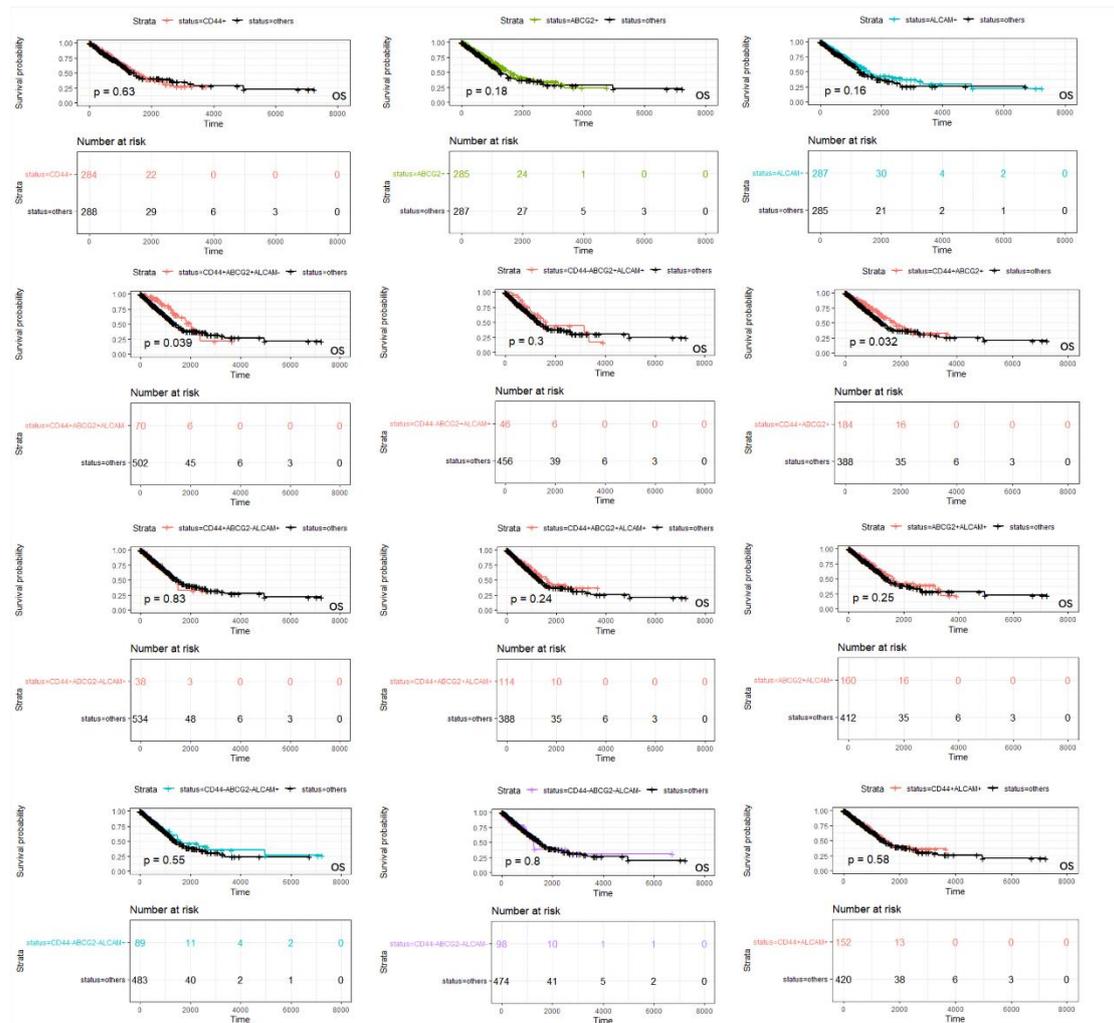


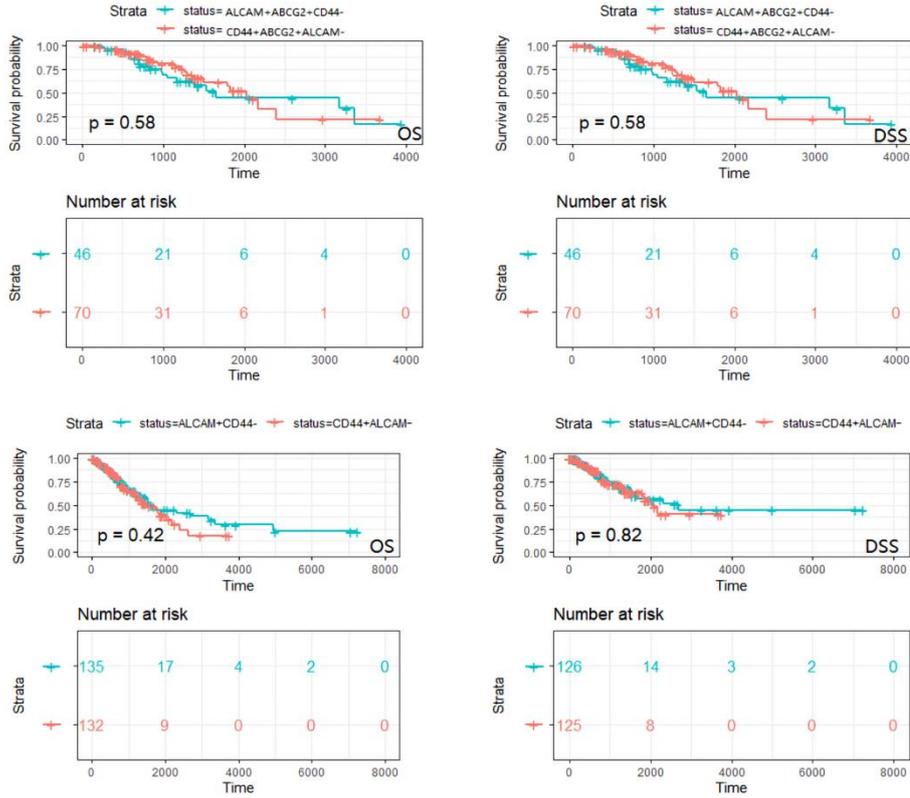
**Figure S1.** UMAP projection of PC-9s cells and PC-9 cells (GSE149383) before and after batch effect treatment (A). Based on expression of three cancer stem-like cell markers (CD44, ABCG2, ALCAM), the UMAP plot shows that the cell populations after batch effect treatment were divided into two groups: CD44+ABCG2-ALCAM-

and CD44-ABCG2-ALCAM+ (B). The mRNA<sub>si</sub> scores of CD44+ABCG2-ALCAM- were significantly higher than CD44-ABCG2-ALCAM+ (Wilcox test, p-value <2.2e-16) (C). Violin plots display that expression of three cancer stem-like cell markers (CD44, ABCG2, ALCAM) between the two groups (D). The number of PC-9 cells and PC-9s cells in the two groups after batch effect treatment. There were 10,710 PC-9 cells and 4,902 PC-9s cells in CD44-ABCG2-ALCAM+, while CD44+ABCG2-ALCAM- only owned 6 PC-9 cells and 2,418 PC-9s cells (E).

