Figure S4: Transcriptome traits in distinct TME clusters of validation cohorts
(a-b) Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of differentially expressed genes (DEGs) presented a higher carcinogenic pathway in TMEclusterA (a) and higher immune cell activation in TMEclusterB (b) in GSE22153. **(c-d)** KEGG analysis of differentially expressed genes (DEGs) presented a higher carcinogenic pathway in TMEclusterA (c) and higher immune cell activation in TMEclusterB (d) in GSE54467. **(e-f)** KEGG analysis of differentially expressed genes (DEGs) presented a higher carcinogenic pathway in TMEclusterA (e) and higher immune cell activation in TMEclusterB (f) in GSE65904.