PACid:23564983	orange1.1g022373m|PACid:18136830
NuCpOT	TOC64-III	translocon at the outer membrane of chloroplasts 64-III	Q9LVH5	AT3G17970.1	GSVIVT01008433001|PACid:17821034	Gorai.007G003700.2|PACid:26785262	Eucgr.K02274.1|PACid:23603826	orange1.1g008025m|PACid:18133978
NuCpOT	TSA1	tryptophan synthase alpha chain	Q42529	AT3G54640.1	GSVIVT01000716001|PACid:17817114	Gorai.004G218800.1|PACid:26773573	Eucgr.G01098.3|PACid:23586709	orange1.1g021527m|PACid:18093093
NuCpOT	TSB1	tryptophan synthase beta-subunit 1	P14671	AT5G54810.1	GSVIVT01001997001|PACid:17817953	Gorai.013G161300.1|PACid:26786795	Eucgr.F03443.1|PACid:23584524	orange1.1g012341m|PACid:18098393
NuCpRP	PSRP-1	Plastid-specific ribosomal protein 1	Q94K97	AT5G24490.1	GSVIVT01038643001|PACid:17842866	Gorai.004G125000.1|PACid:26774818	Eucgr.A01406.1|PACid:23563165	orange1.1g020955m|PACid:18119458
NuCpRP	PSRP-2	Plastid-specific ribosomal protein 2	Q8VYM4	AT3G52150.1	GSVIVT01032039001|PACid:17838080	Gorai.009G264000.3|PACid:26767920	Eucgr.J01250.1|PACid:23599219	orange1.1g025070m|PACid:18102026
NuCpRP	RPL1	50S ribosomal protein L1	Q9LY66	AT3G63490.1	GSVIVT01032196001|PACid:17838199	Gorai.004G170500.1|PACid:26775568	Eucgr.G03333.1|PACid:23589199	orange1.1g017710m|PACid:18102866
NuCpRP	RPL11	50S ribosomal protein L11	Q9MAP3	AT1G32990.1	GSVIVT01019689001|PACid:17829269	Gorai.007G018600.1|PACid:26780423	Eucgr.D01648.1|PACid:23575396	orange1.1g042478m|PACid:18118570
NuCpRP	RPL13	50S ribosomal protein L13	Q9SYL9	AT1G78630.1	GSVIVT01014101001|PACid:17825159	Gorai.002G048000.1|PACid:26795195	Eucgr.F01365.1|PACid:23582036	orange1.1g026067m|PACid:18130212
NuCpRP	RPL15	50S ribosomal protein L15	P25873	AT3G25920.1	GSVIVT01011891001|PACid:17823646	Gorai.005G191400.2|PACid:26803125	Eucgr.G02317.1|PACid:23587913	orange1.1g024515m|PACid:18138875

NuCpRP	RPL17	50S ribosomal protein L17	Q9M385	AT3G54210.1	GSVIVT01037929001|PACid:17842417	Gorai.004G255400.1|PACid:26774838	Eucgr.A00878.1|PACid:23562581	orange1.1g041707m|PACid:18106960
NuCpRP	RPL18-1	50S ribosomal protein L18	Q9SX68	AT1G48350.1	GSVIVT01017720001|PACid:17827843	Gorai.004G096600.2|PACid:26772256	Eucgr.L01079.1|PACid:23606135	orange1.1g030804m|PACid:18122212
NuCpRP	RPL18-2	Ribosomal L18p/L5e family protein	Q9LJX6	AT3G20230.1	GSVIVT01026787001|PACid:17834368	Gorai.005G145200.1|PACid:26802010	Eucgr.F02580.1|PACid:23583420	orange1.1g048206m|PACid:18115723
NuCpRP	RPL19	50S ribosomal protein L19-2	Q8RXX5	AT5G47190.1	GSVIVT01002112001|PACid:17818010	Gorai.003G177300.2|PACid:26798453	Eucgr.D02125.1|PACid:23575955	orange1.1g026573m|PACid:18103360
NuCpRP	RPL21	50S ribosomal protein L21	P51412	AT1G35680.1	GSVIVT01026890001|PACid:17834444	Gorai.009G290100.1|PACid:26769294	Eucgr.F02613.1|PACid:23583455	orange1.1g027519m|PACid:18092311
NuCpRP	RPL24	50S ribosomal protein L24	P92959	AT5G54600.1	GSVIVT01014572001|PACid:17825530	Gorai.002G080800.1|PACid:26791820	Eucgr.F03416.1|PACid:23584479	orange1.1g029417m|PACid:18126228
NuCpRP	RPL27	50S ribosomal protein L27	Q9FLN4	AT5G40950.1	GSVIVT01033086001|PACid:17838894	Gorai.006G042400.2|PACid:26830759	Eucgr.I01643.1|PACid:23596287	orange1.1g029509m|PACid:18117563
NuCpRP	RPL28	50S ribosomal protein L28	O22795	AT2G33450.1	GSVIVT01027870001|PACid:17835144	Gorai.005G052000.1|PACid:26801668	Eucgr.H02995.1|PACid:23592322	orange1.1g031725m|PACid:18130178
NuCpRP	RPL29	50S ribosomal protein L29	Q9FJP3	AT5G65220.1	GSVIVT01013304001|PACid:17824605	Gorai.007G237100.1|PACid:26782310	Eucgr.I00441.1|PACid:23594992	orange1.1g030809m|PACid:18128335
NuCpRP	RPL3	50S ribosomal protein L3-1	Q9SKX4	AT2G43030.1	GSVIVT01019355001|PACid:17828994	Gorai.013G198500.1|PACid:26789431	Eucgr.D01115.1|PACid:23574885	orange1.1g023905m|PACid:18110898
NuCpRP	RPL31	50S ribosomal protein L31	Q9FWS4	AT1G75350.1	GSVIVT01009748001|PACid:17822106	Gorai.009G200300.1|PACid:26764750	Eucgr.F01878.1|PACid:23582638	orange1.1g032493m|PACid:18092575
NuCpRP	RPL34	50S ribosomal protein L34	Q9LP37	AT1G29070.1	GSVIVT01021193001|PACid:17830354	Gorai.010G158700.1|PACid:26758135	Eucgr.D00519.3|PACid:23574290	orange1.1g031306m|PACid:18112475
NuCpRP	RPL35	50S ribosomal protein L35	Q8VZ55	AT2G24090.1	GSVIVT01012574001|PACid:17824132	Gorai.004G106500.1|PACid:26773615	Eucgr.C02515.1|PACid:23571992	orange1.1g031865m|PACid:18104157
NuCpRP	RPL4	50S ribosomal protein L4	O50061	AT1G07320.1	GSVIVT01024788001|PACid:17832913	Gorai.004G006900.1|PACid:26772945	Eucgr.J01939.1|PACid:23599973	orange1.1g023024m|PACid:18111429

