Supplementary Tables Legends

Supplementary Table 1. Summary of the average RSCU in *Citrus* species and *P. trifoliata*. AA represents amino acid. The highest RSCU of codons for each amino acid is indicated with asterik (*), evaluated using a χ^2 contingency test. Species are in the following order: A=*C. sinensis*; B=*C. aurantifolia*; C=*C. aurantium*; D=*C. clementina*; E=*C. clementina* × *C. tangerina*; F=*C. jambhiri*; G=*C. japonica var margarita*; H= *C. limettioides*; I=*C. limonia*; J=*C. medica*; K=*C. reshni*; L=*C. reticulata*; M=*C. reticulata* × *C. temple*; N=*C. sinensis* × *P. trifoliata*; O=*C. sunki*; P=*P. trifoliata*; Q=*C. unshiu*; R=*C. paradisi*; S=*C. paradisi* × *P. trifoliata*.

Supplementary Table 2. GC_3 variation and stress association across *Citrus* species and *P. trifoliata*.

Supplementary Figures Legends

Supplementary Figure 1. Plot for coordinates of first two major axes of correspondence analysis on RSCU for *Citrus* species and *P. trifoliata* genes. The genes have been classified according to the GC_{3s} richness. Species are in the following order: A=*C. sinensis*; B=*C. aurantifolia*; C=*C. aurantium*; D=*C. clementina*; E=*C. clementina* × *C. tangerina*; F= *C. jambhiri*; G=*C. japonica var margarita*; H=*C. limettioides*; I=*C. limonia*; J=*C. medica*; K=*C. reshni*; L=*C. reticulata*; M=*C. reticulata* × *C. temple*; N=*C. sinensis* × *P. trifoliata*; O=*C. sunki*; P=*P. trifoliata*; Q=*C. unshiu*; R=*C. paradisi*; S=*C. paradisi* × *P. trifoliata*.

Supplementary Figure 2. CG_3 skew across *Citrus* species and *P.trifoliata*. Species order: A=*C. sinensis*; B= *C. aurantifolia*; C= *C. aurantium*; D=*C. clementina*; E=*C. clementina* × *C.tangerina*; F=*C. jambhiri*; G=*C japonica var margarita*; H=*C. limettioides*; I=*C. limonia*; J=*C. medica*; K=*C. reshni*; L=*C. reticulata*; M=*C. reticulata* × *C. temple*; N=*C. sinensis* × *P. trifoliata*; O=*C. sunki*; P=*P. trifoliata*; Q=*C. unshiu*; R=*C. paradisi*; S=*C. paradisi* × *P.trifoliata*. These plots show gradients of CG_3 skew for 5% of GC_3-rich and GC_3-poor genes for all analyzed genomes. Gradients from 5' and 3' ends of the CDS are shown in the same plot, separated by a vertical line.

Supplementary Figure 3A. An overview of *Citrus* phylogeny using the genome and frame corrected coding regions: All the proteins were compared and a suggestive phylogeny was build on the basis of the co-orthologous proteins. In the figure, branch labels show the number of common genes in the subtrees. Branch lengths represent the number of new common genes since the last node.

Supplementary Figure 3B. An overview of *Citrus* phylogeny using the genome and frame corrected coding regions: Phylogenetic tree obtained in figure 3 A was re-rooted using *P. trifoliata* as an out-group species. In the figure, branch labels show the number of common genes in the subtrees. Branch lengths represent the number of new common genes since the last node.

Supplementary Table 1. Summary of the average RSCU in *Citrus* species and *P.trifoliata*. AA represents amino acid. The highest RSCU of codons for each amino acid is indicated with asterisk (*), evaluated using a χ^2 contingency test. Species are in the following order: A=*C. sinensis*; B=*C. aurantifolia*; C=*C. aurantium*; D=*C. clementina*; E=*C. clementina* × *C. tangerina*; F=*C. jambhiri*; G=*C. japonica var margarita*; H=*C. limettioides*; I=*C. limonia*; J=*C. medica*; K=*C. reshni*; L=*C. reticulata*; M=*C. reticulata* × *C. temple*; N=*C. sinensis* × *P. trifoliata*; O=*C. sunki*; P=*P. trifoliata*; Q=*C. unshiu*; R=*C. paradisi*; and S=*C. paradisi* × *P. trifoliata*.

