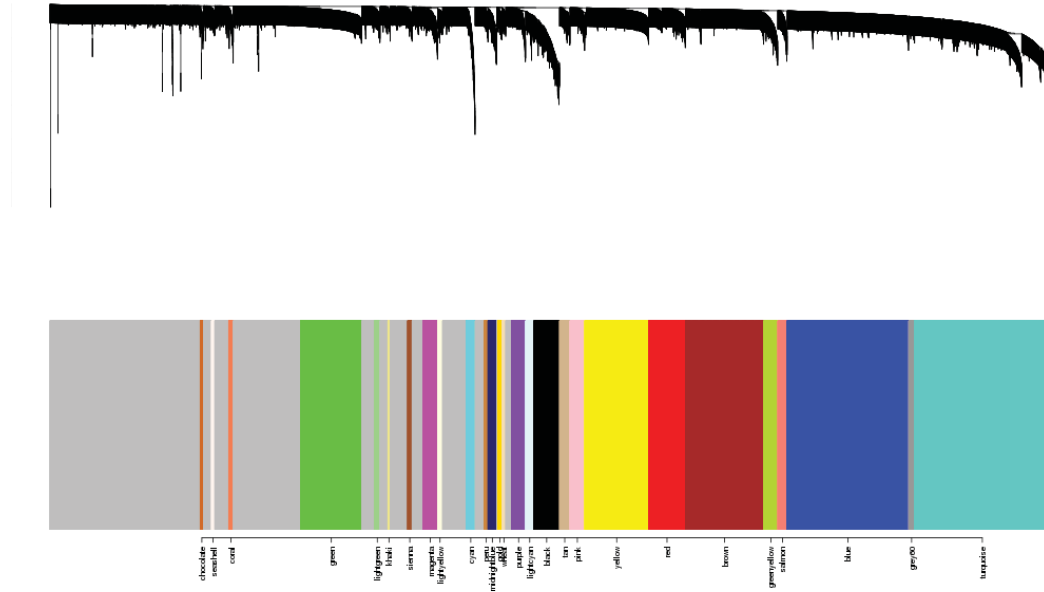**Supplementary Fig S2: Dynamic tree-cut plots of the coexperssion networks using gene expression data adjusted and unadjusted for cell counts, respectively.** A) network from cell count adjusted analysis; B) network from cell count unadjusted analysis. The gene clustering tree (dendrogram) was obtained from an average linkage hierarchical clustering of adjacency-based dissimilarity metric. The dynamic tree-cut algorithm was then used to choose the cut-off for module identification. The modules are highlighted as color blocks. The height of the tree (dendrogram) indicates the dissimilarity score among genes.

A

B