NuCpRP	RPL5	50S ribosomal protein L5	O04603	AT4G01310.1	GSVIVT01027006001|PACid:17834540	Gorai.001G158300.1|PACid:26819956	Eucgr.D02319.1|PACid:23576205	orange1.1g024440m|PACid:18137634
NuCpRP	RPL6	50S ribosomal protein L6	O23049	AT1G05190.1	GSVIVT01030599001|PACid:17837072	Gorai.013G101000.1|PACid:26787029	Eucgr.A01711.1|PACid:23563493	orange1.1g027306m|PACid:18134331
NuCpRP	RPS1	30S ribosomal protein S1	Q93VC7	AT5G30510.1	GSVIVT01034940001|PACid:17840233	Gorai.005G069200.2|PACid:26804540	Eucgr.H04084.2|PACid:23593370	orange1.1g015066m|PACid:18109752
NuCpRP	RPS10	30S ribosomal protein S10	Q9LK61	AT3G13120.1	GSVIVT01014640001|PACid:17825582	Gorai.007G310400.1|PACid:26778146	Eucgr.F03697.1|PACid:23584853	orange1.1g041275m|PACid:18114020
NuCpRP	RPS13	30S ribosomal protein S13	P42732	AT5G14320.1	GSVIVT01008933001|PACid:17821451	Gorai.005G091500.1|PACid:26802809	Eucgr.F03746.2|PACid:23584921	orange1.1g030930m|PACid:18107910
NuCpRP	RPS20	30S ribosomal protein S20	Q9ASV6	AT3G15190.1	GSVIVT01014290001|PACid:17825306	Gorai.009G375600.1|PACid:26771393	Eucgr.F01167.2|PACid:23581851	orange1.1g029900m|PACid:18100947
NuCpRP	RPS5	30S ribosomal protein S5	P93014	AT2G33800.1	GSVIVT01021083001|PACid:17830272	Gorai.010G256400.3|PACid:26758859	Eucgr.D00609.1|PACid:23574371	orange1.1g021869m|PACid:18112187
NuCpRP	RPS6	30S ribosomal protein S6	Q8VY91	AT1G64510.1	GSVIVT01019593001|PACid:17829186	Gorai.008G256400.1|PACid:26816845	Eucgr.D01771.1|PACid:23575531	orange1.1g027743m|PACid:18118695
NuCpRP	RPS9	30S ribosomal protein S9	Q9XJ27	AT1G74970.1	GSVIVT01009628001|PACid:17822000	Gorai.010G013000.1|PACid:26759486	Eucgr.A00474.2|PACid:23562154	orange1.1g042358m|PACid:18092513

[1] Uniprot IDs for NuCpRP and NuCyRP are listed.

[2] Accession numbers for TAIR database (https://www.arabidopsis.org).

[3] Accession number for Phytozome v9.1 (Goodstain et al., 2012).

Supplementary Table S3. Likelihood ratio test results for rate comparison between Geraniaceae and outgroups

