

**SUPPLEMENTARY TABLE 4.** — *Zea luxurians* diversity statistics at silent sites for all loci.

locus	bp	n	S	$\eta_1$	H	$\theta_\pi$	D	RM	$\rho$
<i>adh1</i>	921	8	26	8	0.964	0.012	0.305	6	0.030
<i>asg11</i>	346	5	9	6	1.000	0.012	-0.197	1	0.096
<i>asg35</i>	496	10	5	0	0.511	0.004	1.032	0	0.002
<i>asg64</i>	585	11	21	3	0.891	0.016	1.518	1	0.000
<i>asg65</i>	528	11	9	3	0.600	0.006	0.423	0	0.002
<i>bnl7-13</i>	760	11	7	7	0.727	0.002	-1.897	0	0.000
<i>bz2</i>	206	11	8	4	0.927	0.012	-0.392	2	0.091
<i>c1</i>	450	7	17	3	0.952	0.019	1.310	1	0.005
<i>csu1132</i>	335	10	17	10	0.978	0.015	-0.867	2	0.015
<i>csu1138</i>	186	10	6	5	0.533	0.007	-1.493	0	0.000
<i>csu1171</i>	462	8	10	5	0.929	0.008	-0.229	0	0.000
<i>csu381</i>	921	9	7	3	0.972	0.002	-0.612	1	0.108
<i>csu636</i>	643	9	2	2	0.417	0.001	-1.362	0	0.021
<i>csu838</i>	253	11	13	6	0.927	0.018	0.213	1	0.169
<i>d8</i>	206	8	7	2	0.857	0.014	0.466	0	0.000
<i>fus6</i>	157	12	1	1	0.167	0.001	-1.141		
<i>gl1510</i>	490	12	5	1	0.803	0.004	0.395	0	0.000
<i>glb1</i>	532	6	18	7	0.933	0.016	0.355	1	0.018
<i>mgs3020</i>	179	12	4	1	0.742	0.009	0.707	1	0.055
<i>pepc1070</i>	718	10	6	2	0.889	0.003	-0.193	0	0.000
<i>pepc1150</i>	237	11	8	0	0.582	0.011	-0.171	0	0.000
<i>tb1</i>	1710	11	46	40	0.945	0.006	-1.711	1	0.001
<i>ts2</i>	309	8	10	3	0.964	0.015	0.917	3	0.032
<i>vp1010</i>	168	6	3	1	0.933	0.008	0.338	1	0.592
<i>wipl</i>	298	9	16	5	0.889	0.020	0.139	0	0.002
<i>wx1</i>	515	21	13	5	0.943	0.007	0.015	3	0.080

bp: number of silent sites; n: sample size; S: segregating sites  $\eta_1$ : number of singletons; H: haplotype

diversity;  $\theta_\pi$ : nucleotide diversity per bp; RM: minimum number of recombination events;  $\rho$ : recombination

rate per bp