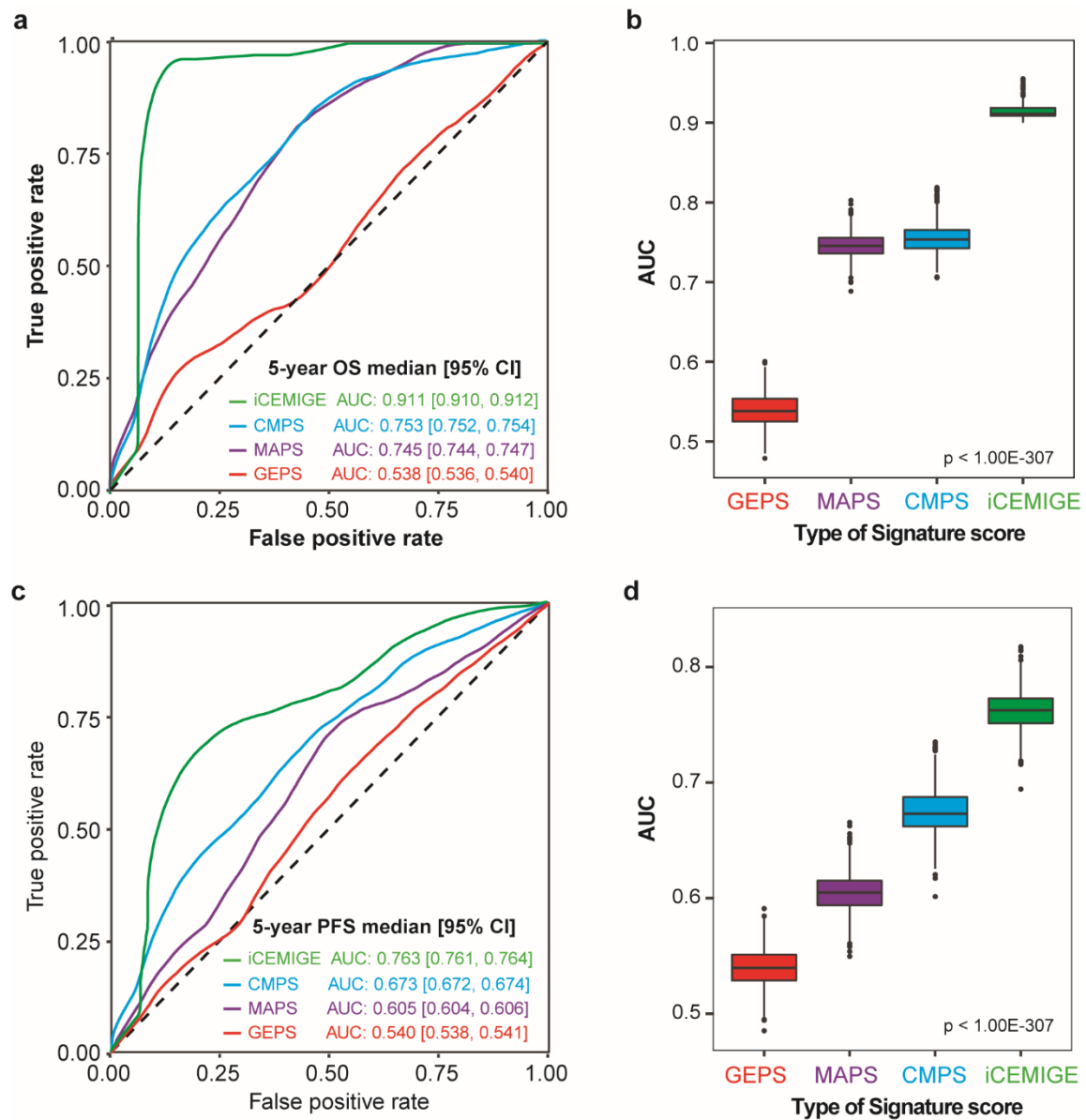
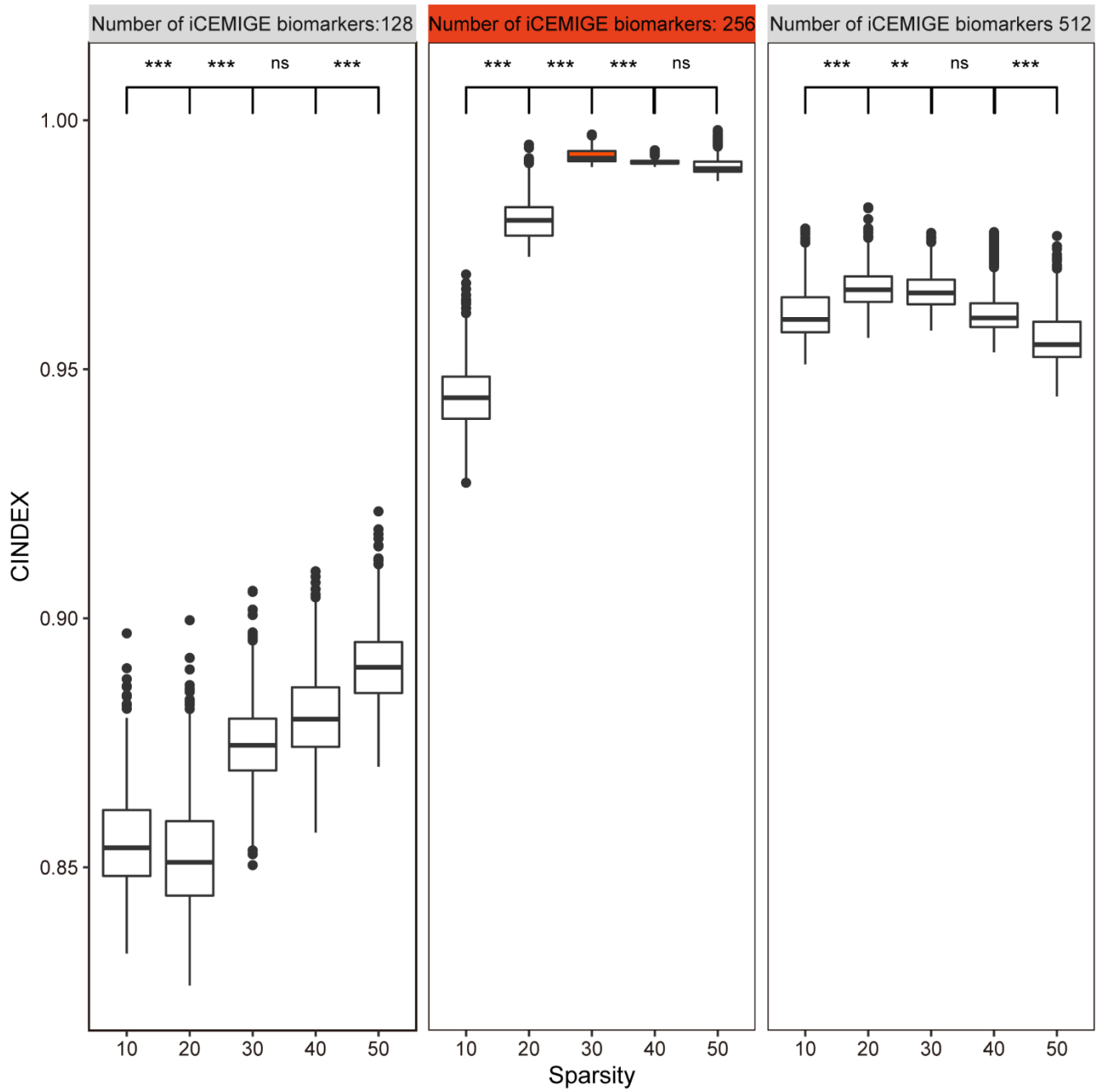


