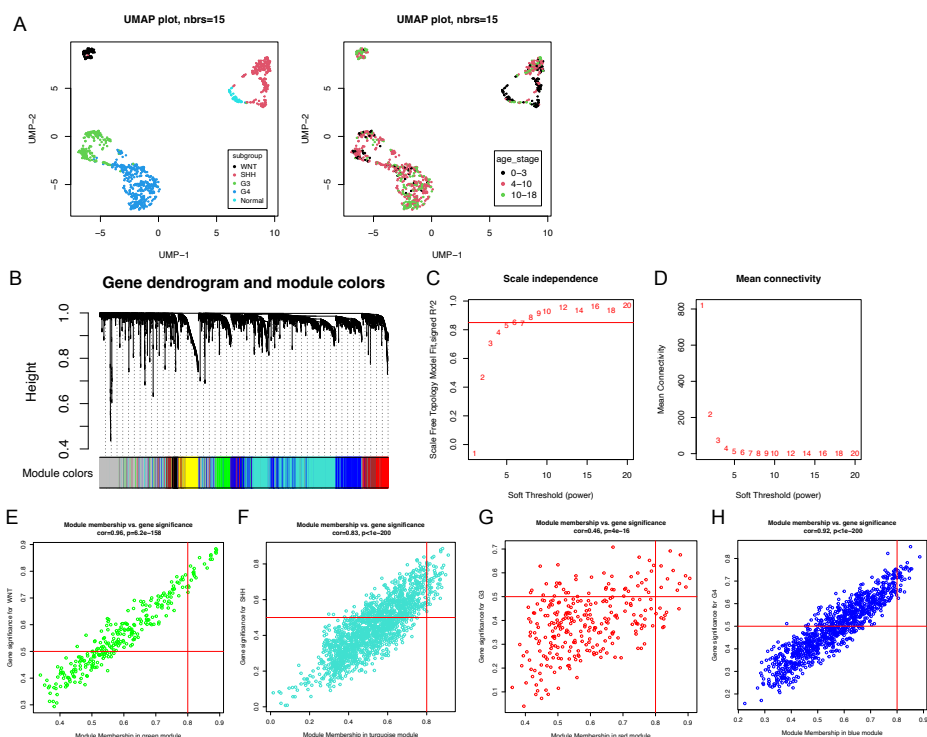
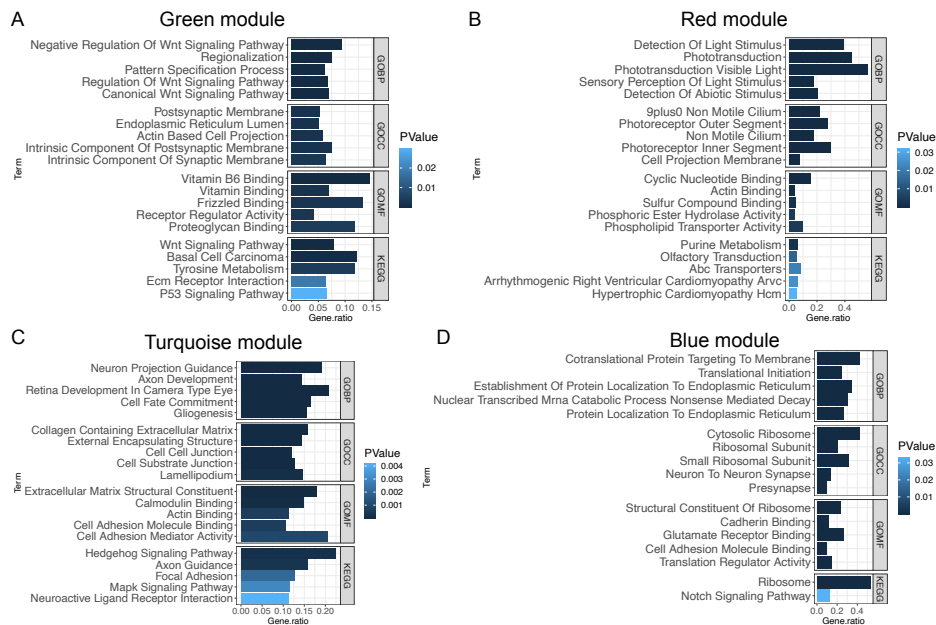
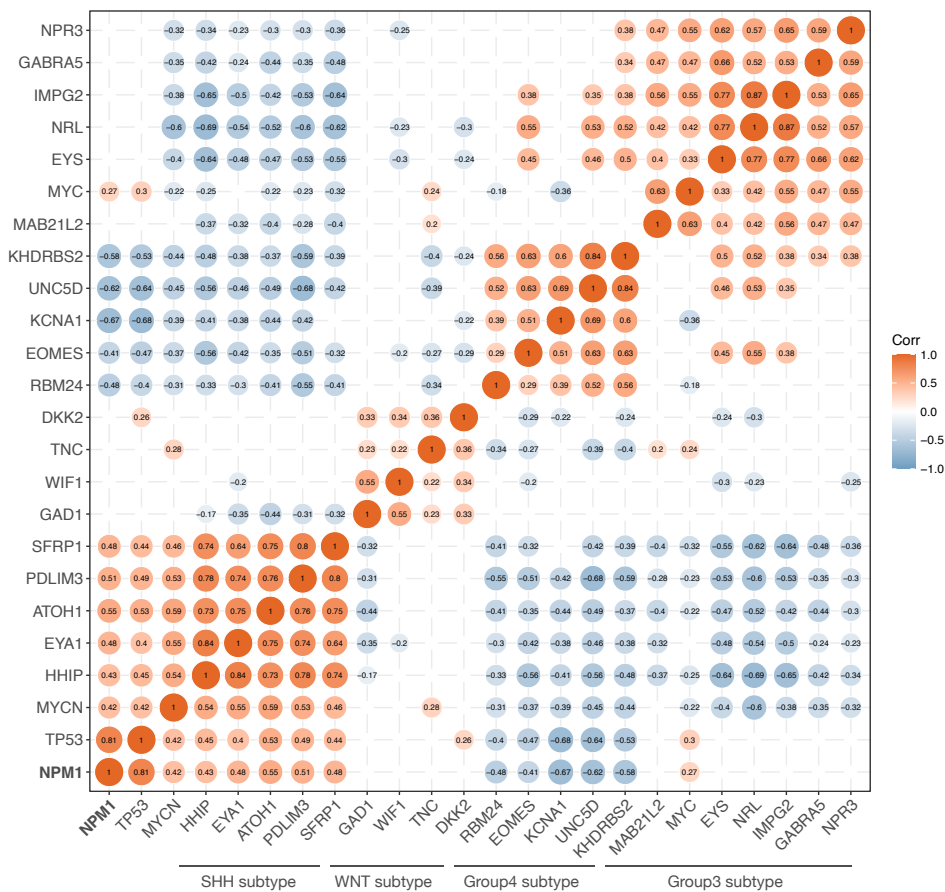




