



Figure S6. (A) PANTHER and (B) WikiPathways cancer pathway enrichment analyses of 13 EZH2-associated immuno-inhibitor genes, 14 EZH2-associated immuno-stimulator genes, and the top 50 co-expressed genes using WebGestalt. (C) Network shows a comprehensive pathway and process enrichment analysis of the abovementioned 77 genes using Metascape.