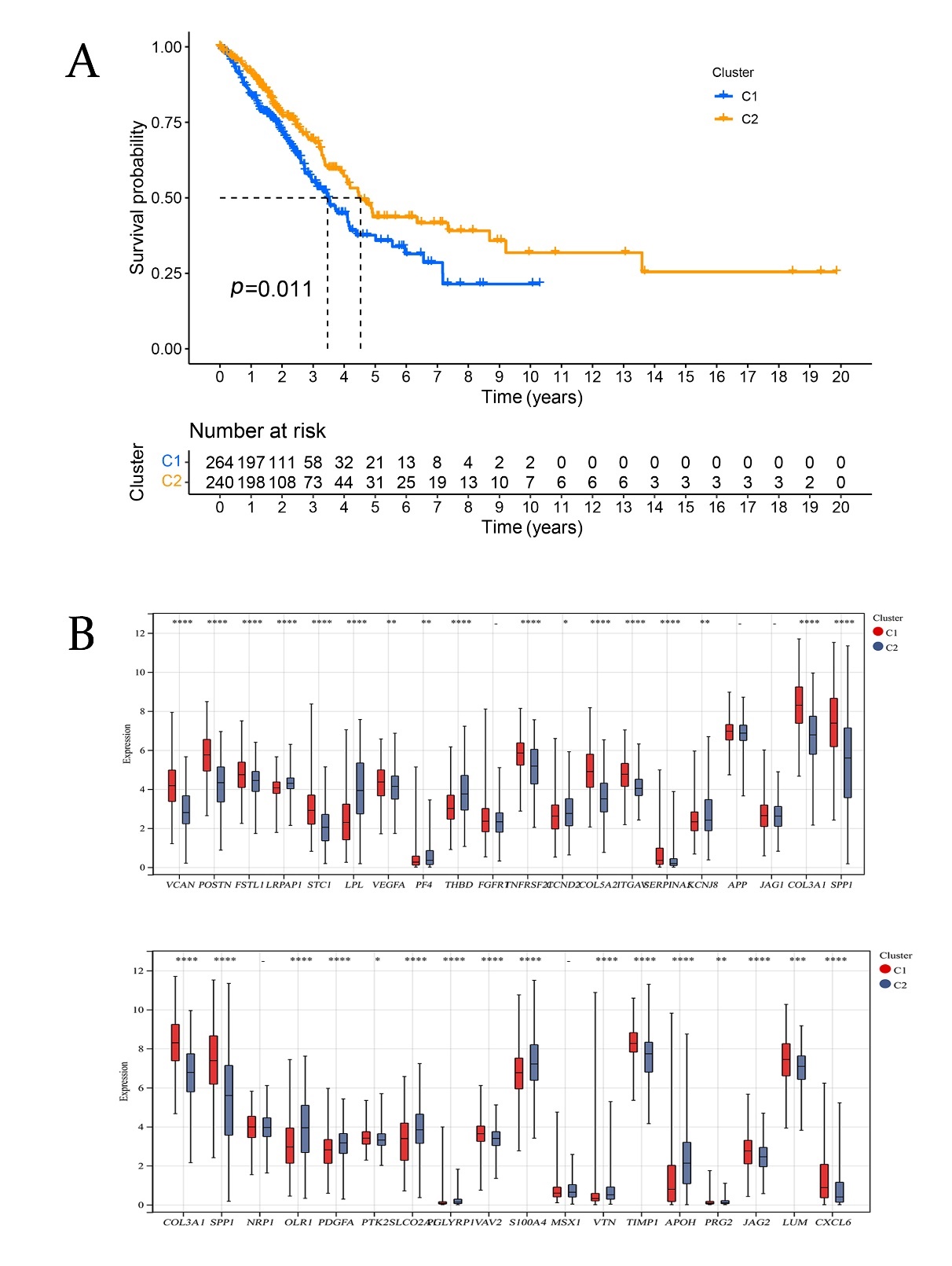
