Supplementary Information

Genomic analysis reveals major determinants of *cis*-regulatory variation in *Capsella grandiflora*

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Supplementary Figures

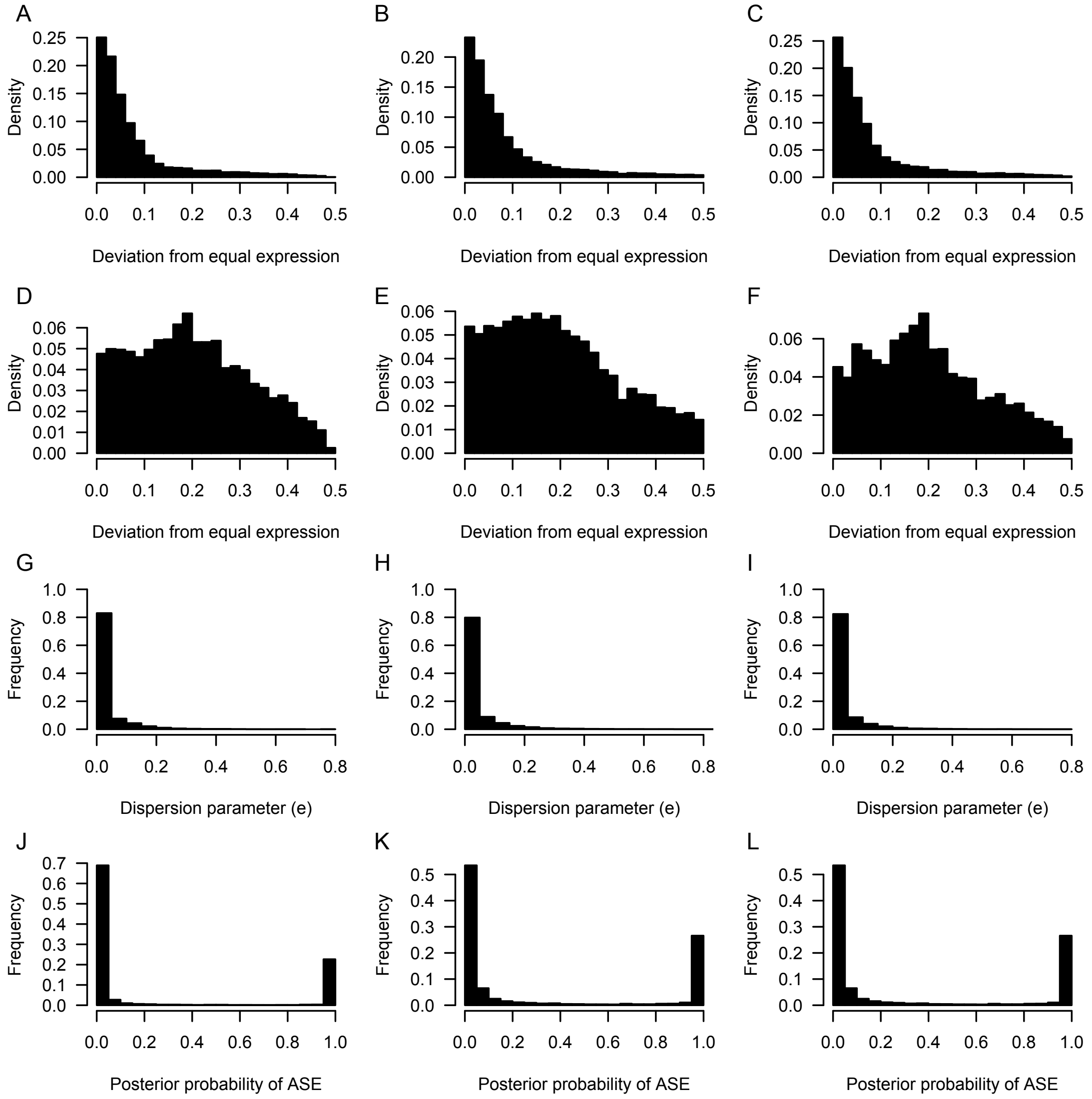

Figure S1. ASE in flower buds of three intraspecific *C. grandiflora* F1s. Distributions of the deviation from equal expression for all assayed genes (A-C) and for genes with at least 0.95 posterior probability of ASE (D-F), estimates of the dispersion parameter (G-I), and the posterior probability of ASE (J-L). All distributions are shown for each of the three intraspecific F1s intra6.3 (left), intra7.2 (middle) and intra8.2 (right).

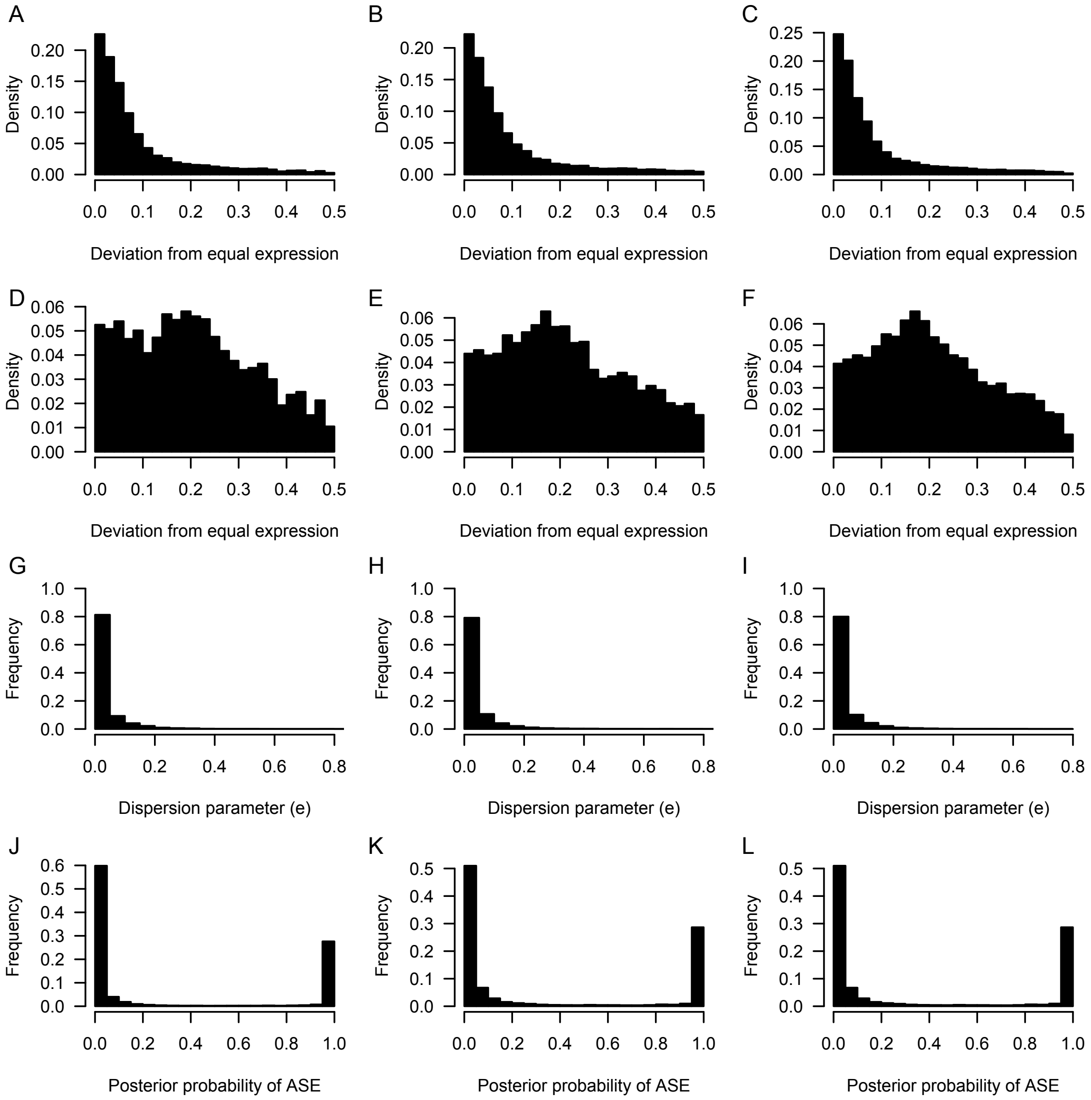

Figure S2. ASE in leaves of three intraspecific *C. grandiflora* F1s. Distributions of the deviation from equal expression for all assayed genes (A-C) and for genes with at least 0.95 posterior probability of ASE (D-F), estimates of the dispersion parameter (G-I), and the posterior probability of ASE (J-L). All distributions are shown for each of the three intraspecific F1s intra6.3 (left), intra7.2 (middle) and intra8.2 (right).

Figure S3. Venn diagram of genes with ASE (posterior probability of ASE ≥ 0.95) in leaves and flower buds of all three F1s. There were a total of 10,522 genes that were amenable to analyses of ASE that did not show evidence for ASE, whereas a total of 1,010 had ASE in either leaves or flower buds.

