



Supplemental Figure 3. Functional enrichment analysis for EBNA2-dependent differentially expressed genes. Gene set enrichment analyses of EBNA2-dependent differentially expressed genes for GO Biological Process. The X-axis indicates the normalized ratio of the number of input genes to the total number of annotated genes times 100. The Y-axis is sorted by significance (i.e., lower p-values are at the top of the plot). Analysis was performed using ToppFun from ToppGene Suite (<https://toppgene.cchmc.org/enrichment.jsp>). Bonferroni correction was used to adjust the *p*-values.