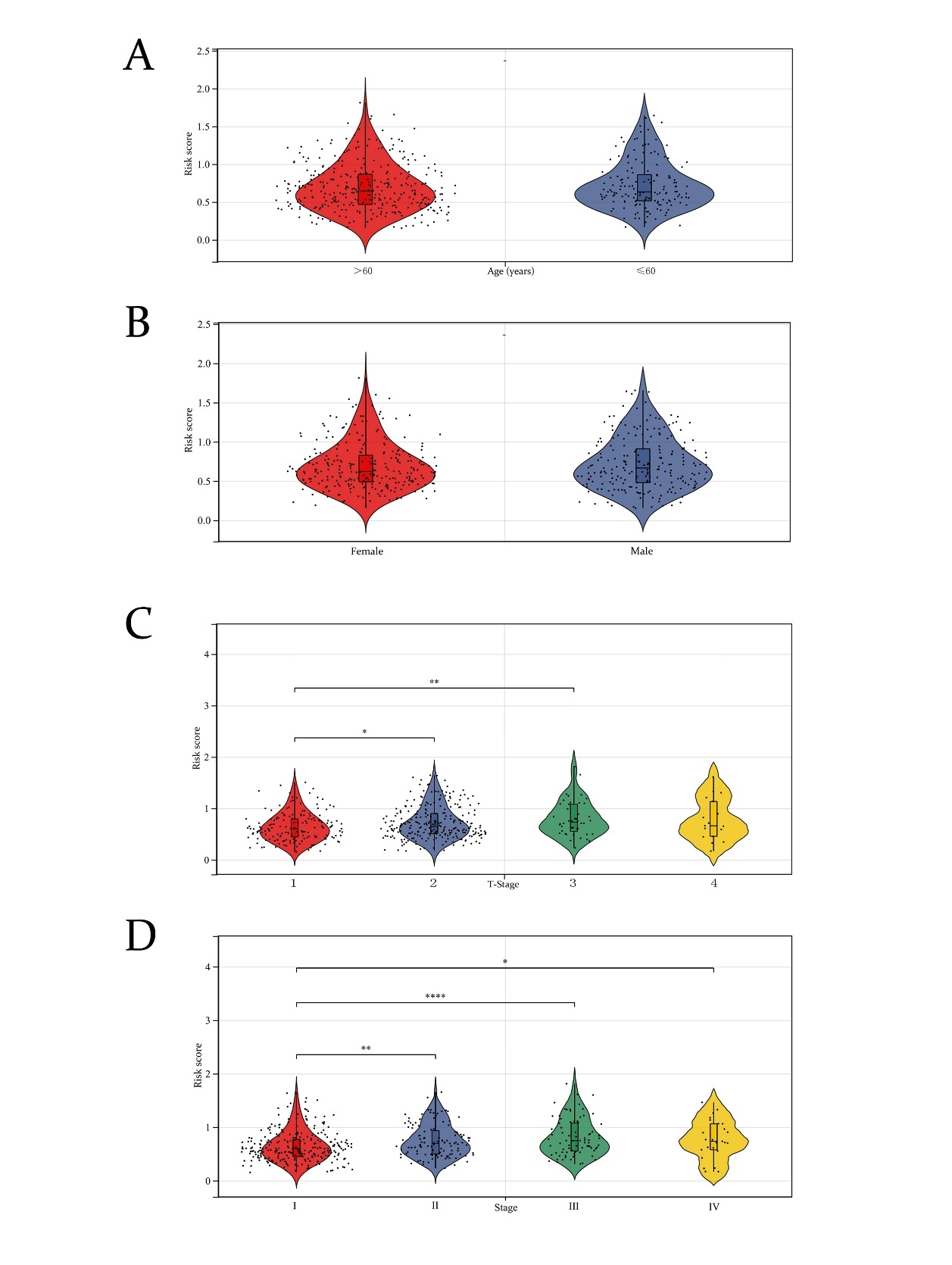
**Supplementary Figure 1**

