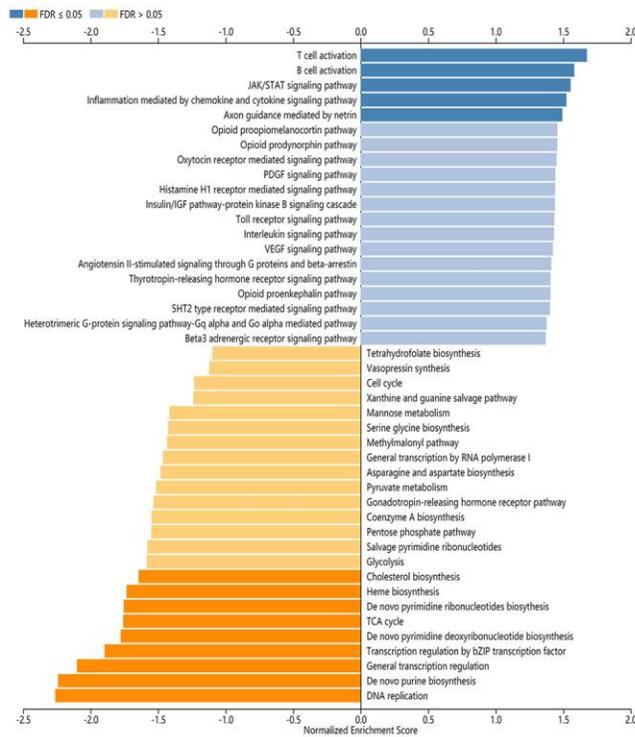
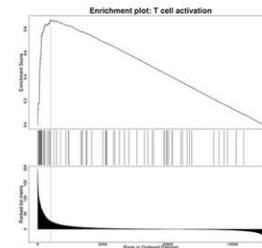


SUPPLEMENTARY FIGURES

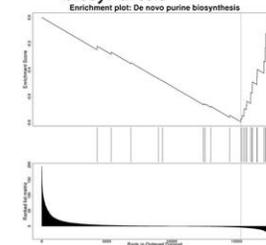
**A** The bar chart of panther pathway based GSEA of ARHGAP30 in lung adenocarcinoma



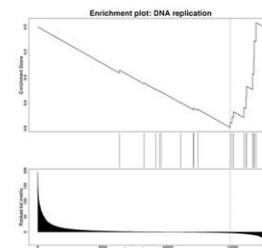
**B1** P00053: T cell activation



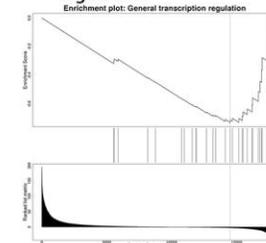
**B2** P02738: De novo purine biosynthesis



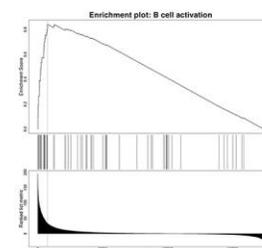
**B3** P00017: DNA replication



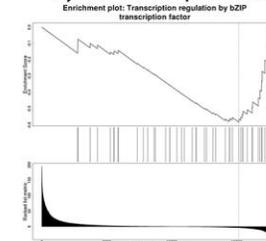
**B4** P00023: General transcription regulation



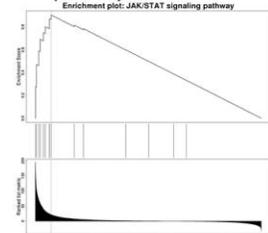
**B5** P00010: B cell activation



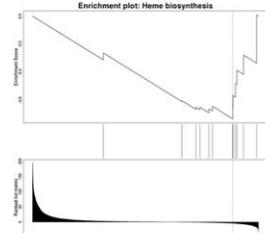
**B6** P00055: Transcription regulation by bZIP transcription factor



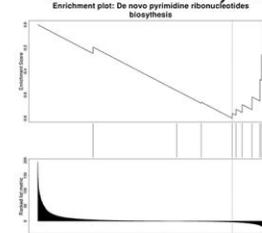
**B7** P00038: JAK/STAT signaling pathway



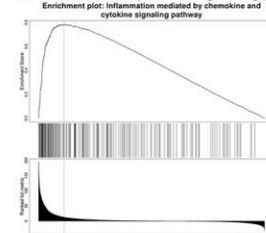
**B8** P02746: Heme biosynthesis



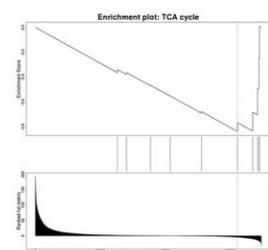
**B9** P02740: De novo pyrimidine ribonucleotides biosynthesis



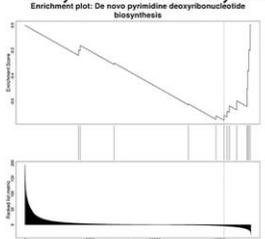
**B10** P00031: Inflammation mediated by chemokine and cytokine signaling pathway



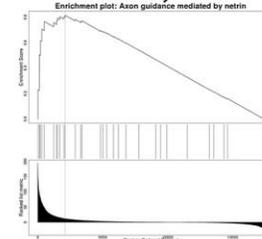
**B11** P00051: TCA cycle



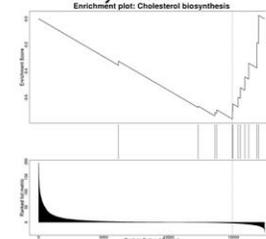
**B12** P02739: De novo pyrimidine deoxyribonucleotide biosynthesis



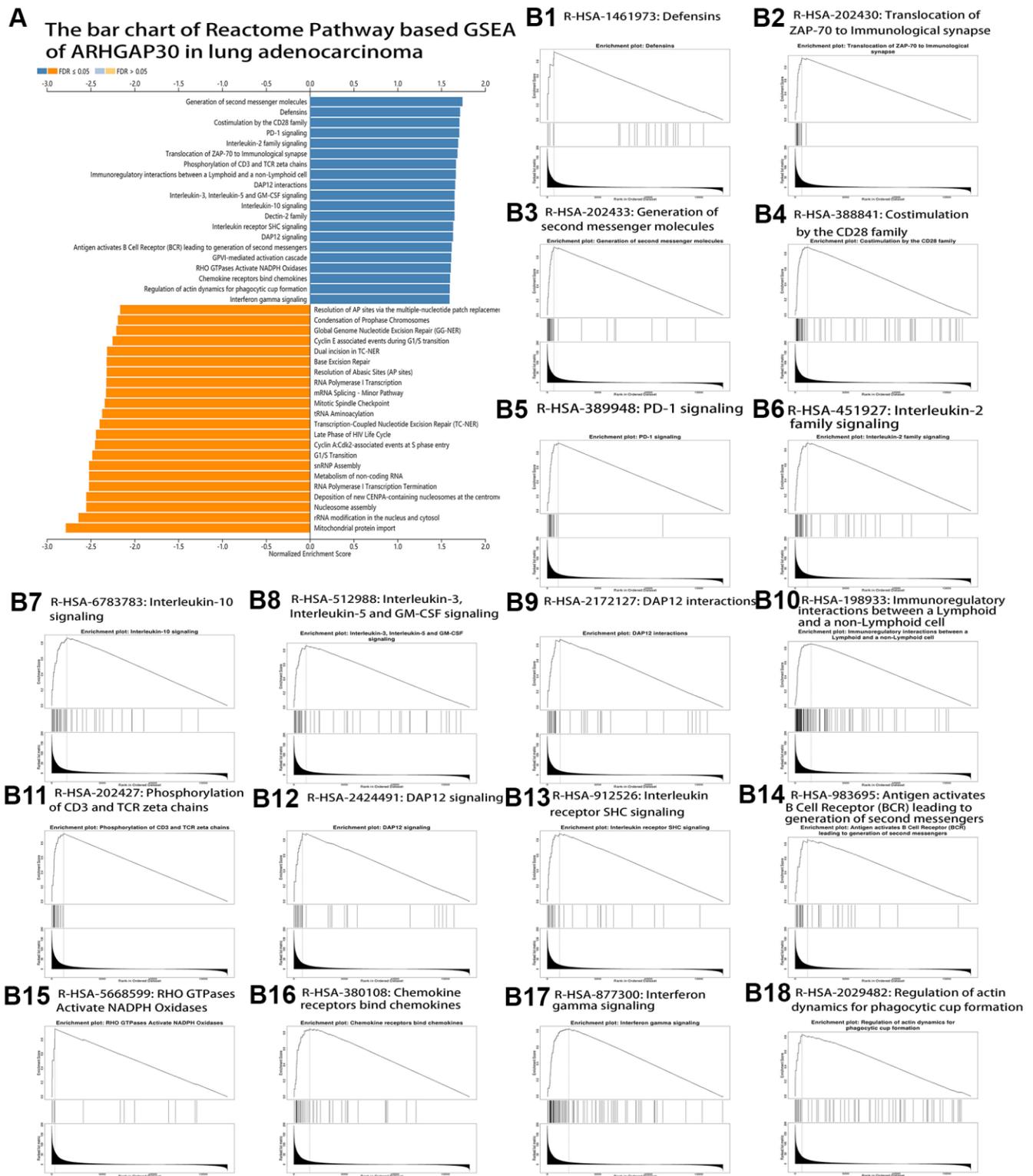
**B13** P00009: Axon guidance mediated by netrin