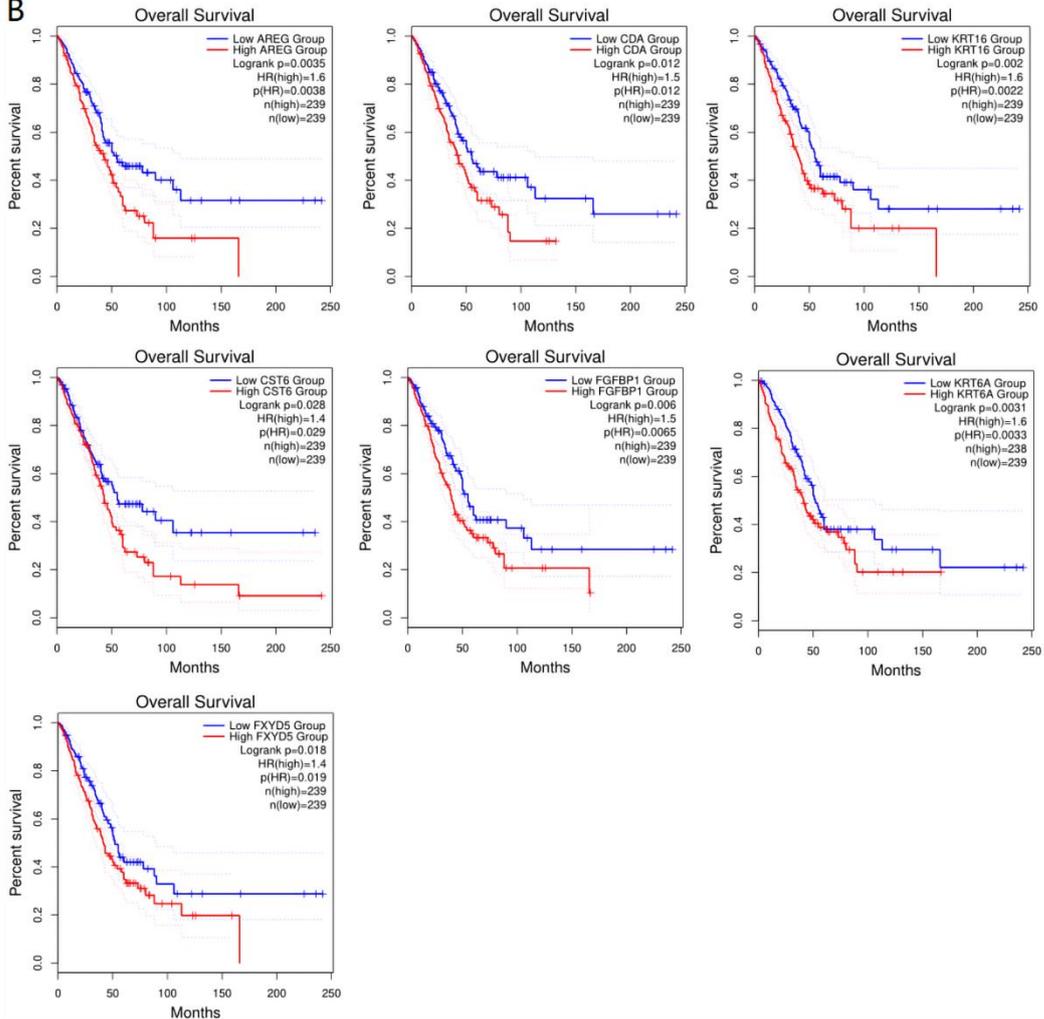


**Figure S2.** OS survival analyses of TCGA LUAD patients. High level (+) and low level (-) with the median of each marker gene expression across all patients as the threshold. Groups include: CD44+, ABCG2+, ALCAM+, CD44+ABCG2+ALCAM-, CD44-ABCG2+ALCAM+, CD44+ABCG2+, CD44+ABCG2-ALCAM+, CD44+ABCG2+ALCAM+, ABCG2+ALCAM+, CD44-ABCG2-ALCAM+, CD44-ABCG2-ALCAM- and CD44+ALCAM+.

