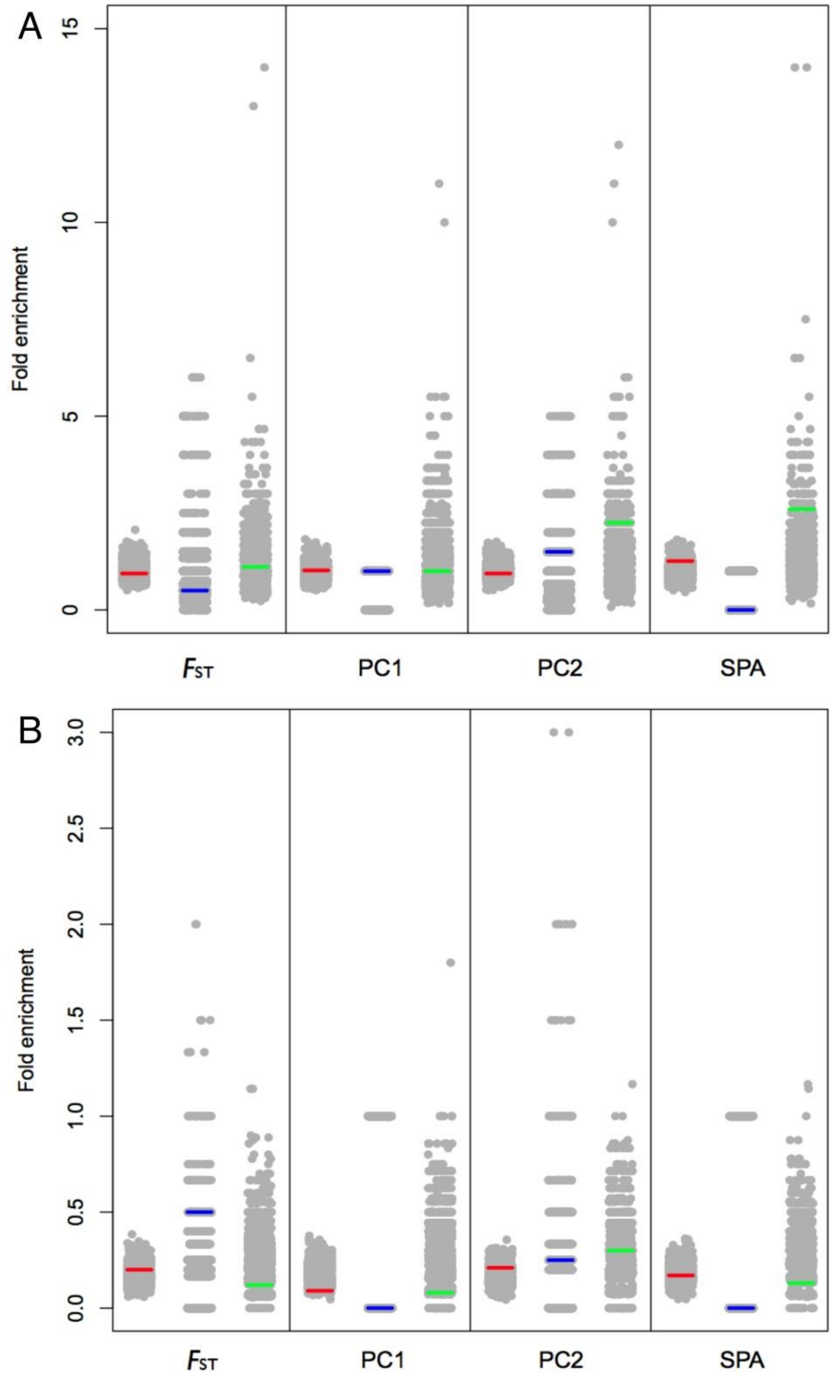

Figure S6 Enrichment analysis for (A) genic versus non-genic and (B) nonsynonymous versus synonymous SNPs. Enrichment analysis for candidates involved resampling the number of SNPs in each candidate list (outliers in F_{ST}, environmental association or SPA analyses) randomly from the genome 1000 times. Enrichment analysis was performed for all SNPs genome-wide, centromeric regions, and the two putative translocations or inversions. The observed values from the data is indicated by the colored horizontal line, red: genome-wide; blue: centromeric regions; green: the two putative structural rearrangements.