**Supplementary Table 1. Patient demographic and clinical characteristics.**

**Supplementary Table 2. Immune-related gene list.** Immune related molecules demonstrating roles in tumor microenvironment based on publications were listed in the table and used in this study.

**Supplementary Table 3.** Common mutational events in “epithelial” and “mesenchymal” lung adenocarcinomas versus EMT status. Commonly observed mutations in TCGA samples were analyzed by dividing the patients into either EMT high or low based on the mRNA EMT score. Patients with gene expression levels of EMT score ≥ highest 1/3 are defined as “mesenchymal” (M) and patients with gene expression levels of EMT score ≤ lowest 1/3 are defined as “epithelial” (E).

**Supplementary Figure 1. Validation of anti-PD-L1 antibody E1L3N (Cell Signaling Technology). (A)** Western blot of PD-L1 expression using E1L3N on whole cell line lysates of U293 and U293 cells transduced with a vector expressing PD-L1. (**B)** PD-L1IHC staining of U293 cell pellets. (**C)** PD-L1 IHC staining of U293 cells transduced with a vector expressing PD-L1. (**D)** Example of negative PD-L1 IHC staining on PC3 cell pellets (SignalSlide negative control, Cell Signaling Technology). (**E)** Example of positive PD-L1 IHC staining on HDLM-2 pellets (SignalSlide positive control, Cell Signaling Technology). (**F)** Example of positive PD-L1 IHC staining on placenta. (**G)** Example of positive PD-L1 IHC staining on human tonsil. Antibody E1L3N has been used in IHC analysis of PD-L1 expression in this current study.

**Supplementary Figure 2. Validation of anti-PD-L1 antibody ab174838 (Abcam).** 5 H1 antibody was initially developed in Dr Lieping Chen’s lab and has been used as control to validate ab174838 (Abcam). **(A)** Western blot of PD-L1 expression using either 5H1 or ab174838 on cell line lysates. (**B)** PD-L1IHC staining of U293 cell pellets. (**C)** PD-L1 IHC staining of U293 cells transduced with a vector expressing PD-L1. (**D)** PD-L1 IHC staining of placenta. (**E)** Example of negative PD-L1 IHC staining on NSCLC tumor tissue. (**F)** Example of low level PD-L1 IHC staining on NSCLC tumor tissue. (**G)** Example of high level PD-L1 IHC staining on NSCLC tumor tissue, with membrane accentuation. (**H)** Example of positive PD-L1 IHC staining on tumor infiltrating immune cells. Panels E-H are staining with antibody ab174838 (Abcam). Antibody ab174838 has been used in RPPA analysis of PD-L1 expression in this current study.

**Supplementary Figure 3.** Elevation of multiple immune molecules in “mesenchymal” compared to “epithelial” lung adenocarcinoma. Supervised cluster heatmap of immune related molecules in lung adenocarcinoma from TCGA (A), and PROSPECT (B) respectively. The tumor specimens were first grouped as EMT low (EMT score < lowest 1/3), EMT intermediate (EMT score ≥ lowest 1/3, but ≤ highest 1/3) and EMT high (EMT scores > highest 1/3). Expression levels of immune related molecules are shown on the heatmaps. Expression levels of immune checkpoint molecules, co-stimulatory molecules, CXCL10 and IDO in lung adenocarcinomas with EMT low, intermediate and high from TCGA (**C**) and PROSPECT(**D**) respectively.

**Supplementary Figure 4. B7-H3 is associated with poor OS and RFS in lung adenocarcinoma.** The probability of overall survival and recurrence free survival of patients from PROSPECTwere analyzed by dividing the patients into either high or low group based on the expression levels of each immune checkpoint molecule or EMT score. Patients with gene expression levels ≥ highest 1/3 are considered as high and gene expression levels ≤ lowest 1/3 are considered as low respectively. (**A)** Overall survival, (**B)** Recurrence free survival. Both are from PROSPECT.

**Supplementary Figure 5. The association between EMT and inflammatory tumor microenvironment in advanced lung adenocarcinoma. A.** Supervised cluster heatmap of immune related molecules in “epithelial” (N = 14) versus “mesenchymal” (N = 43) lung adenocarcinoma from BATTLE-1 dataset. Geneexpression levels of immune checkpoint molecules (**B**), co-stimulatory molecules (**C**) and CXCL10 and IDO (**D**) in “mesenchymal” lung adenocarcinoma in comparison to “epithelial” lung adenocarcinoma in tumor tissues from BATTLE-1 dataset.