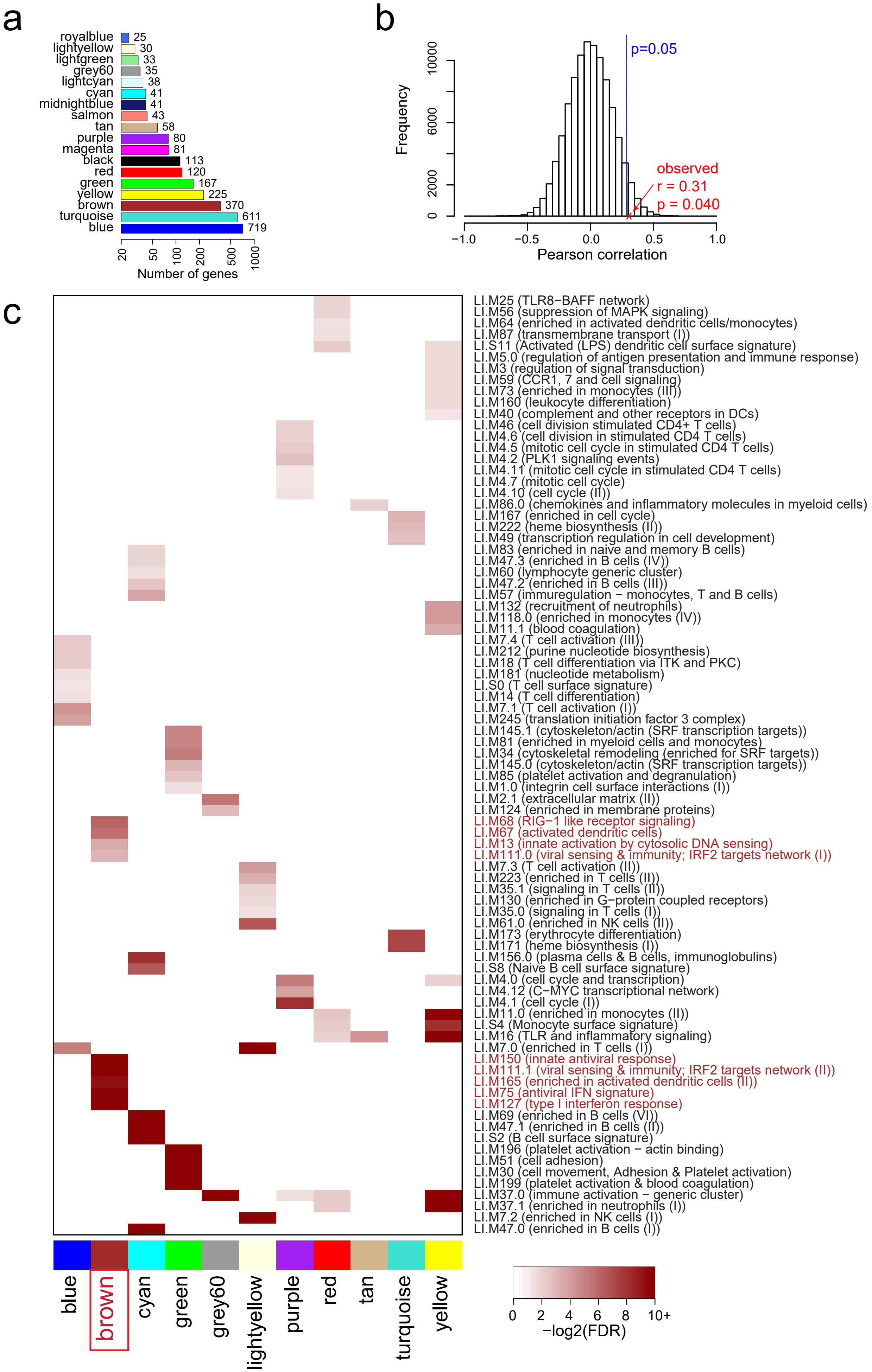
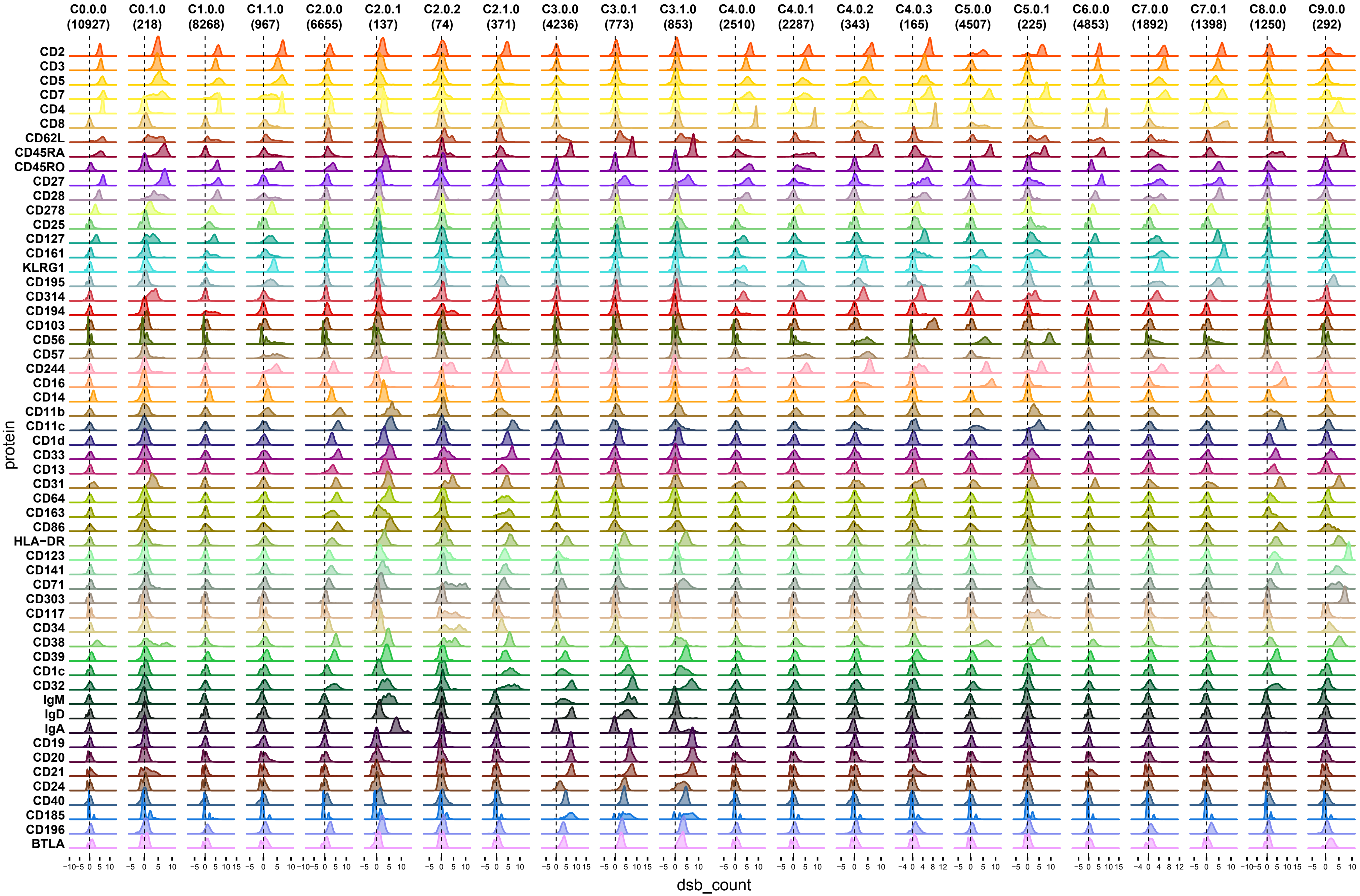
Supplementary Figure 1