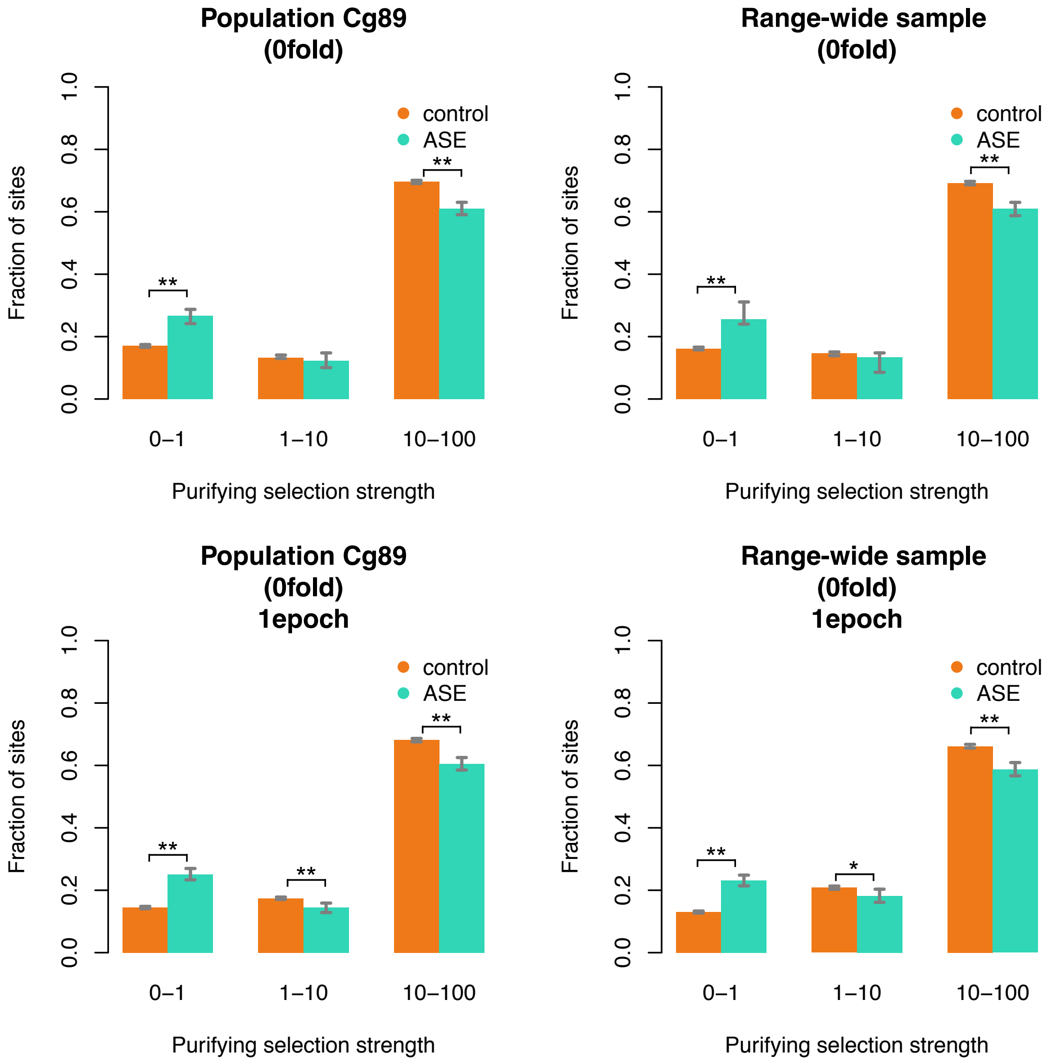

Figure S4. DFE-alpha results for 0-fold degenerate sites. The estimated proportion of new mutations in the selected class in each bin of the distribution of negative fitness effects is shown, with whiskers corresponding to 95% confidence intervals based on 200 bootstrap replicates, separately for genes with ASE and control genes. The top panels show results under the stepwise population size change model and the lower panels show results for the constant population size model. Panels on the left show results for the population sample, and those on the right for the scattered range-wide sample. Significance levels of the p-value: * ≤ 0.05; ** ≤ 0.01.

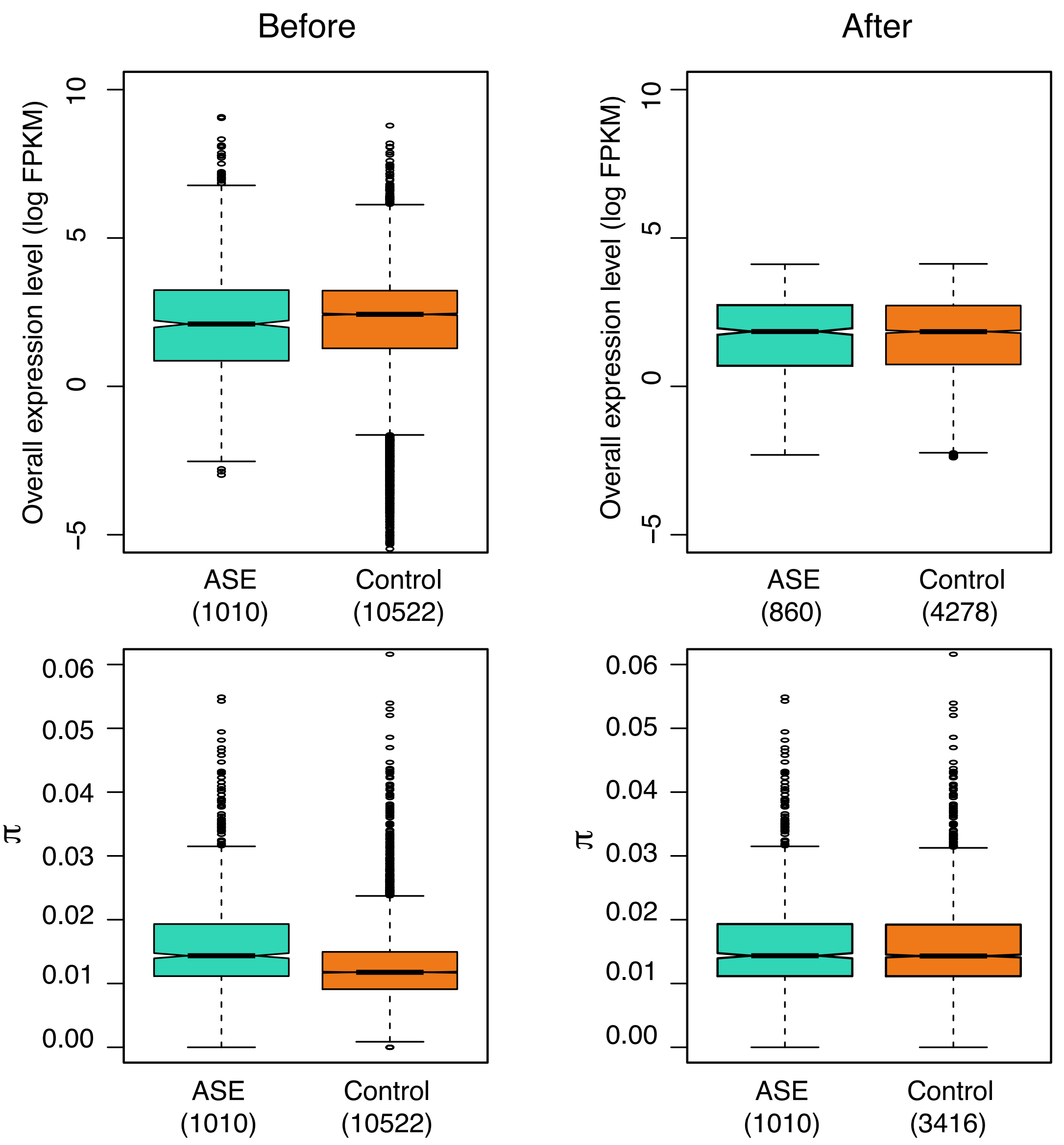

Figure S5. Top panels show the distributions of overall expression level (log FPKM) before and after the subsampling procedure (see Methods) of ASE and Control genes. Bottom panels similarly show the distribution for polymorphism level (π).

