**Figure S1. Histograms of P-value distributions for distortion** in the direction of containing more *L. serriola* or *L. sativa* alleles based on a Monte Carlo algorithm, 50,000x drawing N virtual plants from the expected distribution per locus. The observed distribution was compared to these confidence intervals. Each locus was independently drawn per virtual plant. Left-above: control population grown in the greenhouse, Right-above: $S_1$ generation under field exposure; Left-middle: $BC_1$ generation under field exposure. Right-middle: $BC_{1S1}$ generation under field exposure. Left-below: P-value distribution for all 3 populations for significant alterations in LD compared to the control generation; note the $10^x$ scaling of x-axis. Chi-square testing was used for testing of statistical significance, using LD and (1-LD) for both expected (control) and observed (one of the populations) as variables (df = 1).