

Figure S1. Differential gene expression analyses in neuroblastoma: (A) The dotplot illustrates the most statistically and biologically significant processes associated with the total spectrum of 286 uDEGs, as defined by GOs. The metabolism-related ontologies are highlighted within boxes. (B) The heatmap depicts the transcriptional profile of TF-encoding genes side by side in non-MYCIN-amplified and MYCIN-amplified neuroblastoma cell lines.

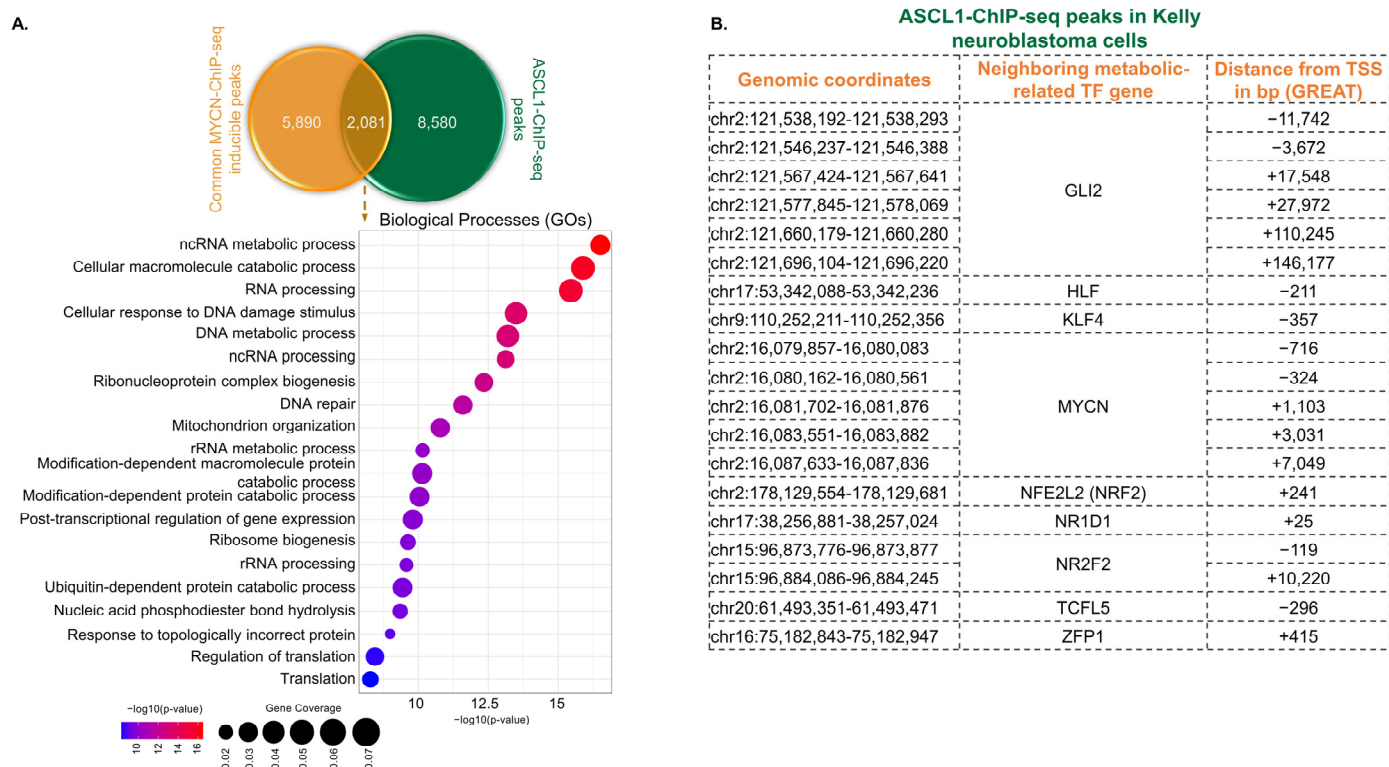


Figure S2. ASCL1-binding profile and correlation with neuroblastoma metabolism. (A) Intersection of ASCL1- and MYCN-ChIP-seq peaks and GOs on their common spectrum. Metabolism-related processes are highlighted. (B) The distribution of ASCL1 proximal to metabolism-related TFs in Kelly neuroblastoma cells. Several binding events are captured proximal to the TSSs of *GLI2*, *HLF*, *KLF4*, *NRF2*, *NR1D1*, *NR2F2*, *TCFL5*, *ZFP1*, and *MYCN*.