**B14** P00014: Cholesterol biosynthesis

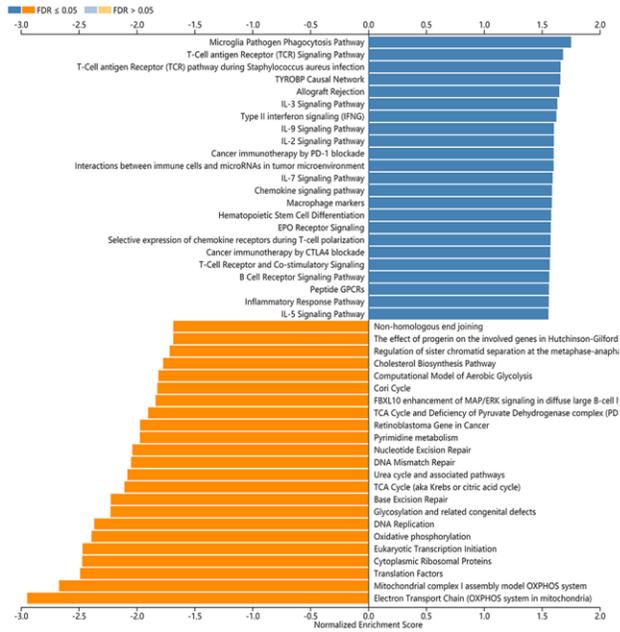


**Supplementary Figure 1. Panther pathway-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD).** (A) Bar chart of Panther Pathway-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B14) GSEA enrichment analysis Plots of 14 tumor immune-related Panther Pathway gene sets (FDR < 0.05).

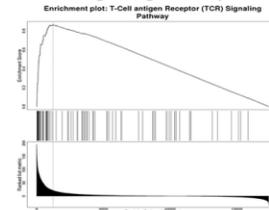


**Supplementary Figure 2. Reactome pathway-based GSEA of *ARHGAP30* in lung adenocarcinoma (LUAD).** (A) Bar chart of Reactome Pathway-based GSEA of *ARHGAP30* in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis Plots of 18 tumor immune-related Reactome Pathway gene sets (FDR < 0.05).

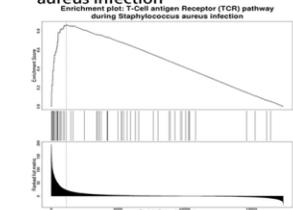
**A** The bar chart of Wikipathway based GSEA of *ARHGAP30* in lung adenocarcinoma



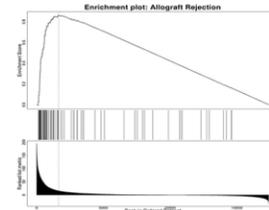
**B1** WP69: T-Cell antigen Receptor (TCR) Signaling Pathway



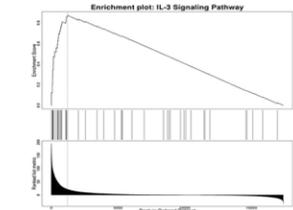
**B2** WP3863: T-Cell antigen Receptor (TCR) pathway during *Staphylococcus aureus* infection



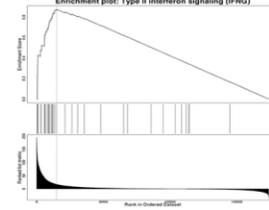
**B3** WP2328: Allograft Rejection



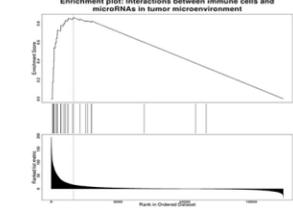
**B4** WP286: IL-3 Signaling Pathway



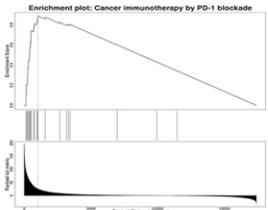
**B5** WP619: Type II Interferon signaling (IFNG)



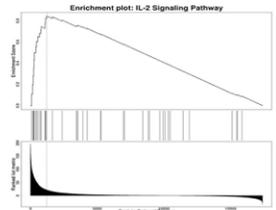
**B6** WP4559: Interactions between immune cells and microRNAs in tumor microenvironment



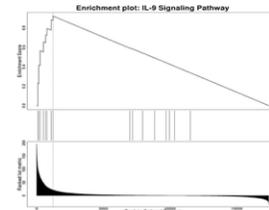
**B7** WP4585: Cancer immunotherapy by PD-1 blockade



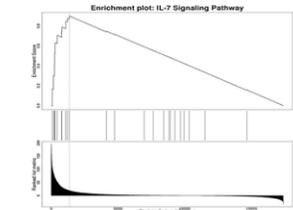
**B8** WP49: IL-2 Signaling Pathway



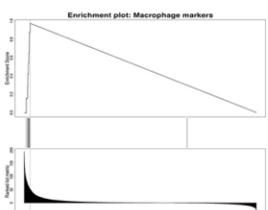
**B9** WP22: IL-9 Signaling Pathway



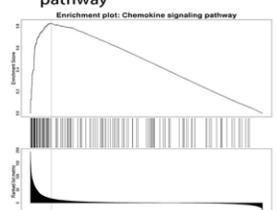
**B10** WP205: IL-7 Signaling Pathway



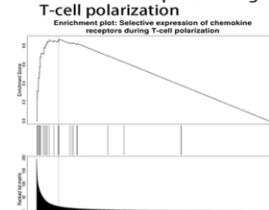
**B11** WP4146: Macrophage markers



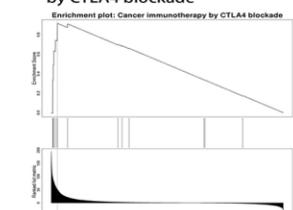
**B12** WP3929: Chemokine signaling pathway



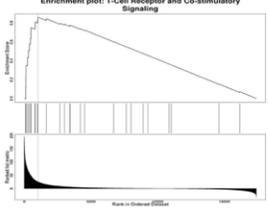
**B13** WP4494: Selective expression of chemokine receptors during T-cell polarization



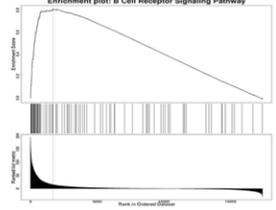
**B14** WP4582: Cancer immunotherapy by CTLA4 blockade