			dN						dS					
Gene_group	gene	lnL_Null	lnL_Alt	LRT	p-value_Bonferroni	dN_out*	dN_Ger*	High_rate_lineage**	lnL_Alt	LRT	p-value_Bonferroni	dS_out*	dS_Ger*	High_rate_lineage**
CpRP	rpl2	-4246.1230	-4242.1774	7.89	4.97E-01	0.0754	0.6250	Geraniaceae	-4246.0438	0.1585	6.91E+01	0.3319	1.7096	Geraniaceae
CpRP	rpl14	-2595.8938	-2592.8299	6.13	1.33E+00	0.1794	1.4440	Geraniaceae	-2564.6290	62.5296	2.66E-13	1.8009	2.1881	**Geraniaceae**
CpRP	rpl16	-2572.8792	-2572.8067	0.15	7.03E+01	0.1393	0.6093	Geraniaceae	-2520.5030	104.7526	0.00E+00	2.2984	2.3290	**Geraniaceae**
CpRP	rpl20	-4270.1197	-4269.2462	1.75	1.86E+01	0.5076	2.9041	Geraniaceae	-4264.6355	10.9684	9.27E-02	1.5917	4.5400	Geraniaceae
CpRP	rpl23	-2939.8645	-2912.1126	55.50	9.33E-12	0.0986	2.2255	**Geraniaceae**	-2934.6176	10.4937	1.20E-01	0.1102	1.8846	Geraniaceae
CpRP	rpl32	-3816.3165	-3808.9854	14.66	1.29E-02	0.4578	3.9472	**Geraniaceae**	-3813.4442	5.7446	1.65E+00	2.0647	6.3980	Geraniaceae
CpRP	rpl33	-1714.1555	-1712.7492	2.81	9.35E+00	0.4569	1.5392	Geraniaceae	-1701.8659	24.5793	7.13E-05	1.9706	3.3032	**Geraniaceae**
CpRP	rpl36	-739.2057	-736.0253	6.36	1.17E+00	0.0582	1.2010	Geraniaceae	-730.0196	18.3722	1.82E-03	2.2591	3.2445	**Geraniaceae**
CpRP	rps2	-5839.9532	-5829.3765	21.15	4.24E-04	0.2199	1.9326	**Geraniaceae**	-5783.8484	112.2096	0.00E+00	1.5824	1.8230	**Geraniaceae**
CpRP	rps3	-7608.6796	-7590.9375	35.48	2.57E-07	0.2673	2.5315	**Geraniaceae**	-7559.0957	99.1678	0.00E+00	2.2080	3.4833	**Geraniaceae**
CpRP	rps4	-5479.5922	-5477.1011	4.98	2.56E+00	0.2861	1.8232	Geraniaceae	-5466.9571	25.2702	4.98E-05	1.1017	2.6004	**Geraniaceae**
CpRP	rps7	-3114.8068	-3083.1368	63.34	1.78E-13	0.0375	1.4927	**Geraniaceae**	-3110.1943	9.2251	2.39E-01	0.1312	1.6782	Geraniaceae
CpRP	rps8	-3071.5018	-3063.9558	15.09	1.02E-02	0.4640	1.2035	**Geraniaceae**	-3035.2124	72.5787	0.00E+00	1.9491	2.5361	**Geraniaceae**
CpRP	rps11	-4205.3380	-4197.0080	16.66	4.47E-03	0.2644	2.4132	**Geraniaceae**	-4189.1871	32.3017	1.32E-06	1.8817	3.9909	**Geraniaceae**
CpRP	rps12	-2169.9354	-2162.0266	15.82	6.98E-03	0.0498	0.8319	**Geraniaceae**	-2169.7724	0.3260	5.68E+01	0.5247	2.2266	Geraniaceae
CpRP	rps14	-1608.1426	-1606.7348	2.82	9.33E+00	0.2716	0.8669	Geraniaceae	-1581.0652	54.1549	1.85E-11	1.4484	1.3382	**Outgroup**
CpRP	rps15	-2455.4898	-2452.1400	6.70	9.64E-01	0.5763	1.8159	Geraniaceae	-2435.0351	40.9093	1.59E-08	1.9482	2.7707	**Geraniaceae**
CpRP	rps16	-2560.6320	-2559.7539	1.76	1.85E+01	0.4249	1.6223	Geraniaceae	-2555.4206	10.4229	1.24E-01	1.2953	3.2667	Geraniaceae
CpRP	rps18	-7257.0909	-7180.4052	153.37	0.00E+00	0.1924	5.2020	**Geraniaceae**	-7246.3883	21.4052	3.72E-04	0.4877	5.6604	**Geraniaceae**
CpRP	rps19	-2855.3564	-2855.1152	0.48	4.87E+01	0.2515	1.3732	Geraniaceae	-2835.8492	39.0143	4.21E-08	1.6220	2.4920	**Geraniaceae**
NuCpRP	PSRP-1	-9188.1112	-9109.0462	158.13	0.00E+00	0.9896	1.6693	**Geraniaceae**	-8907.6892	560.8440	0.00E+00	7.0169	5.1738	**Outgroup**
NuCpRP	PSRP-2	-8393.5167	-8341.6641	103.71	0.00E+00	1.0161	1.9638	**Geraniaceae**	-8076.3650	634.3036	0.00E+00	8.5647	4.7815	**Outgroup**
NuCpRP	RPL1	-10418.4135	-10332.5851	171.66	0.00E+00	0.8804	1.4761	**Geraniaceae**	-10055.9192	724.9887	0.00E+00	6.6535	4.5710	**Outgroup**
NuCpRP	RPL3	-7331.6543	-7291.5994	80.11	0.00E+00	0.4744	0.7573	**Geraniaceae**	-6996.3309	670.6470	0.00E+00	10.8779	6.9182	**Outgroup**
