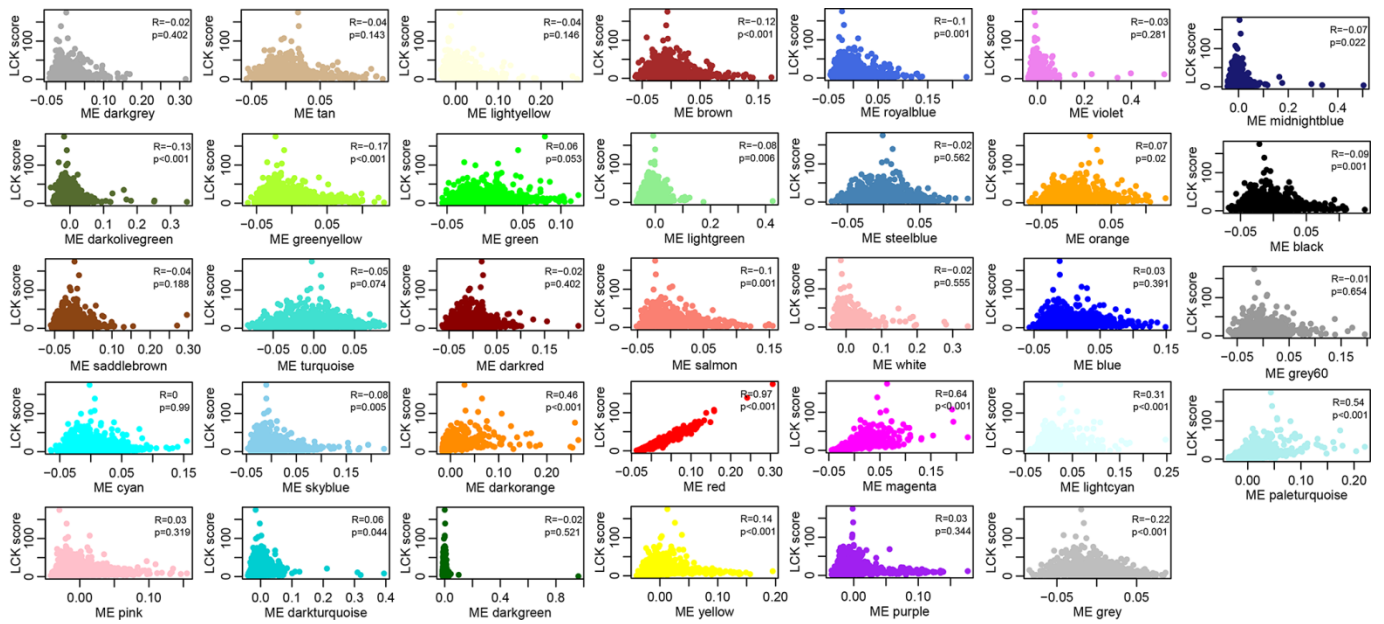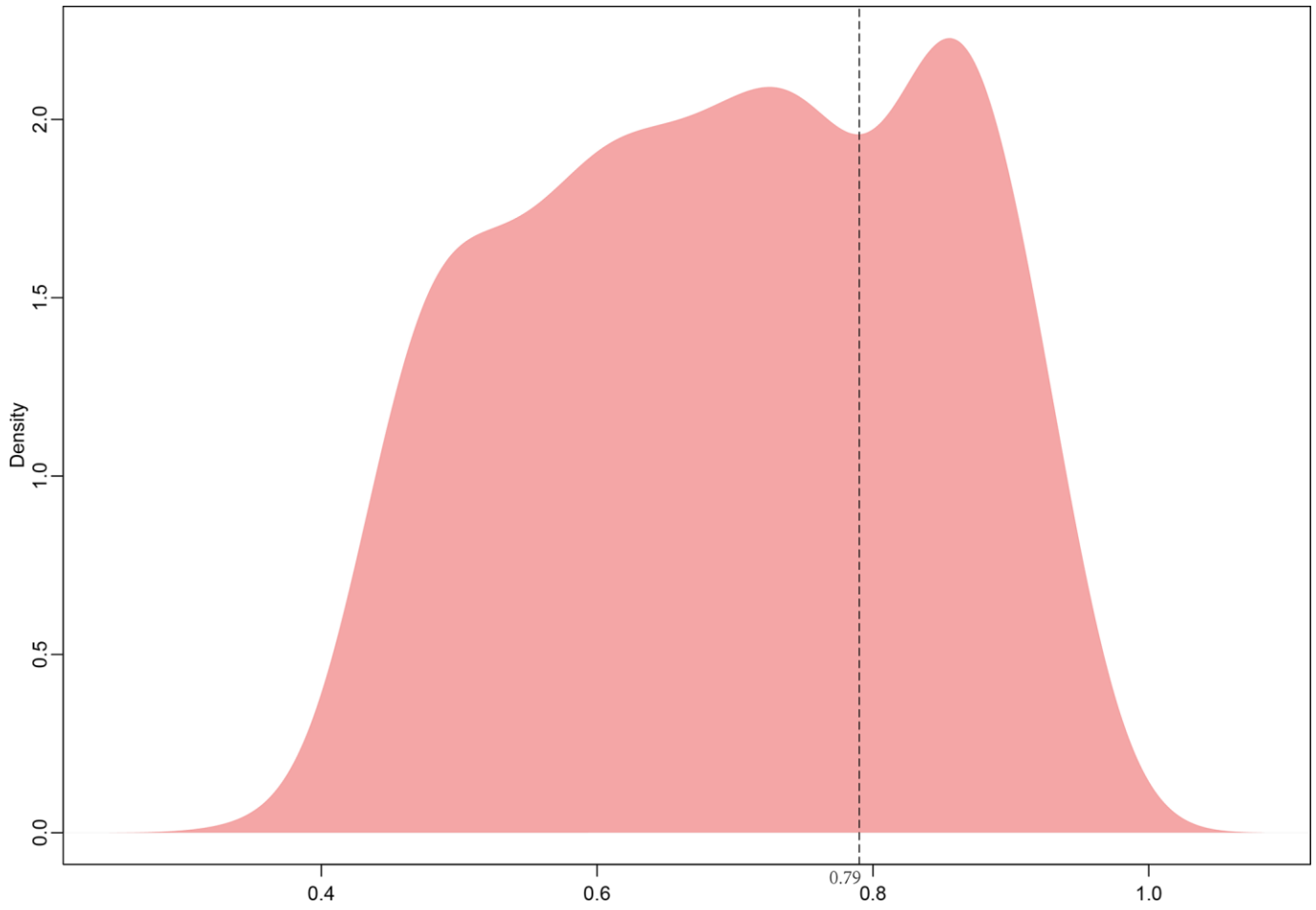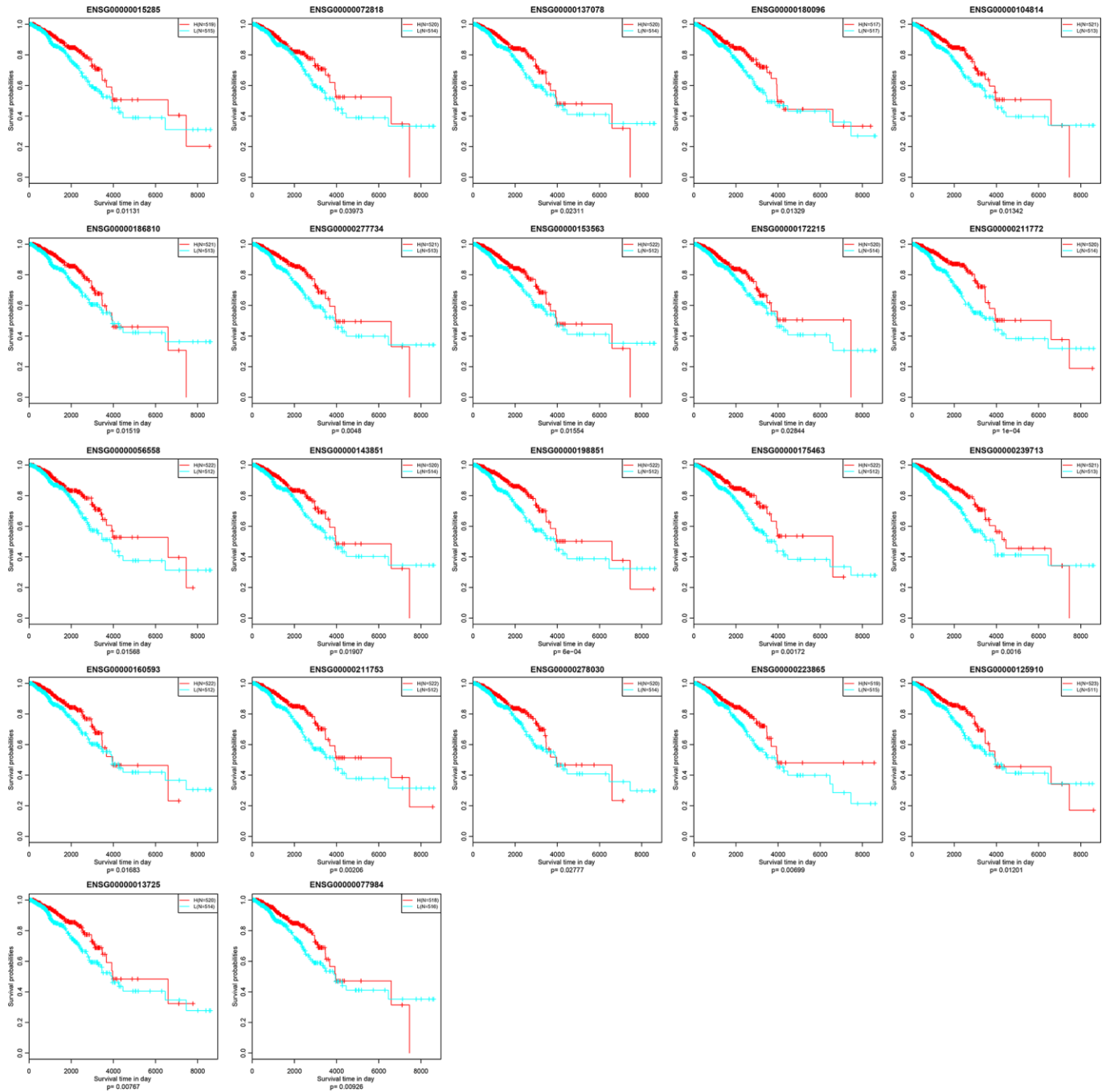Supplementary Figure 1. LCK metagenes-related gene modules mined through WGCNA. (A) Sample clustering analysis. (B, C) Analysis of network topology under various soft-thresholding powers. (D) Gene dendrogram and module colors.
