

Supplementary Figure 6. Transcriptomic characterization of urethane-induced lung adenocarcinoma (LUAD) cell lines. A-C, RNA of mouse urethane-induced LUAD cell lines, lungs obtained pre- and one week post-urethane treatment (n = 2 each), and airway epithelial cells (AEC), alveolar type II cells [ATII; data from [36]], and bone marrow-derived macrophages (BMDM) was examined by Affymetrix Mouse Gene ST2.0 microarrays (n = 4/group). A, Number of genes out of the 30 top-represented transcripts of AEC, ATII, and BMDM within the top-2000-expressed genes of lungs and LUAD cells. **B** and **C**, Mean expression levels of selected transcripts, including lineage markers and markers of histologic subtype in LUAD compared with lungs pre- and one week posturethane treatment (B, microarray, n = 2/group; C, qPCR, n = 3/group). AD, adenocarcinoma; SQ, squamous cell carcinoma; SC, small cell carcinoma. **D** and **E**, Differentially expressed genes between six different lung adenocarcinoma cell lines cultured from urethane-induced lung tumors and six benign respiratory mouse samples, including lungs of saline- and urethane-treated mice obtained at one week post-treatment, as well as primary mouse tracheal epithelial cells. **D**, Whole heat map showing the accurate hierarchical clustering of the samples according to differentially expressed genes, as well as the top over- and under-represented genes. Note the universal loss of expression of lineage markers by lung adenocarcinoma cells (genes in red font). E, Volcano plot showing selected top over- and under-represented genes (arrows). ANOVA, analysis of variance; FDR, false discovery rate. Data are given as mean \pm SD and two-way ANOVA (graphs) or χ^2 test (table) P values. ns, *, and ***: P > 0.05, P < 0.05, and P < 0.001 for the comparisons indicated (A) or for comparison of all genes (B, D) and of Krt20 (C) with naïve lungs by Bonferroni post-tests (graphs) or Fischer's exact test (table).