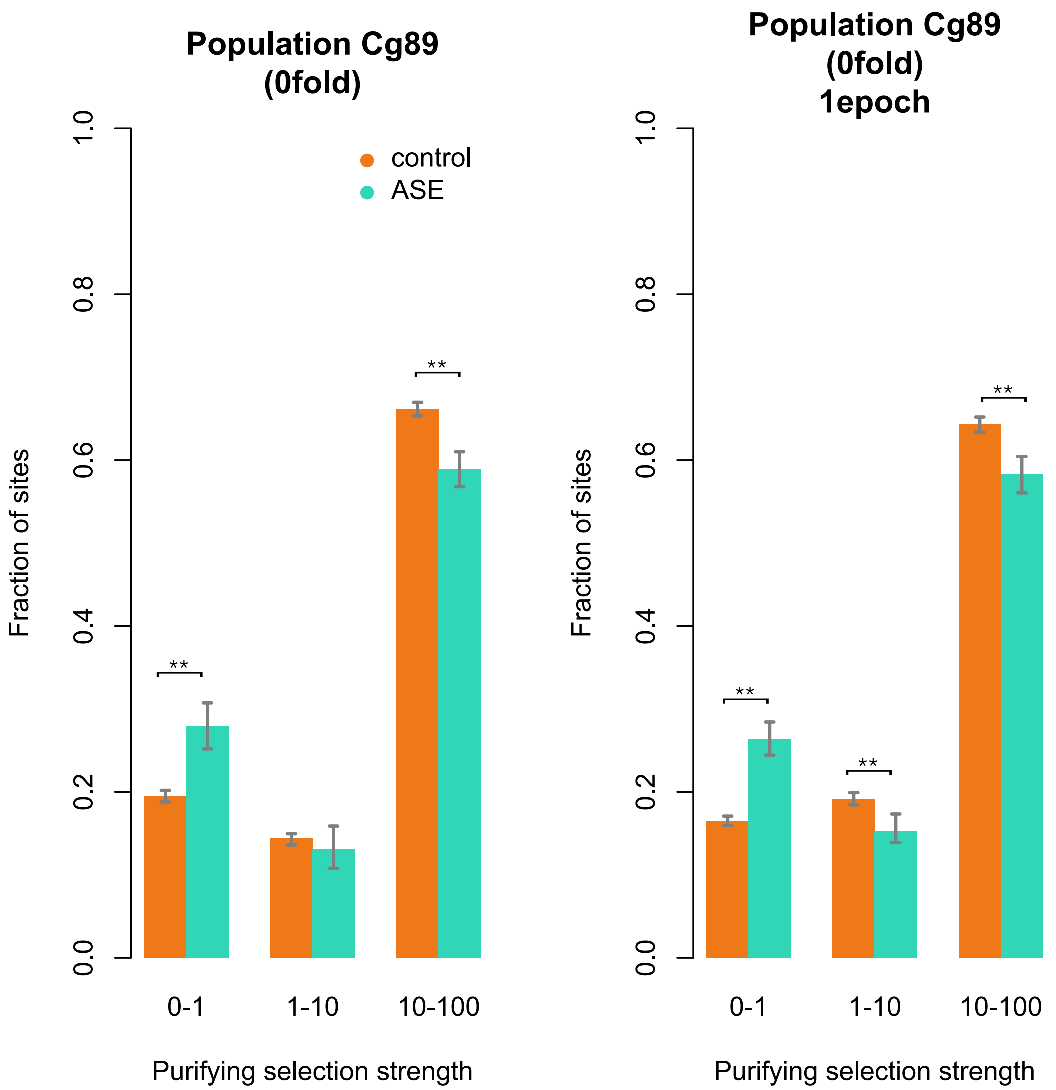

Figure S6. DFE-alpha results for 0-fold degenerate sites, after correction for expression level differences among control and ASE genes. The estimated proportion of new mutations in the selected class in each bin of the distribution of negative fitness effects is shown, with whiskers corresponding to 95% confidence intervals based on 200 bootstrap replicates, separately for genes with ASE and control genes. The left panel shows results under the stepwise population size change model and the right panel shows results for the constant population size model. Significance levels of the p-value: * ≤ 0.05; ** ≤ 0.01.

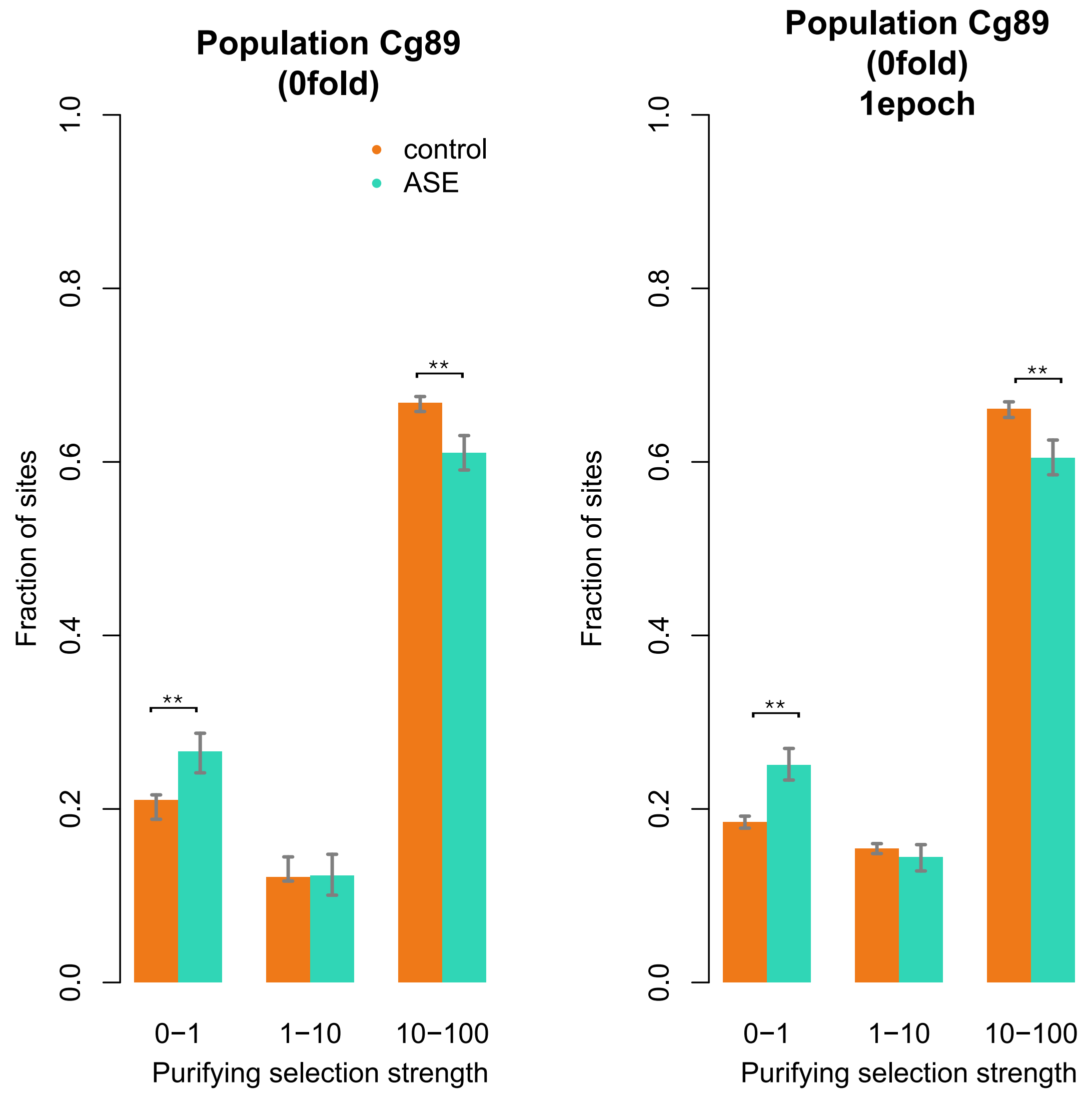

Figure S7. DFE-alpha results for 0-fold degenerate sites, after correction for polymorphism level differences among control and ASE genes. The estimated proportion of new mutations in the selected class in each bin of the distribution of negative fitness effects is shown, with whiskers corresponding to 95% confidence intervals based on 200 bootstrap replicates, separately for genes with ASE and control genes. The left panel shows results under the stepwise population size change model and the right panel shows results for the constant population size model. Significance levels of the p-value: * ≤ 0.05; ** ≤ 0.01.

