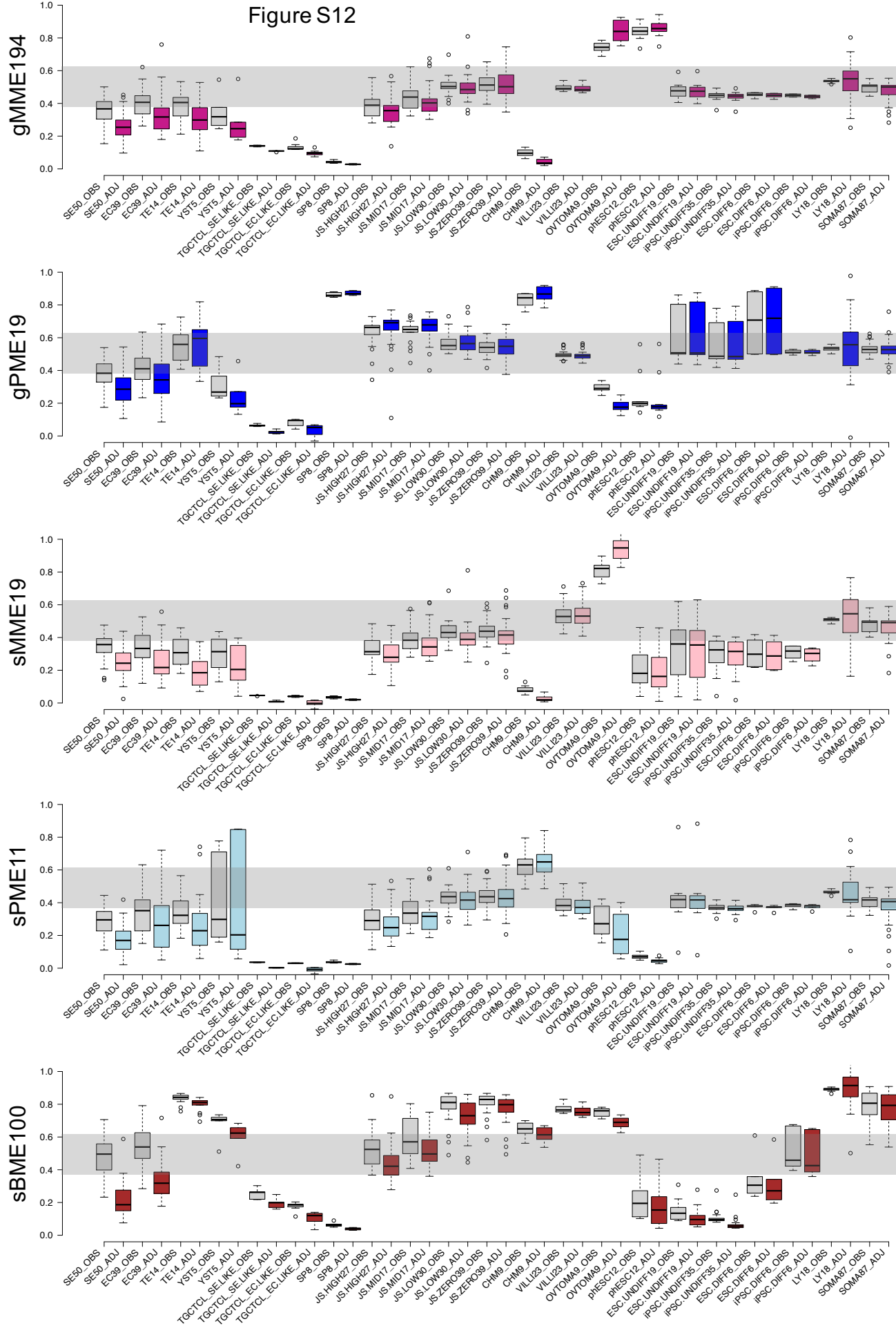Figure S12

Supplemental Fig. S12. Methylation modules comparison across 21 different sample groups, without (gray boxes) and with (colored boxes) lymphoid adjustment. Boxplots display the average module methylation level of each sample within the respective group. Abbreviations: Obs: observed average beta; Adj: adjusted average beta; SE: seminoma (n=50); EC: embryonal carcinoma (n=39); TE: teratoma (n=14); YST: yolk sac tumor (n=5); TGCTCL_SE-like: seminoma-like TGCT cell line (n=5); TGCTCL_EC-like: embryonal carcinoma-like TGCT cell line (n=7); SP: sperm (n=8); JS.HIGH: high Johnsen score (JS) benign adjacent testis (BNT) (n=27); JS.MID: mid JS BNT (n=17); JS.LOW: low JS BNT (n=30); JS.zero: zero JS BNT (n=39); CHM: complete hydatidiform mole (n=9); villi (n=23); OVTOMA: mature ovarian teratoma (n=9); phESC: parthenogenetic embryonic stem cell (ESC) (n=12); ESC.undiff: undifferentiated ESC (n=19); iPSC.undiff: undifferentiated induced pluripotent stem cell (iPSC) (n=35); ESC.diff: differentiated ESC (n=6); iPSC.diff: differentiated iPSC (n=6); LY: purified lymphoid cells (n=18); SOMA: somatic tissue and culture samples (n=87).