Figure S3. Enrichment analysis of paralogs (ab) and repetitive sequences (c) within RH hotspot regions. (a) The paralogs tagged by polymorphic markers to specifically evaluate the possible bias in identifying RH hotspots per population were chosen. (b) The subset of paralogs in (a) whose similarity were higher than 80% between target and query genes. The binomial distribution was used to test the null hypothesis that both proportions within RH hotspot, the observed paralogs and repetitive sequences proportion (red bar) and the proportion expected by chance (blue bar), come from the same distribution ($P<0.05$; right tail).