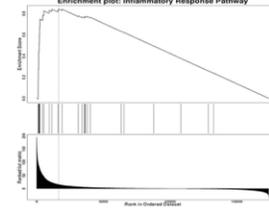
**B15** WP2583: T-Cell Receptor and Co-stimulatory Signaling



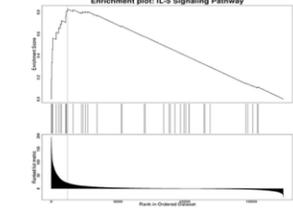
**B16** WP23: B Cell Receptor Signaling Pathway



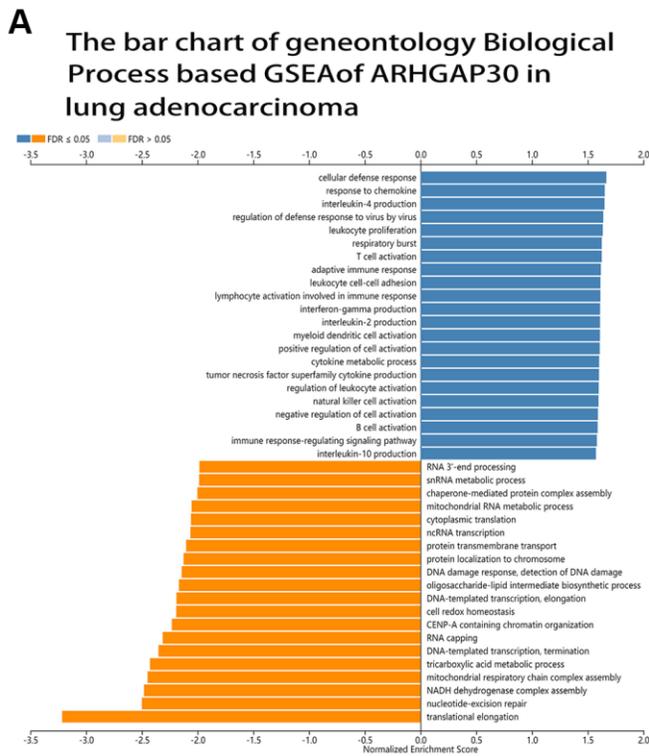
**B17** WP453: Inflammatory Response Pathway



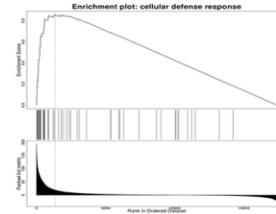
**B18** WP127: IL-5 Signaling Pathway



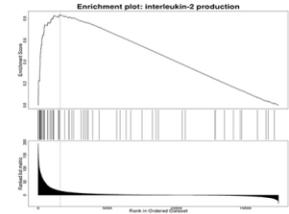
**Supplementary Figure 3. Wikipathway-based GSEA of *ARHGAP30* in lung adenocarcinoma (LUAD). (A)** Bar chart of Wikipathway-based GSEA of *ARHGAP30* in LUAD (FDR < 0.05). **(B1–B18)** GSEA enrichment analysis Plots of 18 tumor immune-related Wikipathway gene sets (FDR < 0.05).



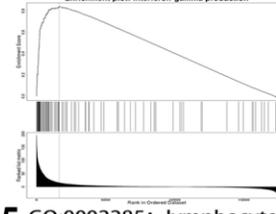
**B1** GO:0006968: cellular defense response



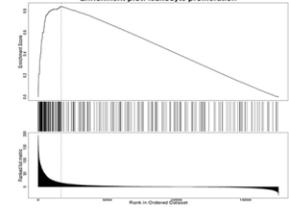
**B2** GO:0032623: interleukin-2 production



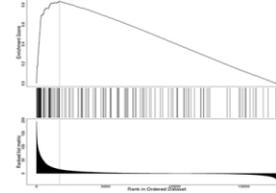
**B3** GO:0032609: interferon-gamma production



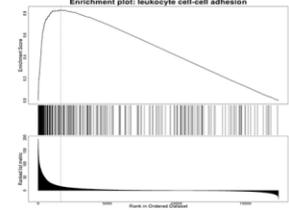
**B4** GO:0070661: leukocyte proliferation



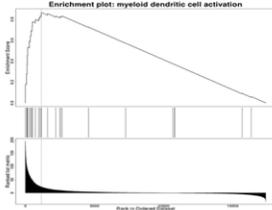
**B5** GO:0002285: lymphocyte activation involved in immune response



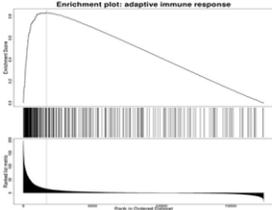
**B6** GO:0007159: leukocyte cell-cell adhesion



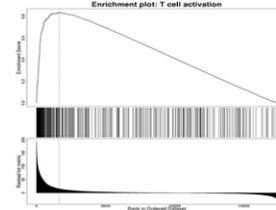
**B7** GO:0001773: myeloid dendritic cell activation



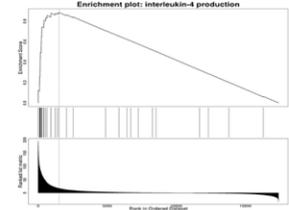
**B8** GO:0002250: adaptive immune response



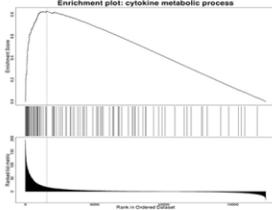
**B9** GO:0042110: T cell activation



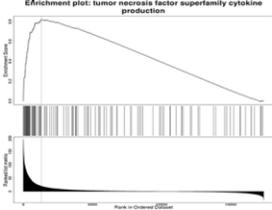
**B10** GO:0032633: interleukin-4 production



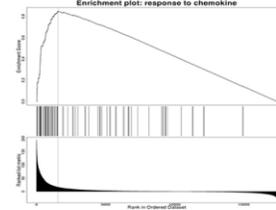
**B11** GO:0042107: cytokine metabolic process



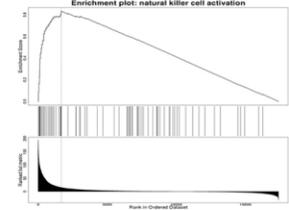
**B12** GO:0071706: tumor necrosis factor superfamily cytokine production



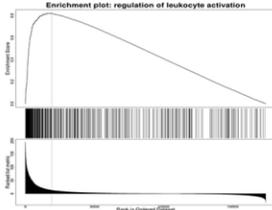
**B13** GO:1990868: response to chemokine



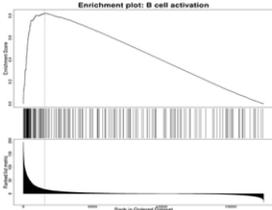
**B14** GO:0030101: natural killer cell activation



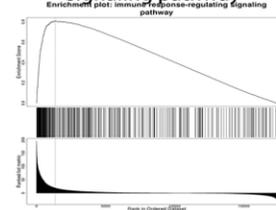
**B15** GO:0002694: regulation of leukocyte activation