NuCpRP	RPL4	-9139.0156	-9015.1034	247.82	0.00E+00	0.9347	1.1106	**Geraniaceae**	-8812.5886	652.8539	0.00E+00	8.8880	5.7524	**Outgroup**
NuCpRP	RPL5	-8699.3806	-8665.0094	68.74	1.11E-14	0.8017	1.7945	**Geraniaceae**	-8426.8193	545.1226	0.00E+00	7.4617	5.7662	**Outgroup**
NuCpRP	RPL6	-6800.6383	-6750.7752	99.73	0.00E+00	0.8000	1.3155	**Geraniaceae**	-6553.8113	493.6540	0.00E+00	7.4655	5.2619	**Outgroup**
NuCpRP	RPL11	-4979.0873	-4965.5900	26.99	2.04E-05	0.3923	0.8473	**Geraniaceae**	-4755.6212	446.9323	0.00E+00	8.0631	5.4469	**Outgroup**
NuCpRP	RPL13	-6768.9737	-6715.6398	106.67	0.00E+00	0.6947	1.0076	**Geraniaceae**	-6576.8149	384.3176	0.00E+00	6.3923	5.4247	**Outgroup**
NuCpRP	RPL15	-8232.5029	-8135.2295	194.55	0.00E+00	0.7603	0.8810	**Geraniaceae**	-7948.1989	568.6080	0.00E+00	6.6624	4.9300	**Outgroup**
NuCpRP	RPL17	-5515.3433	-5501.6585	27.37	1.68E-05	0.5792	1.3747	**Geraniaceae**	-5278.2852	474.1162	0.00E+00	9.5650	6.1766	**Outgroup**
NuCpRP	RPL18_1	-3755.3401	-3727.4421	55.80	8.04E-12	0.5657	0.8379	**Geraniaceae**	-3586.0542	338.5718	0.00E+00	6.9155	4.5887	**Outgroup**
NuCpRP	RPL18_2	-4415.1684	-4374.1810	81.97	0.00E+00	0.6972	0.9051	**Geraniaceae**	-4253.9708	322.3952	0.00E+00	8.9141	6.6030	**Outgroup**
NuCpRP	RPL19	-6484.7894	-6462.3458	44.89	2.09E-09	0.8848	2.1540	**Geraniaceae**	-6213.7110	542.1567	0.00E+00	7.9271	3.8315	**Outgroup**
NuCpRP	RPL21	-5844.8948	-5800.7805	88.23	0.00E+00	0.9929	1.7580	**Geraniaceae**	-5636.7943	416.2010	0.00E+00	7.2573	4.5408	**Outgroup**
NuCpRP	RPL24	-5695.5313	-5671.7485	47.57	5.32E-10	0.8422	1.8541	**Geraniaceae**	-5476.7949	437.4728	0.00E+00	8.5192	5.1088	**Outgroup**
NuCpRP	RPL27	-6437.6359	-6391.7522	91.77	0.00E+00	0.8166	1.4064	**Geraniaceae**	-6198.4150	478.4418	0.00E+00	7.8134	4.9747	**Outgroup**
NuCpRP	RPL28	-4073.3217	-4056.9029	32.84	1.00E-06	0.8290	1.8394	**Geraniaceae**	-3969.6235	207.3964	0.00E+00	6.2782	5.2817	**Outgroup**
NuCpRP	RPL29	-4537.7180	-4537.1733	1.09	2.97E+01	0.4088	2.2782	Geraniaceae	-4397.2919	280.8523	0.00E+00	7.2794	5.2579	**Outgroup**
NuCpRP	RPL31	-5168.6856	-5125.6399	86.09	0.00E+00	1.0158	1.7349	**Geraniaceae**	-4967.8686	401.6339	0.00E+00	11.8868	6.0312	**Outgroup**
NuCpRP	RPL34	-3545.3754	-3545.2870	0.18	6.74E+01	0.5166	2.3058	Geraniaceae	-3491.3121	108.1266	0.00E+00	5.8446	7.1117	**Geraniaceae**
NuCpRP	RPL35	-2636.8852	-2627.0194	19.73	8.91E-04	0.5377	1.0687	**Geraniaceae**	-2536.1637	201.4430	0.00E+00	6.9287	4.8150	**Outgroup**
NuCpRP	RPS1	-13055.0923	-13054.1273	1.93	1.65E+01	0.4044	1.7295	Geraniaceae	-12673.4324	763.3199	0.00E+00	5.6460	4.5925	**Outgroup**
NuCpRP	RPS5	-13438.8029	-13432.7342	12.14	4.94E-02	0.5831	3.6590	**Geraniaceae**	-13235.7022	406.2015	0.00E+00	7.2984	8.3098	**Geraniaceae**
NuCpRP	RPS6	-9373.5634	-9373.1480	0.83	3.62E+01	0.9154	4.0447	Geraniaceae	-9234.6139	277.8990	0.00E+00	8.2625	8.1512	**Outgroup**
NuCpRP	RPS9	-5849.9406	-5839.5616	20.76	5.21E-04	0.5751	1.5602	**Geraniaceae**	-5580.4181	539.0452	0.00E+00	8.9696	5.3919	**Outgroup**
NuCpRP	RPS10	-4637.2741	-4617.3442	39.86	2.73E-08	0.7212	1.5232	**Geraniaceae**	-4413.2656	448.0169	0.00E+00	7.6229	3.7289	**Outgroup**
NuCpRP	RPS13	-4315.9983	-4310.5127	10.97	9.25E-02	0.5244	1.5020	Geraniaceae	-4156.6385	318.7196	0.00E+00	6.8869	4.8930	**Outgroup**
NuCpRP	RPS20	-5401.1954	-5400.9553	0.48	4.88E+01	0.6418	2.8378	Geraniaceae	-5297.5792	207.2324	0.00E+00	6.0208	6.2438	**Geraniaceae**
NuCpOT	CAO	-15997.2572	-15830.4603	333.59	0.00E+00	0.7179	0.8543	**Geraniaceae**	-15613.3596	767.7952	0.00E+00	6.6309	7.6124	**Geraniaceae**
