



**Supplemental Figure 4. Enhanced transcriptional signatures of angiogenesis and tumor vascularity in MPNST.** **(A)** Volcano plot illustrating the top differentially expressed genes in Cluster 3 (n=11) versus Cluster 1 (n=14) lesions. The x-axis represents the  $\log_2$  fold change in gene expression, whereas the y-axis represents the  $-\log_{10}$  Benjamini Hochberg adjusted p-value. An adjusted p-value of 0.05 was set as the false discovery threshold as denoted by the dotted line. Genes with  $\log_2$  fold changes  $\geq 1$  are colored red, whereas those with  $\log_2$  fold changes  $\leq -1$  are colored blue. **(B)** Volcano plot showing the top differentially expressed genes in MPNST (n=6) vs PNF (n=10). **(C)** Lollipop plot demonstrating the  $\log_2$  fold changes in angiogenesis signature genes comparing MPNST (n=6) versus PNF (n=10). **(D)** Representative photomicrographs of immunohistochemical staining of CD31+ vessels per high power field in PNF, ANNUBP, and MPNST. Magnification is denoted by 100  $\mu\text{m}$  scale bars with inset high-power magnification as shown. **(E)** Box plot of CD31+/vessels per high power field (HPF) in PNF (n=6), ANNUBP(n=5), and MPNST (n=6). Five independent HPFs were analyzed for each tumor slide. Whiskers extend from the minima to maxima. The center line represents the median. The box spans the 25<sup>th</sup> to 75<sup>th</sup> percentiles. Dots represent individual data points. P-values represent unpaired, two-tailed t-tests between groups. **(F)** UMAP visualization of integrated scRNAseq data from four patients with NF1-associated MPNST (n=21,969 cells) annotated by cell type. **(G)** UMAP plots of normalized gene expression values for angiogenesis markers including *MMP9*, *FGF18*, *VEGFA*, *SERPINH1*, *HEY1*, and *FGFR1*.