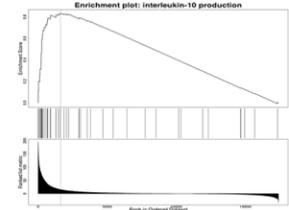
**B16** GO:0042113: B cell activation



**B17** GO:0002764: immune response-regulating signaling pathway

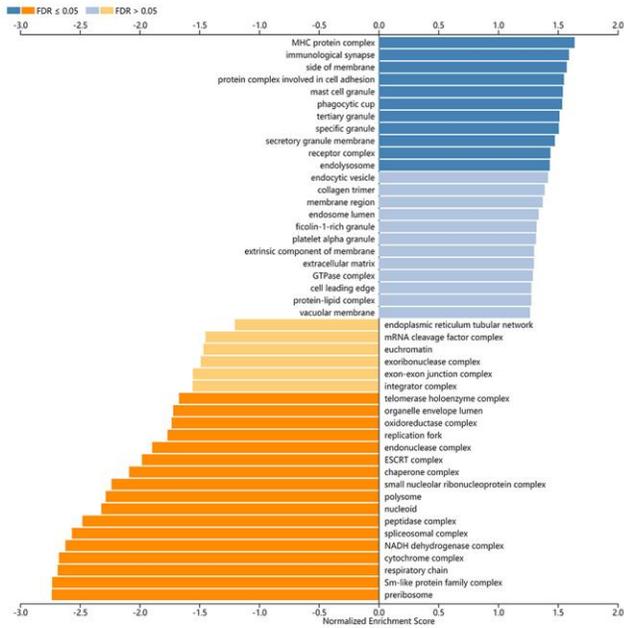


**B18** GO:0032613: interleukin-10 production

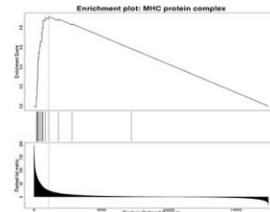


**Supplementary Figure 4. Gene ontology biological process-based GSEA of *ARHGAP30* in lung adenocarcinoma (LUAD).** (A) Bar chart of Gene Ontology Biological Process-based GSEA of *ARHGAP30* in LUAD (FDR  $<$  0.05). (B1–B18) GSEA enrichment analysis plots of 18 tumors immune-related Gene Ontology Biological Process gene sets (FDR  $<$  0.05).

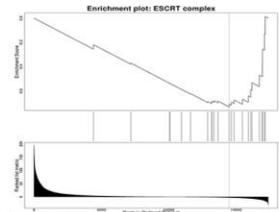
**A** The bar chart of geneontology Cellular Component based GSEA of ARHGAP30 in lung adenocarcinoma



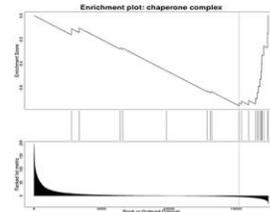
**B1** GO:0042611: MHC protein complex



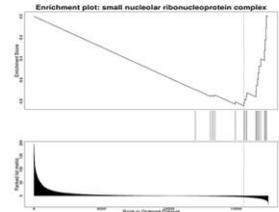
**B2** GO:0036452: ESCRT complex



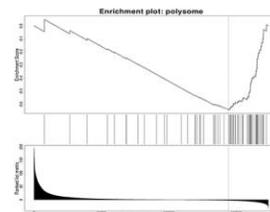
**B3** GO:0101031: chaperone complex



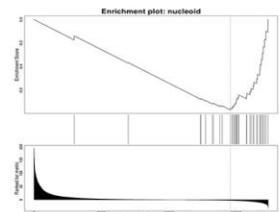
**B4** GO:0005732: small nucleolar ribonucleoprotein complex



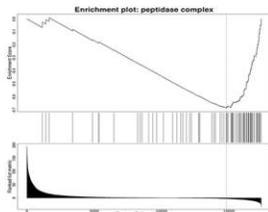
**B5** GO:0005844: polysome



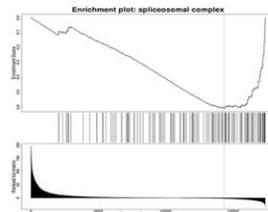
**B6** GO:0009295: nucleoid



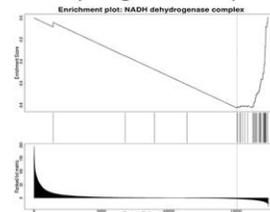
**B7** GO:1905368: peptidase complex



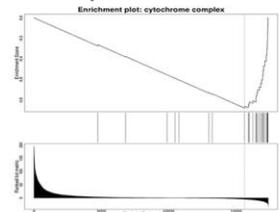
**B8** GO:0005681: spliceosomal complex



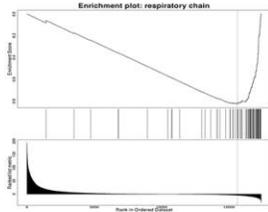
**B9** GO:0030964: NADH dehydrogenase complex



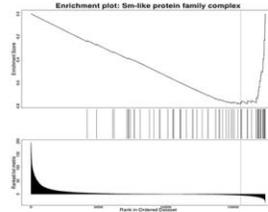
**B10** GO:0070069: cytochrome complex



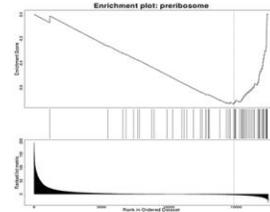
**B11** GO:0070469: respiratory chain



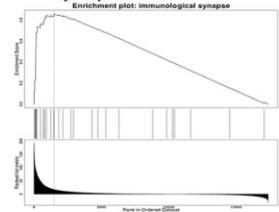
**B12** GO:0120114: Sm-like protein family complex



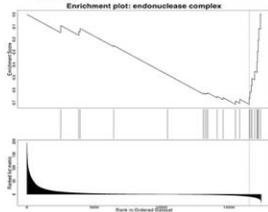
**B13** GO:0030684: preribosome



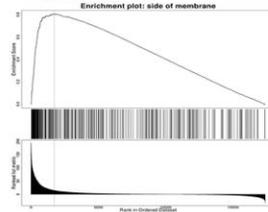
**B14** GO:0001772: immunological synapse



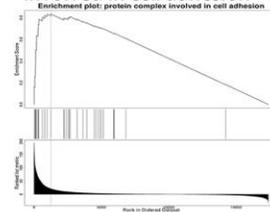
**B15** GO:1905348: endonuclease complex



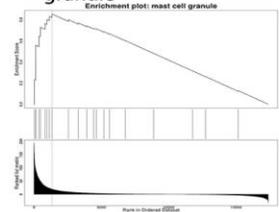
**B16** GO:0098552: side of membrane



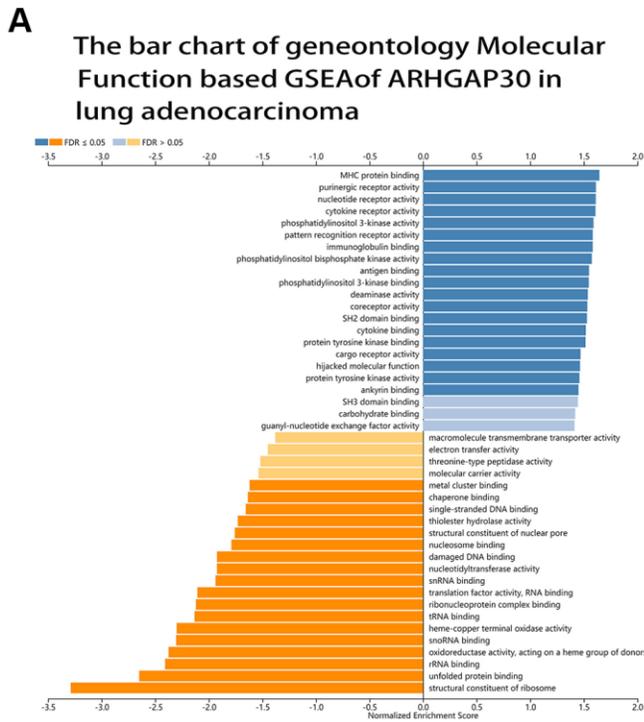
**B17** GO:0098636: protein complex involved in cell adhesion



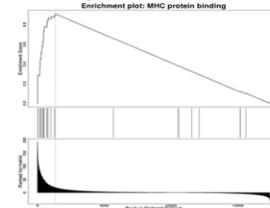
**B18** GO:0042629: mast cell granule



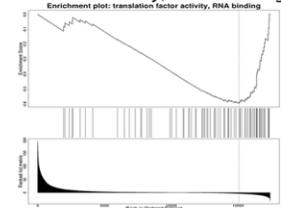
**Supplementary Figure 5. Gene ontology cellular component-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A)** Bar chart of Gene Ontology Cellular Component-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). **(B1–B18)** GSEA enrichment analysis plots of 18 tumors immune-related Gene Ontology Cellular Component gene sets (FDR < 0.05).