AA	Codon	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
Phe	TTT*	1.23	1.11	1.12	1.15	1.18	1.11	1.14	1.29	1.30	1.15	1.15	1.15	1.12	1.12	1.32	1.13	1.12	1.15	1.18
	TTC	0.77	0.89	0.88	0.85	0.82	0.89	0.86	0.71	0.70	0.85	0.85	0.85	0.88	0.88	0.68	0.87	0.88	0.85	0.82
Leu	TTA	0.86	0.66	0.67	0.71	0.69	0.64	0.65	0.79	0.76	0.64	0.69	0.69	0.66	0.69	0.82	0.70	0.67	0.69	0.70
	TTG*	1.54	1.46	1.50	1.47	1.52	1.43	1.45	1.50	1.54	1.52	1.49	1.46	1.52	1.46	1.40	1.46	1.53	1.53	1.55
	CTT	1.50	1.49	1.49	1.37	1.58	1.46	1.59	1.47	1.47	1.54	1.54	1.50	1.49	1.50	1.42	1.49	1.48	1.54	1.54
	CTC	0.71	0.96	0.95	1.09	0.79	0.99	0.91	0.88	0.78	0.92	0.91	0.94	0.89	0.93	0.82	0.96	0.93	0.85	0.81
	CTA	0.57	0.51	0.50	0.48	0.52	0.51	0.52	0.45	0.47	0.50	0.49	0.50	0.51	0.49	0.47	0.51	0.50	0.51	0.51
	CTG	0.82	0.92	0.89	0.87	0.90	0.97	0.88	0.91	0.99	0.88	0.88	0.91	0.93	0.92	1.08	0.88	0.89	0.88	0.88
Ile	ATT*	1.51	1.45	1.45	1.41	1.49	1.47	1.49	1.48	1.51	1.45	1.46	1.46	1.47	1.48	1.45	1.46	1.47	1.48	1.49
	ATC	0.73	0.89	0.93	0.95	0.86	0.92	0.90	0.89	0.85	0.89	0.89	0.90	0.91	0.89	0.91	0.90	0.88	0.85	0.84
	ATA	0.77	0.66	0.62	0.64	0.65	0.61	0.61	0.63	0.64	0.66	0.65	0.64	0.62	0.63	0.64	0.64	0.65	0.67	0.67
Val	GTT*	1.65	1.55	1.58	1.51	1.64	1.62	1.61	1.56	1.59	1.64	1.62	1.55	1.55	1.61	1.52	1.55	1.57	1.60	1.62
	GTC	0.64	0.82	0.81	0.85	0.68	0.81	0.78	0.81	0.76	0.75	0.76	0.82	0.76	0.73	0.79	0.81	0.74	0.72	0.71
	GTA	0.65	0.53	0.53	0.51	0.56	0.51	0.52	0.53	0.54	0.52	0.54	0.53	0.53	0.52	0.54	0.53	0.56	0.58	0.56
	GTG	1.06	1.11	1.08	1.13	1.12	1.05	1.09	1.11	1.11	1.09	1.08	1.10	1.16	1.14	1.15	1.11	1.13	1.10	1.11
Ser	TCT*	1.57	1.46	1.47	1.41	1.53	1.58	1.47	1.42	1.42	1.50	1.55	1.51	1.47	1.47	1.37	1.45	1.48	1.52	1.48
	TCC	0.72	1.00	0.98	1.10	0.76	0.87	0.85	1.20	1.08	0.83	0.84	1.01	0.81	0.91	1.29	1.02	0.83	0.78	0.76
	TCA	1.45	1.30	1.32	1.22	1.41	1.38	1.39	1.23	1.33	1.38	1.37	1.30	1.37	1.26	1.17	1.32	1.39	1.38	1.43
	TCG	0.43	0.49	0.49	0.66	0.42	0.49	0.50	0.49	0.47	0.50	0.49	0.51	0.52	0.59	0.55	0.51	0.50	0.48	0.47