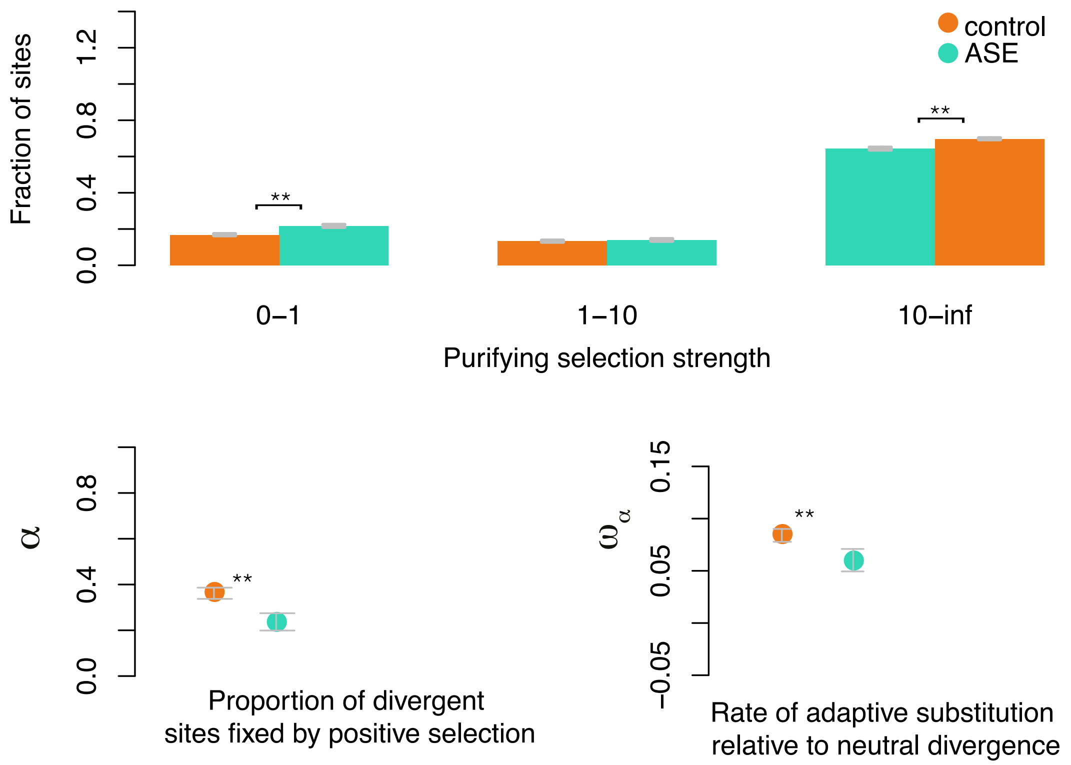

Figure S8. Purifying and positive selection on 0-fold degenerate sites, with ASE vs. control status determined based on F1 individual intra7.2, under the two-epoch model of DFE-alpha and for the population sample (similar results were obtained for the 1-epoch model and the range-wide sample). The estimated proportion of new nonsynonymous mutations in each bin of the distribution of negative fitness effects is shown in the top panel, with whiskers corresponding to 95% confidence intervals based on 200 bootstrap replicates, separately for genes with ASE and control genes. The lower two panels show the proportion of divergent nonsynonymous sites fixed by positive selection (α) and the rate of adaptive nonsynonymous substitutions relative to neutral divergence (ω_α). Significance levels of the p-value: * ≤ 0.05; ** ≤ 0.01.

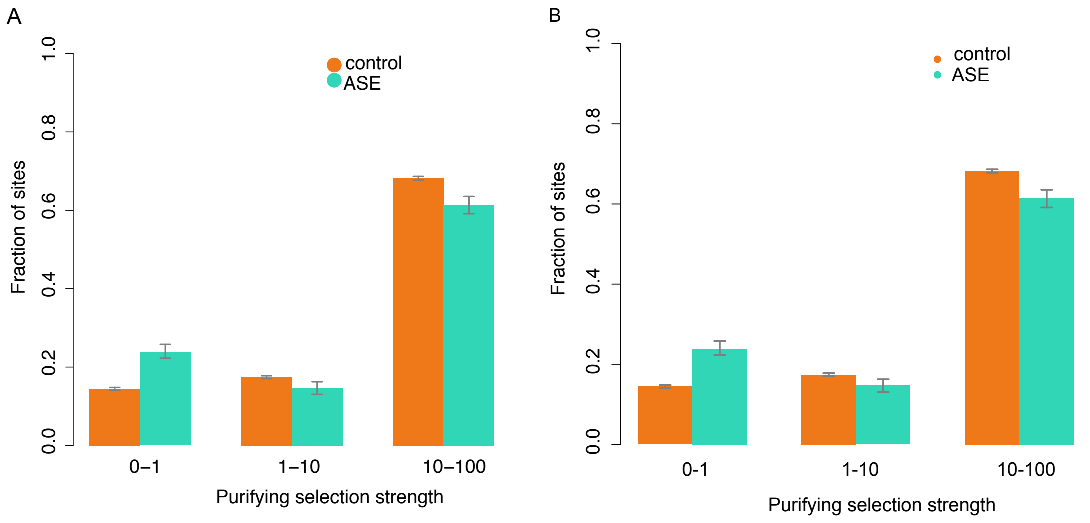

Figure S9. DFE-alpha results for 0-fold degenerate sites, after removing genes annotated as being involved in defense response ("GO:0006952"). The estimated proportion of new mutations in the selected class in each bin of the distribution of negative fitness effects is shown, with whiskers corresponding to 95% confidence intervals based on 200 bootstrap replicates, separately for genes with ASE and control genes. The left panel shows results under the stepwise population size change model and the right panel shows results for the constant population size model, for analyses of the population sample. Similar results were obtained for the range-wide sample.

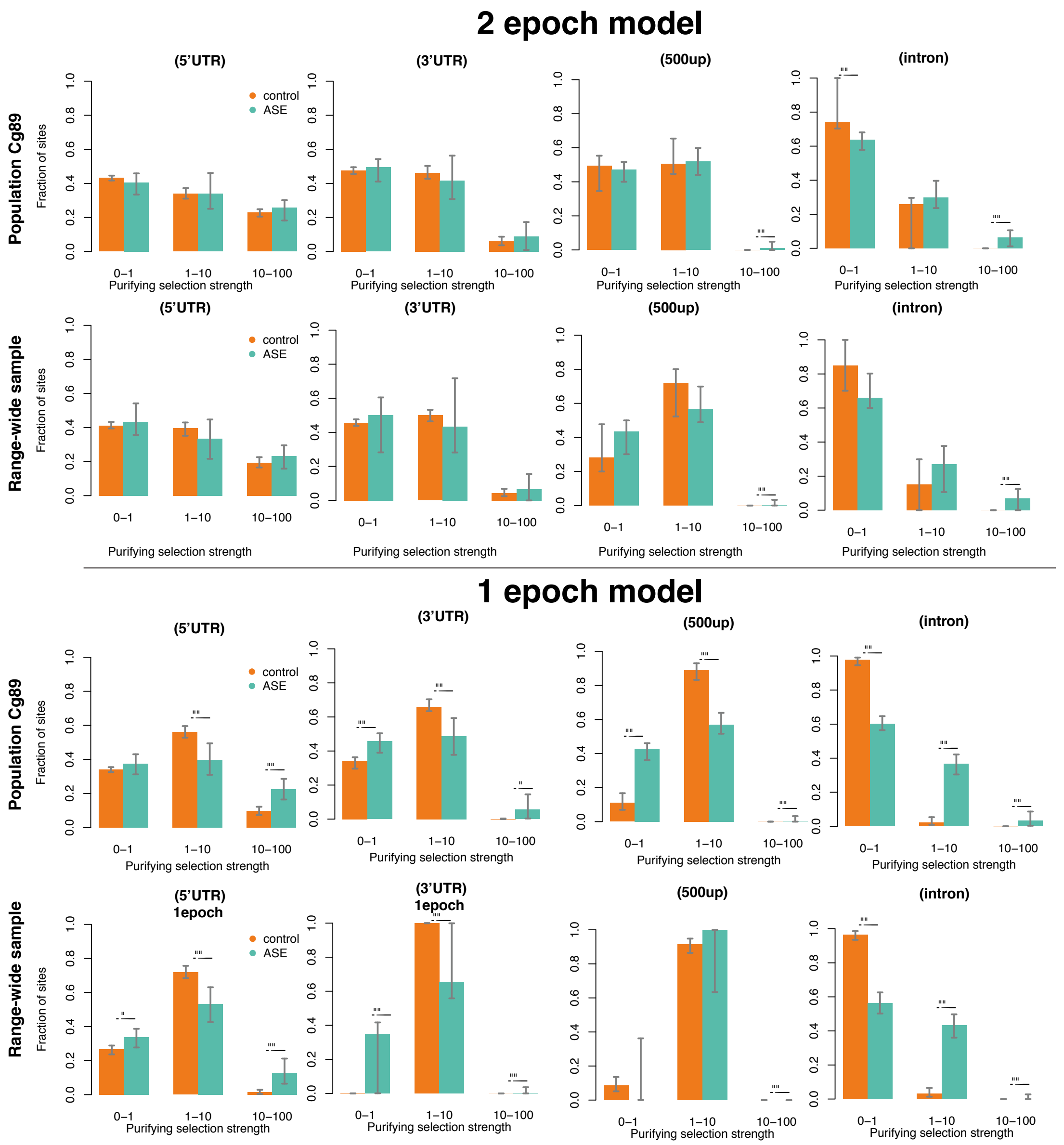

Figure S10. DFE-alpha results for 5'UTRs, 3'UTRs, promoter polymorphism (500up) and introns. The estimated proportion of new mutations in the selected class in each bin of the distribution of negative fitness effects is shown, with whiskers corresponding to 95% confidence intervals based on 200 bootstrap replicates, separately for genes with ASE and control genes. The top panels show results under the stepwise population size change model and the lower panels show results for the constant population size model. Panels on the left show results for the population sample, and those on the right for the scattered range-wide sample. Significance levels of the p-value: * ≤ 0.05; ** ≤ 0.01.