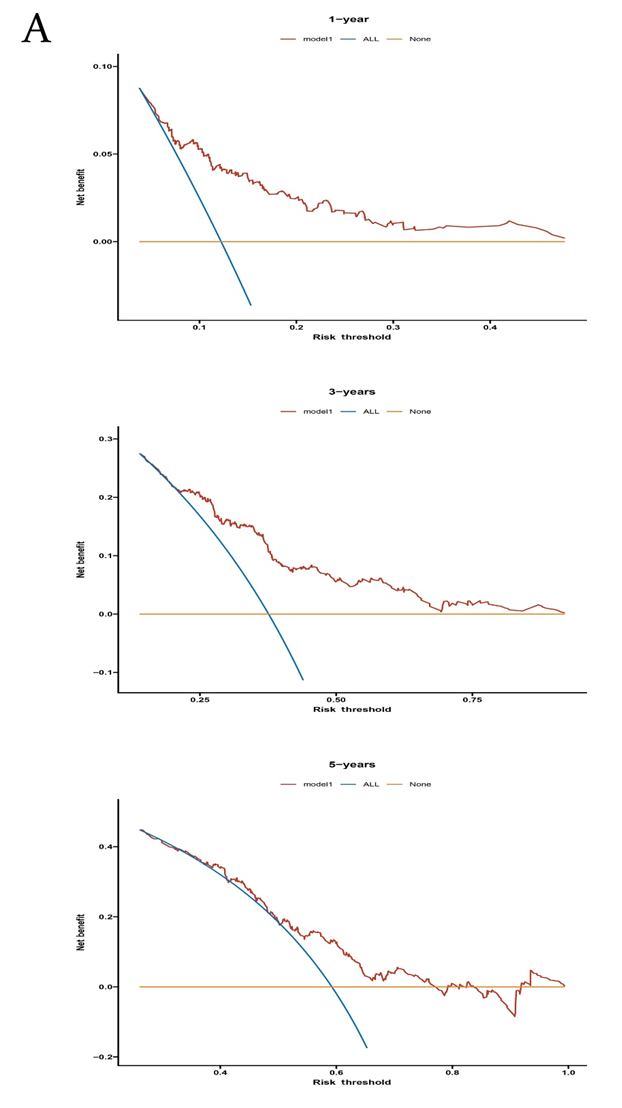
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**Supplementary Figure 1.** Retyping based on differentially expressed genes. A: Survival according to differentially expressed gene cluster. Patients in the two DEG clusters had significantly different survival (*p*=0.011). B: Differences in the expression of angiogenesis-related genes among the two clusters of differentially expressed genes. Significantly different at: \**p*<0.05,\*\**p*<0.01, \*\*\**p*<0.001 and \*\*\*\**p*<0.0001.