	AGT*	1.06	0.81	0.84	0.81	1.03	0.84	0.90	0.81	0.86	0.92	0.90	0.83	0.92	0.85	0.71	0.86	0.92	0.97	1.00
	AGC	0.77	0.96	0.90	0.80	0.87	0.84	0.89	0.87	0.84	0.87	0.85	0.83	0.91	0.91	0.92	0.84	0.87	0.88	0.85
Pro	CCT*	1.51	1.07	1.17	1.18	1.47	1.45	1.44	1.04	1.08	1.42	1.42	1.24	1.40	1.29	0.92	1.28	1.40	1.48	1.48
	CCC	0.59	1.07	1.01	1.09	0.63	0.74	0.71	1.39	1.29	0.68	0.73	0.98	0.66	0.79	1.60	0.92	0.68	0.64	0.65
	CCA	1.45	1.27	1.25	1.07	1.44	1.30	1.34	1.04	1.09	1.37	1.32	1.21	1.34	1.30	0.94	1.23	1.38	1.38	1.38
	CCG	0.45	0.59	0.57	0.66	0.45	0.51	0.51	0.54	0.54	0.53	0.53	0.58	0.60	0.62	0.54	0.58	0.54	0.50	0.48
Thr	ACT*	1.49	1.16	1.25	1.28	1.46	1.51	1.43	1.15	1.27	1.43	1.45	1.32	1.44	1.35	1.09	1.36	1.42	1.45	1.45
	ACC	0.75	1.10	1.08	1.08	0.85	0.97	0.92	1.19	1.14	0.93	0.89	1.04	0.93	0.93	1.30	0.99	0.91	0.90	0.87
	ACA	1.34	1.21	1.16	1.05	1.30	1.11	1.21	1.14	1.14	1.18	1.20	1.13	1.16	1.12	1.11	1.15	1.21	1.23	1.25
	ACG	0.41	0.53	0.51	0.58	0.40	0.41	0.45	0.53	0.44	0.46	0.46	0.51	0.47	0.60	0.49	0.50	0.46	0.42	0.43
Ala	GCT*	1.66	1.44	1.54	1.49	1.71	1.66	1.61	1.42	1.45	1.66	1.68	1.55	1.62	1.64	1.26	1.54	1.62	1.69	1.66
	GCC	0.70	0.96	0.93	1.03	0.72	0.94	0.85	1.06	1.00	0.85	0.82	0.91	0.84	0.84	1.20	0.90	0.83	0.79	0.77
	GCA	1.33	1.13	1.11	1.00	1.27	1.06	1.13	1.04	1.11	1.14	1.16	1.08	1.19	1.16	1.00	1.12	1.20	1.21	1.24
	GCG	0.32	0.48	0.42	0.48	0.30	0.34	0.42	0.47	0.44	0.34	0.34	0.45	0.34	0.36	0.55	0.44	0.35	0.32	0.32
Tyr	TAT*	1.22	1.07	1.07	1.04	1.17	1.09	1.13	1.07	1.10	1.11	1.13	1.09	1.08	1.12	1.07	1.06	1.10	1.13	1.12