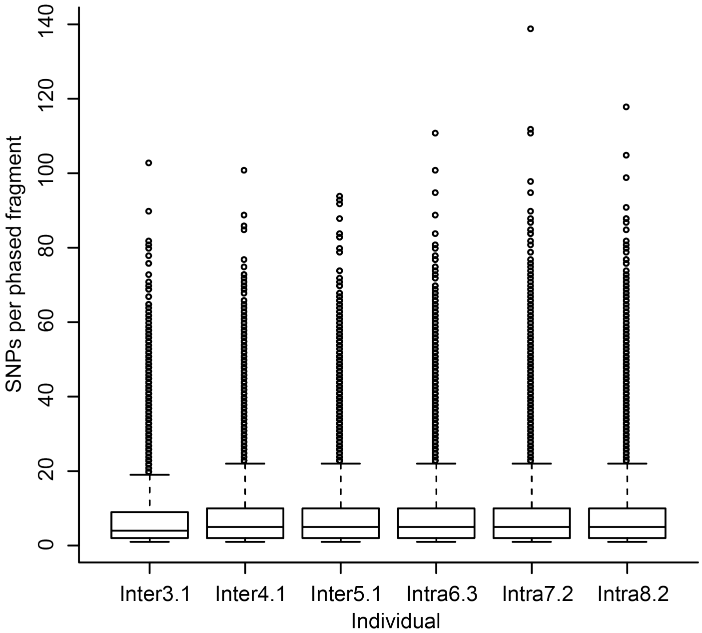

Figure S11. Boxplots showing the number of phased SNPs per fragment for interspecific *C. grandiflora* x *C. rubella* F1s (inter3.1, inter4.1 and inter5.1) and for intraspecific *C. grandiflora* F1s (intra6.3, intra7.2, and intra8.2). The median number SNPs per phased fragment is 5 for both inter- and intraspecific F1s.

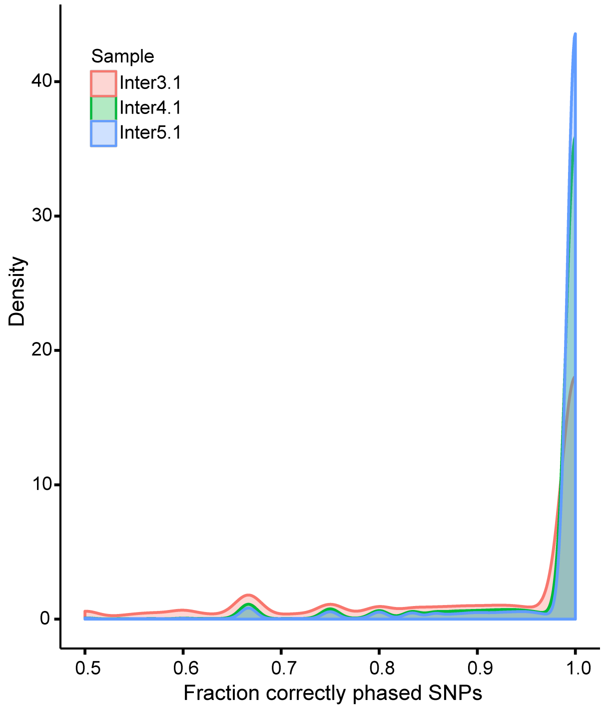

Figure S12. Success of read-back phasing. The distribution of the proportion of correctly read-back phased SNPs for three interspecific F1s (inter3.1, inter4.1 and inter5.1) with known haplotypes.

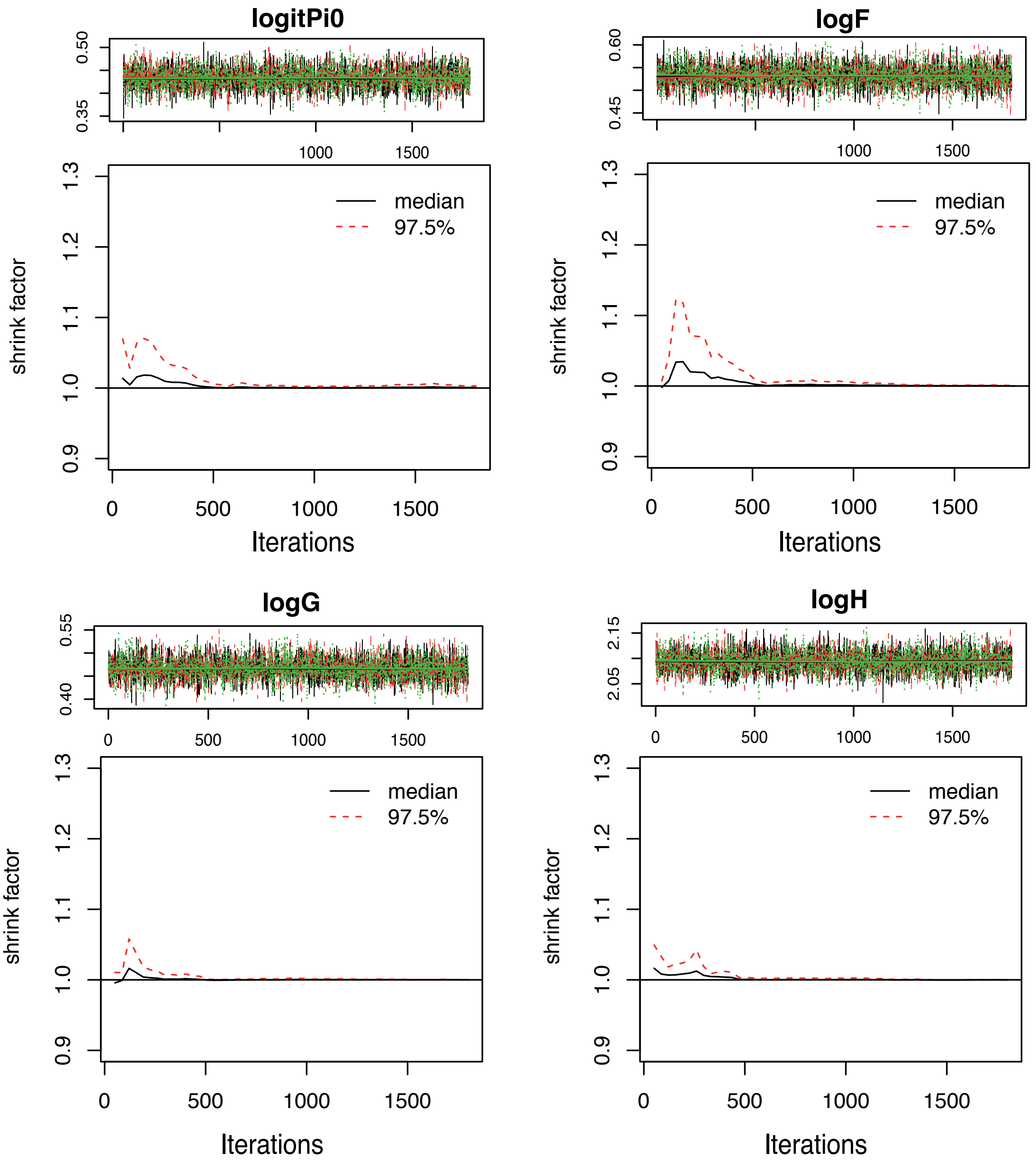

Figure S13. Trace plot and Gelman-Rubin-Brooks convergence plot of the parameters estimated during three independent MCMC chains of ASE analysis for one F1s leaf tissues. The shrink factor estimates when the chain “have forgotten” their state and value below 1.1 support among chain convergence. Results were consistent for the 3 F1s (not shown) and tissues with low shrink factors always below 1.1.

Supplementary Tables

Supplementary Table S1. Yield of RNAseq data analyzed in this study.

Sample designation	Replicate	Sample type	Yield (Gbp)	Yield Q≥30 (Gbp)
Intra6.3	1	flower buds	1.8	1.6
Intra6.3	1	leaves	9.2	8.3
Intra7.2	1	flower buds	9.2	8.5
Intra7.2	1	leaves	14.6	13.5
Intra7.2	2	flower buds	16.8	15.5
Intra7.2	2	leaves	11	10.1
Intra7.2	3	flower buds	8	7.4
Intra7.2	3	leaves	11	10.1
Intra8.2	1	flower buds	11	10.1
Intra8.2	1	leaves	11	10.1
Total			103.6	95.2

Supplementary Table S2. Yield of DNA sequence data analyzed in this study.

Sample designation	**Sample type**	**Yield (Gbp)**	**Yield Q≥30 (Gbp)**
Cg5a-KS2	Range-wide	8.2	7.5
Cg7h-KS2	Range-wide	7	6.4
Cg85_3-KS2	Range-wide	7.8	7
Cg86_15-KS2	Range-wide	8.8	8
Cg87_19-KS2	Range-wide	8.4	7.5
Cg89_1-KS2	Population	10	9.1
Cg89_11-KS3	Population	8.8	8.1
Cg89_14-KS2	Population	8	7.4
Cg89_18-KS3	Population	7.6	6.7
Cg89_19-KS2	Population	8.2	7.4
Cg89_2-KS1	Population	8	7.2
Cg89_21-KS2	Population	8.2	7.4
Cg89_25-KS2	Population	8.4	7.6
Cg89_26-KS2	Population/ Range-wide	8.8	8
Cg89_3-KS2	Population	7	6.5
Cg89-12-KS2	Population	6.6	6.1
Cg89-13-KS3	Population	7.4	6.5
Cg89-15-KS3	Population	7.4	6.8
Cg89-16-KS3	Population	7.6	6.8
Cg89-20-KS2	Population	8.4	7.7
Cg89-22-KS2	Population	7.6	7.1
Cg89-23-KS2	Population	7.6	6.8
Cg89-27-KS2	Population	7.4	6.6
Cg89-4-KS3	Population	7.8	7
Cg89-5-KS3	Population	7.2	6.4
Cg89-9-KS3	Population	8.4	7.7
Cg8d-KS3	Range-wide	8.6	8
Cg92_11-KS3	Range-wide	8	7.4
Cg93_9-KS3	Range-wide	8.6	7.9
Cg96_7-KS3	Range-wide	8	7.3
Cg98_8-KS1	Range-wide	7.8	7.3
Cg99-15-KS2	Range-wide	8.8	8
Intra6.3	F1	8	7
Intra7.2	F1	11.6	10.2
Intra8.2	F1	10.4	9.4
Total		286.4	259.8

Supplementary Table S3. Results from TopGO analyses for enrichment of Biological Process Gene Ontology terms among genes with evidence for ASE (posterior probability ≥ 0.95) in leaves. Only terms with FDR ≤ 0.01 are shown. No terms met this criterion in flower samples.