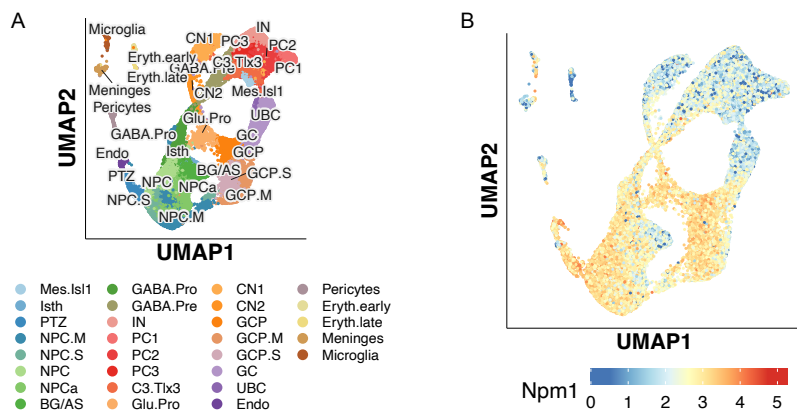
Supplementary Figure S1. Cluster visualization of pediatric patients and gene significance of subtype highly correlated modules in GSE124814 dataset. (A) Uniform manifold approximation and projection (UMAP) plots of GSE124814 bulk RNA-seq data annotated with molecular subtypes (left) and age subgroups (right). (B) Topological clustering dendrogram of gene mRNA expression levels. Eight co-expression modules were generated and labeled in different colors. (C) Topology model analysis of different weighting coefficients. The red line is corresponding for 0.85. (D) Average connectivity with various soft-thresholding powers. (E-H) Scatterplots of gene significance for different molecular subtypes in green(E), turquoise(F), red(G) and blue(H) modules.



