

Figure S7. Correlations among Interleukin signaling components. The three plots show the average relative transcript abundance (log base 2 scale) for the indicated genes in the Urban (U: Anza), Nomadic (N: Bedouin), and Rural (R: Sebt-Nabor) locations. *P* values in brackets indicate the significance of the 3-way location term from mixed model ANOVA. Across all 46 individuals, IL-8 is negatively correlated with IRAK2 ($P = 0.0008$), IRAK1 is negatively correlated with IRAKBP1 ($P = 0.008$), and IRAK3 is positively correlated with IRAK4 ($P = 0.004$).

