

**Figure S5. Genomewide genetic and gene expression differentiation.** Average  $F_{st}$  measures plotted against  $\log_2$  fold change (A) and negative  $\log_{10}$  probability resulting from differential expression analyses with SVA (B), for each of the 10,177 expressed genes and for each population pairwise comparison (Green, Nomadic vs. Rural; Blue, Nomadic vs. Urban; Red, Urban vs. Rural). Each open circle represents a gene. Gene-specific  $F_{st}$  values were calculated for each gene by averaging  $F_{st}$  values for all segregating SNPs located within 1-Mb upstream and downstream of the expression probe. The percent variance explained is less than 0.001 with  $p > 0.05$  for all six regressions represented by these plots.