NuCpOT	CRTISO	-15544.2583	-15211.3669	665.78	0.00E+00	0.8622	0.6275	**Outgroup**	-14896.7106	1295.0955	0.00E+00	6.2256	4.0533	**Outgroup**
NuCpOT	OEP80	-19202.0270	-18952.5643	498.93	0.00E+00	0.7231	0.7258	**Geraniaceae**	-18318.8881	1766.2776	0.00E+00	7.6506	4.5131	**Outgroup**
NuCpOT	PDH-E1_BETA	-10407.3146	-10345.0520	124.53	0.00E+00	0.3474	0.4034	**Geraniaceae**	-10110.1429	594.3434	0.00E+00	7.3794	8.2908	**Geraniaceae**
NuCpOT	PSAK	-2495.1646	-2489.5165	11.30	7.77E-02	0.2330	0.4419	Geraniaceae	-2393.1797	203.9698	0.00E+00	7.5415	6.4886	**Outgroup**
NuCpOT	PSAL	-5815.8771	-5776.7384	78.28	0.00E+00	0.4222	0.5135	**Geraniaceae**	-5649.4667	332.8207	0.00E+00	7.8066	8.6736	**Geraniaceae**
NuCpOT	PSBO2	-8368.7137	-8268.6784	200.07	0.00E+00	0.5066	0.4625	**Outgroup**	-8022.5448	692.3379	0.00E+00	8.0262	5.8845	**Outgroup**
NuCpOT	PSBQ-2	-6398.0167	-6314.3358	167.36	0.00E+00	0.8646	1.0366	**Geraniaceae**	-6184.8568	426.3198	0.00E+00	7.1387	5.8142	**Outgroup**
NuCpOT	PSBR	-3934.3425	-3897.6896	73.31	0.00E+00	0.7901	1.0113	**Geraniaceae**	-3854.5307	159.6236	0.00E+00	5.8391	6.7976	**Geraniaceae**
NuCpOT	PSY	-13895.1689	-13674.1761	441.99	0.00E+00	0.9539	0.8853	**Outgroup**	-13447.5557	895.2264	0.00E+00	8.8344	7.1782	**Outgroup**
NuCpOT	SS1	-20539.3179	-19934.4215	1209.79	0.00E+00	1.4233	0.9282	**Outgroup**	-19830.1589	1418.3181	0.00E+00	8.0314	6.1006	**Outgroup**
NuCpOT	TOC33	-11622.7512	-11394.8723	455.76	0.00E+00	1.3466	1.2901	**Outgroup**	-11209.5536	826.3953	0.00E+00	8.6462	5.6513	**Outgroup**
NuCpOT	TOC64-III	-18657.1966	-18225.3050	863.78	0.00E+00	1.2211	1.0040	**Outgroup**	-17806.3858	1701.6216	0.00E+00	8.3884	4.5328	**Outgroup**
NuCpOT	TSA1	-8507.9815	-8366.9046	282.15	0.00E+00	0.8529	0.7679	**Outgroup**	-8093.4173	829.1284	0.00E+00	7.6412	4.6694	**Outgroup**
NuCpOT	TSB1	-12163.5862	-12037.6198	251.93	0.00E+00	0.4883	0.4497	**Outgroup**	-11740.5049	846.1625	0.00E+00	7.6204	7.0692	**Outgroup**
NuCyRP	RPL10AA	-5782.0211	-5704.6738	154.69	0.00E+00	0.4146	0.2421	**Outgroup**	-5647.6175	268.8071	0.00E+00	7.0951	9.0853	**Geraniaceae**
NuCyRP	RPL12A	-4816.8677	-4771.3757	90.98	0.00E+00	0.2912	0.1918	**Outgroup**	-4658.6792	316.3770	0.00E+00	11.4539	11.4142	**Outgroup**
NuCyRP	RPL17A	-5077.7806	-5018.4827	118.60	0.00E+00	0.3452	0.2015	**Outgroup**	-4874.6355	406.2902	0.00E+00	8.9787	7.9732	**Outgroup**
NuCyRP	RPL23AA	-4076.5281	-4030.1174	92.82	0.00E+00	0.3580	0.2530	**Outgroup**	-3930.4903	292.0756	0.00E+00	7.6292	7.4322	**Outgroup**
NuCyRP	RPL26B	-4035.5273	-3976.2887	118.48	0.00E+00	0.3843	0.2117	**Outgroup**	-3824.1510	422.7525	0.00E+00	15.0789	8.4034	**Outgroup**
NuCyRP	RPL3A	-10349.5465	-10268.5168	162.06	0.00E+00	0.3221	0.3246	**Outgroup**	-10147.1906	404.7118	0.00E+00	5.8129	8.0575	**Geraniaceae**
NuCyRP	RPL3B	-10371.7454	-10293.5136	156.46	0.00E+00	0.2883	0.2863	**Outgroup**	-10008.4036	726.6837	0.00E+00	7.3141	7.1623	**Outgroup**
NuCyRP	RPL4A	-12777.8152	-12645.3757	264.88	0.00E+00	0.4582	0.4286	**Outgroup**	-12425.5852	704.4600	0.00E+00	9.0859	9.2341	**Geraniaceae**
NuCyRP	RPL7A	-9138.8829	-8708.9869	859.79	0.00E+00	2.0216	0.8872	**Outgroup**	-8742.3673	793.0311	0.00E+00	10.5883	5.7800	**Outgroup**
NuCyRP	RPL8B	-7622.0684	-7546.1274	151.88	0.00E+00	0.2249	0.1273	**Outgroup**	-7408.5261	427.0847	0.00E+00	6.9683	7.8825	**Geraniaceae**
NuCyRP	RPP0C	-9608.7511	-9506.5240	204.45	0.00E+00	0.3813	0.3669	**Outgroup**	-9330.1724	557.1575	0.00E+00	5.8442	6.0745	**Geraniaceae**
