



Supplemental Figure 6

Supplemental Figure 6. Upregulation of cell proliferation and survival/apoptosis gene signatures in MPNST and Cluster 3 tumors. (A) Box and whisker plot of normalized cell proliferation signature scores in PNF (n=10), NF with atypia (n=6), ANNUBP (n=10) and MPNST (n=6). Dots represent individual samples. Whiskers extend from the minima to maxima that are no further than 1.5x the inter-quartile range spanning the first to third quartiles. The center line represents the median. The box spans the 25th to 75th percentiles. Data beyond the whiskers are outliers and are plotted as individual points. P-values represent unpaired, two-tailed t-tests between groups as shown. **(B)** Box and whisker plot of normalized DNA damage repair signatures scores in Cluster 1 (n=14), Cluster 2 (n=10), and Cluster 3 (n=11) tumors. P-values represent unpaired, two-tailed t-tests for pairwise comparisons between groups as shown. **(C)** Box and whisker plot of normalized apoptosis signature scores in PNF (n=10), NF with atypia (n=6), ANNUBP (n=10) and MPNST (n=6). P-values represent unpaired, two-tailed t-tests for pairwise comparisons between groups as shown. **(D)** Box and whisker plot of normalized apoptosis signature scores in Cluster 1 (n=14), Cluster 2 (n=10), and Cluster 3 (n=11) tumors. P-values represent unpaired, two-tailed t-tests for pairwise comparisons between groups as shown. **(E)** Lollipop plot demonstrating the log₂ fold changes in apoptosis signature genes in MPNST (n=6) vs PNF (n=10).