

Supplementary Fig. 1. Mutational landscape of LUAD somatic genes in TCGA

(A) At-a-glance view of all gene mutations; (B) Mutations of common 9 drug target genes. SNP, single nucleotide polymorphism; INS, insertion; DEL, deletion; SNV, single nucleotide variant; TTN, titin; MUC16, mucin 16; RYR2, ryanodine receptor 2; CSMD3, CUB and Sushi multiple domains 3; TP53, tumor protein p53; LRP1B, low-density lipoprotein receptor-related protein 1B; USH2A, usherin; ZFHX4, zinc finger homeobox 4; XIRP2, xin actin-binding repeat-containing protein 2; KRAS, KRAS proto-oncogene, GTPase; EGFR, epidermal growth factor receptor; BRAF, B-Raf proto-oncogene, serine/threonine kinase; ROS1, ROS proto-oncogene 1, receptor tyrosine kinase; ALK, anaplastic lymphoma kinase; RET, ret proto-oncogene; MET, mesenchymal–epithelial transition factor.



Supplementary Fig. 2. Model construction and gene expression in the model

(A) Variation of variables with the number of operations during model construction (green: important variables; red: unimportant variables; blue: shadow variables; yellow: tentative variables); (B) Important variables and their IMPORTANCE values in the model (the yellow section represents the genes used for model construction, while the remaining are shadow variables; the vertical axis indicates importance values, with higher values denoting greater contributions). AURKA, Aurora kinase A; EIF2S1, eukaryotic translation initiation factor 2 subunit 1; STMN1, stathmin-1; ALOX15B, arachidonate 15-lipoxygenase type B; ZNF419, zinc finger protein 419; FANCD2, fanconi anemia group D2 protein.



Supplementary Fig. 3. Immune infiltration analysis

(A) Immune infiltration in tumor tissues versus normal tissues; (B) Comparison of immune infiltration between high and low AURKA expression groups. (C) Correlation between PDCD1 and AURKA expression; (D) Correlation between CD274 and AURKA expression; (E) Correlation between CTLA4 and AURKA expression. Note: “tumor” indicates tumor tissue; “normal” indicates normal tissue; AURKA-H indicates high AURKA expression; AURKA-L indicates low AURKA expression. PDCD1, programmed cell death 1; CD274, cluster of differentiation 274 (also known as PD-L1); CTLA4, cytotoxic T-lymphocyte-associated protein 4.