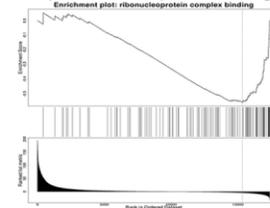
**B1** GO:0042287: MHC protein binding



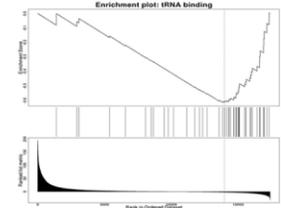
**B2** GO:0008135: translation factor activity, RNA binding



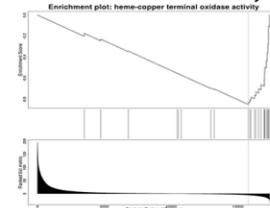
**B3** GO:0043021: ribonucleoprotein complex binding



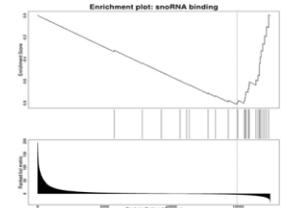
**B4** GO:0000049: tRNA binding



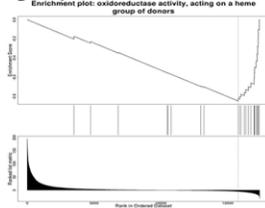
**B5** GO:0015002: heme-copper terminal oxidase activity



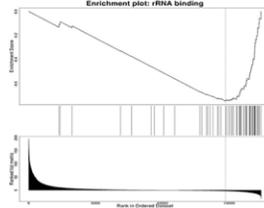
**B6** GO:0030515: snoRNA binding



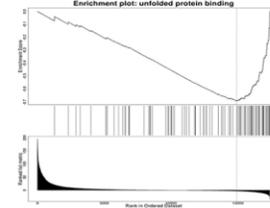
**B7** GO:0016675: oxidoreductase activity, acting on a heme group of donors



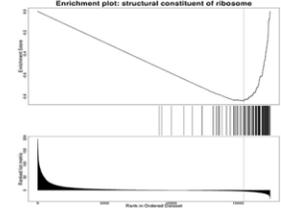
**B8** GO:0019843: rRNA binding



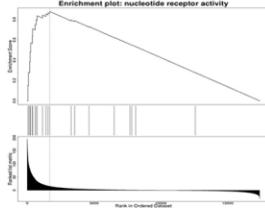
**B9** GO:0051082: unfolded protein binding



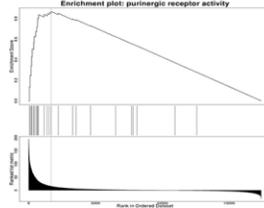
**B10** GO:0003735: structural constituent of ribosome



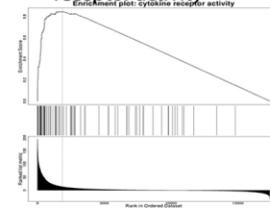
**B11** GO:0016502: nucleotide receptor activity



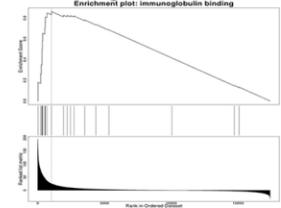
**B12** GO:0035586: purinergic receptor activity



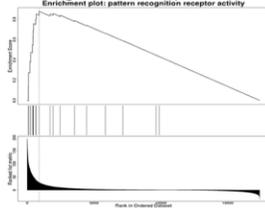
**B13** GO:0004896: cytokine receptor activity



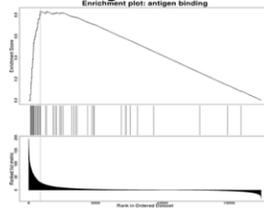
**B14** GO:0019865: immunoglobulin binding



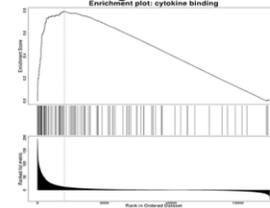
**B15** GO:0038187: pattern recognition receptor activity



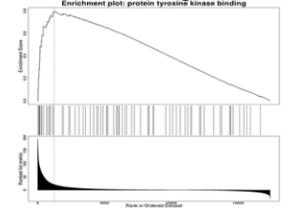
**B16** GO:0003823: antigen binding



**B17** GO:0019955: cytokine binding

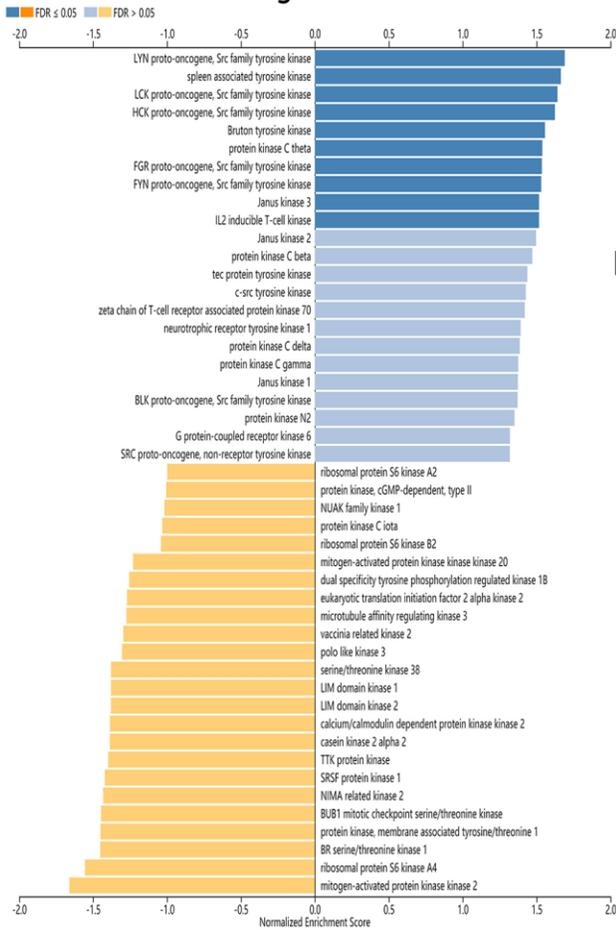


**B18** GO:1990782: protein tyrosine kinase binding

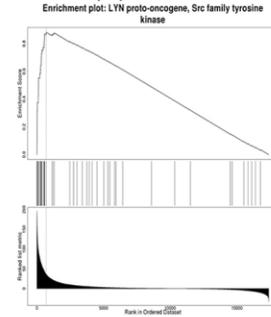


**Supplementary Figure 6. Gene ontology molecular function-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD). (A)** Bar chart of Gene Ontology Molecular Function-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). **(B1–B18)** GSEA enrichment analysis plots of 18 tumors immune-related Gene Ontology Molecular Function gene sets (FDR < 0.05).