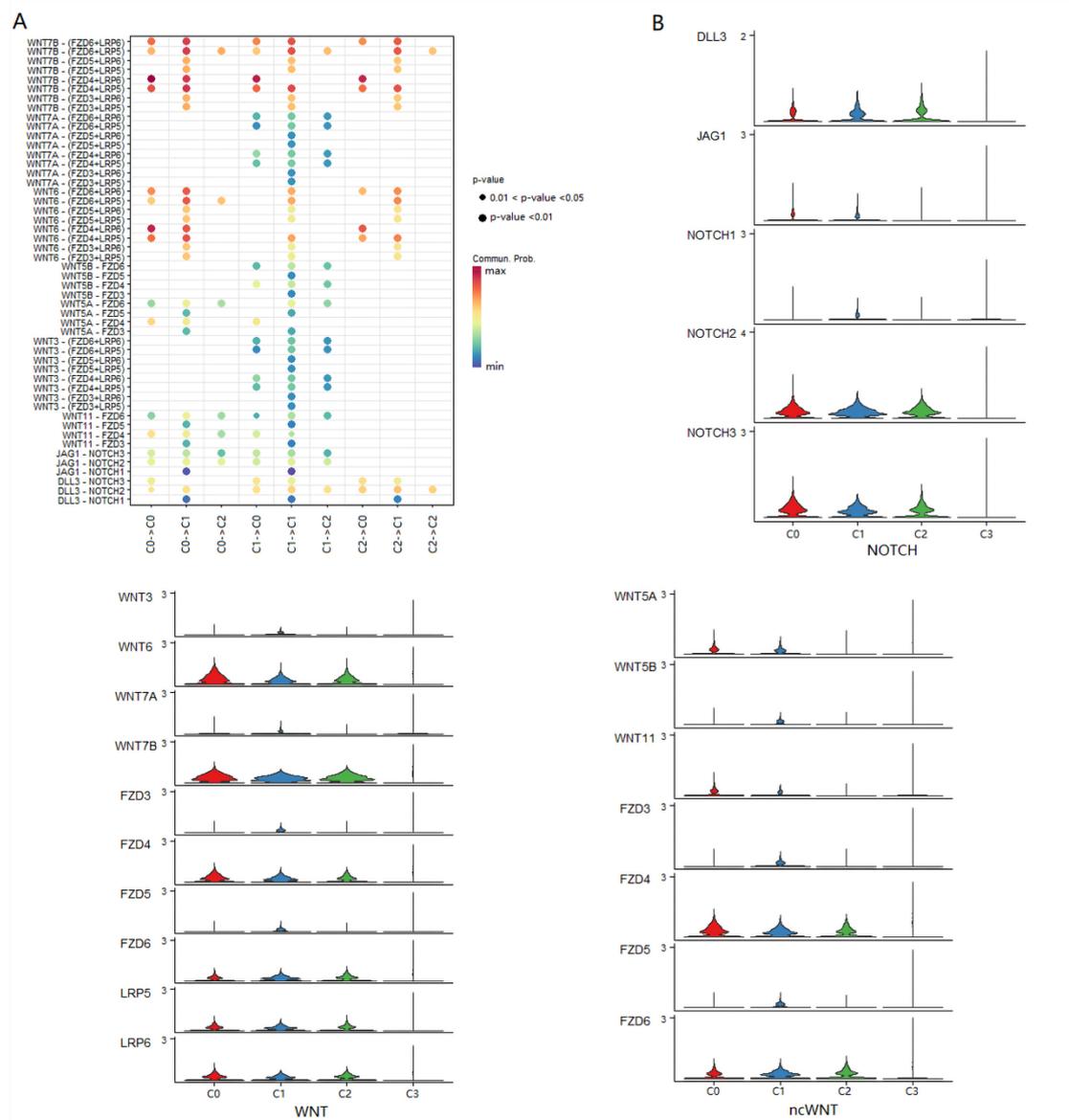
**A**



**B**



**Figure S3.** Survival curves (OS and DSS) of TCGA LUAD patients. High level (+) and low level (-) with the median of each marker gene expression across all patients as the threshold (A). The OS plots were obtained for intersected DEGs from table S3 were analyzed by GEPIA2 (<http://gepia2.cancer-pku.cn/>) (B).



**Figure S4.** Bubble plot reveals contribution of each ligand receptor to the overall signaling pathway among three signaling pathways from figure 5A (p-value < 0.05; A). Violin plots show the gene expression level related three signaling pathways in different cell clusters (B).