Figure S1 The interaction between mesothelial cells and fibroblasts. (A) Ligand-receptor pairs between mesothelial cells and fibroblasts with means >0.5 inferred by CellphoneDB; (B) the interactions between mesothelial cells and fibroblasts predicted by Nichenet. The expression levels of top predicted ligands in mesothelial cells from different subtypes were shown in the left heatmap. The middle and right upper heatmap displayed the ligand-receptor and ligand-target interaction potential, respectively. The right lower heatmap displayed the expression levels of target genes in fibroblasts from the cancer and normal subtypes. Meso, mesothelial cells; Fib, fibroblasts.
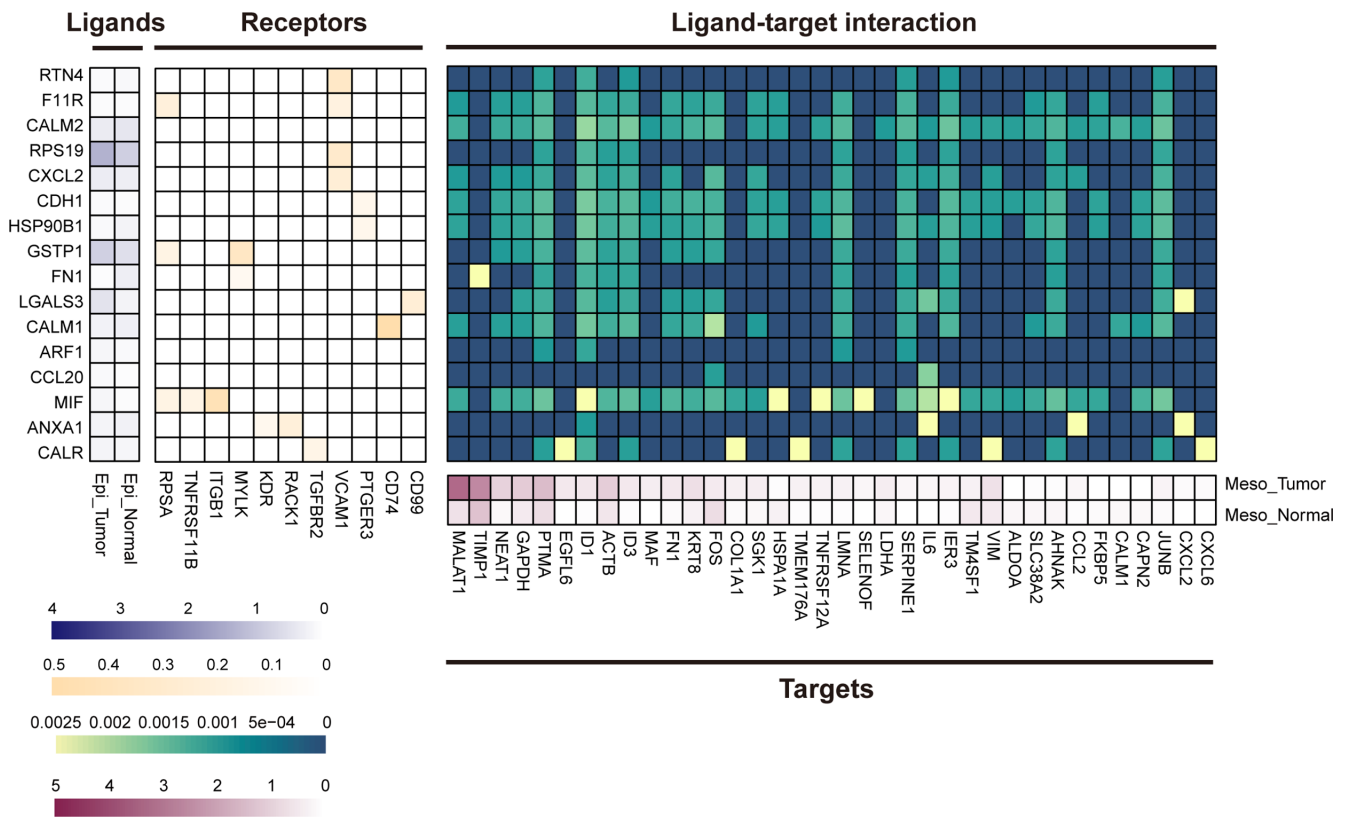
Figure S2 The interactions between mesothelial cells and epithelial cells predicted by Nichenet. The expression levels of top predicted ligands in epithelial cells from different subtypes were shown in the left heatmap. The middle and right upper heatmap displayed the ligand-receptor and ligand-target interaction potential, respectively. The right lower heatmap displayed the expression levels of target genes in mesothelial cells from the cancer and normal subtypes. Epi, epithelial cells; Meso, mesothelial cells.
