



Figure S24. Genome-wide variation associated with environmental variable (bio19). (a) KEGG enrichment analysis for genes containing selective candidate SNPs. Horizontal axis shows enrichment fold change. Bubble size indicates gene count per pathway; color gradient represents p -value significance (blue to red means less to more significant). (b) Manhattan plot shows the genotype-environment association estimated with LFMM. Vertical axis shows the p -value of the relationship between SNPs and bio19, ranging from $p = 1$ to $p = 10^{-60}$. The light blue and pink dots indicate threshold values of $p = 10^{-5}$ and $p = 10^{-10}$, respectively. The colored strips with a red-blue gradient represent the density of SNPs on the chromosome.