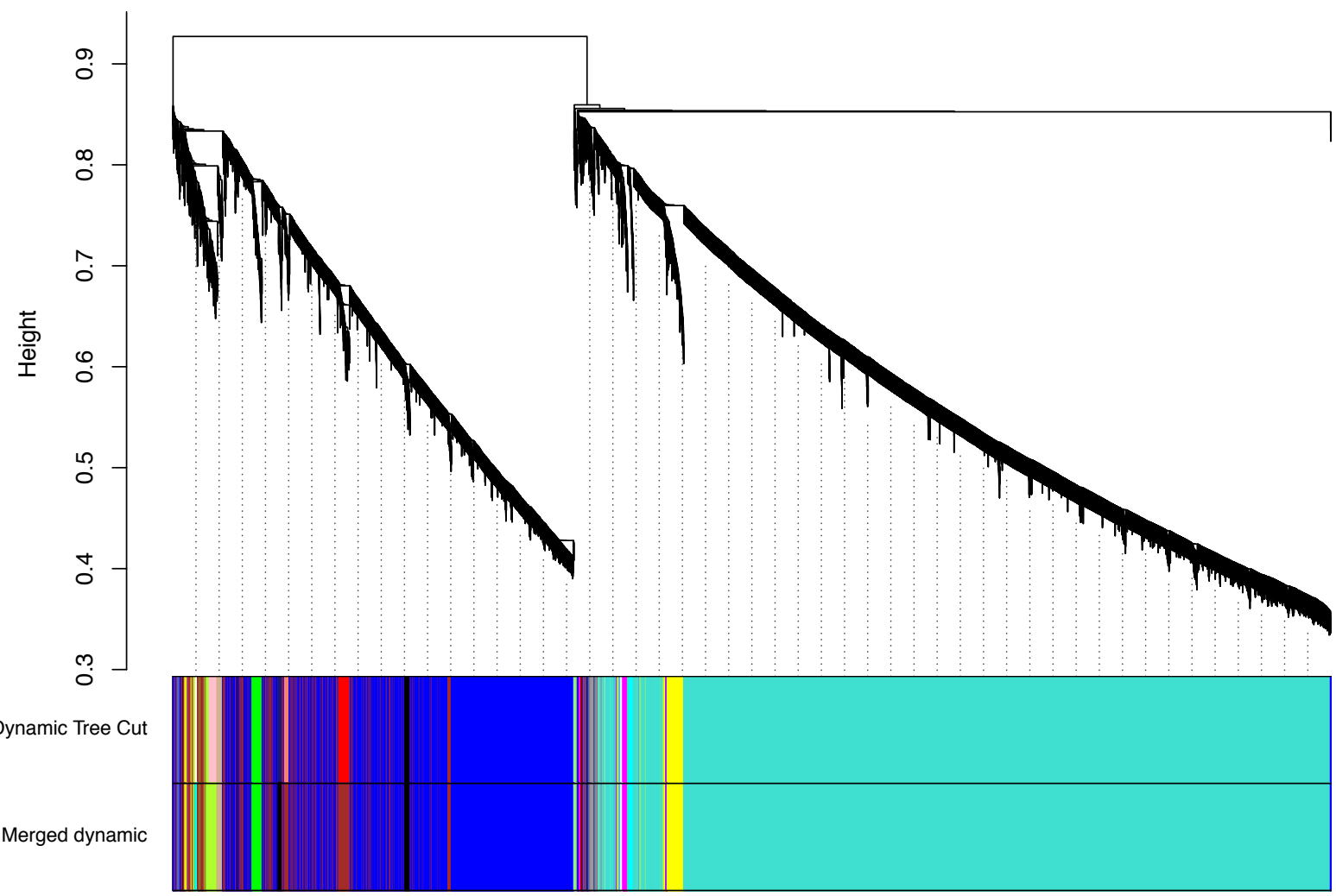


Cluster Dendrogram



Supplementary Figure S2 shows the results of the hierarchical clustering algorithm and the dynamic tree cut. The y-axis represents a dissimilarity measurement based on topological overlap, with the more similar topological overlaps corresponding to lower heights. Each branch of the dendrogram represents one gene. Branches of the dendrogram are “pruned” into modules, corresponding to each color in the bottom rows. The top color row shows the module grouping after the initial dynamic tree cut (21 modules), while the bottom color row shows the module grouping after merging similar modules (16 remaining modules).