	TAC	0.78	0.93	0.93	0.96	0.83	0.91	0.87	0.93	0.90	0.89	0.87	0.91	0.92	0.88	0.93	0.94	0.90	0.87	0.88
His	CAT*	1.31	0.96	1.01	1.05	1.20	1.19	1.18	1.05	1.12	1.17	1.20	1.09	1.18	1.15	1.02	1.09	1.17	1.20	1.23
	CAC	0.69	1.04	0.99	0.95	0.80	0.81	0.82	0.95	0.88	0.83	0.80	0.91	0.82	0.85	0.98	0.91	0.83	0.80	0.77
Gln	CAA*	1.09	1.09	1.06	1.06	1.01	1.02	1.01	1.15	1.13	1.00	1.02	1.06	0.97	1.02	1.18	1.05	1.01	1.01	1.01
	CAG	0.91	0.91	0.94	0.94	0.99	0.98	0.99	0.85	0.87	1.00	0.98	0.94	1.03	0.98	0.82	0.95	0.99	0.99	0.99
Asn	AAT*	1.30	1.06	1.09	1.11	1.23	1.14	1.17	1.09	1.15	1.19	1.16	1.14	1.17	1.15	1.04	1.11	1.17	1.20	1.22
	AAC	0.70	0.94	0.91	0.89	0.77	0.86	0.83	0.91	0.85	0.81	0.84	0.86	0.83	0.85	0.96	0.89	0.83	0.80	0.78
Lys	AAA	0.99	0.99	0.95	1.07	0.86	0.87	0.87	1.30	1.26	0.86	0.90	1.02	0.83	0.94	1.35	1.00	0.88	0.87	0.88
	AAG*	1.01	1.01	1.05	0.93	1.14	1.13	1.13	0.70	0.74	1.14	1.10	0.98	1.17	1.06	0.65	1.00	1.12	1.13	1.12
Asp	GAT*	1.42	1.25	1.27	1.25	1.37	1.32	1.34	1.24	1.30	1.33	1.35	1.29	1.33	1.32	1.17	1.31	1.34	1.36	1.37
	GAC	0.58	0.75	0.73	0.75	0.63	0.68	0.66	0.76	0.70	0.67	0.65	0.71	0.67	0.68	0.83	0.69	0.66	0.64	0.63
Glu	GAA*	1.09	1.03	1.04	1.03	1.03	0.99	1.03	1.15	1.14	0.99	1.02	1.06	0.98	1.03	1.17	1.04	1.01	1.01	1.02
	GAG	0.91	0.97	0.96	0.97	0.97	1.01	0.97	0.85	0.86	1.01	0.98	0.94	1.02	0.97	0.83	0.96	0.99	0.99	0.98
Cys	TGT*	1.13	0.95	0.97	1.00	1.07	0.95	1.10	0.98	1.03	1.00	1.03	1.00	0.99	1.01	0.96	0.97	0.99	1.04	1.04