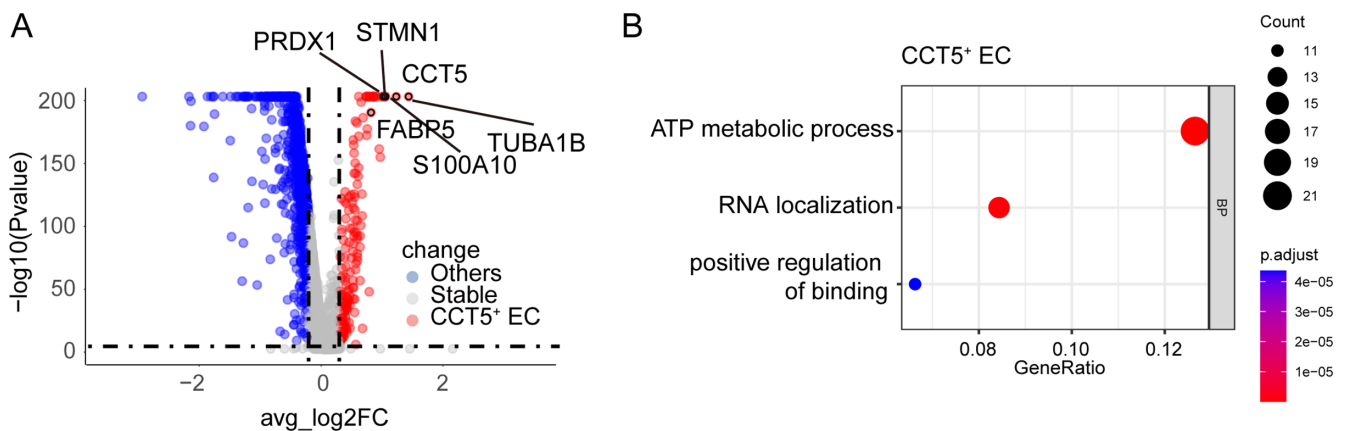

Figure S3 Highly expressed genes in CCT5^{+} EC. (A) Volcano plot displaying the DEGs between CCT5^{+} EC and other clusters of epithelial cells. (B) GO enrichment analysis of increased DEGs in CCT5^{+} EC. DEG, differentially expressed genes; GO, gene ontology.
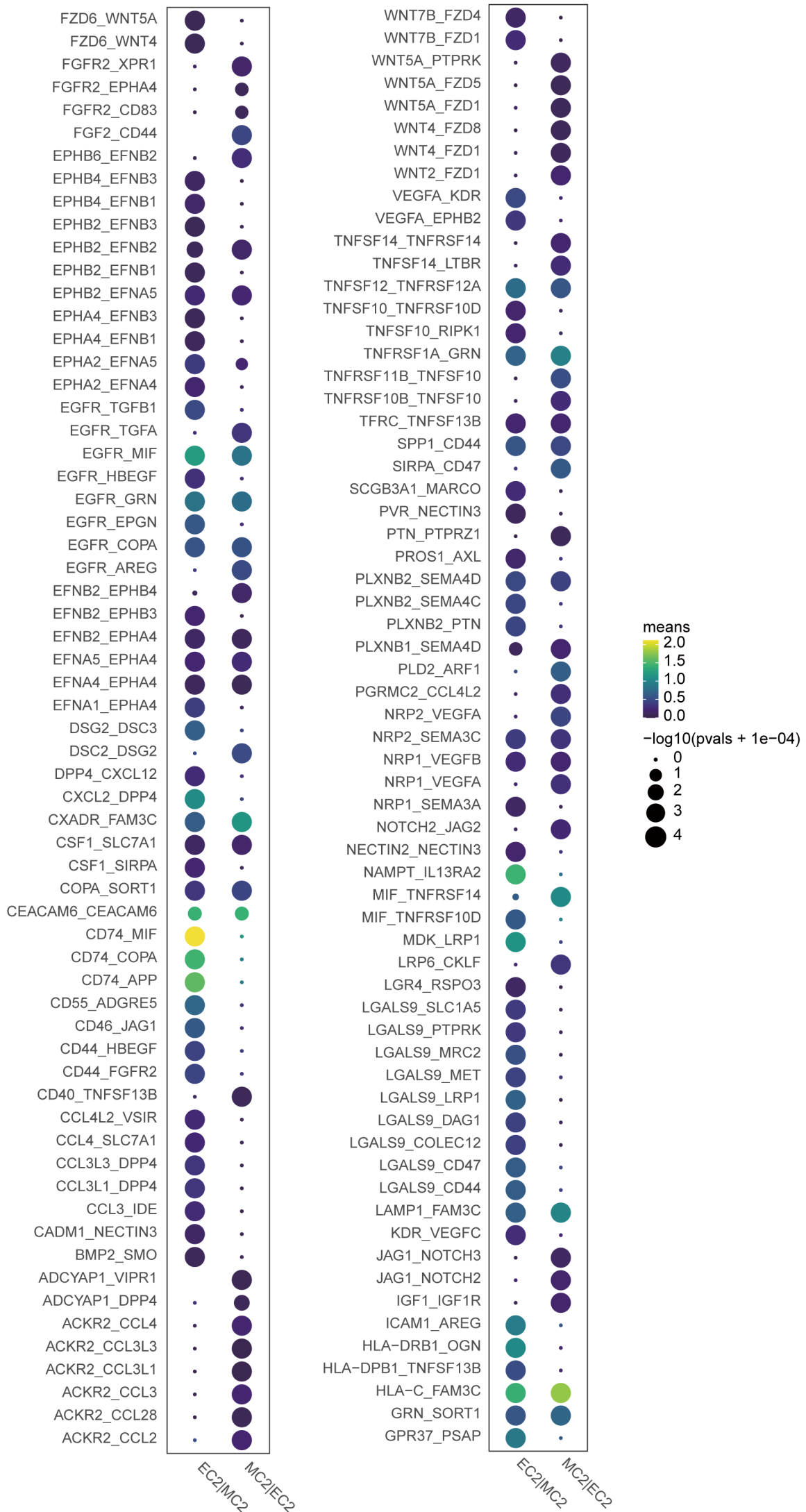
Figure S4 Ligand-receptor pairs between CEMIP+ MC and MUC21+ EC were inferred by CellphoneDB.
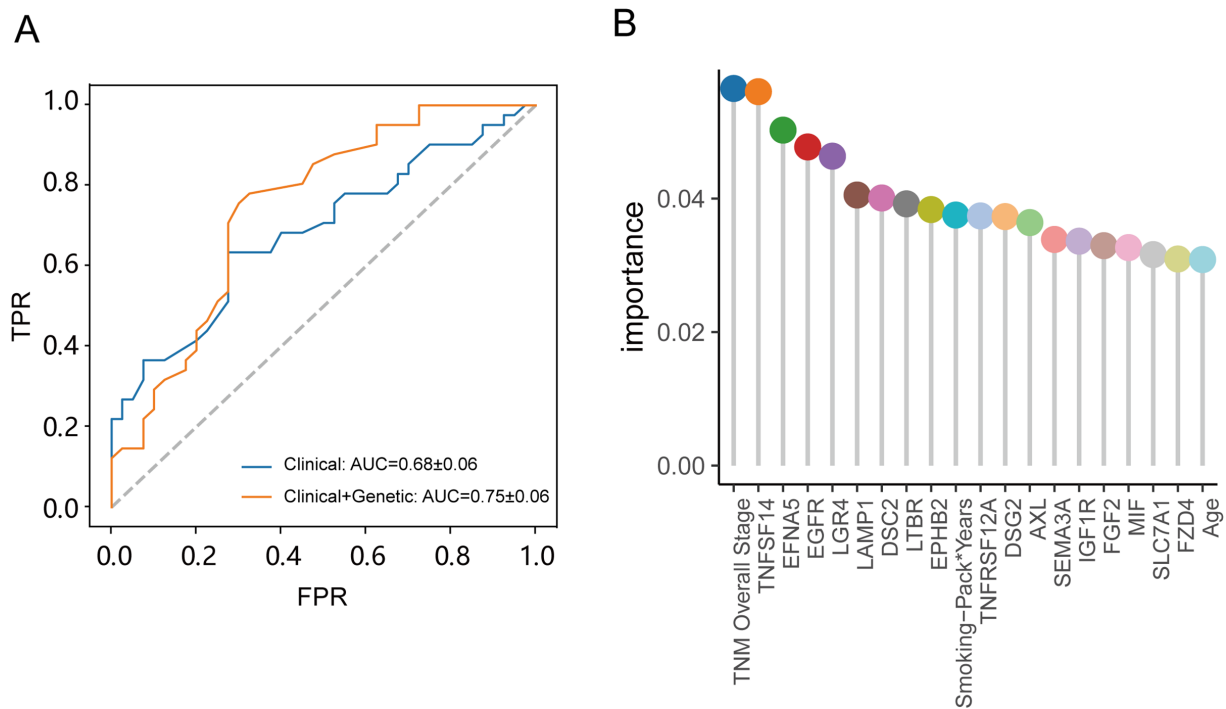
Figure S5 A Prediction model constructed based on the interaction genes between CAMCs and epithelial cells. (A) The comparison between the AUC of 3-year OS based on our model constructed by 21 candidate genes and clinical information and the model built by clinical information only; (B) feature importance (Gini coefficients) of our random forest model was ranked. AUC, area under the curve; OS, overall survival; TPR, true positive rate; FPR, false positive rate.
