Table S4. Statistics specific to the S-locus used in the IMfor2 analyses.

Gene	Comparison	S	S1	S2	Ss	Sf	Fst	MinDist[1]	K_S [2]	Recombination [3]
lal2-1	crassa vs ala	1	0	0	0	1	1	0.0078125	0.00785	No
	crassa vs 19	1	0	0	0	1	1	0.0078125	0.00785	No
	crassa vs waco	1	0	0	0	1	1	0.0078125	0.00785	No
	19 vs waco	0	0	0	0	0	0	0	0	No
lal2-2	crassa vs ala	1	0	0	0	1	1	0.008	0.00804	No
	crassa vs 19	1	0	0	0	1	1	0.008	0.00804	No
	crassa vs waco	1	0	0	0	1	1	0.008	0.00804	No
	19 vs waco	0	0	0	0	0	0	0	0	No
lal2-3	19 vs waco	2	0	2	0	0	0.625	0	0.01002	No
lal2-4	19 vs waco	0	0	0	0	0	0	0	0	No
lal2-5	19 vs waco	0	0	0	0	0	0	0	0	No
lal2-6	crassa vs ala	2	0	1	0	1	0.861538	0.00775194	0.0086	No
	crassa vs 19	2	0	1	0	1	0.777778	0.00775194	0.01163	No
	crassa vs waco	1	0	0	0	1	1	0.00775194	0.00773	No
	19 vs waco	1	1	0	0	0	0.333333	0	0.00386	No
lal2-7	crassa vs ala	0	0	0	0	0	0	0	0	No
	crassa vs 19	0	0	0	0	0	0	0	0	No
lal2-8	crassa vs ala	1	0	0	0	1	1	0.00740741	0.00744	No
	crassa vs waco	1	0	0	0	1	1	0.00740741	0.00744	No
lal2-9	19 vs waco	0	0	0	0	0	0	0	0	No
Average [4]	crassa vs ala	5	0	1	0	4	0.772308	0.00619437	0.00639	
	crassa vs 19	4	0	1	0	3	0.694444	0.00589111	0.00688	
	crassa vs waco	4	0	0	0	4	1	0.00774296	0.00777	
	19 vs waco	3	1	2	0	0	0.136905	0	0.00198	

Notes: statistics calculated on synonymous sites.

[1] Minimum pairwise sequence divergence between the two species (populations).

[2] Average number of nucleotide substitutions per site between populations with Jukes and Cantor correction.

[3] According to the Hudson and Kaplan test.

[4] The S statistics represent the sum of all genes and not the average.