



Supplementary Fig. S6: Defining mesenchymal vs adrenergic lncRNAs in two NBL cohorts. (A) Heatmap of the expression of genes previously shown to be associated with either the MES or ADRN cell lineage in the TARGET NBL cohort. Samples were assigned into three groups using hierarchical clustering based on whether they had more expression of MES or ADRN genes. **(B)** *MYCN* expression in TARGET and GMKF samples predicted to have either ADRN or MES phenotype. *MYCN* expression is observed to be higher in ADRN samples.

(C) Expression of lncRNAs with significant correlation ($|r| > 0.6$) to the MES or ADRN score in the GMKF NBL cohort. lncRNAs were then correlated with protein coding genes on the same chromosome and subsequent gene set enrichment analysis was performed for MES and ADRN protein coding genes separately. Gene set enrichment results for each group are shown to the right of the heatmap. **(D)** Correlation of lncRNAs to the MES and ADRN score in the TARGET (x-axis) and GMKF (y-axis) NBL cohort respectively. Numbered points represent lncRNAs that had a significant correlation to the MES or ADRN score in both cohorts.