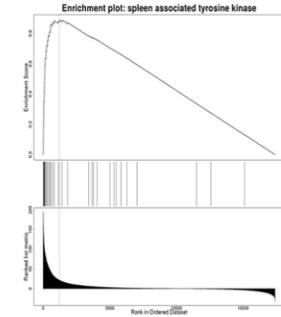
**A** The bar chart of geneontology Kinase target network based GSEA of ARHGAP30 in lung adenocarcinoma



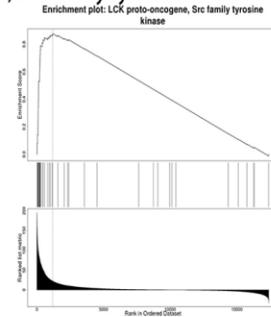
**B1** Kinase\_LYN: LYN proto-oncogene, Src family tyrosine kinase



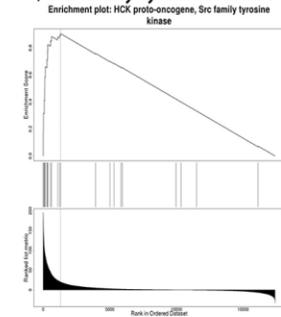
**B2** Kinase\_SYK: spleen associated tyrosine kinase



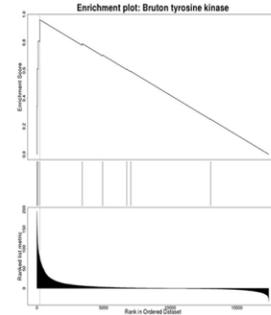
**B3** Kinase\_LCK: LCK proto-oncogene, Src family tyrosine kinase



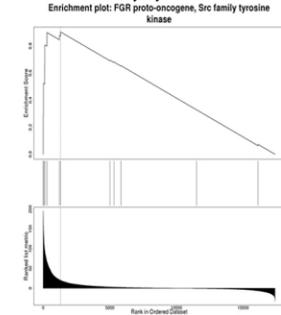
**B4** Kinase\_HCK: HCK proto-oncogene, Src family tyrosine kinase



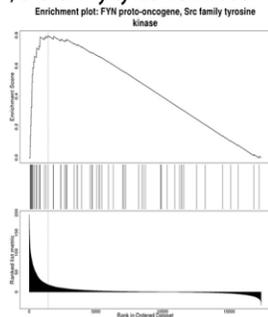
**B5** Kinase\_BTK: Bruton tyrosine kinase



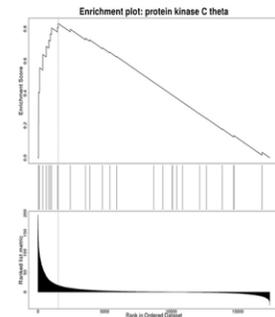
**B6** Kinase\_FGR: FGR proto-oncogene, Src family tyrosine kinase



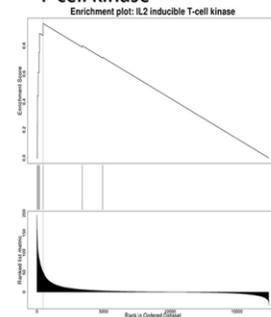
**B7** Kinase\_FYN: FYN proto-oncogene, Src family tyrosine kinase



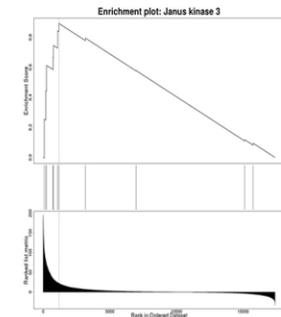
**B8** Kinase\_PRKCO: protein kinase C theta



**B9** Kinase\_ITK: IL2 inducible T-cell kinase

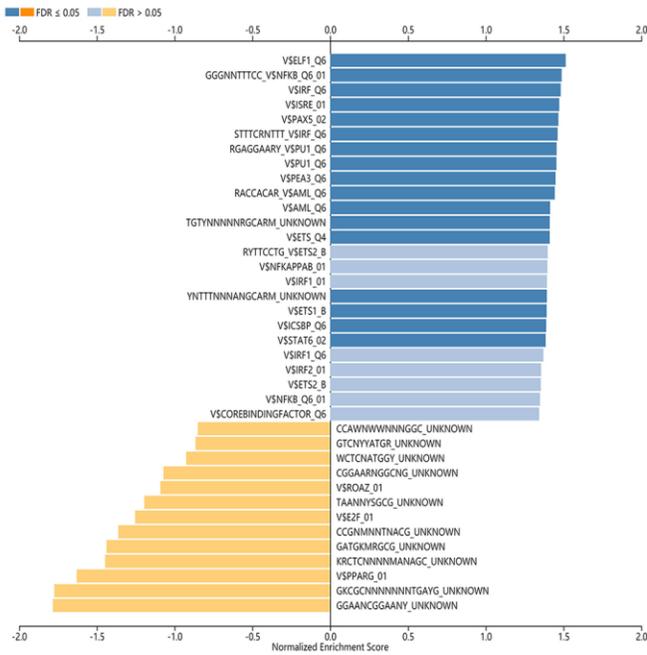


**B10** Kinase\_JAK3: Janus kinase 3

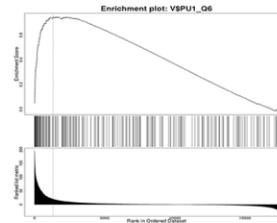


**Supplementary Figure 7. Kinase target network-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD).** (A) Bar chart of Kinase Target Network-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B10) GSEA enrichment analysis plots of 10 tumor immune-related Kinase Target Network gene sets (FDR < 0.05).

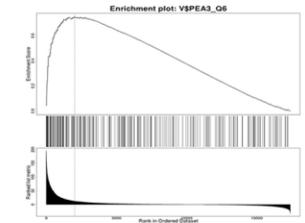
**A** The bar chart of geneontology Transcription Factor network based GSEA of ARHGAP30 in lung adenocarcinoma