	TGC	0.87	1.05	1.03	1.00	0.93	1.05	0.90	1.02	0.97	1.00	0.97	1.00	1.01	0.99	1.04	1.03	1.01	0.96	0.96
Arg	CGT	0.80	0.78	0.83	0.84	0.83	0.87	0.79	0.74	0.80	0.90	0.85	0.85	0.84	0.87	0.73	0.85	0.86	0.92	0.88
	CGC	0.49	0.97	0.87	0.80	0.53	0.64	0.78	0.72	0.75	0.63	0.63	0.83	0.61	0.65	0.80	0.81	0.61	0.57	0.58
	CGA	0.70	0.71	0.68	0.65	0.71	0.61	0.66	0.56	0.58	0.66	0.65	0.67	0.61	0.66	0.54	0.68	0.66	0.68	0.64
	CGG	0.56	0.66	0.65	0.73	0.51	0.57	0.61	0.79	0.78	0.54	0.55	0.70	0.68	0.60	0.96	0.63	0.55	0.54	0.54
	AGA*	1.96	1.54	1.58	1.54	1.83	1.76	1.62	1.58	1.47	1.76	1.80	1.54	1.62	1.63	1.40	1.64	1.78	1.76	1.78
	AGG	1.49	1.35	1.39	1.45	1.59	1.56	1.53	1.61	1.63	1.51	1.53	1.41	1.63	1.58	1.58	1.40	1.55	1.54	1.59
Gly	GGT	1.21	1.01	1.10	1.05	1.21	1.24	1.14	0.83	0.94	1.22	1.20	1.05	1.12	1.13	0.76	1.05	1.18	1.21	1.22
	GGC	0.74	0.84	0.85	0.90	0.80	0.90	0.89	0.73	0.77	0.85	0.85	0.82	0.89	0.85	0.81	0.88	0.85	0.80	0.79
	GGA*	1.28	1.20	1.15	1.05	1.31	1.14	1.23	1.03	1.04	1.21	1.22	1.16	1.20	1.20	0.92	1.17	1.22	1.25	1.23
	GGG	0.77	0.96	0.90	0.99	0.68	0.72	0.74	1.41	1.25	0.72	0.73	0.97	0.79	0.82	1.51	0.90	0.75	0.75	0.75

