Figure S1. (A) CDF curve indicated consensus clustering of liquid-liquid phase separation-related genes in oral squamous cell carcinoma. (B) GO pathway enrichment analysis of identified DEGs between clusters C1 and C2. (C) KEGG pathway enrichment analysis of identified DEGs between clusters C1 and C2. CDF, cumulative distribution function; DEGs, differentially expressed genes; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

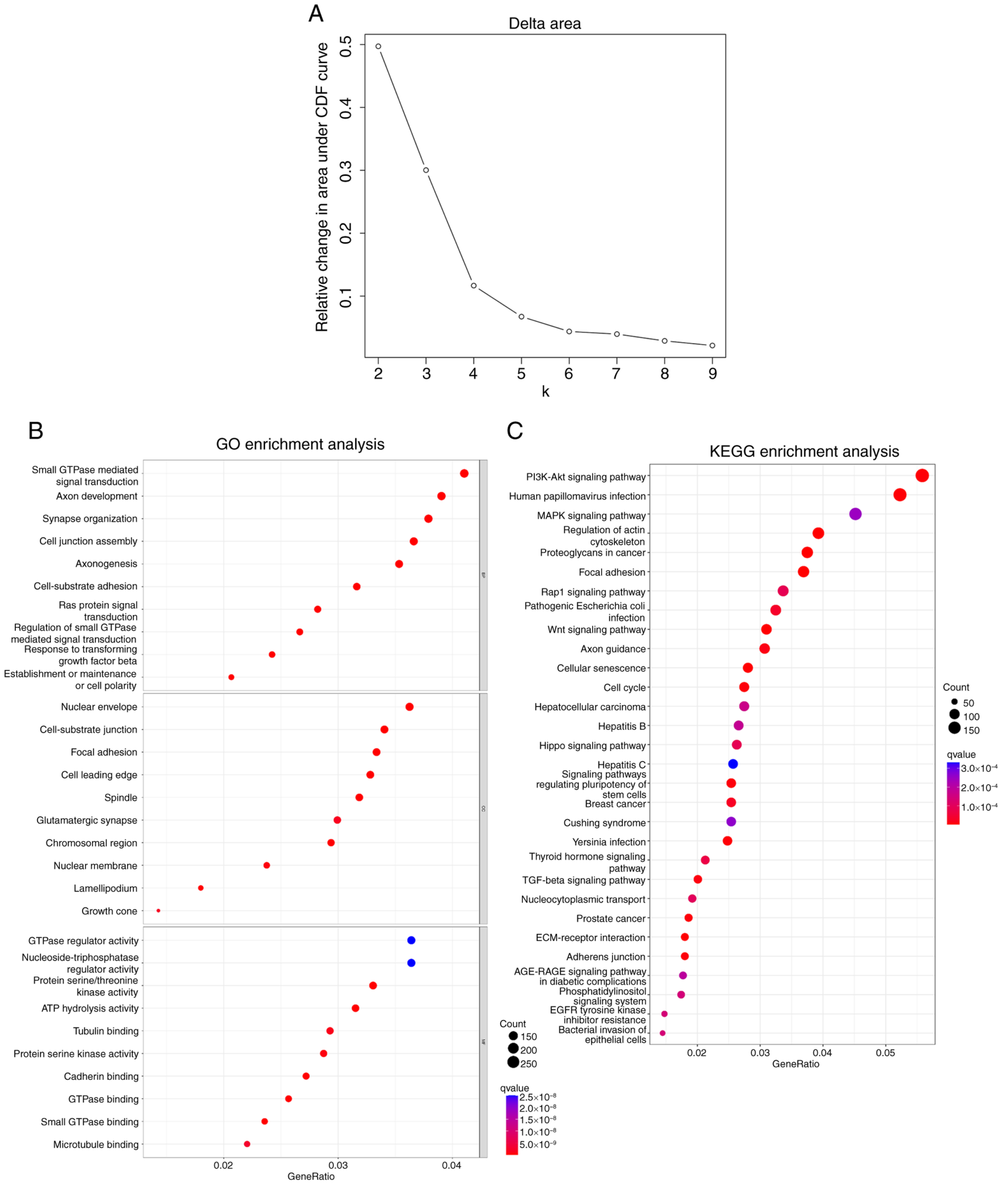

Figure S2. (A) PCA for the high- and low-risk groups in the training set. (B) tSNE analysis for the high- and low-risk groups in the training set. (C) PCA for the high- and low-risk groups in the validation set. (D) tSNE analysis for the high- and low-risk groups in the validation set. PCA, principal component analysis; tSNE, t-distributed stochastic neighbor embedding.

