Supplementary Figure 1. Subcellular mapping of the KIAA0101 human proteome in lung adenocarcinoma cells. (A–H) Represent the subcellular mapping of the KIAA0101 human proteome (RH-30, HPA047929), respectively. (A) Antibody. (B) Nucleus and intensity. (C) Microtubule and intensity. (D) Microtubule. (E) Antibody and microtubule. (F) Antibody, nucleus, and microtubule. (G) Microtubule and endoplasmic reticulum. (H) Microtubule and endoplasmic reticulum. The cell structure sections were based on representative images of antibody-stained human cancer cell lines. Each sample was stained with an in-house generated HPA-antibody and counterstained with markers for microtubules, the endoplasmic reticulum, and the nucleus.
Supplementary Figure 2. Enrichment plot of pathways in the enrichment results of figure 3A with the top 8 and the bottom 8 genes according to the normalized enrichment score. (A) hsa04110, Cell cycle; (B) hsa03010, Ribosome; (C) hsa03050, Proteasome; (D) hsa03040, Spliceosome; (E) hsa03030, DNA replication; (F) hsa03013, RNA transport; (G) hsa00240, Pyrimidine metabolism; (H) hsa03008, Ribosome biogenesis in eukaryotes; (I) hsa04514, Cell adhesion molecules (CAMs); (J) hsa04970, Salivary secretion; (K) hsa04972, Pancreatic secretion; (L) hsa05412, Arrhythogenic right ventricular cardiomyopathy (ARVC); (M) hsa04659, Th17 cell differentiation; (N) hsa04070, Phosphatidylinositol signaling system; (O) hsa04640, Hematopoietic cell lineage; (P) hsa04928, Parathyroid hormone synthesis secretion and action.
Supplementary Figure 3. KEGG pathway annotations of the ribosome pathway (HSA03010). Red denotes leading edge genes; green denotes the remaining genes.
Supplementary Figure 4. KEGG pathway annotations of the Proteasome pathway (hsa03050). Red denotes leading edge genes; green denotes the remaining genes.
Supplementary Figure 5. KEGG pathway annotations of the Spliceosome pathway (hsa03040). Red denotes leading edge genes; green denotes the remaining genes.
Supplementary Figure 6. KEGG pathway annotations of the DNA replication pathway (hsa03030). Red denotes leading edge genes; green denotes the remaining genes.
Supplementary Figure 7. The scatter diagram of KIAA0101 and the first 16 genes highly related to KIAA0101 (Pearson correlation coefficient > 0.8). (A) CCNB2; (B) RAD51; (C) OIP5; (D) CDK1; (E) NUSAP1; (F) SPC25; (G) CCNB1; (H) BIRC5; (I) PBK; (J) NCAPG; (K) ZWINT; (L) MAD2L1; (M) SKA3; (N) CDC45; (O) RRM2; (P) UBE2T.
Supplementary Figure 8. Expression of KIAA0101 and correlation scatter diagram of miRNAs. (A1–A10) Positive correlations between the expression of KIAA0101 and miRNAs. (B1–B10) Negative correlations between the expression of KIAA0101 and miRNAs.
Supplementary Figure 9. Correlations between the expression of KIAA0101 and immunoinhibitors. (A1–A12) are scatter plots of the negative correlations between KIAA0101 expression and immunoinhibitors in the treatment of lung adenocarcinoma. (B1–B8) are scatter plots of the positive correlations between KIAA0101 expression and immunoinhibitors in the treatment of lung adenocarcinoma.
Supplementary Figure 10. The correlation between the expression of KIAA0101 and immunostimulators. (A1–A29) are scatter plots of the negative correlations between KIAA0101 expression and Immunostimulators in the treatment of lung adenocarcinoma. (B1–B15) are scatter plots of the positive correlations between KIAA0101 expression and Immunostimulators in the treatment of lung adenocarcinoma.
Supplementary Figure 11. The correlation between the expression of *KIAA0101* and MHC molecules. (A1–A17) are scatter plots of the negative correlations between *KIAA0101* expression and MHC molecules in the treatment of lung adenocarcinoma. (B1–B3) are scatter plots of the positive correlations between *KIAA0101* expression and MHC molecules in the treatment of lung adenocarcinoma.
Supplementary Figure 12. The correlation between the expression of KIAA0101 and chemokines. (A1–A17) are scatter plots of the negative correlations between KIAA0101 expression and chemokines in the treatment of lung adenocarcinoma. (B1–B19) are scatter plots of the positive correlations between KIAA0101 expression and chemokines in the treatment of lung adenocarcinoma.
Supplementary Figure 13. The correlation between the expression of KIAA0101 and receptors. (A1–A14) are scatter plots of the negative correlation between KIAA0101 expression and receptors in the treatment of lung adenocarcinoma. (B1–B2) are scatter plots of the positive correlation between KIAA0101 expression and receptors in the treatment of lung adenocarcinoma.
Supplementary Figure 14. KIAA0101 transcription in subgroups of patients with lung adenocarcinoma, stratified based on sex, age, and other criteria (UALCAN). (A) Individual cancer stages; (B) patient’s ethnicity; (C) patient’s sex; (D) patient’s age; (E) patient’s smoking habits; (F) patient’s metastasis status. ※ P>0.05, ☆ P < 0.05; ☆☆, P < 0.01; ☆☆☆, P < 0.001.