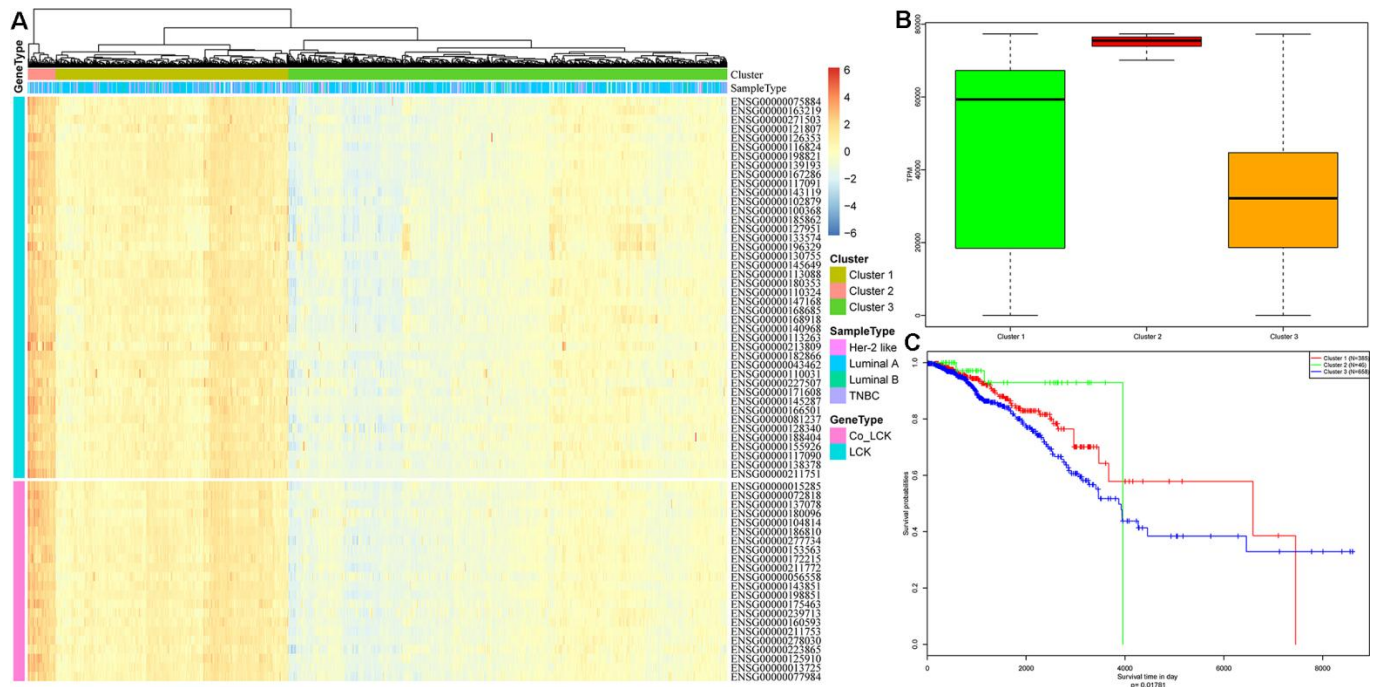

Supplementary Figure 2. Correlation between eigenvectors of 34 gene modules and LCK metagenes.

Supplementary Figure 3. Screening of module-related genes.

Supplementary Figure 4. Relationship between 22 immune microenvironment-related genes and prognosis. Kaplan-Meier survival curve between high expression and Low expression group of breast cancer patients.

Supplementary Figure 5. Correlations of 22 immune microenvironment-related prognostic genes and LCK metagenes. (**A**) Expression profiles of 22 immune microenvironment-related prognostic genes and 42 gene members in LCK metagenes. (**B**) LCK metagenes scores in the three clusters. (**C**) Kaplan-Meier survival curves for the three clusters.
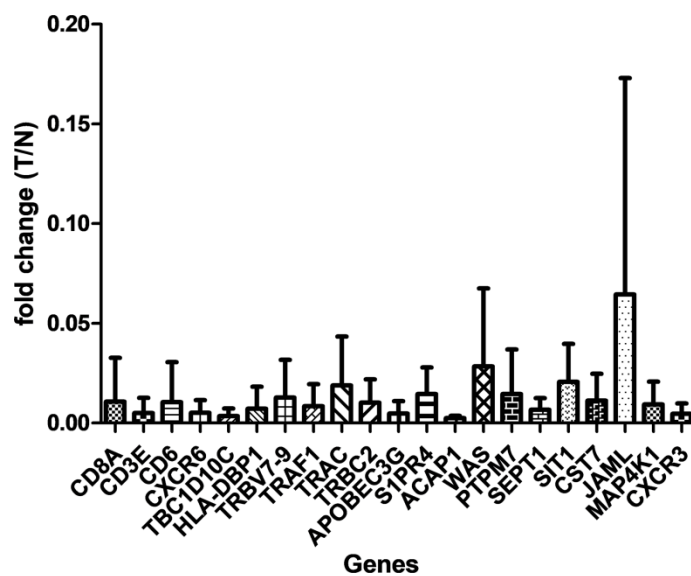
Supplementary Figure 6. Fold change of 22 genes. Data are represented as mean +/- SD.