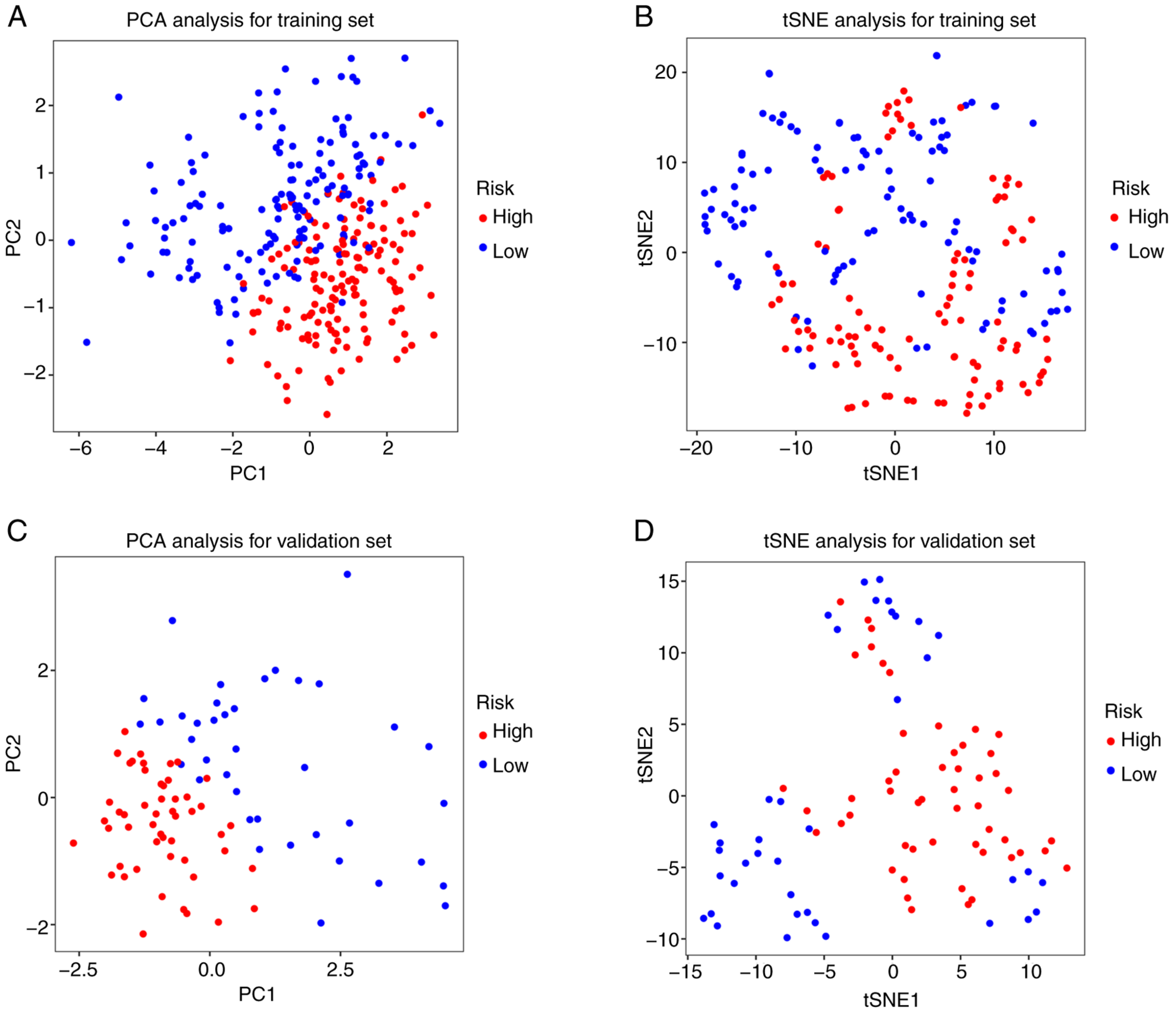

Figure S3. (A) GEPIA2 website displayed relative expression of the seven model genes in TCGA-OSCC. Reverse transcription-quantitative PCR detected expression of the seven model genes relative to MYO1B in (B) HSC3 and (C) SCC1 cells. Gene expression data were normalized to GAPDH for all quantitative calculations. For visualization purposes only, data were normalized to MYO1B to prevent axis compression from highly expressed GAPDH and to improve biological variation display. (D) GEPIA2 website generated a survival map of the seven model genes in TCGA-OSCC. The IUPred2A platform identified disordered protein regions (IUPred2) and disordered binding regions (ANCHOR2) of (E) MYO1B and (F) CDH13. PhaSePred scored liquid-liquid phase separation potential of (G) MYO1B and (H) CDH13. OSCC, oral squamous cell carcinoma.