**Supplementary Figure 2**

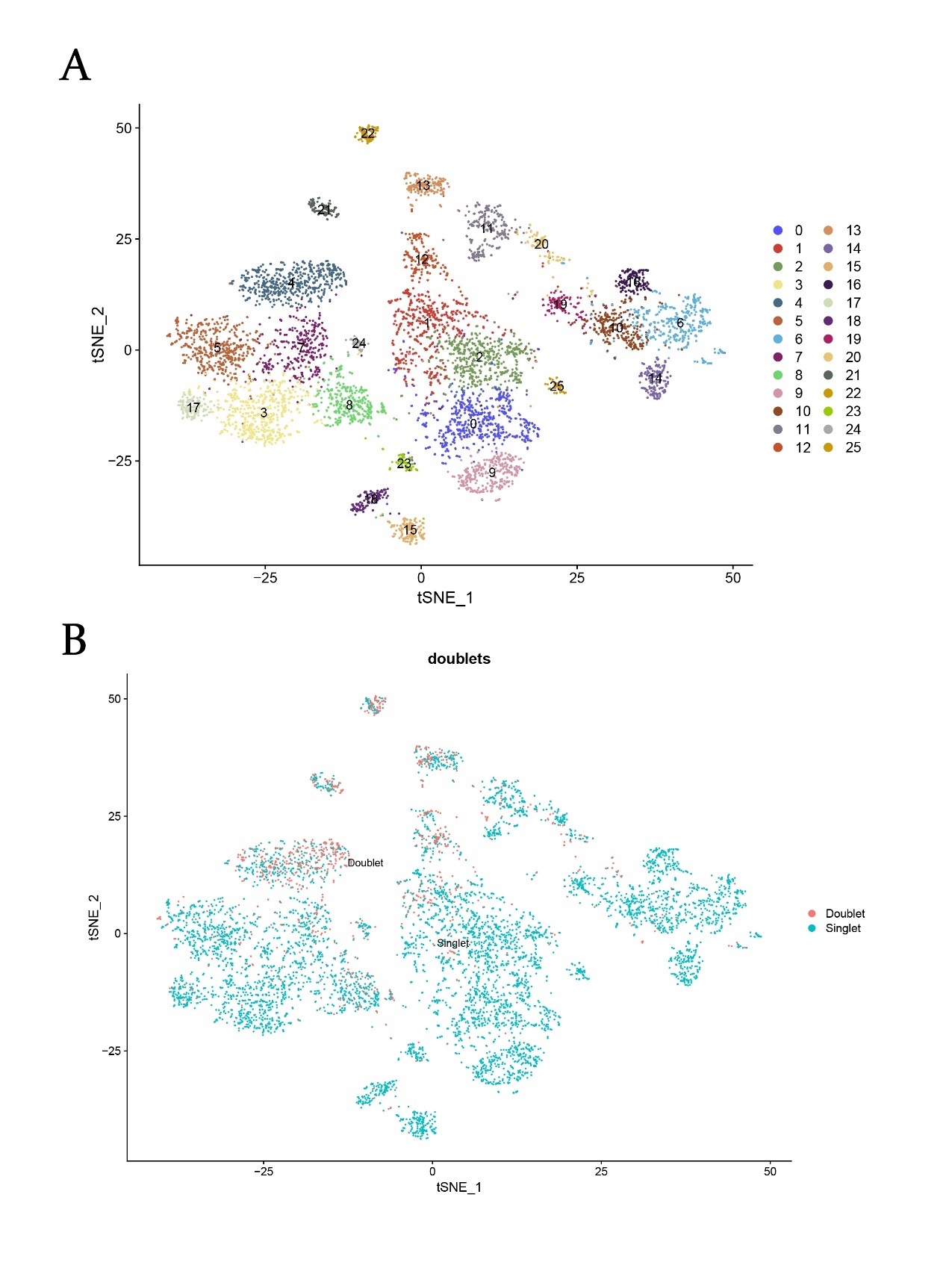


**Supplementary Figure 2.** Correlation of risk score with clinical features. A: Differences in risk scores between ages. B: Differences in risk scores between sexes. C: Differences in risk scores between tumor stages. D: Differences in risk scores between stages. Significantly different at: \**p*<0.05,\*\**p*<0.01 and \*\*\*\**p*<0.0001.