GO.ID	Term	Annotated	Significant	Expected	FDR (Fisher test)
GO:0015979	photosynthesis	152	28	9.29	0.00024
GO:0019684	photosynthesis, light reaction	117	24	7.15	0.00024
GO:0006952	defense response	745	78	45.55	0.00169
GO:0006950	response to stress	1874	159	114.58	0.00285
GO:0006091	generation of precursor metabolites and energy	256	35	15.65	0.00446
GO:0009765	photosynthesis, light harvesting	15	7	0.92	0.00849

Table S4. Population genetic summary statistics (nucleotide diversity: π, Watterson's theta: θ_W and Tajima's D: D_T), confidence intervals (CI), and *P*-values of Wilcoxon rank sum test of a difference between ASE and control genes.

Site class	Gene set	Mean π	π *P-value*	π CI		Mean θ_W	θ_W *P*-value	θ_W CI		Mean D_T	D_T *P-value*	D_T CI	
4-fold	ASE	0.029	<0.001	0.003	0.080	0.029	1.50293E-21	0.008	0.068	-0.024	5.93202E-09	-1.45	1.46
	control	0.023		0.003	0.054	0.024		0.008	0.049	-0.170		-1.49	1.29
0-fold	ASE	0.009	<0.001	0.000	0.033	0.011	1.03963E-48	0.001	0.033	-0.345	4.54597E-18	-1.29	0.89
	control	0.005		0.000	0.018	0.007		0.001	0.020	-0.501		-1.34	0.47
3'UTR	ASE	0.018	<0.001	0.001	0.041	0.021	1.45389E-10	0.006	0.045	-0.344	2.38782E-18	-1.28	0.90
	control	0.014		0.002	0.034	0.018		0.005	0.041	-0.501		-1.34	0.48
5'UTR	ASE	0.016	<0.001	0.000	0.050	0.016	3.31541E-08	0.004	0.049	-0.344	5.00495E-18	-1.28	0.90
	control	0.012		0.000	0.038	0.012		0.004	0.041	-0.501		-1.34	0.48
500 bp upstream	ASE	0.017	<0.001	0.005	0.037	0.020	1.18006E-11	0.008	0.039	-0.395	1.6763E-19	-1.24	0.77
	control	0.015		0.004	0.032	0.019		0.007	0.035	-0.543		-1.31	0.36
intron	ASE	0.020	<0.001	0.005	0.041	0.022	8.24546E-09	0.009	0.043	-0.345	3.49223E-18	-1.29	0.87
	control	0.018		0.005	0.035	0.020		0.009	0.035	-0.502		-1.34	0.47

Table S5. DFE-alpha estimates for all site classes analyzed, for the stepwise population size change model and the constant population size model, respectively. Four-fold synonymous sites were used as the neutral category in all analyses. Site categories analyzed were 0-fold degenerate sites, 5'UTRs, 3'UTRs, promoter regions (500 bp upstream of the TSS), and introns. Significance levels of the p-value: * ≤ 0.05; ** ≤ 0.01.

Demographic model	**Site class**	**Gene set**	**Estimate (95%CI)**
Population Cg89			
Stepwise population change			
0-fold	ASE	L	-256954.87 (-271144.26, -244811.06)
		n2	119 (89, 158.4)
		n1	101.1 (93.89, 158.4)
		t2	12 (12, 4567.06)
		beta	0.17 (0.13, 0.2)
		Es	-7.7 (-29.15, -2.68)
		f0	0.83 (0.82, 0.84)
		α	-0.01 (-0.13, 0.11)
		ω_α	0 (-0.03, 0.03)
0-fold	Control	L	-2175110.15 (-2208379.47, -2142390.58)
		n2	144 (131, 144)
		n1	105.34 (104.49, 106.44)
		t2	26.36 (21.87, 40.04)
		beta	0.25 (0.24, 0.27)
		Es	-4.07 (-4.59, -3.06)
		f0	0.84 (0.84, 0.85)
		α	0.35 (0.34, 0.39)
		ω_α	0.08 (0.08, 0.09)
3’UTR	ASE	L	-152589.24 (-158890.56, -146076.55)
		n2	119 (98, 232.2)
		n1	101.1 (99.14, 232.13)
		t2	12 (12, 4779.98)
		beta	0.36 (0.23, 0.8)
		Es	-0.03 (-0.06, -0.01)
		f0	0.83 (0.81, 0.84)
		α	0.56 (0.48, 0.66)
		ω_α	0.53 (0.44, 0.65)
3’UTR	Control	L	-1445345.39 (-1462311.3, -1426852.15)

		n2	144 (144, 144)
		n1	105.39 (104.43, 106.58)
		t2	26.66 (21.31, 34.43)
		beta	0.44 (0.38, 0.55)
		Es	-0.03 (-0.03, -0.02)
		f0	0.84 (0.84, 0.85)
		α	0.56 (0.53, 0.59)
		ω_α	0.5 (0.47, 0.54)
5'UTR	ASE	L	-126534.44 (-133412.2, -120318.31)
		n2	119 (89, 231)
		n1	101.1 (94.02, 231)
		t2	12 (12, 4779.99)
		beta	0.29 (0.2, 0.45)
		Es	-0.09 (-0.15, -0.03)
		f0	0.83 (0.81, 0.84)
		α	0.62 (0.53, 0.73)
		ω_α	0.58 (0.46, 0.75)
5'UTR	Control	L	-1206613.76 (-1219801.39, -1191971.01)
		n2	144 (144, 144)
		n1	105.41 (104.61, 106.53)
		t2	26.73 (22.52, 34.39)
		beta	0.28 (0.25, 0.32)
		Es	-0.08 (-0.09, -0.06)
		f0	0.84 (0.84, 0.85)
		α	0.59 (0.57, 0.61)
		ω_α	0.54 (0.51, 0.57)
500bp upstream	ASE	L	-239037.42 (-246708.38, -231910.82)
		n2	119 (98, 231)
		n1	101.1 (99.14, 231)
		t2	12 (12, 4779.98)
		beta	0.74 (0.44, 1.62)
		Es	-0.02 (-0.03, -0.01)
		f0	0.83 (0.81, 0.84)
		α	0.71 (0.65, 0.77)
		ω_α	0.88 (0.81, 0.99)
500bp upstream	Control	L	-2399129.99 (-2416962.54, -2382243.06)
		n2	144 (144, 144)

		n1	105.44 (104.57, 106.79)
		t2	26.9 (22.29, 34.84)
		beta	9.11 (1.7, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.84 (0.84, 0.85)
		α	0.72 (0.68, 0.75)
		ω_α	0.85 (0.79, 0.89)
intron	ASE	L	-320600.37 (-343516.35, -301306.64)
		n2	119 (89, 191)
		n1	101.1 (94.78, 191)
		t2	12 (12, 4779.88)
		beta	0.22 (0.15, 0.46)
		Es	-0.02 (-0.04, -0.01)
		f0	0.83 (0.82, 0.84)
		α	0.49 (0.43, 0.58)
		ω_α	0.54 (0.46, 0.66)
intron	Control	L	-3747727.32 (-3813864.92, -3678864.68)
		n2	144 (144, 144)
		n1	105.53 (104.62, 106.91)
		t2	27.42 (22.57, 35.28)
		beta	1.56 (0.56, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.84 (0.84, 0.85)
		α	0.5 (0.44, 0.56)
		ω_α	0.51 (0.45, 0.58)
Constant population size			
0-fold	ASE	L	-256962.28 (-271148.6, -244813.4)
		n1	100 (100, 100)
		beta	0.2 (0.17, 0.22)
		Es	-3.29 (-6.08, -2.11)
		f0	0.84 (0.83, 0.84)
		α	0.08 (-0.01, 0.17)
		ω_α	0.02 (0, 0.05)
0-fold	Control	L	-2175899.69 (-2209232.68, -2143257.99)
		n1	100 (100, 100)
		beta	0.35 (0.34, 0.35)
		Es	-1.29 (-1.38, -1.19)