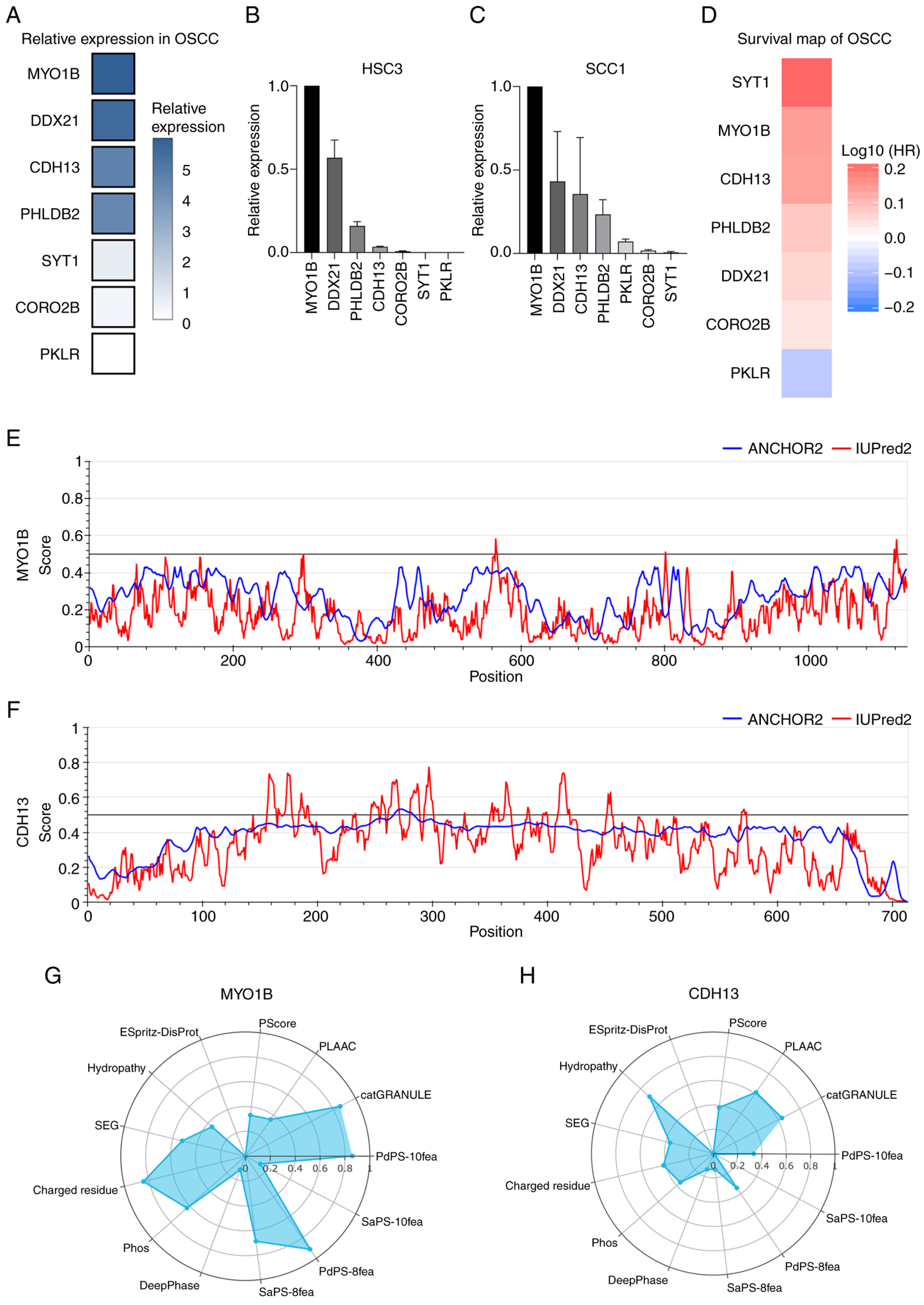

Figure S4. (A) Western blotting of PHLDB2, GAPDH and EMT biomarkers (N-cadherin, vimentin and E-cadherin) in the control-si group and PHLDB2-si group. (B) Relative expression levels of EMT biomarkers (N-cadherin, vimentin and E-cadherin) and PHLDB2 in the control-si group and PHLDB2-si group, as determined by