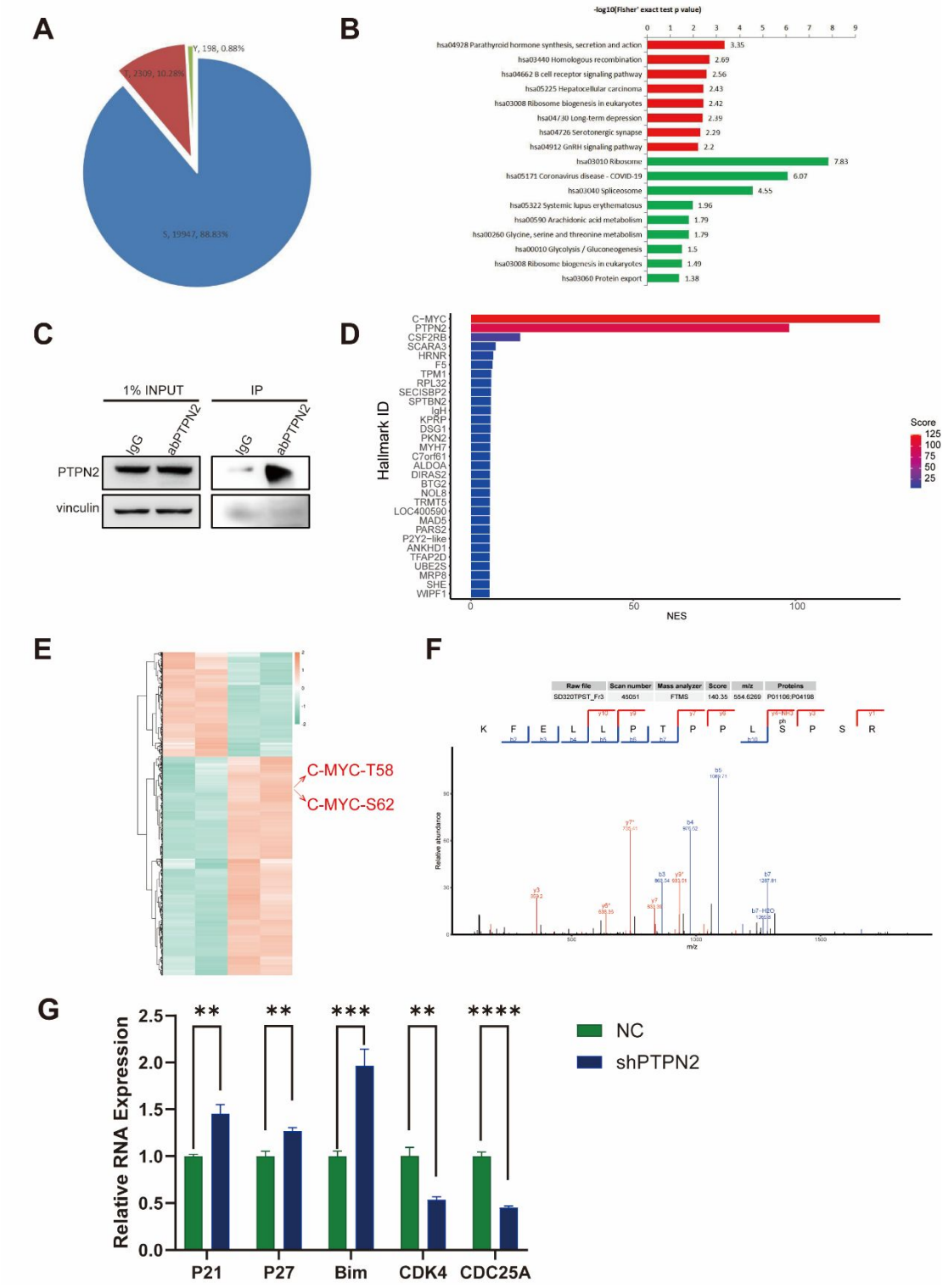


Supplementary Figure 2. IP and quantitative phosphoproteomic analysis of PTPN2 knock down MOLM13 cells. (A) Distribution of the assigned amino acid residues for all identified phosphorylation sites (B) Bar graphs show the significantly up-regulated and down-regulated phosphoproteins (C) Co-IP analysis of protein extracts from MOLM13 cells. IP was performed with a PTPN2 antibody, followed by WB analysis of PTPN2 pull down products using PTPN2 and vinculin antibodies (D) Matching score of proteins specifically bound to PTPN2 in immunoprecipitated by mass spectrometry (E) Heat map showing up-regulation of c-MYC (T58) and c-MYC (S62) phosphorylation (F) MS/MS spectra of the phosphosites of potential PTPN2 substrates, pS62 of c-MYC (G) Quantitative real-time PCR (qRT-PCR) analysis the expression of c-MYC downstream target genes. Statistical analysis was performed using two-tailed unpaired Student's t-test. **, $P < 0.01$, ***, $P < 0.001$, ****, $P < 0.0001$.