**Supplementary Figure 3**

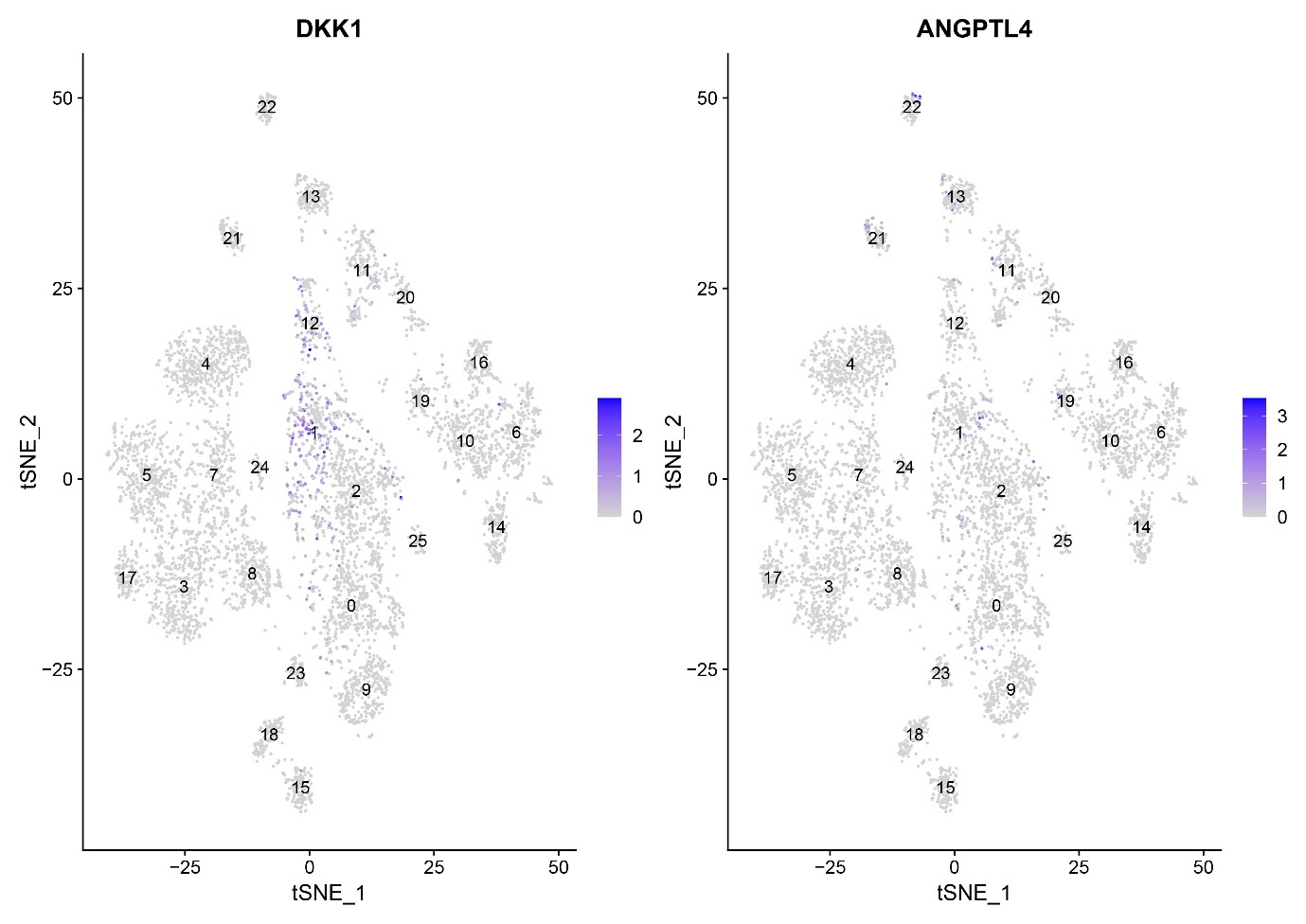
**Supplementary Figure 3.** Decision curve analysis for the nomograms compared for 1-, 3-, and 5-year overall survival. Blue line represents all positive. Yellow line represents all negative.

**Supplementary Figure 4**

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**Supplementary Figure 4.** Clustering single-cell sequencing data of lung adenocarcinoma and normal tissue. A: Samples were clustered into 25 groups. B: Doublets *versus* singlets in samples.**Supplementary Figure 5**





**Supplementary Figure 5.** The predicted genes were significantly over-represented in basal cells and luminal cells.