		f0	0.86 (0.86, 0.87)
		α	0.49 (0.48, 0.5)
		ω_α	0.12 (0.11, 0.12)
3’UTR	ASE	L	-152603.26 (-158909.62, -146103.69)
		n1	100 (100, 100)
		beta	0.49 (0.31, 1.02)
		Es	-0.03 (-0.05, -0.02)
		f0	0.84 (0.83, 0.84)
		α	0.62 (0.56, 0.69)
		ω_α	0.6 (0.51, 0.69)
3’UTR	Control	L	-1446572.18 (-1463360.56, -1428060.67)
		n1	100 (100, 100)
		beta	1.6 (1.22, 2.45)
		Es	-0.02 (-0.02, -0.02)
		f0	0.86 (0.86, 0.87)
		α	0.72 (0.7, 0.75)
		ω_α	0.67 (0.64, 0.71)
5’UTR	ASE	L	-126541.88 (-133412.96, -120329.83)
		n1	100 (100, 100)
		beta	0.36 (0.26, 0.5)
		Es	-0.07 (-0.11, -0.05)
		f0	0.84 (0.83, 0.84)
		α	0.67 (0.58, 0.75)
		ω_α	0.63 (0.51, 0.8)
5’UTR	Control	L	-1207495.86 (-1220673.48, -1192858.6)
		n1	100 (100, 100)
		beta	0.62 (0.55, 0.7)
		Es	-0.04 (-0.04, -0.03)
		f0	0.86 (0.86, 0.87)
		α	0.71 (0.69, 0.73)
		ω_α	0.67 (0.65, 0.69)
500bp upstream	ASE	L	-239088.58 (-246751.2, -231991.05)
		n1	100 (100, 100)
		beta	1.05 (0.59, 3.34)
		Es	-0.02 (-0.02, -0.01)
		f0	0.84 (0.83, 0.84)

		α	0.75 (0.71, 0.79)
		ω_α	0.95 (0.88, 1.05)
500bp upstream	Control	L	-2401990.44 (-2419373.47, -2384878.95)
		n1	100 (100, 100)
		beta	100 (100, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.86 (0.86, 0.87)
		α	0.78 (0.77, 0.79)
		ω_α	0.94 (0.92, 0.96)
intron	ASE	L	-320649.35 (-343558.52, -301334.71)
		n1	100 (100, 100)
		beta	0.34 (0.22, 0.61)
		Es	-0.02 (-0.03, -0.01)
		f0	0.84 (0.83, 0.84)
		α	0.55 (0.49, 0.61)
		ω_α	0.62 (0.54, 0.71)
intron	Control	L	-3751129.56 (-3817573.88, -3681960.11)
		n1	100 (100, 100)
		beta	100 (100, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.86 (0.86, 0.87)
		α	0.63 (0.61, 0.64)
		ω_α	0.66 (0.64, 0.68)
Range-wide sample			
Stepwise population change			
0-fold	ASE	L	-228831.52 (-239793.9, -215937.1)
		n2	158 (131, 307.77)
		n1	103.34 (102.54, 111.87)
		t2	12 (12, 23.71)
		beta	0.18 (0.11, 0.21)
		Es	-4.62 (-100.3, -2.84)
		f0	0.79 (0.72, 0.81)
		α	0.06 (-0.24, 0.14)
		ω_α	0.01 (-0.06, 0.04)
0-fold	Control	L	-1921169.23 (-1955228.74, -1889955.17)
		n2	158 (158, 174)

		n1	112.15 (110.59, 113.62)
		t2	48.98 (32.84, 56.07)
		beta	0.28 (0.26, 0.29)
		Es	-2.32 (-3.07, -2.1)
		f0	0.83 (0.82, 0.83)
		α	0.41 (0.38, 0.42)
		ω_α	0.1 (0.09, 0.1)
3’UTR	ASE	L	-134539.4 (-140342.97, -129761.8)
		n2	231 (144, 660)
		n1	107.51 (103.34, 131.83)
		t2	12 (12, 20.01)
		beta	0.4 (0.2, 100)
		Es	-0.03 (-0.05, -0.01)
		f0	0.75 (0.59, 0.8)
		α	0.57 (0.45, 0.73)
		ω_α	0.56 (0.43, 0.74)
3’UTR	Control	L	-1279054.76 (-1299259.06, -1260535.93)
		n2	158 (158, 174)
		n1	112.27 (110.59, 113.91)
		t2	49.54 (33.07, 57.52)
		beta	0.54 (0.45, 0.65)
		Es	-0.02 (-0.03, -0.02)
		f0	0.83 (0.82, 0.83)
		α	0.59 (0.57, 0.62)
		ω_α	0.53 (0.51, 0.56)
5’UTR	ASE	L	-113525.53 (-118689.59, -107393.46)
		n2	231 (158, 661.65)
		n1	107.51 (103.34, 131.92)
		t2	12 (12, 17.05)
		beta	0.28 (0.15, 0.42)
		Es	-0.08 (-0.17, -0.04)
		f0	0.76 (0.59, 0.79)
		α	0.6 (0.45, 0.71)
		ω_α	0.57 (0.38, 0.76)
5’UTR	Control	L	-1080942.2 (-1094594.88, -1065935.39)
		n2	158 (158, 174)
		n1	112.09 (110.64, 113.63)

		t2	48.69 (32.78, 56.1)
		beta	0.34 (0.29, 0.39)
		Es	-0.05 (-0.07, -0.05)
		f0	0.83 (0.82, 0.83)
		α	0.62 (0.59, 0.64)
		ω_α	0.57 (0.55, 0.6)
500bp upstream	ASE	L	-211757.76 (-218720.28, -205932.29)
		n2	144 (131, 231)
		n1	103.24 (101.9, 107.51)
		t2	15.45 (12, 31.21)
		beta	1.04 (0.55, 5.69)
		Es	-0.02 (-0.02, -0.01)
		f0	0.8 (0.76, 0.81)
		α	0.75 (0.69, 0.8)
		ω_α	0.96 (0.85, 1.07)
500bp upstream	Control	L	-2113038.25 (-2129886.18, -2096361.1)
		n2	158 (158, 174)
		n1	111.98 (110.68, 113.61)
		t2	48.19 (33.07, 56)
		beta	99.99 (4.87, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.83 (0.82, 0.83)
		α	0.75 (0.73, 0.76)
		ω_α	0.89 (0.85, 0.91)
intron	ASE	L	-282833.62 (-303379.94, -264364.89)
		n2	191 (131, 409)
		n1	105.23 (102.54, 117.61)
		t2	12 (12, 23.01)
		beta	0.19 (0.07, 0.94)
		Es	-0.02 (-0.06, -0.01)
		f0	0.77 (0.68, 0.8)
		α	0.47 (0.33, 0.57)
		ω_α	0.53 (0.36, 0.64)
intron	Control	L	-3273883.1 (-3330916.44, -3218921.67)
		n2	158 (158, 174)
		n1	111.95 (110.23, 113.37)
		t2	48.02 (31.56, 54.61)

		beta	7.64 (0.89, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.83 (0.82, 0.83)
		α	0.55 (0.48, 0.58)
		ω_α	0.57 (0.5, 0.6)
Constant population size			
0-fold	ASE	L	-228892.46 (-239843.29, -215994.66)
		n1	100 (100, 100)
		beta	0.25 (0.22, 0.29)
		Es	-1.19 (-1.97, -0.8)
		f0	0.83 (0.82, 0.83)
		α	0.2 (0.1, 0.28)
		ω_α	0.05 (0.02, 0.07)
0-fold	Control	L	-1922427.06 (-1956510.48, -1891226.11)
		n1	100 (100, 100)
		beta	0.42 (0.41, 0.43)
		Es	-0.7 (-0.76, -0.65)
		f0	0.86 (0.86, 0.86)
		α	0.56 (0.55, 0.57)
		ω_α	0.14 (0.13, 0.14)
3’UTR	ASE	L	-134598.17 (-140412.09, -129783.88)
		n1	100 (100, 100)
		beta	1.56 (0.67, 100)
		Es	-0.02 (-0.03, -0.01)
		f0	0.83 (0.82, 0.83)
		α	0.74 (0.67, 0.83)
		ω_α	0.75 (0.65, 0.89)
3’UTR	Control	L	-1280785.37 (-1300998.02, -1262315.36)
		n1	100 (100, 100)
		beta	100 (100, 100)
		Es	-0.01 (-0.02, -0.01)
		f0	0.86 (0.86, 0.86)
		α	0.83 (0.81, 0.84)
		ω_α	0.79 (0.77, 0.81)
5’UTR	ASE	L	-113585.64 (-118760.57, -107468.66)
		n1	100 (100, 100)
		beta	0.56 (0.39, 0.81)