Supplementary Table 2. GC_3 variation and stress association across *Citrus* species and *P. trifoliata*.

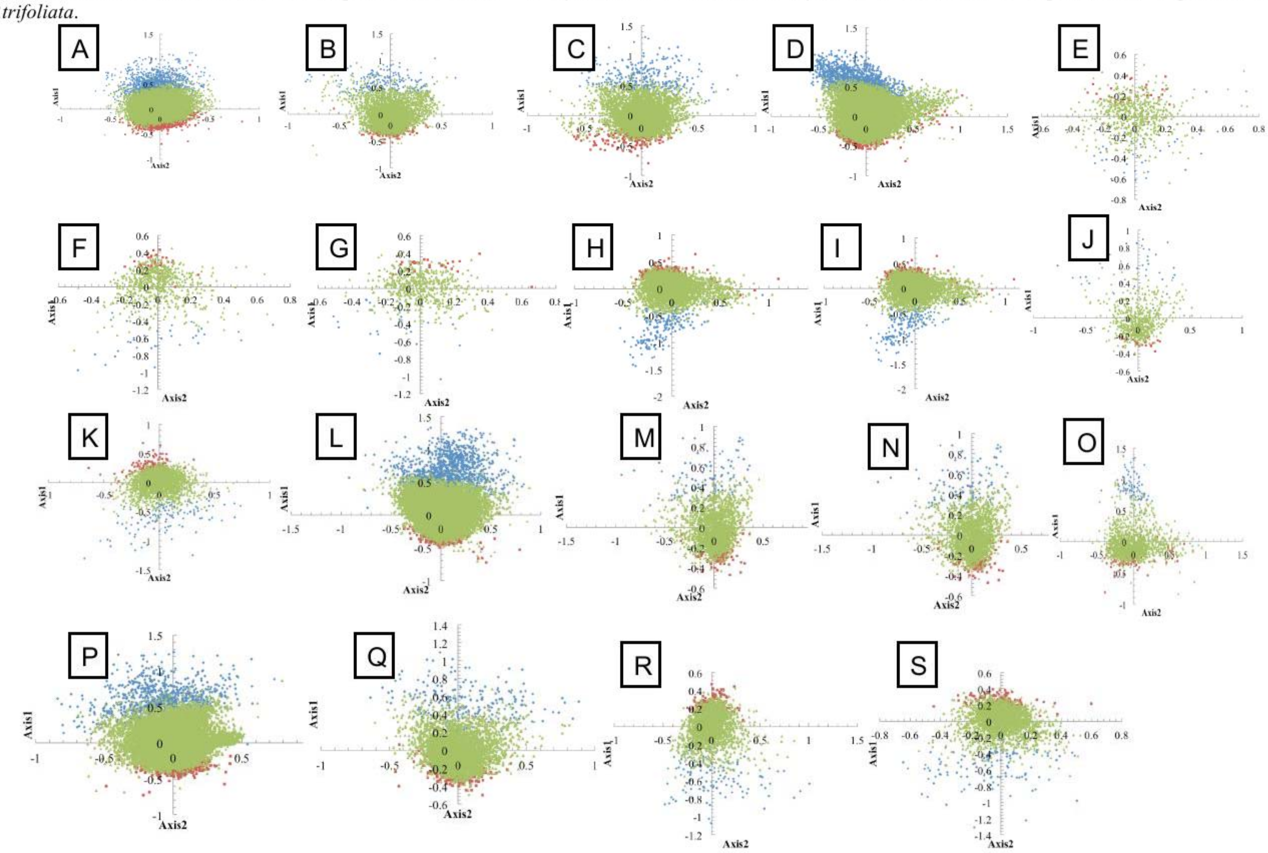
Organism	GC_3^*	Stress (S)	Not associated with stress (NS)	Ratio S/NS
C. sinensis	High	945	4289	0.22033108
C. sinensis	Mid	1857	9534	0.194776589
C. sinensis	Low	1699	9944	0.170856798
P. trifoliata	High	951	2562	0.371194379
P. trifoliata	Mid	591	2594	0.227833462
P. trifoliata	Low	281	1492	0.188337802
C. reticulata	High	1718	4251	0.404140202
C. reticulata	Mid	1067	4010	0.266084788
C. reticulata	Low	541	2590	0.208880309
C. aurantiifolia	High	338	744	0.454301075
C. aurantiifolia	Mid	126	512	0.24609375
C. aurantiifolia	Low	63	360	0.175
C. aurantium	High	331	860	0.384883721
C. aurantium	Mid	150	723	0.20746888
C. aurantium	Low	102	415	0.245783133
C. japonica var margarita	High	13	28	0.464285714
C. japonica var margarita	Mid	9	35	0.257142857
C. japonica var margarita	Low	4	19	0.210526316
C. clementina × *C. tangerina*	High	22	63	0.349206349
C. clementina × *C. tangerina*	Mid	12	57	0.210526316