NuCyRP	RPS13B	-3698.2384	-3678.5258	39.43	3.41E-08	0.1308	0.0836	**Outgroup**	-3543.2236	310.0295	0.00E+00	8.4072	7.4694	**Outgroup**
NuCyRP	RPS15AE	-4370.7942	-4211.6876	318.21	0.00E+00	1.3356	0.6719	**Outgroup**	-4170.5516	400.4853	0.00E+00	9.7172	5.3883	**Outgroup**
NuCyRP	RPS20C	-2995.6665	-2990.9732	9.39	2.19E-01	0.1614	0.3555	Geraniaceae	-2887.7444	215.8441	0.00E+00	5.5722	5.2649	**Outgroup**
NuCyRP	RPS5B	-6202.8534	-6119.9320	165.84	0.00E+00	0.4601	0.3606	**Outgroup**	-5950.9408	503.8251	0.00E+00	7.7743	6.2240	**Outgroup**
NuCyRP	RPS9C	-5189.9369	-5105.8458	168.18	0.00E+00	0.3294	0.1119	**Outgroup**	-4988.5679	402.7381	0.00E+00	7.7642	7.2773	**Outgroup**
NuCyRP	RPSaA	-12382.9510	-12199.7805	366.34	0.00E+00	1.0212	1.1682	**Geraniaceae**	-12081.0110	603.8801	0.00E+00	8.1019	7.6659	**Outgroup**
CpPS	psaA	-8589.2907	-8575.6941	27.19	1.84E-05	0.0580	0.0980	**Geraniaceae**	-8450.5086	277.5642	0.00E+00	1.3570	1.7958	**Geraniaceae**
CpPS	psaB	-8356.3536	-8346.0418	20.62	5.59E-04	0.0596	0.1134	**Geraniaceae**	-8203.5425	305.6223	0.00E+00	1.5411	1.8897	**Geraniaceae**
CpPS	psaC	-954.1048	-953.1146	1.98	1.59E+01	0.0000	0.0745	Geraniaceae	-933.0840	42.0417	8.93E-09	2.4923	3.1660	**Geraniaceae**
CpPS	psaI	-646.8000	-630.7716	32.06	1.50E-06	0.6260	0.4884	**Outgroup**	-643.8034	5.9933	1.44E+00	0.9751	1.8939	Geraniaceae
CpPS	psaJ	-747.2063	-746.1177	2.18	1.40E+01	0.1656	0.4000	Geraniaceae	-734.3188	25.7750	3.84E-05	1.8759	2.3728	**Geraniaceae**
CpPS	psbA	-3717.1302	-3713.5121	7.24	7.15E-01	0.0309	0.0456	Geraniaceae	-3684.0218	66.2167	4.44E-14	1.1809	2.2046	**Geraniaceae**
CpPS	psbB	-6635.0133	-6631.1102	7.81	5.21E-01	0.0713	0.1869	Geraniaceae	-6497.1524	275.7219	0.00E+00	2.1667	2.5691	**Geraniaceae**
CpPS	psbC	-5700.0183	-5696.7150	6.61	1.02E+00	0.0445	0.1043	Geraniaceae	-5611.1583	177.7200	0.00E+00	1.4809	2.0840	**Geraniaceae**
CpPS	psbD	-3680.3886	-3676.0206	8.74	3.12E-01	0.0300	0.0406	Geraniaceae	-3630.5578	99.6616	0.00E+00	1.2022	1.8043	**Geraniaceae**
CpPS	psbE	-756.6164	-753.4030	6.43	1.12E+00	0.0575	0.0310	Outgroup	-744.9305	23.3718	1.34E-04	1.1501	1.4531	**Geraniaceae**
CpPS	psbF	-379.4486	-379.3878	0.12	7.27E+01	0.0237	0.0748	Geraniaceae	-377.5662	3.7649	5.23E+00	0.6451	1.4035	Geraniaceae
CpPS	psbH	-1238.0128	-1221.1312	33.76	6.22E-07	0.3854	0.3457	**Outgroup**	-1223.0731	29.8793	4.60E-06	1.7886	2.6222	**Geraniaceae**
CpPS	psbI	-530.0374	-528.8419	2.39	1.22E+01	0.0000	0.1857	Geraniaceae	-521.7156	16.6435	4.51E-03	2.2486	3.5407	**Geraniaceae**
CpPS	psbJ	-460.6276	-456.1902	8.87	2.89E-01	0.1708	0.1159	Outgroup	-448.3111	24.6329	6.94E-05	1.8122	1.6692	**Outgroup**
CpPS	psbK	-1031.6398	-1021.7976	19.68	9.13E-04	0.2944	0.4215	**Geraniaceae**	-1019.1856	24.9084	6.01E-05	1.0845	1.3041	**Geraniaceae**
CpPS	psbL	-343.4525	-341.2852	4.33	3.73E+00	0.1015	0.0716	Outgroup	-339.7414	7.4222	6.44E-01	0.9488	1.4561	Geraniaceae
CpPS	psbM	-483.9357	-481.8543	4.16	4.13E+00	0.1776	0.2717	Geraniaceae	-475.4608	16.9498	3.84E-03	1.9806	2.3251	**Geraniaceae**
CpPS	psbN	-410.3770	-408.2026	4.35	3.70E+00	0.0927	0.0651	Outgroup	-404.2886	12.1768	4.84E-02	1.2030	1.5539	**Geraniaceae**
CpPS	psbT	-462.3817	-461.9926	0.78	3.78E+01	0.0650	0.1646	Geraniaceae	-460.4701	3.8232	5.05E+00	0.9025	2.1878	Geraniaceae
CpPS	psbZ	-863.5684	-863.5668	0.00	9.56E+01	0.0983	0.4837	Geraniaceae	-845.2989	36.5389	1.50E-07	1.8223	1.8257	**Geraniaceae**