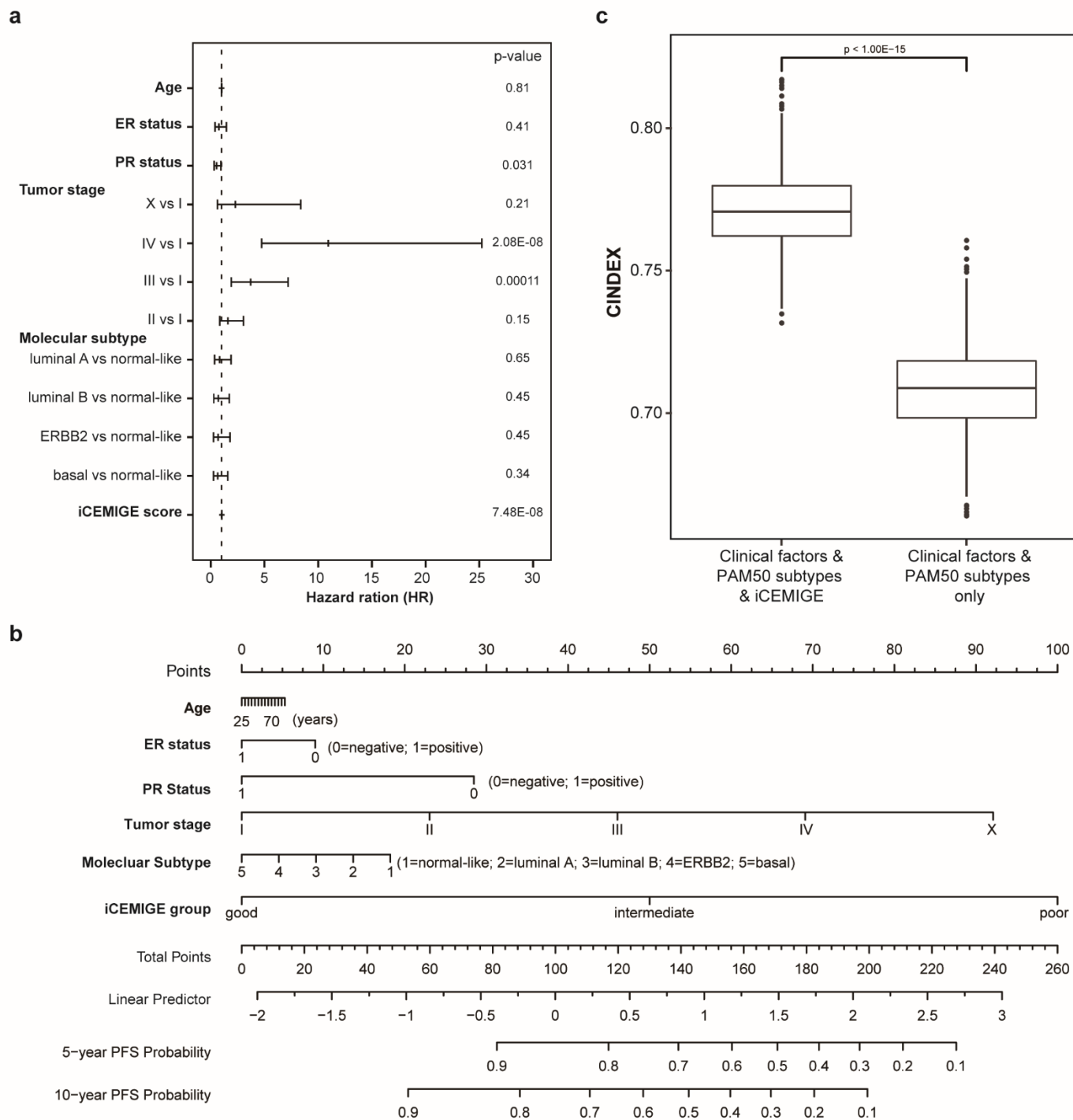
Supplementary Figure 1. Representative histopathologic image for 39-cellular morphometric biomarker signature and their corresponding Kaplan Meier curves demonstrating their significant association with overall survival in the TCGA-BRCA cohort.



