Table S3. Summary statistics for each population.

Population ID	SNPs	π	N_e	T_D	Θ	ρ/Θ
G1_R	1410448	0.0017	22032	0.5693	0.0013	4.676
G1_L	1599340	0.0019	25081	0.3792	0.0015	3.639
G2_R	1597865	0.0019	25157	0.3321	0.0015	4.685
G2_L	1871737	0.0021	29255	0.1324	0.0017	5.500
No_R	965465	0.0012	14991	0.5461	0.0009	7.233
No_L	1859884	0.0021	29023	0.0922	0.0017	8.162
Ca_R	1710748	0.0020	26615	0.2985	0.0016	9.786
Ca_L	2426796	0.0029	37607	0.3471	0.0022	4.987
Us_R	2979553	0.0033	45634	0.0428	0.0027	6.732
Us_L	2755107	0.0031	41977	0.0601	0.0025	6.940

SNPs with a minor allele frequency above 5% are given.

Nucleotide diversity is given as an average across the autosomes.

Effective population size was estimated on the basis of Watterson's theta evaluated at intergenic regions assuming a mutation rate of 1.7×10^{-8}.