		Es	-0.04 (-0.07, -0.03)
		f0	0.83 (0.82, 0.83)
		α	0.72 (0.64, 0.8)
		ω_α	0.71 (0.57, 0.87)
5’UTR	Control	L	-1082319.23 (-1095962.67, -1067305.2)
		n1	100 (100, 100)
		beta	1.26 (1.04, 1.64)
		Es	-0.03 (-0.03, -0.02)
		f0	0.86 (0.86, 0.86)
		α	0.79 (0.77, 0.81)
		ω_α	0.76 (0.74, 0.79)
500bp upstream	ASE	L	-211880.82 (-218796.62, -206062.17)
		n1	100 (100, 100)
		beta	100 (1.81, 100)
		Es	-0.01 (-0.02, -0.01)
		f0	0.83 (0.82, 0.83)
		α	0.85 (0.8, 0.86)
		ω_α	1.13 (1.03, 1.2)
500bp upstream	Control	L	-2117145.16 (-2133978.09, -2100465.44)
		n1	100 (100, 100)
		beta	100 (100, 100)
		Es	-0.01 (-0.01, -0.01)
		f0	0.86 (0.86, 0.86)
		α	0.79 (0.78, 0.8)
		ω_α	0.96 (0.94, 0.98)
intron	ASE	L	-282950.23 (-303525.7, -264529.84)
		n1	100 (100, 100)
		beta	0.8 (0.34, 100)
		Es	-0.01 (-0.02, -0.01)
		f0	0.83 (0.82, 0.83)
		α	0.63 (0.55, 0.72)
		ω_α	0.73 (0.62, 0.85)
intron	Control	L	-3278975.81 (-3336542.74, -3224367.68)
		n1	100 (100, 100)
		beta	100 (100, 100)
		Es	-0.01 (-0.01, -0.01)

f0	0.86 (0.86, 0.86)
α	0.64 (0.62, 0.65)
ω_α	0.68 (0.66, 0.7)

Table S6. Predictor importance in logistic regression best-fit model predicting ASE from genomic features using BIC (BIC=3093.1). Regression coefficients and their standard error, z-statistics and associated P-values, and odds ratios (OR) are shown

Model parameter	Coeff. (SE)	z value	P-value	OR
Gene-body methylation	-0.62 (0.18)	-3.45	$<10^{-3}$	0.54
Expression level	0.20 (0.05)	-3.45	$<10^{-3}$	1.22
Promoter polymorphism	0.20 (0.05)	4.37	$<10^{-3}$	1.23
Tissue specificity	0.20 (0.05)	5.12	$<10^{-3}$	1.35
Intercept	-2.55 (0.05)	-46.81	$<10^{-3}$	0.08

Table S7. Predictors importance in logistic regression model predicting ASE from genomic features using model averaging with AIC and BIC criterion. Conditional averages for regression coefficients and their standard error, z-statistics and associated P-values, odds ratios (OR) and predictor relative importance are shown.

	AIC				**BIC**			
Model parameter	**Coeff (SE)**	**P-value**	**OR**	**Importance**	**Coeff (SE)**	**P-value**	**OR**	**Importance**
Gene-body methylation	-0.64 (0.20)	0.001	0.51	0.99	-0.62 (0.18)	$<10^{-3}$	0.54	0.92
π_N/π_S	0.08 (0.04)	0.029	1.09	0.73	0.07 (0.04)	0.044	1.08	0.07
Expression level	0.20 (0.06)	$<10^{-3}$	1.22	0.99	0.20 (0.06)	$<10^{-3}$	1.22	0.80
Promoter polymorphism	0.20 (0.05)	$<10^{-3}$	1.23	1	0.20 (0.05)	$<10^{-3}$	1.23	0.99
Tissue specificity	0.30 (0.06)	$<10^{-3}$	1.35	1	0.28 (0.07)	$<10^{-3}$	1.35	0.99
TE within 1 kb	0.32 (0.13)	0.012	1.38	0.88	0.32 (0.13)	0.011	1.38	0.20
Co-expression module size	-0.08 (0.05)	NS	0.92	0.55	-0.09 (0.05)	NS	0.91	0.05
Gene length	0.08 (0.06)	NS	1.09	0.51	0.07 (0.06)	NS	1.08	0.03
Recombination rates	0.06 (0.05)	NS	1.06	0.46	0.06 (0.05)	NS	1.06	0.03
Gene density	0.04 (0.05)	NS	1.04	0.32	0.025 (0.05)	NS	1.02	0.01
Synonymous divergence	0.03 (0.05)	NS	1.03	0.31	0.03 (0.05)	NS	1.03	0.01
Alpha paralog present	0.02 (0.11)	NS	1.02	0.27	0.02 (0.11)	NS	1.02	0.01
Beta/gamma paralog present	-0.12 (0.15)	NS	0.87	0.34	-0.12 (0.15)	NS	0.89	0.02

Table S8. Percent contributions of each continuous variable to each PC. Variables with higher than 20% contribution are highlighted in bold.

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Recombination rate	0.1	0.8	**30.1**	5.8	4.2	9.5	**26.8**	8.9	2.3
Tissue specificity	**27.7**	5.7	5.4	6.8	7.7	7.3	3.3	0.1	**40.6**
Gene length	16.0	19.3	5.3	12.4	5.5	0.4	10.4	**31.1**	5.3
Expression level	**26.4**	11.2	5.9	4.7	10.0	1.3	6.5	2.8	**39.6**
Gene density	6.1	2.8	24.5	17.7	12.7	16.2	12.3	**20.6**	1.0
Synonymous divergence	11.0	**22.3**	3.6	1.9	1.4	**30.0**	1.9	**20.8**	1.8
Promoter polymorphism	1.4	1.2	14.2	**32.2**	1.3	5.2	**23.2**	1.0	3.0
π_N/π_S	10.3	13.6	8.6	4.4	**43.1**	2.8	2.6	6.4	0.4
Coexpression module size	1.0	**23.1**	2.7	14.2	14.1	**27.4**	13.0	8.3	6.0

Table S9. Results of the best fit logistic regression including principal components of the continuous variables as well as the binary variables TE presence within 1 kb and gene-body methylation using stepwise AIC. PC1 and PC7 improved model fit and are therefore included despite having individually non-significant effects.

Model parameter	Coefficient	Std. Error	z value	P-value	OR
Gene-body methylation	-0.67	0.19	-3.59	0.0003	0.51
TE within 1 kb	0.32	0.13	2.48	0.0132	1.37
PC1	0.06	0.04	1.52	NS	1.06
PC3	-0.10	0.04	-2.28	0.0229	0.91
PC4	0.11	0.05	2.38	0.0174	1.11
PC5	-0.08	0.04	-1.97	0.0485	0.92
PC6	-0.11	0.05	-2.13	0.0328	0.89
PC7	0.09	0.06	1.57	NS	1.09
PC8	-0.14	0.06	-2.25	0.0244	0.87
PC9	0.36	0.08	4.68	$<10^{-3}$	1.43
Intercept	-2.60	0.06	-43.29	$<10^{-3}$	0.07

Table S10. Results of the best fit logistic regression including principal components of the continuous variables as well as the binary variables TE presence within 1 kb and gene-body methylation using stepwise BIC.

Model parameter	Coefficient	Std. Error	z value	P-value	OR
Gene-body methylation	-0.69	0.18	-3.91	$<10^{-3}$	0.51
PC9	0.36	0.08	4.68	$<10^{-3}$	1.43
Intercept	-2.52	0.06	-43.29	$<10^{-3}$	0.08

Table S11. Intraspecific *C. grandiflora* F1 samples for analysis of allele-specific expression

Designation	Seed parent	Geographical origin, seed parent	Pollen parent	Geographical origin, pollen parent
Intra6.3	Cg89.30-1	Greece, Zagory, Koukouli	Cg935/13-2	Greece, Corfu, Sokraki
Intra7.2	Cg94-6-1	Greece, Zagory, Mikro Papingo	Cg5d-1	Greece, Corfu, Near Troumpeta
Intra8.2	Cg2k-1	Greece, Corfu, Paleokastritsas	Cg88.14-1	Greece, Zagory, Monodendri

Table S12. Geographic origin of samples for population genomic analyses.

Species	**Designation**	**Geographical origin**
C. grandiflora	Cg5a-KS2	Greece, Corfu, Troumpeta
C. grandiflora	Cg7h-KS2	Greece, Lefkas, Exanthia
C. grandiflora	Cg85.3-KS2	Greece, south of Ioannina
C. grandiflora	Cg86.15-KS2	Greece, Zagory
C. grandiflora	Cg87.19-KS2	Greece, Zagory
C. grandiflora	Cg89.1-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.11-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg89.12-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.13-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg89.14-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.15-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg89.16-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg89.18-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg89.19-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.2-KS1	Greece, Zagory, Koukouli
C. grandiflora	Cg89.20-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.21-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.22-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.23-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.25-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.26-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.27-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.3-KS2	Greece, Zagory, Koukouli
C. grandiflora	Cg89.4-KS3	Greece, Zagory, Koukouli

C. grandiflora	Cg89.5-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg89.9-KS3	Greece, Zagory, Koukouli
C. grandiflora	Cg8d-KS3	Greece, Sterea Ellada, Thirio
C. grandiflora	Cg92.11-KS3	Greece, Zagory
C. grandiflora	Cg93.9-KS3	Greece, Zagory
C. grandiflora	Cg96.7-KS3	Greece, Zagory, Mikro Papingo
C. grandiflora	Cg98.8-KS1	Greece, Katara Pass
C. grandiflora	Cg99.15-KS2	Greece, near Panagia northeast of Metsovo