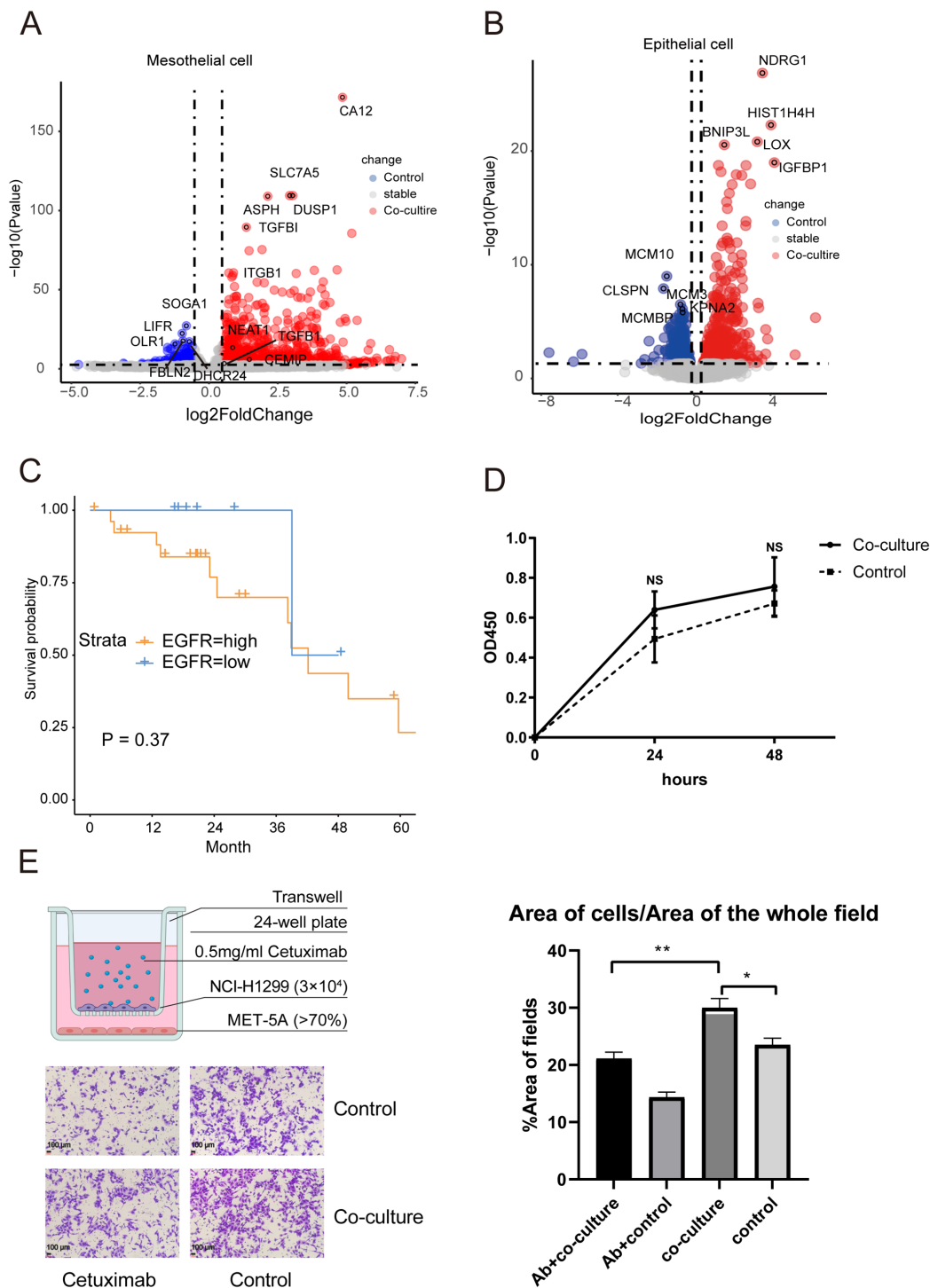
Figure S6 The co-culture of mesothelial cells and epithelial cells (A) Volcano plot displaying the DEGs between control and co-culture groups of mesothelial cells. (B) Volcano plot displaying the DEGs between control and co-culture groups of epithelial cells. (C) The survival curve of the EGFR expression in TCGA-LUAD patients with EGFR mutations. (D) The proliferation assay of A549 cells. (E) Left up: The illustration of invasion assay of H1299 cells co-culturing with mesothelial cells. Scale bar: 100 μm. Staining: crystal violet. Left down: upper left: Cetuximab. Upper right: control. Lower left: cetuximab + mesothelial cells. Lower right: mesothelial cells. Right: the area of cells/area of the filed in different groups. *, P<0.05; **, P<0.01. DEG, differentially expressed genes; EGFR, epidermal growth factor receptor.