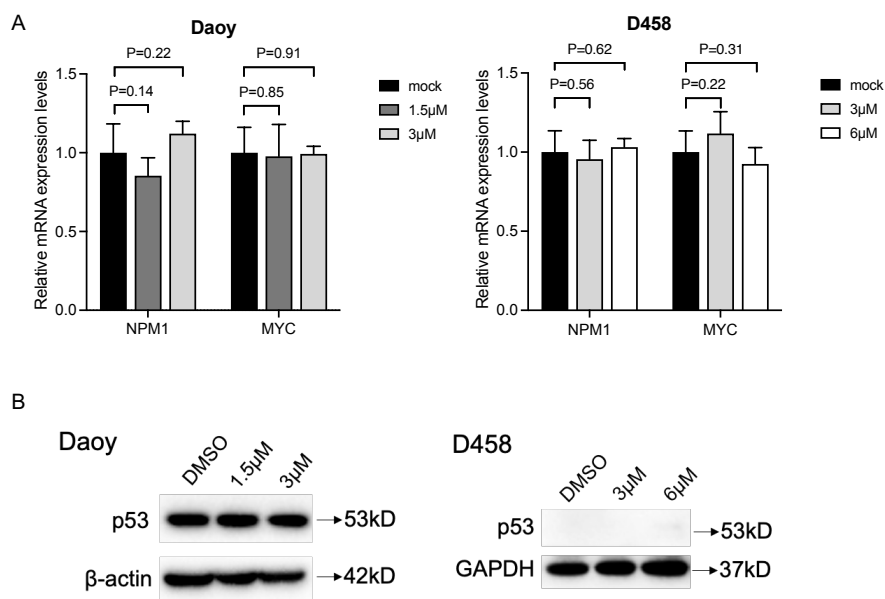
Supplementary Figure S2. GO and KEGG function enrichment of four molecular subtype highly correlated modules. Top five GO and KEGG pathways in Green (A), red (B), turquoise (C) and blue (D) modules were shown.



Supplementary Figure S3. Spearman correlation analysis of NPM1 and MB subtype marker genes in GSE164677 cohort. Correlations with P -value < 0.05 were shown on circles, blue and orange represented negative and positive correlations, respectively.



Supplementary Figure S5. Single cell RNA-seq analysis of *Npm1* in GSE187546. (A) UMAP visualization of mouse cerebellar single cell populations from E10.5 to E17.5. (B) Expression patterns of *Npm1* during mouse embryonic cerebellum development.



Supplementary Figure S6. (A) Real-time qPCR analysis of MYC and NPM1 in Daoy (left) and D458 (right) cells treated with NSC348884 for 9h; bar plots show mean $\pm$ SD, n=3; significance was calculated by unpaired two-tailed Student's t-test. (B) Representative immunoblotting images of p53 treated with NSC348884 for 9 hours; concentrations were referenced by the drug IC₅₀ values of Daoy (left) and D458 (right) cells.