* Substitution rates were adjusted by the number of species in the lineage

** The significantly high rate lineage was in bold (Bonferroni corrected p-value <0.05)

Supplementary Table S4. Tests for relaxed selection using RELAX

Gene_group	Gene	p-value	k*	ω1_test	ω1_Ref	ω1_percentage	ω2_test	ω2_Ref	ω2_percentage	ω3_test	ω3_Ref	ω3_percentage
CpRP	rpl2	8.07E-01	0.96	0.1824	0.1693	76.06	0.2521	0.2373	21.58	6.6486	7.2260	2.36
CpRP	rpl14	9.52E-01	1.04	0.0000	0.0000	66.82	1.0000	1.0000	32.85	1907.0834	1466.4695	0.33
CpRP	rpl16	6.78E-05	**0.61**	0.1618	0.0493	92.95	0.1694	0.0532	6.64	42.1912	485.1908	0.41
CpRP	rpl20	6.61E-01	1.06	0.0000	0.0000	54.46	1.0000	1.0000	44.36	502.1716	357.7103	1.18
CpRP	rpl23	9.70E-03	**2.90**	0.9026	0.9653	70.04	1.0000	1.0000	25.02	63.1791	4.1767	4.94
CpRP	rpl32	2.88E-02	**0.69**	0.0000	0.0000	36.08	0.4470	0.3136	55.87	83.7336	587.1441	8.06
CpRP	rpl33	1.90E-02	**12.03**	0.0000	0.0272	74.22	0.9699	0.9975	0.00	2.0866	1.0630	25.78
CpRP	rpl36	3.11E-04	**17.94**	0.0000	0.0000	90.54	0.3816	0.9477	0.00	4.8668	1.0922	9.46
CpRP	rps2	9.73E-01	1.00	1.0000	1.0000	54.82	0.0000	0.0000	44.88	1445.4338	1466.4695	0.30
CpRP	rps3	0.00E+00	**0.39**	0.4088	0.1019	82.60	0.4102	0.1028	15.33	36.8950	10000.0000	2.06
CpRP	rps4	3.91E-08	**7.56**	0.0000	0.0000	59.00	1.0000	1.0000	39.07	87.6580	1.8068	1.93
CpRP	rps7	1.56E-02	**3.88**	0.0000	0.0000	47.22	0.9205	0.9789	45.80	13.0631	1.9408	6.98
CpRP	rps8	2.93E-02	**0.69**	0.3154	0.1899	86.77	0.3208	0.1946	11.58	7.7792	19.1747	1.65
CpRP	rps11	4.39E-03	**0.65**	0.2759	0.1372	80.86	0.2802	0.1405	16.18	7.7333	23.4589	2.96
CpRP	rps12	3.90E-05	**7.75**	0.0000	0.0000	85.93	0.8637	0.9813	8.96	17.5034	1.4470	5.12
CpRP	rps14	3.89E-04	**0.34**	0.5391	0.1613	5.47	0.5700	0.1901	94.53	1.0923	1.2977	0.00
CpRP	rps15	5.21E-04	**12.07**	0.0000	0.0000	56.84	1.0000	1.0000	37.49	13.2218	1.2384	5.67
CpRP	rps16	2.37E-03	**3.44**	0.0000	0.0001	61.18	0.7586	0.9228	36.26	79.0601	3.5643	2.57
CpRP	rps18	2.45E-12	**4.65**	0.1220	0.6359	52.72	1.0000	1.0000	35.93	72.3561	2.5127	11.36
CpRP	rps19	1.75E-06	**9.82**	0.0000	0.0000	73.66	1.0000	1.0000	23.56	54.9700	1.5038	2.78
NuCpRP	PSRP-1	4.70E-04	**0.38**	0.0286	0.0001	72.92	0.8658	0.6823	26.05	17.0340	1851.8382	1.03
NuCpRP	PSRP-2	0.00E+00	**0.22**	0.0898	0.0000	62.07	0.7714	0.3006	36.40	5.1134	1911.9642	1.53
NuCpRP	RPL1	2.45E-09	**0.57**	0.1295	0.0277	84.26	0.8027	0.6802	13.61	8.4410	42.1770	2.13
NuCpRP	RPL3	9.70E-04	**0.65**	0.0341	0.0055	91.39	0.6546	0.5205	7.91	16.6437	76.2835	0.70
NuCpRP	RPL4	6.43E-01	1.07	0.0242	0.0309	87.17	1.0000	1.0000	12.63	2439.0218	1466.2234	0.20
NuCpRP	RPL5	6.91E-13	**0.59**	0.1953	0.0640	93.05	0.6792	0.5216	5.32	14.3512	88.4655	1.63
NuCpRP	RPL6	5.69E-01	1.09	0.0407	0.0529	86.39	0.0886	0.1080	7.16	3.6251	3.2629	6.45
NuCpRP	RPL11	1.59E-03	**0.63**	0.0623	0.0124	94.14	0.9709	0.9544	5.30	28.1204	195.2725	0.55
NuCpRP	RPL13	9.84E-03	**0.49**	0.0000	0.0000	85.84	0.9597	0.9199	12.80	8.6897	80.0320	1.36
NuCpRP	RPL15	9.54E-01	1.00	0.0000	0.0000	83.71	1.0000	1.0000	15.91	165.0443	164.2793	0.38
NuCpRP	RPL17	2.74E-04	**0.61**	0.0329	0.0037	0.84	0.1309	0.0357	96.71	6.1198	19.4691	2.46
NuCpRP	RPL18_1	6.48E-02	**0.77**	0.0668	0.0301	88.62	0.6348	0.5554	10.35	8.5461	16.0618	1.03
NuCpRP	RPL18_2	2.86E-01	0.84	0.0404	0.0222	91.19	1.0000	1.0000	8.17	17.7134	30.2782	0.64
NuCpRP	RPL19	3.70E-09	**0.46**	0.2632	0.0553	89.70	0.2910	0.0687	5.17	9.3785	128.4471	5.13
NuCpRP	RPL21	1.42E-06	**0.53**	0.1608	0.0326	88.36	1.0000	1.0000	9.50	26.1457	451.8318	2.14
NuCpRP	RPL24	2.61E-09	**0.55**	0.2270	0.0687	89.74	0.4092	0.1992	8.26	12.8419	100.5052	2.01
NuCpRP	RPL27	4.68E-03	**0.64**	0.0914	0.0237	86.33	0.8170	0.7288	11.85	13.7312	60.3146	1.82
NuCpRP	RPL28	1.44E-02	**2.36**	0.0000	0.0000	84.41	0.0000	0.0001	0.07	2.7150	1.5278	15.51
NuCpRP	RPL29	0.00E+00	**0.34**	0.0000	0.0000	30.37	0.4272	0.0800	68.39	22.2187	10000.0000	1.23
NuCpRP	RPL31	4.73E-03	**0.57**	0.0328	0.0025	76.02	0.3899	0.1914	17.60	3.0360	7.0228	6.38
NuCpRP	RPL34	4.96E-06	**0.50**	0.1328	0.0172	82.70	0.6890	0.4725	15.67	29.2288	891.4019	1.64
NuCpRP	RPL35	7.62E-01	1.11	0.0000	0.0000	88.74	1.0000	1.0000	9.64	25.3522	18.5287	1.62
NuCpRP	RPS1	0.00E+00	**0.43**	0.2485	0.0390	96.72	1.0000	1.0000	1.83	17.4456	780.1329	1.45
NuCpRP	RPS5	3.29E-13	**11.50**	0.0000	0.0000	84.50	0.5800	0.9537	0.00	3.3745	1.1116	15.50
NuCpRP	RPS6	0.00E+00	**0.34**	0.1420	0.0034	66.62	0.5488	0.1747	30.42	23.7551	10000.0000	2.96
NuCpRP	RPS9	4.67E-08	**0.56**	0.1508	0.0334	94.92	0.1702	0.0416	2.21	13.6074	108.8033	2.87
NuCpRP	RPS10	1.42E-04	**0.51**	0.1476	0.0236	1.97	0.1479	0.0237	92.33	5.8875	32.2430	5.69
NuCpRP	RPS13	6.47E-03	**0.67**	0.1209	0.0422	0.82	0.1210	0.0423	95.37	4.7939	10.4671	3.81
NuCpRP	RPS20	5.57E-10	**13.99**	0.0000	0.0000	80.03	0.7608	0.9806	0.00	3.1889	1.0864	19.97

* selection intensity parameter (k) significantly deviated from one was in bold

Supplementary Table S5. Proportion of ribosome protein identified as contact residues.