Supplementary Figure 1: Evaluation of the brown module. a, Size distribution of the 18 transcriptomic modules shown in Fig. 3a. **b,** Empirical null distribution generated by randomly permuting DaCP subject labels and recalculating the Pearson correlation with the brown module eigengene. Empirical p-values were determined by comparing the observed correlations with the null distribution generated by permutation. This allowed assessment of the statistical significance of the observed correlation in Fig. 3b (p=0.04 permutation test). The blue line indicates p=0.05 significance level based on the null distribution, and the red cross denotes the observed correlation. **c,** Enrichment of blood transcriptomic modules[21] (BTMs) in WGCNA modules shown in (**a**) using the hyper-geometric test (9601 genes were used as the background); the heatmap color indicates the -log10 of the BH-adjusted one-tailed p-value (FDR); only modules enriched for at least one BTM are shown (FDR<0.05). The brown BTM labels denote those that are enriched in the brown module.

Supplementary Figure 2



Supplementary Figure 2: The distribution of denoised and background rescaled (see Methods) counts for the surface proteins shown in Fig. 4c. Only clusters formed by spectral clustering at resolution 1.0 (level 3 clusters) are shown. Each column corresponds to a cluster (see Fig. 4b,c); the number of cells in each cluster is shown in parentheses. Each protein (row) is labeled with a single color. Proteins are ordered according to Fig. 4c; cell clusters are ordered according to Fig. 4b.