C. clementina × *C. tangerina*	Low	7	47	0.14893617
C. sunki	High	72	163	0.441717791
C. sunki	Mid	49	154	0.318181818
C. sunki	Low	13	53	0.245283019
C. jambhiri	High	19	55	0.345454545
C. jambhiri	Mid	10	46	0.217391304
C. jambhiri	Low	8	53	0.150943396
C. limonia	High	110	320	0.34375
C. limonia	Mid	88	424	0.20754717
C. limonia	Low	54	231	0.233766234
C. limettioides	High	176	425	0.414117647
C. limettioides	Mid	99	359	0.275766017
C. limettioides	Low	53	218	0.243119266
C. reshni	High	104	304	0.342105263
C. reshni	Mid	74	281	0.263345196
C. reshni	Low	47	177	0.265536723
C. medica	High	23	56	0.410714286
C. medica	Mid	13	54	0.240740741
C. medica	Low	10	42	0.238095238
C. sinensis × *P. trifoliata*	High	47	139	0.338129496
C. sinensis × *P. trifoliata*	Mid	32	138	0.231884058
C. sinensis × *P. trifoliata*	Low	6	62	0.096774194
C. reticulata × *C. temple*	High	135	441	0.306122449

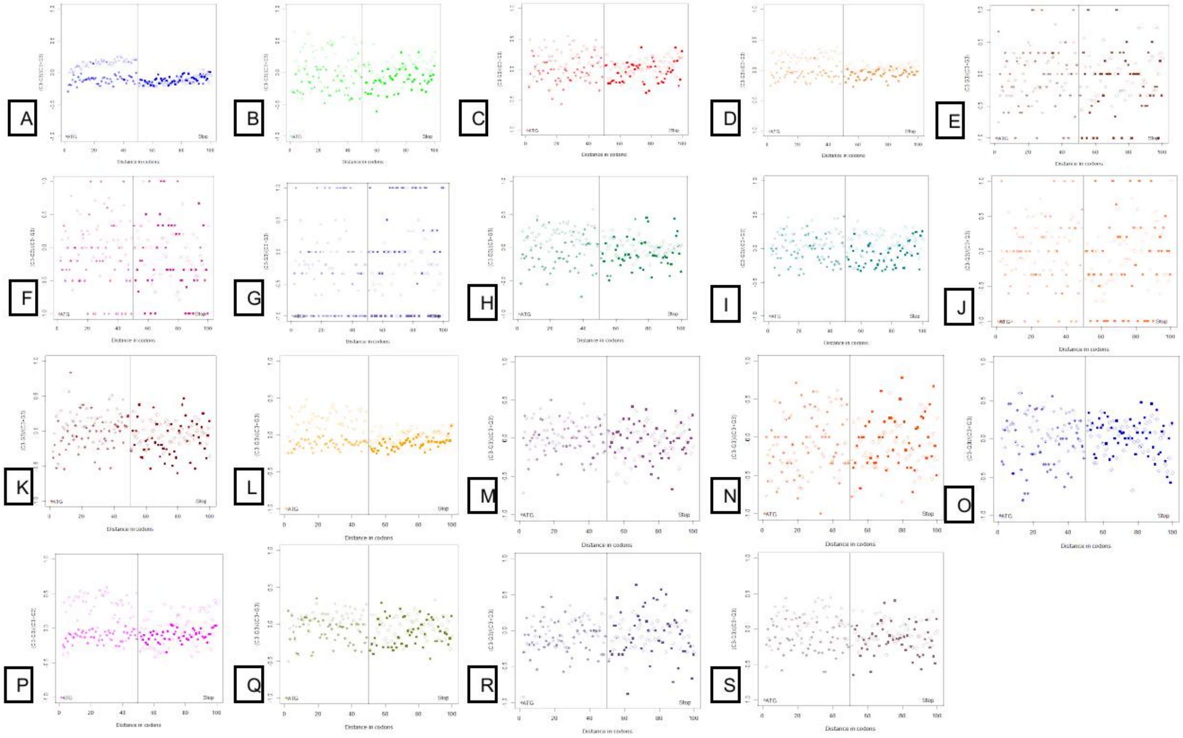
C. reticulata × *C. temple*	Mid	67	276	0.242753623
C. reticulata × *C. temple*	Low	28	148	0.189189189
C. unshiu	High	161	624	0.258012821
C. unshiu	Mid	119	501	0.23752495
C. unshiu	Low	53	308	0.172077922
C. clementina	High	1522	7032	0.216439135
C. clementina	Mid	921	4730	0.194714588
C. clementina	Low	376	2137	0.17594759
C. paradisi	High	72	289	0.249134948
C. paradisi	Mid	54	257	0.210116732
C. paradisi	Low	35	196	0.178571429
C. paradisi × *P. trifoliata*	High	96	213	0.450704225
C. paradisi × *P. trifoliata*	Mid	80	302	0.264900662
C. paradisi × *P. trifoliata*	Low	51	256	0.19921875