			Total contact residue[2]		Protein contact residue[3]		rRNA contact residue[4]	
Gene group	Gene	Sequence length[1]	Count	Percentage[5]	Count	Percentage[5]	Count	Percentage[5]
CpRP	rps2	231	92	39.8	32	13.9	82	35.5
CpRP	rps3	218	141	64.7	95	43.6	92	42.2
CpRP	rps4	201	37	18.4	37	18.4	0	0.0
CpRP	rps7	155	105	67.7	43	27.7	87	56.1
CpRP	rps8	134	128	95.5	67	50.0	94	70.1
CpRP	rps11	140	107	76.4	70	50.0	77	55.0
CpRP	rps12	123	112	91.1	12	9.8	112	91.1
CpRP	rps14	100	98	98.0	66	66.0	86	86.0
CpRP	rps15	90	75	83.3	16	17.8	67	74.4
CpRP	rps16	88	69	78.4	0	0.0	69	78.4
CpRP	rps18	103	57	55.3	44	42.7	44	42.7
CpRP	rps19	92	78	84.8	55	59.8	64	69.6
CpRP	rpl32	57	56	98.2	47	82.5	52	91.2
CpRP	rpl33	66	62	93.9	20	30.3	62	93.9
CpRP	rpl36	104	38	36.5	21	20.2	38	36.5
CpRP	rpl2	269	220	81.8	1	0.4	220	81.8
CpRP	rpl14	121	92	76.0	48	39.7	69	57.0
CpRP	rpl16	135	120	88.9	12	8.9	120	88.9
CpRP	rpl20	119	118	99.2	88	73.9	96	80.7
NuCpRP	rps5	308	136	44.2	96	31.2	92	29.9
NuCpRP	rps6	168	74	44.0	46	27.4	54	32.1
NuCpRP	rps9	197	103	52.3	42	21.3	96	48.7
NuCpRP	rps10	197	80	40.6	54	27.4	69	35.0
NuCpRP	rps13	145	68	46.9	20	13.8	68	46.9
NuCpRP	rps20	202	82	40.6	1	0.5	82	40.6
NuCpRP	rpl31	144	37	25.7	37	25.7	5	3.5
NuCpRP	rpl34	152	37	24.3	1	0.7	37	24.3
NuCpRP	rpl35	159	62	39.0	55	34.6	62	39.0
NuCpRP	rpl1	352	110	31.3	4	1.1	106	30.1
NuCpRP	rpl3	259	130	50.2	39	15.1	120	46.3
NuCpRP	rpl4	293	164	56.0	76	25.9	151	51.5
NuCpRP	rpl5	220	149	67.7	63	28.6	112	50.9
NuCpRP	rpl6	223	103	46.2	12	5.4	102	45.7
NuCpRP	rpl11	224	88	39.3	2	0.9	88	39.3
NuCpRP	rpl13	250	111	44.4	34	13.6	107	42.8
NuCpRP	rpl15	257	134	52.1	52	20.2	130	50.6
NuCpRP	rpl17	205	113	55.1	29	14.1	113	55.1
NuCpRP	rpl18	161	100	62.1	18	11.2	100	62.1
NuCpRP	rpl19	233	93	39.9	64	27.5	58	24.9
NuCpRP	rpl21	257	85	33.1	58	22.6	62	24.1
NuCpRP	rpl24	191	90	47.1	0	0.0	90	47.1
NuCpRP	rpl27	198	81	40.9	29	14.6	79	39.9
NuCpRP	rpl28	151	71	47.0	17	11.3	69	45.7
NuCpRP	rpl29	173	56	32.4	32	18.5	46	26.6
Average				57.5		24.3		50.3

[1] Amino acid sequence length

[2] Residues that are within 10Å distance of either amino acid residues in other proteins or nucleotide residues in rRNAs

[3] Residues that are within 10Å distance of amino acid residues in other proteins

[4] Residues that are within 10Å distance of nucleotide residues in rRNAs

[5] Percentage as (the count of contact residues/sequence length)*100%

Supplementary Table S6. Pair-wise amino acid sequence identity of ribosomal proteins.

Gene group	Gene	Overall	Pair-wise identity All contact sites	Protein contact sites
CpRP	rps2	80.7	83.4	87.8
CpRP	rps3	71.5	77.7	76.5
CpRP	rps4	84.1	86.3	86.3
CpRP	rps7	82.2	83.1	80.6
CpRP	rps8	81.2	80.8	84.5
CpRP	rps11	76.3	79.4	81.6
CpRP	rps12	87.1	87.2	78.9
CpRP	rps14	86.1	86.7	85
CpRP	rps15	80.4	80.6	90.2
CpRP	rps16	84.9	86.8	n/a
CpRP	rps18	68.6	78.8	79.2
CpRP	rps19	75.7	76.4	75.5
CpRP	rpl32	75.6	75.6	73.6
CpRP	rpl33	77	78.1	80
CpRP	rpl36	86.4	86.4	89.1
CpRP	rpl2	90.9	91.2	100
CpRP	rpl14	81.2	82.3	79.8
CpRP	rpl16	90.4	90.6	91.5
CpRP	rpl20	73.4	73.4	74.8
NuCpRP	rps5	70.8	77	75.3
NuCpRP	rps6	76.2	72.8	81
NuCpRP	rps9	79.3	84.6	77.8
NuCpRP	rps10	87.2	87.7	84.9
NuCpRP	rps13	81.7	86.4	85.6
NuCpRP	rps20	71.6	74.8	53.8
NuCpRP	rpl31	72.3	n/a	88.3
NuCpRP	rpl34	83.9	88.5	100
NuCpRP	rpl35	85	83.7	82.6
NuCpRP	rpl1	83.7	92.6	88.7
NuCpRP	rpl3	89.2	92.6	88.8
NuCpRP	rpl4	79.1	81.8	83.9
NuCpRP	rpl5	77	81.6	84.4
NuCpRP	rpl6	84.2	89.1	82.8
NuCpRP	rpl11	89.8	89	61.3
NuCpRP	rpl13	88.6	91.5	92
NuCpRP	rpl15	87.9	90.4	92.5
NuCpRP	rpl17	92.7	93.5	93.5
NuCpRP	rpl18	85.2	86	90
NuCpRP	rpl19	73.8	77.9	75
NuCpRP	rpl21	85	87.3	85.8
NuCpRP	rpl24	80	82.7	n/a
NuCpRP	rpl27	81.9	90.2	89.4
NuCpRP	rpl28	84.7	83.2	77.9
NuCpRP	rpl29	74.1	73.5	67.5
Mean		81.3	83.8	82.8

Reference:

Wertheim JO, Murrell B, Smith MD, Kosakovsky Pond SL, Scheffler K. 2015. RELAX: detecting relaxed selection in a phylogenetic framework. *Mol Biol Evol* 32:820–832.

Yu G, Smith D, Zhu H, Guan Y, Lam TT. submitted. ggtree: an R package for visualization and annotation of phylogenetic tree with different types of meta-data. *Methods Ecol Evol* (Available at https://bioconductor.org/packages/release/bioc/html/ggtree.html)