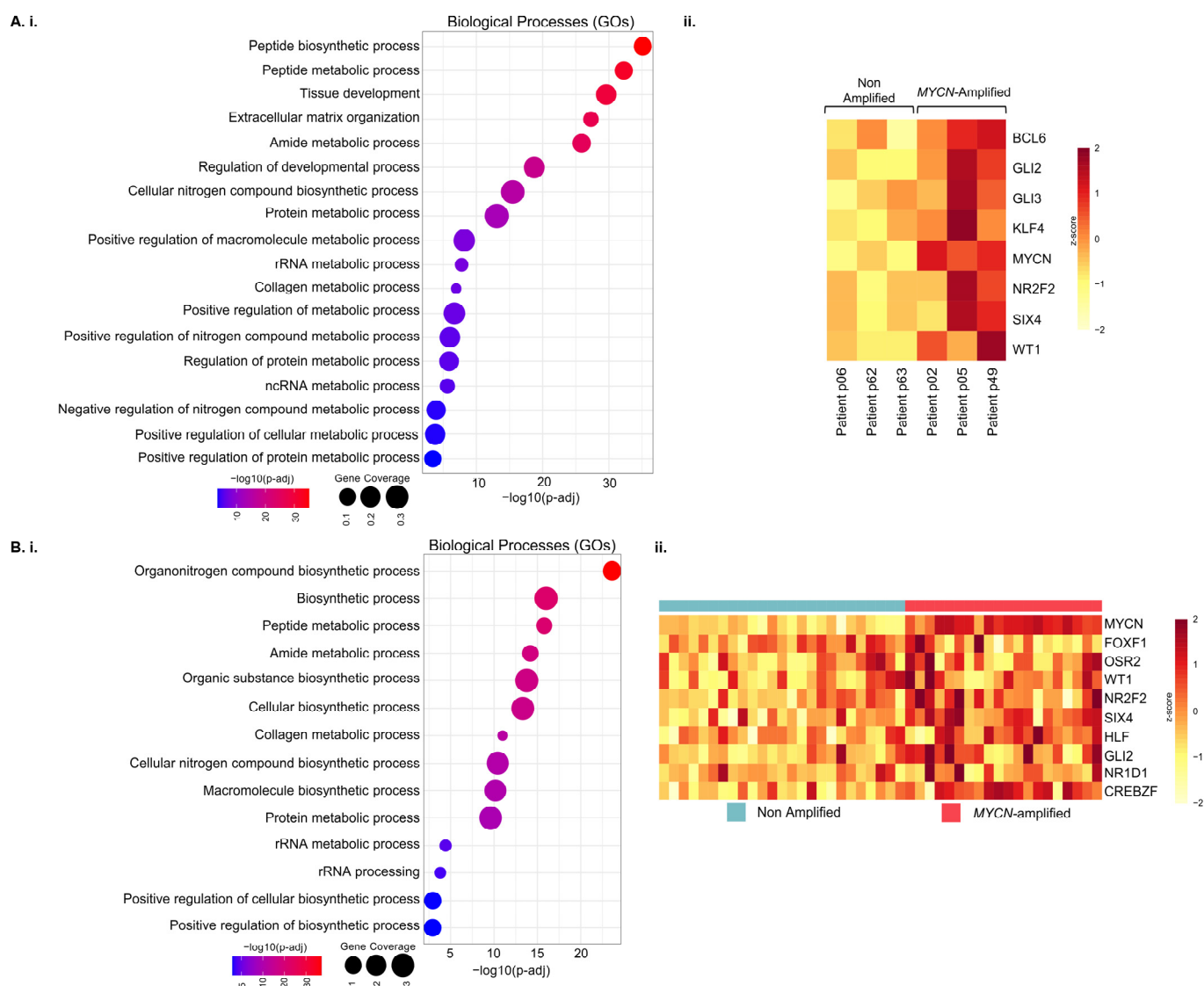


Figure S3. Transcriptional profiling of MYCN-amplified and non-amplified neuroblastoma patient-derived samples. (A) Gene expression investigation on MYCN-amplified and non-MYCN-amplified stage 4/M metastatic neuroblastoma specimens. (i) Selected examples of the most statistically and biologically significant biological processes, as determined by gene ontology analyses (GOs) applied to the 1396 uDEGs, are highlighted. Among these, several ontologies and functions connected to metabolism are depicted. (ii) RNA-seq heatmap illustrating the transcriptional upregulation of MYCN, BCL6, KLF4, SIX4, NR2F2, GLI2, GLI3, and WT1. The heatmap was generated using $\log_2(\text{CPM})$ normalized counts. (B) Gene expression investigation on MYCN-amplified and non-MYCN-amplified primary, undifferentiated or poorly differentiated, high-risk, stage 4, neuroblastoma specimens. (i) Selected examples of the most statistically and biologically significant biological processes, as determined by gene ontology analyses (GOs) applied to the 3424 uDEGs, are highlighted. Among these, several ontologies and functions connected to metabolism are depicted. (ii) RNA-seq heatmap illustrating the transcriptional upregulation of FOXF1, OSR2, WT1, MYCN, NR2F2, SIX4, GLI2, NR1D1, HLF, and CREBZF. The heatmap was generated using $\log_2(\text{CPM})$ normalized counts.