* High GC_3= above 0.46; Middle GC_3 are between 0.39-0.46; Low GC_3 = <0.39

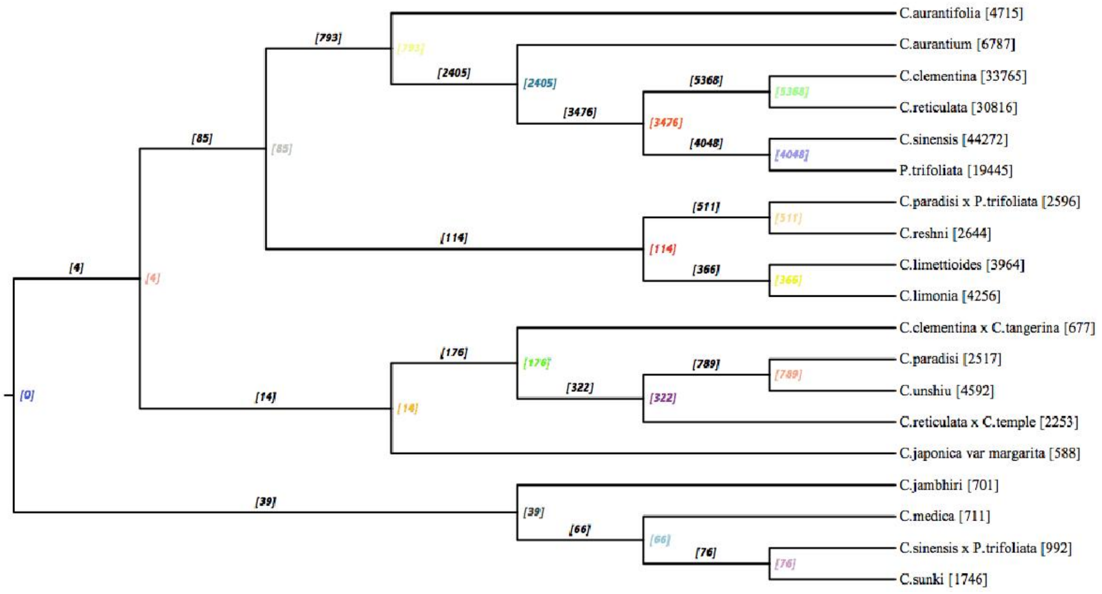
Supplementary Figure 1. Plot for coordinates of first two major axes of correspondence analysis on RSCU for *Citrus* species and *P. trifoliata* genes. The genes have been classified according to the GC_{3s} richness. Species are in the following order: A=*C. sinensis*; B=*C. aurantifolia*; C=*C. aurantium*; D=*C. clementina*; E=*C. clementina* × *C. tangerina*; F= *C. jambhiri*; G=*C. japonica var margarita*; H=*C. limettioides*; I=*C. limonia*; J=*C. medica*; K=*C. reshni*; L=*C. reticulata*; M=*C. reticulata* × *C. temple*; N=*C. sinensis* × *P. trifoliata*; O=*C. sunki*; P=*P. trifoliata*; Q=*C. unshiu*; R=*C. paradisi*; S=*C. paradisi* × *P.trifoliata*.



Supplementary Figure 2. CG_3 skew across *Citrus* species and *P.trifoliata.* Species order: A=*C. sinensis*; B= *C. aurantifolia*; C= *C. aurantium*; D=*C. clementina*; E=*C. clementina × C. tangerina*; F=*C. jambhiri*; G=*C. japonica var margarita*; H=*C. limettioides*; I=*C. limonia*; J=*C. medica*; K=*C. reshni*; L=*C. reticulata*; M=*C. reticulata × C. temple*; N=*C. sinensis × P. trifoliata*; O=*C. sunki*; P=*P. trifoliata*; Q=*C. unshiu*; R=*C. paradisi*; S=*C. paradisi × P. trifoliata*. These plots show gradients of CG_3 skew for 5% of GC_3-rich and GC_3-poor genes for all analyzed genomes. Gradients from 5' and 3' ends of the CDS are shown in the same plot, separated by a vertical line.



Supplementary Figure 3A An overview of *Citrus* phylogeny using the genome and frame corrected coding regions: (A) All the proteins were compared and a suggestive phylogeny was build on the basis of the co-orthologous proteins. In the figure, branch labels show the number of common genes in the subtrees. Branch lengths represent the number of new common genes since the last node.



Supplementary Figure 3B An overview of *Citrus* phylogeny using the genome and frame corrected coding regions: Phylogenetic tree obtained in figure 3A was re-rooted using *P. trifoliata* as an out-group species. In the figure, branch labels show the number of common genes in the subtrees.Branch lengths represent the number of new common genes since the last node.