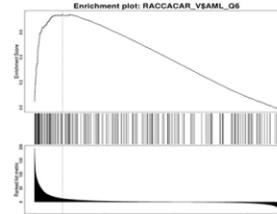
**B1** V\$PU1\_Q6



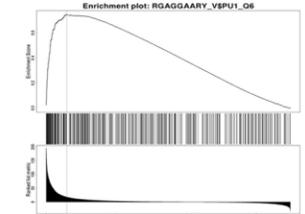
**B2** V\$PEA3\_Q6



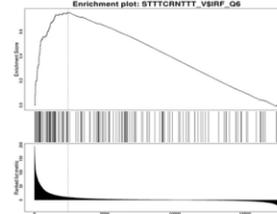
**B3** RACCACAR\_V\$AML\_Q6



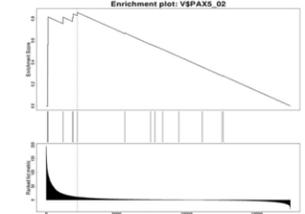
**B4** RGAGGAARY\_V\$PU1\_Q6



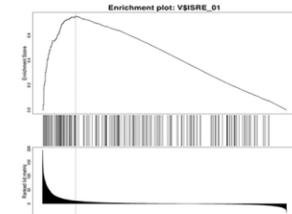
**B5** STTTCRNTTT\_V\$IRF\_Q6



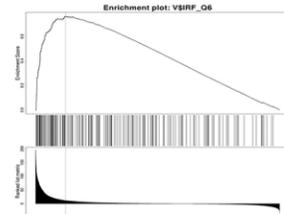
**B6** V\$PAX5\_Q2



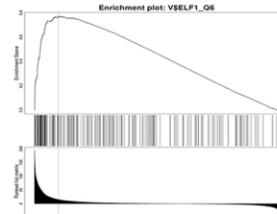
**B7** V\$ISRE\_01



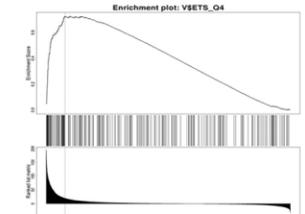
**B8** V\$IRF\_Q6



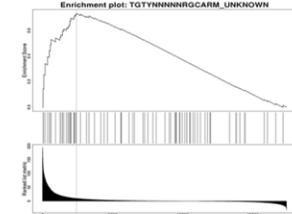
**B9** V\$SELF1\_Q6



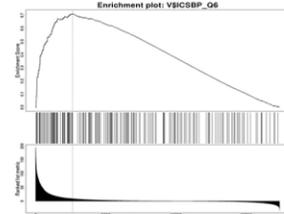
**B10** V\$SETS\_Q4



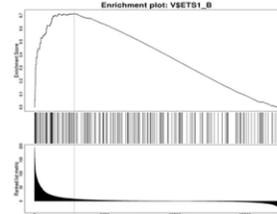
**B11** TGTYNNNNRCARM\_UNKNOW



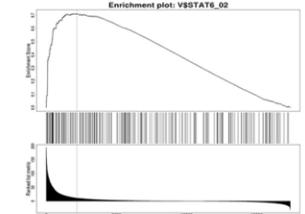
**B12** V\$ICSBP\_Q6



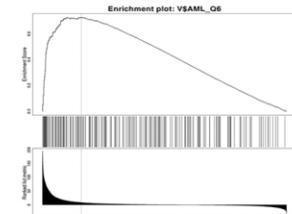
**B13** V\$SETS1\_B



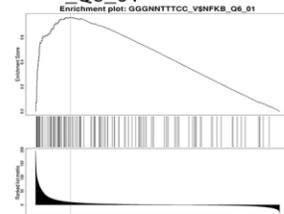
**B14** V\$STAT6\_Q2



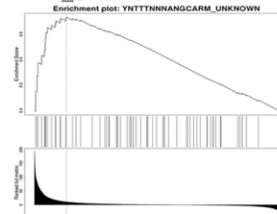
**B15** V\$AML\_Q6



**B16** GGGNNTTCC\_V\$NFKB\_Q6\_01

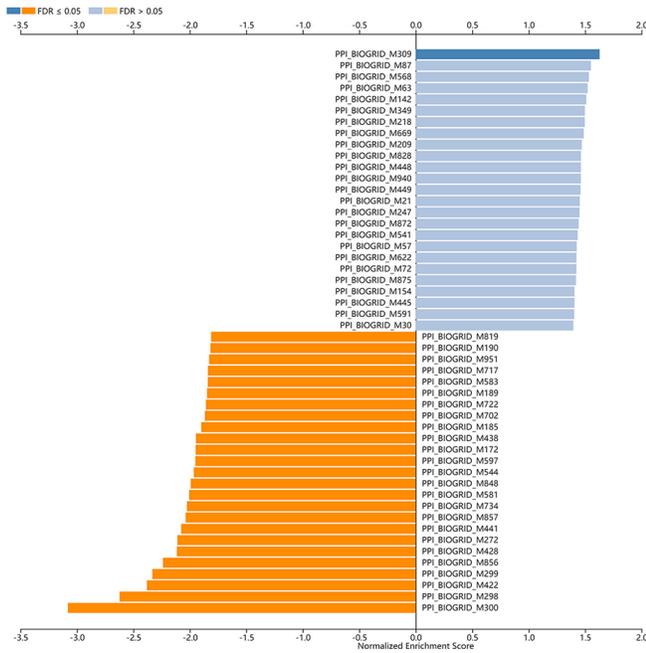


**B17** YNTTTNNNANGCARM\_UNKNOW

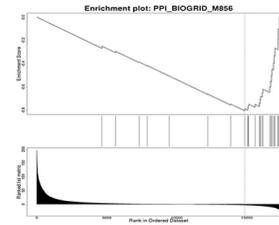


**Supplementary Figure 8. Transcription factor network-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD).** (A) Bar chart of Transcription Factor Network-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B17) GSEA enrichment analysis plots of 17 tumor immune-related Transcription Factor Network gene sets (FDR < 0.05).

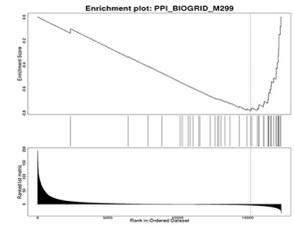
**A** The bar chart of geneontology PPI\_BIOGRID network based GSEA of ARHGAP30 in lung adenocarcinoma