Supplementary Figure 2. iCEMIGE significantly outperforms CMPS, MAPS, and GEPS in prognosis prediction in the TCGA-BRCA cohort. a ROC curves for 5-year OS prediction across different signature scores. **b** AUC of 5-year OS prediction across different signature scores. **c** ROC curves for 5-year PFS prediction across different signature scores. **d** AUC of 5-year PFS prediction across different signature scores.



Supplementary Figure 3. Optimization of multi-modal biomarker mining in iCEMIGE. The optimal number of multi-modal biomarkers (256) and sparsity constraint (30) were experimentally determined with respect to the C-index for OS using iCEMIGE models across different parameter combinations: number of multi-modal biomarkers (128, 256, 512) and sparsity constraint (10, 20, 30, 40, 50). And the C-index was evaluated with an 80% sampling rate and 1000 bootstrapping iterations. The comparison across iCEMIGE models derived with different parameter settings was based on the Mann-Whitney non-parametric test.



Supplementary Figure 4. iCEMIGE provides significant and additional value for PFS prediction. a Multivariate Cox regression analysis of PFS with HR represented as a forest for iCEMIGE score, clinical factors, and PAM50 subtypes. **b** Nomogram for predicting PFS was constructed based on integrating clinical factors and molecular subtype with iCEMIGE. **c** Comparison of C-index for PFS in different nomogram models with and without iCEMIGE. The p-value was obtained from Mann-Whitney non-parametric test.

Supplementary Table 1 Cellular morphometric context representation of patients in the TCGA-BRCA cohort (see a separate excel file).

Supplementary Table 2 Association of CMBs concerning overall survival in the TCGA-BRCA cohort, where the optimal cutpoint per CMB was provided by the survminer package (see a separate excel file).

Supplementary Table 3 Cellular-morphometrics, microbiome, gene, and multi-modal biomarkers for patients in the TCGA-BRCA cohort (see a separate excel file).

Supplementary Table 4 The coefficients of multi-modal biomarkers to calculate iCEMIGE score (see a separate excel file).

Supplementary Table 5 Clinical characteristics and prognostic score and group of patients in the TCGA-BRCA cohort (see a separate excel file).