

Supplemental Information:

Tables:

Site	Latitude	Longitude	Elevation (m)	Tissue	NCBI Accession
Malibu Creek SP	34.10112	-118.71234	185	Mature leaf	SRR1727003
Malibu Creek SP	34.09599	-118.71674	159	Mature leaf	SRR1727008
Malibu Creek SP	34.09455	-118.71642	160	Mature leaf	SRR1727009
Malibu Creek SP	34.09454	-118.71847	166	Expanding leaf bud	SRR1727010
Sedgwick Reserve	34.70143	-120.04046	350	Expanding leaf bud	SRR1727821
Sedgwick Reserve	34.68894	-120.03593	332	Expanding leaf bud	SRR1727822
Sedgwick Reserve	34.70560	-120.04067	358	Expanding leaf bud	SRR1727823
Sedgwick Reserve	34.69640	-120.03815	342	Expanding leaf bud	SRR1727824
Fort Tejon SHP	34.87476	-118.89410	994	Expanding leaf bud	SRR1727826
Fort Tejon SHP	34.87430	-118.89438	994	Expanding leaf bud	SRR1727827
Fort Tejon SHP	34.87446	-118.89432	994	Expanding leaf bud	SRR1727893

Table S1. Sampling information

MAF	Type 1	Type 2	Type 3	Type 4	Type 5	Type 6	Type 7
0.1	0.186(0.002)	0.218(0.003)	0.081(0.003)	0.215(0.003)	0.174(0.008)	0.167(0.004)	0.214(0.006)
0.2	0.182(0.002)	0.231(0.004)	0.077(0.003)	0.242(0.005)	0.168(0.01)	0.164(0.004)	0.231(0.008)
0.3	0.169(0.003)	0.235(0.004)	0.064(0.003)	0.229(0.007)	0.158(0.012)	0.155(0.006)	0.225(0.013)
0.4	0.134(0.003)	0.229(0.006)	0.033(0.003)	0.198(0.012)	0.108(0.018)	0.095(0.008)	0.246(0.031)

Table S2. Mean F_{ST} values (standard error) of contigs stratified by minimum minor allele frequency threshold and contig type. Type1 contain only SNPs; type 2 only CG-SMPs; type 3 only CHG-SMPs; type 4 both SNPs and CG-SMPs; type 5 both CG-SMPs and CHG-SMPs; type 6 both SNPs and CHG-SMPs; type 7 SNPs, CG-SMPs, and CHG-SMPs.

Figures:

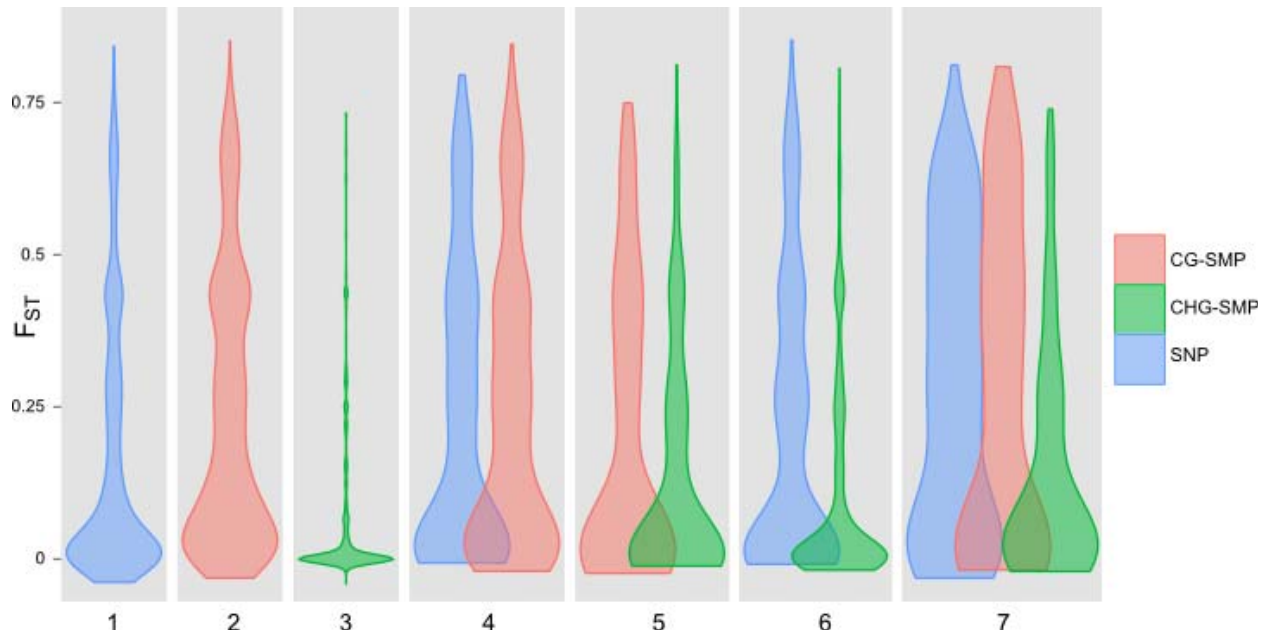


Figure S1. Violin plots of F_{ST} values for polymorphisms in seven categories of loci: those containing 1) only SNPs (8,443 polymorphisms), 2) only CG-SMPs (3,145 polymorphisms), 3) only CHG-SMPs (2,368 polymorphisms), 4) both SNPs and CG-SMPs (1,018 and 661 polymorphisms respectively), 5) both CG-SMPs and CHG-SMPs (160 and 186 polymorphisms respectively), 6) both SNPs and CHG-SMPs (744 and 922 polymorphisms respectively), and 7) SNPs, CG-SMPs, and CHG-SMPs (183, 126, and 162 polymorphisms respectively).

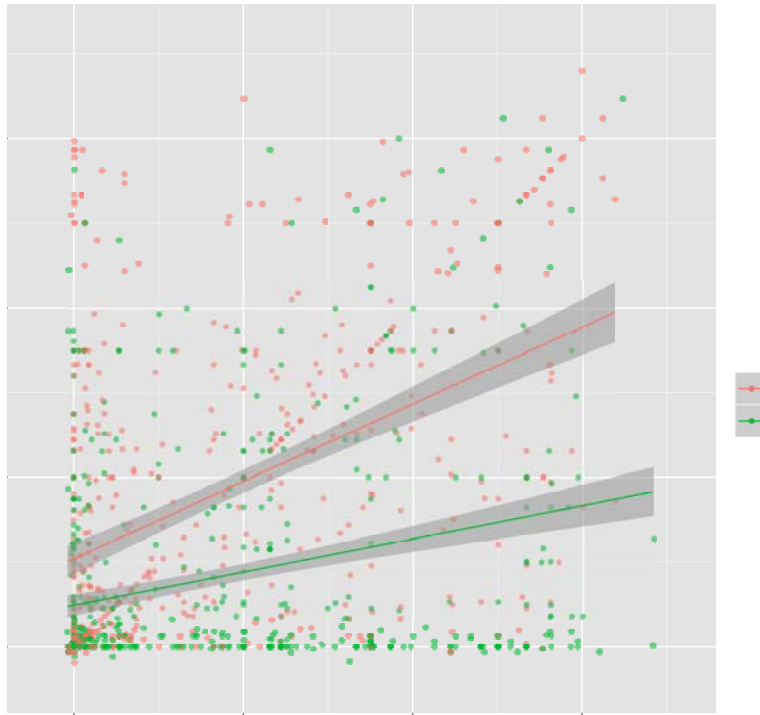


Figure S2. Average F_{ST} values for SNPs and SMPs in each locus containing SNPs and either CG-SMPs or CHG-SMPs but not both. 95% confidence intervals for linear regressions of each type of SMP do not overlap.