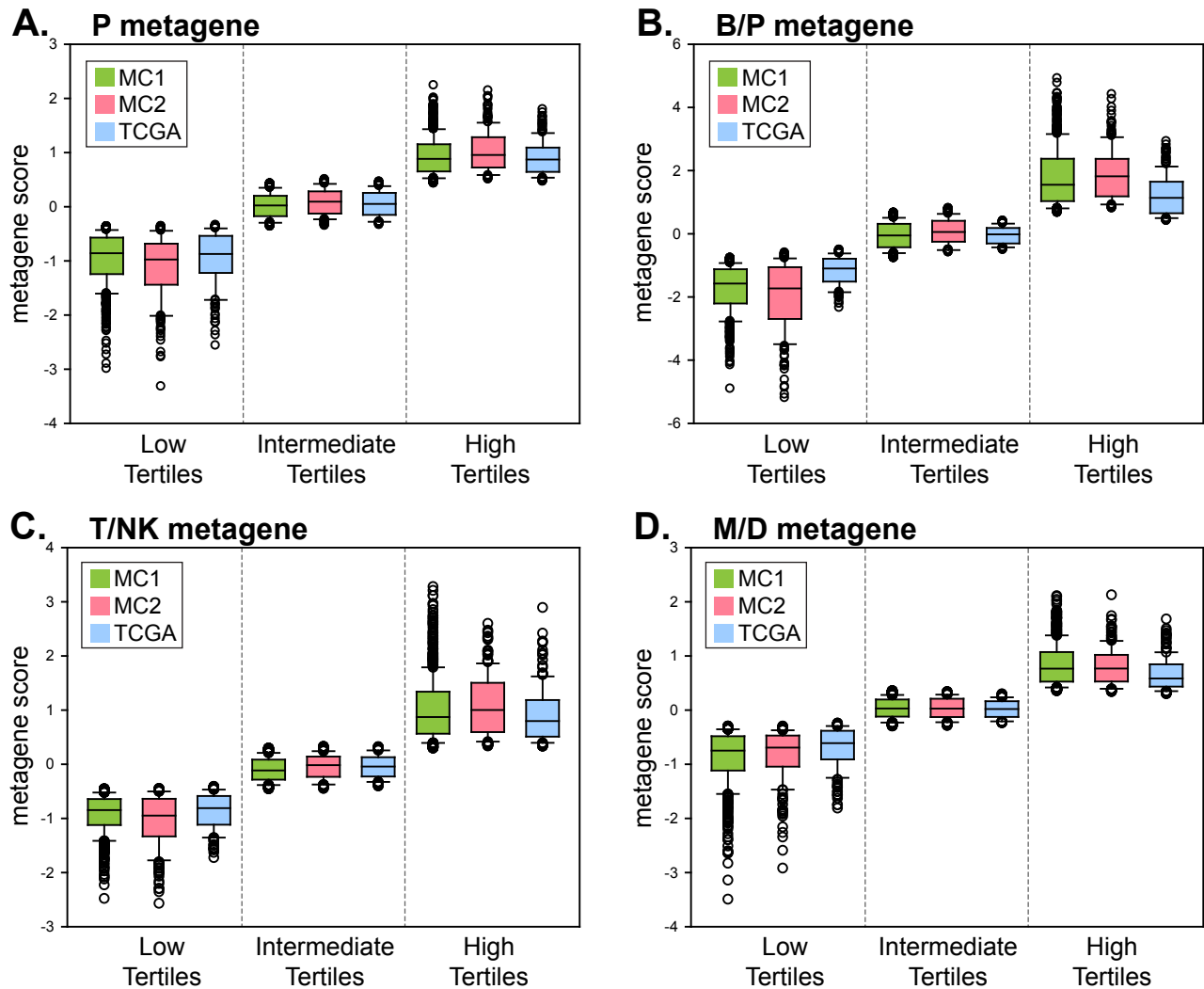


Supplementary Figure S2



Supplementary Figure S2. Cross-cohort comparisons of metagene distributions and tertile thresholds. Metagene scores were computed independently for each meta-cohort (MC1, MC2 and TCGA) from log₂ transformed signal intensities, then mean-centered for cross-cohort comparisons. Shown are box and whisker plots for intra-tertile distributions of metagene scores for the P metagene (A), the B/P metagene (B), the T/NK metagene (C) and the M/D metagene (D). Boxes delineate the interquartile range (25th to 75th percentile). The horizontal line within boxes marks the median. Whiskers (error bars) denote the 5th and 95th percentiles. Open circles represent outliers.