western blotting. $^{*}P<0.05$, $^{**}P<0.01$ and $^{***}P<0.001$ vs. control-si. EMT, epithelial-mesenchymal transition; si, small interfering.

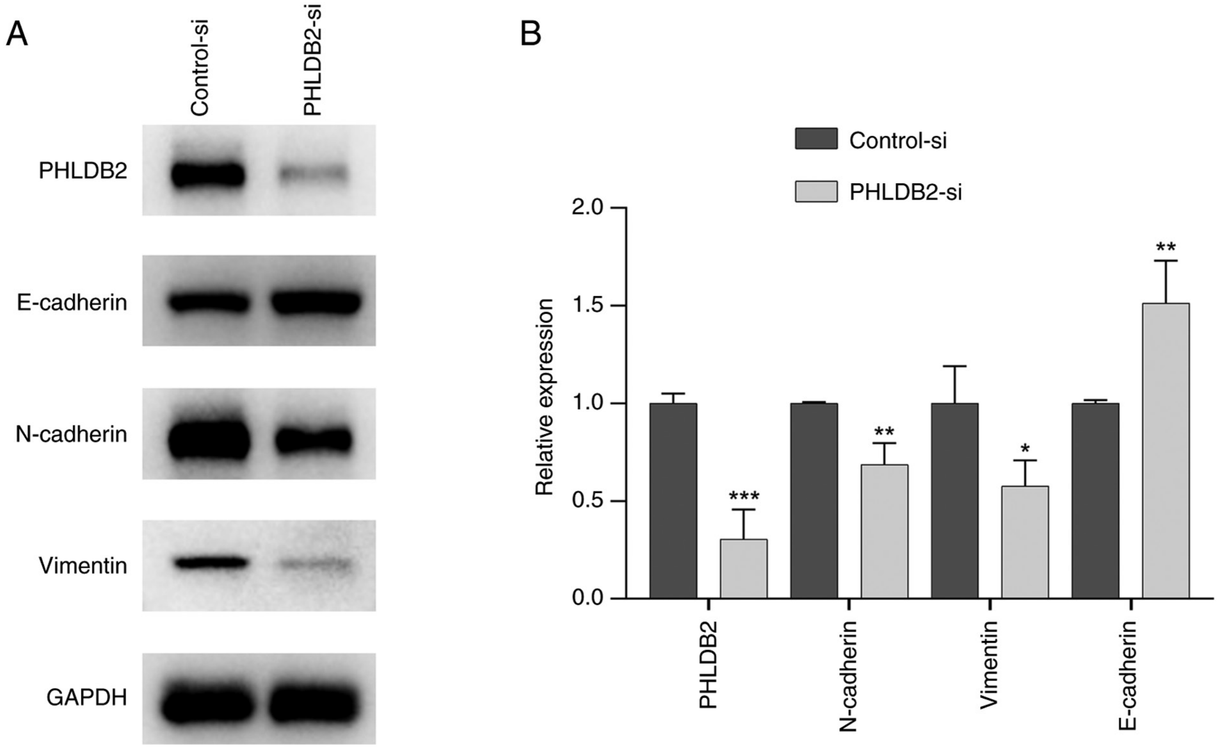

Figure S5. Representative immunohistochemical images of the same field, including (A) IgG negative control staining and (B) anti-PHLDB2 staining. Scale bar, 50 μm.