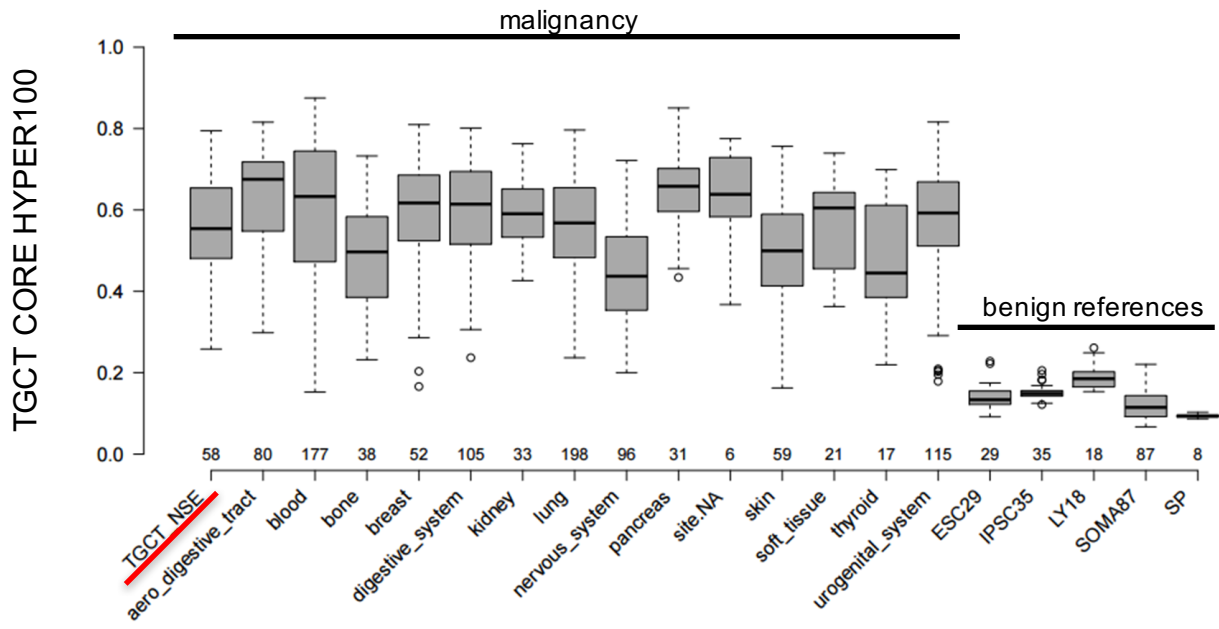
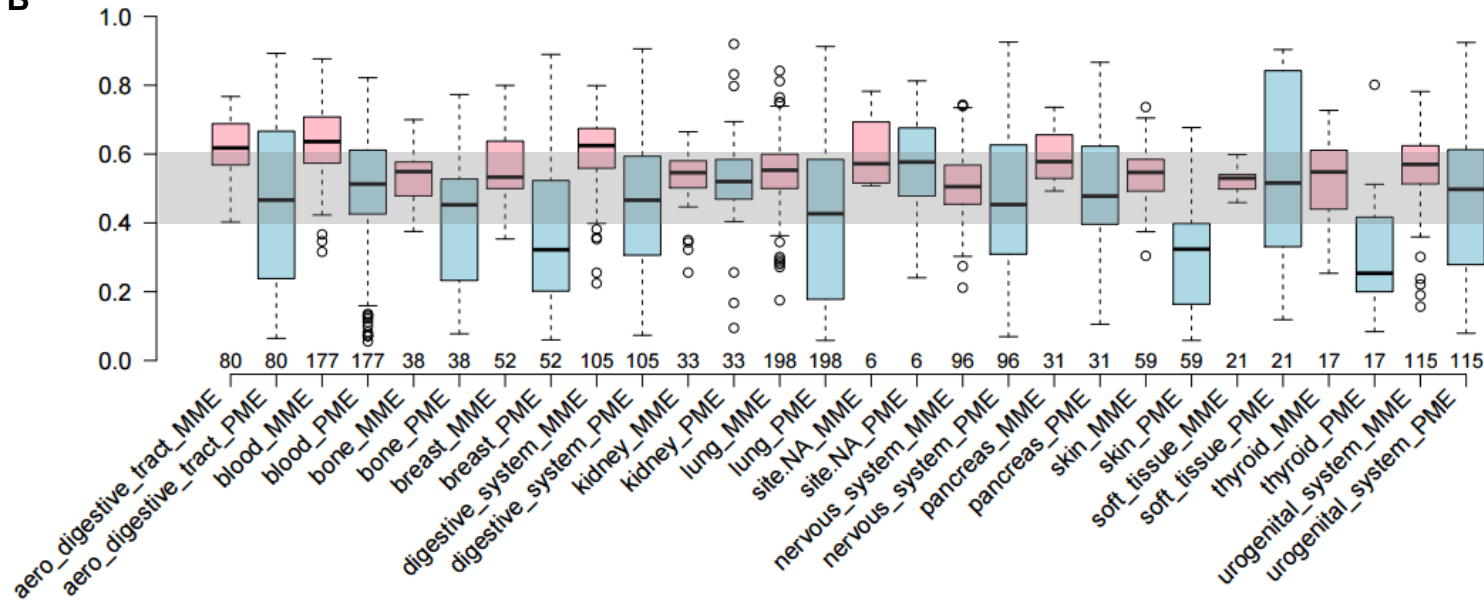


A**B**

Supplemental Fig. S4. **A.** Boxplot of the TGCT core hypermethylation module in a cancer compendium and multiple normal reference groups. X-axis labels: cancer anatomic site; Y-axis: average methylation beta of TGCT core hyper 100. Numbers above X-axis: number of data points in each boxplot. **B.** Boxplot of gMME and gPME methylation levels in same cancer compendium, annotated for sample number, anatomic site, and gMME vs. gPME on x-axis. Y-axis: average methylation level of the module. Y-axis: average beta of the respective module in the respective cancer anatomic site (x-axis category). Blue = gPME; pink = gMME.