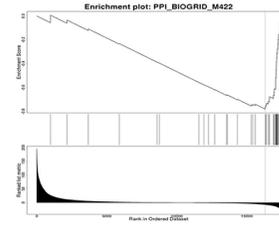
**B1** PPI\_BIOGRID\_M856



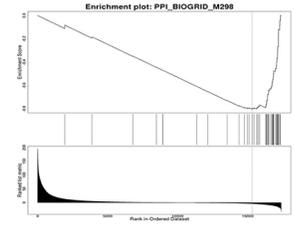
**B2** PPI\_BIOGRID\_M299



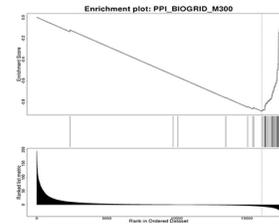
**B3** PPI\_BIOGRID\_M422



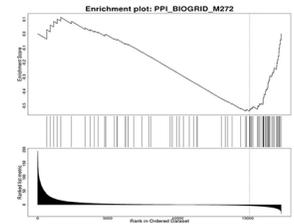
**B4** PPI\_BIOGRID\_M298



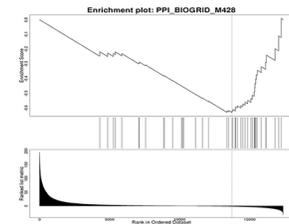
**B5** PPI\_BIOGRID\_M300



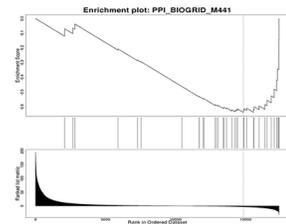
**B6** PPI\_BIOGRID\_M272



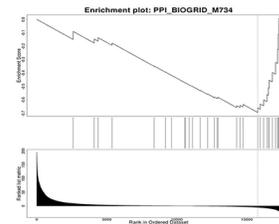
**B7** PPI\_BIOGRID\_M428



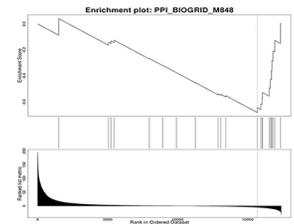
**B8** PPI\_BIOGRID\_M441



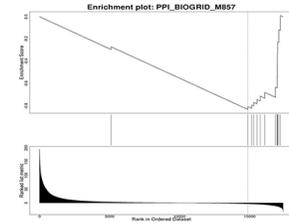
**B9** PPI\_BIOGRID\_M734



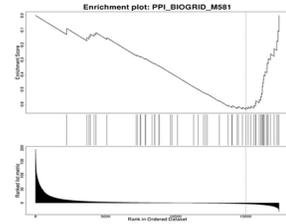
**B10** PPI\_BIOGRID\_M848



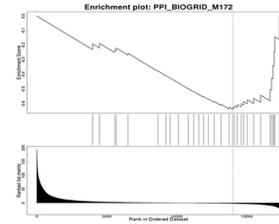
**B11** PPI\_BIOGRID\_M857



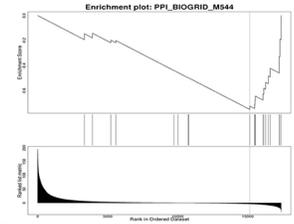
**B12** PPI\_BIOGRID\_M581



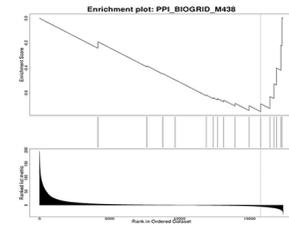
**B13** PPI\_BIOGRID\_M172



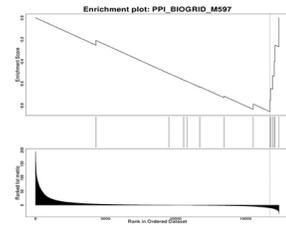
**B14** PPI\_BIOGRID\_M544



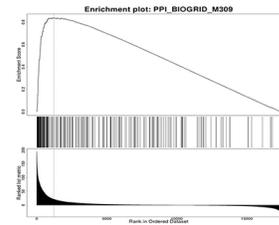
**B15** PPI\_BIOGRID\_M438



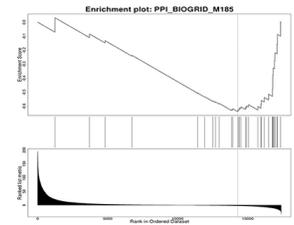
**B16** PPI\_BIOGRID\_M597



**B17** PPI\_BIOGRID\_M309

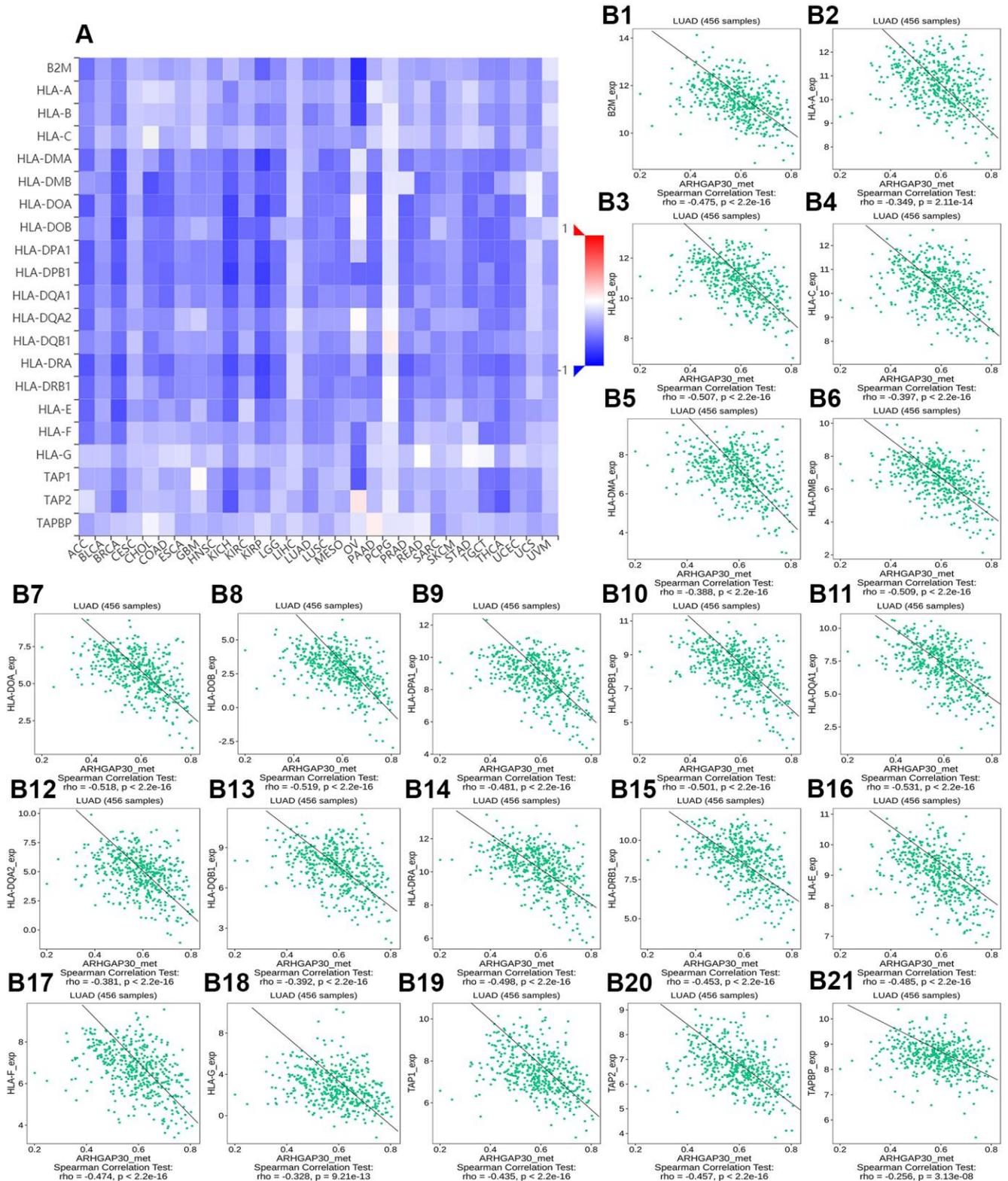


**B18** PPI\_BIOGRID\_M185

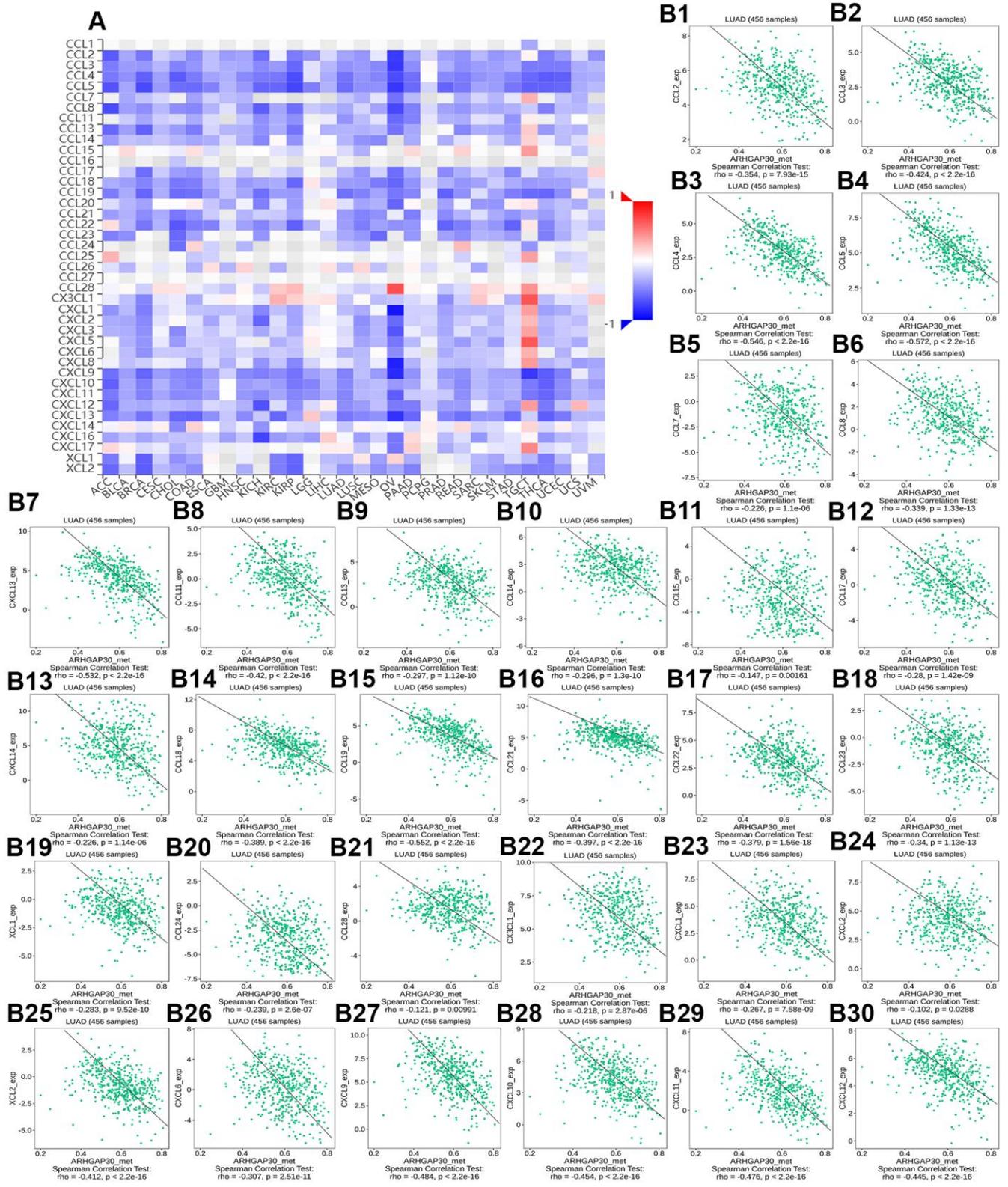


**Supplementary Figure 9. PPI BIOGRID network-based GSEA of ARHGAP30 in lung adenocarcinoma (LUAD).** (A) Bar chart of PPI BIOGRID Network-based GSEA of ARHGAP30 in LUAD (FDR < 0.05). (B1–B18) GSEA enrichment analysis plots of 18 tumor immune-related PPI BIOGRID Network gene sets (FDR < 0.05).





**Supplementary Figure 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.**

