Supplement File 3: Statistical tests for significant heterozygosity (H) excess or deficiency in three populations of *Serolis paradoxa* (PA, AO, FI) assuming three different mutation models (IAM, TPM, SMM). P-values of the Sign Test and Standardized Differences Test and one-tailed probability for heterozygosity deficiency are based on a 1000 permutations. Significant P-values are printed in bold. The TPM was adjusted to allow for 80% mutations according to a SMM and 20% to an IAM model.

Population	Model	Sign Test				Wilcoxon Test
		Expected no of loci with H excess	Observed no. of loci with H excess	observed no of loci with H deficiency	P	P (one tailed for H deficiency)
	IAM	4.00	6	1	0.1212	0.9453
PA	TPM	4.04	4	3	0.6306	0.7109
	SMM	4.03	3	4	0.3360	0.2891
	IAM	4.17	3	4	0.2979	0.2343
AO	TPM	4.10	1	6	**0.0226**	**0.0117**
	SMM	4.09	0	7	**0.0021**	**0.0039**
	IAM	4.06	4	3	0.6244	0.3438
FI	TPM	4.14	2	5	0.1049	0.1484
	SMM	4.16	2	5	0.1024	**0.0195**