Supplementary Figure 1. Panther pathway-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Panther Pathway-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B14) GSEA enrichment analysis plots of 14 tumor immune-related Panther Pathway gene sets (FDR < 0.05).
Supplementary Figure 2. Reactome pathway-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Reactome Pathway-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis Plots of 18 tumor immune-related Reactome Pathway gene sets (FDR < 0.05).
Supplementary Figure 3. Wikipathway-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Wikipathway-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis Plots of 18 tumor immune-related Wikipathway gene sets (FDR < 0.05).
Supplementary Figure 4. Gene ontology biological process-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Gene Ontology Biological Process-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis plots of 18 tumors immune-related Gene Ontology Biological Process gene sets (FDR < 0.05).
Supplementary Figure 5. Gene ontology cellular component-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Gene Ontology Cellular Component-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis plots of 18 tumors immune-related Gene Ontology Cellular Component gene sets (FDR < 0.05).
Supplementary Figure 6. Gene ontology molecular function-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Gene Ontology Molecular Function-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis plots of 18 tumors immune-related Gene Ontology Molecular Function gene sets (FDR < 0.05).
Supplementary Figure 7. Kinase target network-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Kinase Target Network-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B10) GSEA enrichment analysis plots of 10 tumor immune-related Kinase Target Network gene sets (FDR < 0.05).
Supplementary Figure 8. Transcription factor network-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of Transcription Factor Network-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B17) GSEA enrichment analysis plots of 17 tumor immune-related Transcription Factor Network gene sets (FDR < 0.05).
Supplementary Figure 9. PPI BIOGRID network-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A) Bar chart of PPI BIOGRID Network-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis plots of 18 tumor immune-related PPI BIOGRID Network gene sets (FDR < 0.05).
Supplementary Figure 10. The correlation between the expression of ARHGAP30 and MHC molecules. (A) Heat map of Spearman correlations between ARHGAP30 expression and MHC molecules across human cancers. (B1–B39) Scatter plots showing the positive correlation between ARHGAP30 expression and MHC molecules in the treatment of lung adenocarcinoma.
Supplementary Figure 11. The correlation between the DNA methylation of ARHGAP30 and MHC molecules. (A) Heat map of Spearman correlations between DNA methylation of ARHGAP30 and MHC molecules across human cancers. (B1–B21) Scatter plots showing the negative correlation between DNA methylation of ARHGAP30 and MHC molecules in the treatment of lung adenocarcinoma.
Supplementary Figure 12. The correlation between the expression of ARHGAP30 and chemokines. (A) Heat map of Spearman correlations between ARHGAP30 expression and chemokines across human cancers. (B1–B30) Scatter plots showing the positive correlation between ARHGAP30 expression and chemokines in the treatment of lung adenocarcinoma.
Supplementary Figure 13. The correlation between the expression of \textit{ARHGAP30} and Chemokine Receptors. (A) Heat map of Spearman correlations between \textit{ARHGAP30} expression and chemokine receptors across human cancers. (B1–B15) Scatter plots showing the positive correlation between \textit{ARHGAP30} expression and chemokine receptors in the treatment of lung adenocarcinoma.