**File S1. Genomic regions with the highest enrichment in candidate SNPs of selection.**

The genomic regions with genome-wide significant (P<0.01) enrichment in candidate SNPs as estimated using the combined selection scores (CSS, Materials and Methods) confirm various adaptations to recent selective pressures including pathogens, nutrition, and climate (Table S3). For example, we retrieved the well-documented example of positive selection associated with lactase persistence in adulthood (*LCT*) in northern Europe (1st rank in the Northern European populations) and the genomic region of *EDAR* previously found to be under selection in East Asia. The *TLR5* region previously detected under positive selection in YRI (Grossman et al. 2013) has been found to be among the most enriched regions in all African populations except one. We retrieved other examples of well-described candidate regions of selection (Fan et al. 2016; Jeong and Di Rienzo 2014; Vitti et al. 2013), e.g., *APOL1* (resistance to human trypanosomes causing “African sleeping sickness”), *SLC45A2* (lighter pigmentation in Europe), *HERC2* with the rs12913832 associated light skin pigmentation in Europeans (Key et al. 2016), *SPAG4* corresponding to the strongest iHS signal previously found in Europeans (Voight et al. 2006), the *TLR1-6-10* cluster in Europe (Quach et al. 2016), *BBX* (Grossman et al. 2013), *HERC1* (Grossman et al. 2013) and the *ADH* cluster (alcohol dehydrogenase) in East Asians (Barreiro et al. 2008). To quantify the overlap between the genomic regions identified by our selection scan and those identified in other studies we compared with the results obtained by Grossman et al. (2013), a simulation-based selection scan using similar neutrality statistics and the same demography used to estimate *X*. Using the genomic regions identified in YRI, CEU and CHB (Table S3) we retrieved 33%, 36% and 45% of the regions identified by the Grossman’s analysis in the YRI, CEU and CHB+JPT populations, respectively. For comparison, we obtained the same proportion when using the genomic regions identified in the JPT population. Such moderate percentages of genomic regions shared between different studies are expected given the high number of false positives expected in classic selection scans. High false discovery rates are the underlying motivation for our study seeking to provide estimations of numbers of sweeps corrected for false positive signals of selection.

In contrast, some genomic regions previously detected on the basis of large differences in allele frequencies between populations were not identified in this study, such as the *DARC* region (reduced susceptibility to malaria in Africa) (Hamblin and Di Rienzo 2000), because we did not consider neutrality statistics potentially affected by background selection, such as the fixation index *F*st. In the same vein, we did not retrieve the novel selective sweeps identified by Schrider and Kern (2017) except the GRIA2 region in CEU (the GLRB gene close to GRIA2 is present in Table S3), as expected since the neutrality statistics used in our selection scan have low power to individually detect loci evolving under selection on standing variation. This has no incidence on the ABC estimations of *X* as shown by the ability of our method to properly infer the number of sweeps simulated in pseudo-empirical data. Our ABC method captures true adaptive signals that can be missed by selection scans because every selected region enriched in candidate SNPs positively contributes to the ORs and thus provides information for the ABC estimations. Conversely, in selection scans (including ours) only the selected regions with the highest enrichments are identified, the other true adaptive signals with a moderate enrichment below the detection threshold are missed (more explanations are given in the results section).

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