

Supplementary Figures

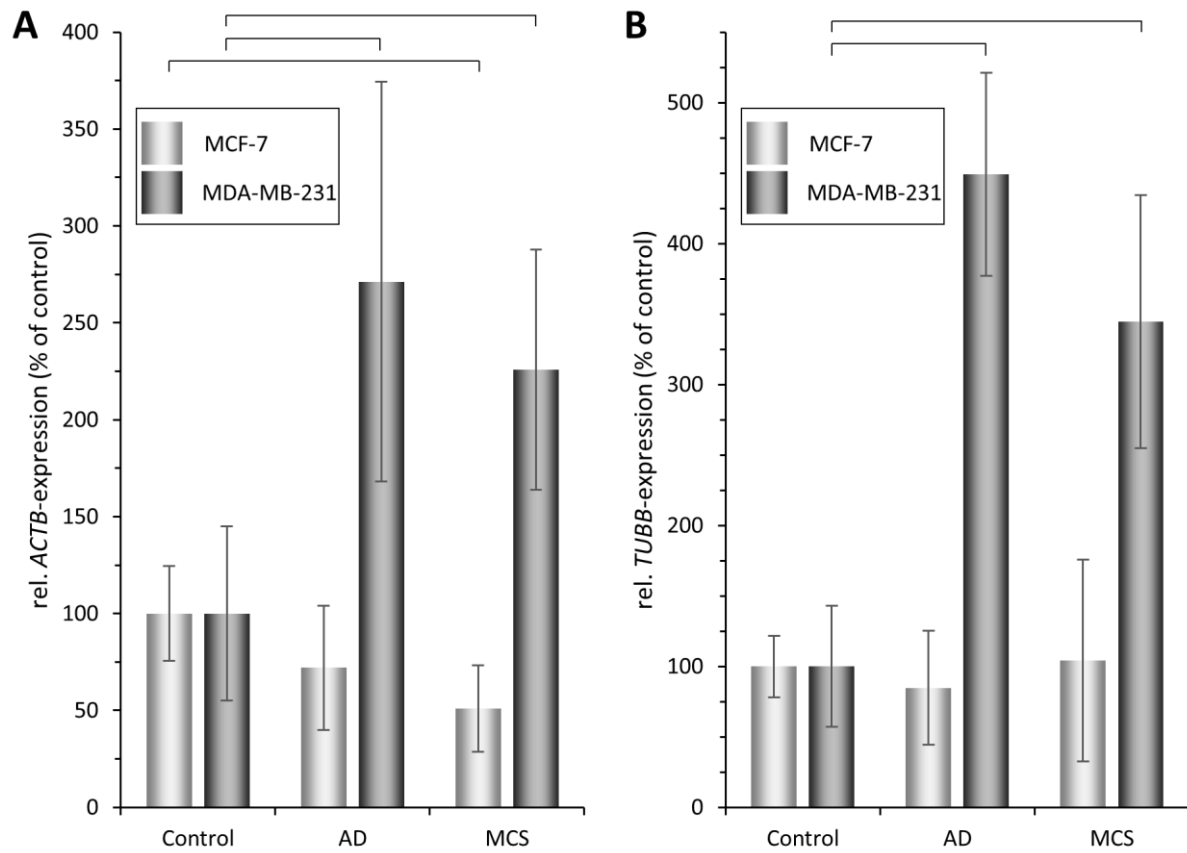


Figure S1: qPCR analysis of cytoskeletal components

A: gene expression of *ACTB*, **B:** gene expression of *TUBB*. n=5. Brackets indicate statistically significant differences with $P < 0.05$.

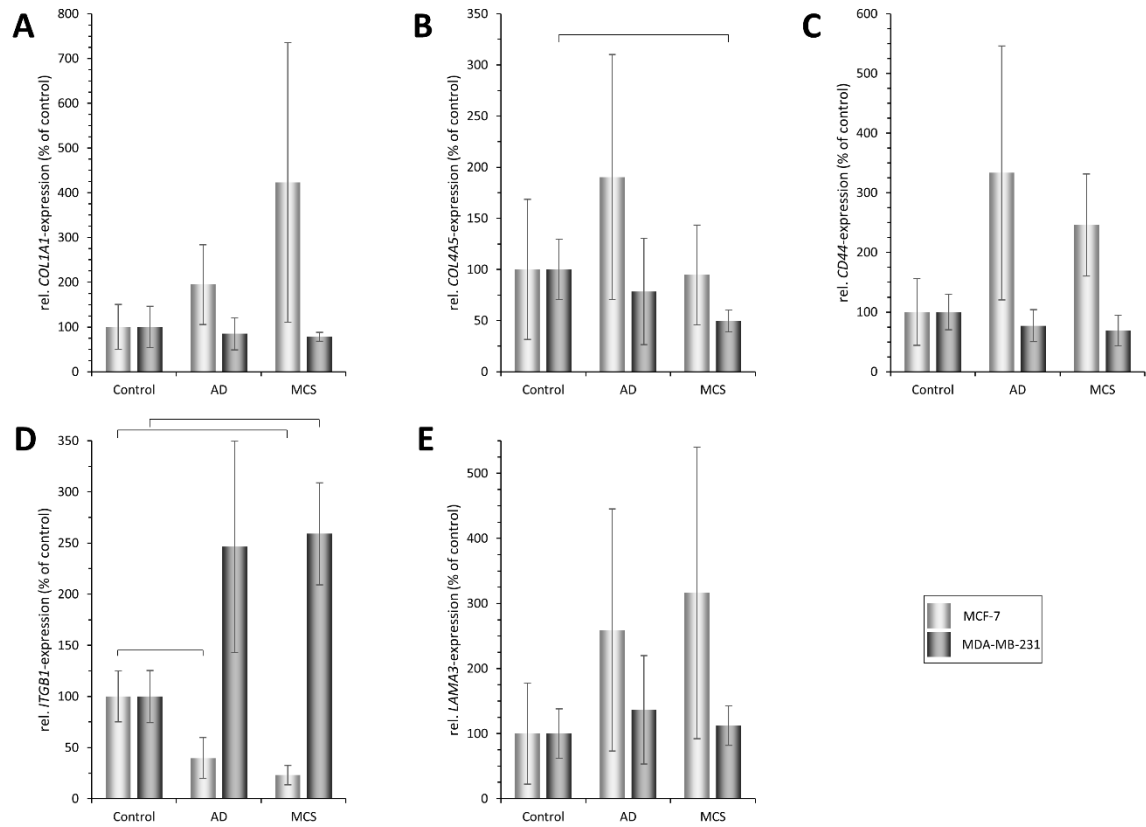


Figure S2: Gene expression of extracellular matrix genes

A: *COL1A1*, **B:** *COL4A5*, **C:** *CD44*, **D:** *ITGB1* and **E:** *LAMA3* gene expression profiles of MCF-7 and MDA-MB-231 BCC exposed to the RPM for 14d. n=5. Brackets indicate statistically significant differences with P < 0.05.

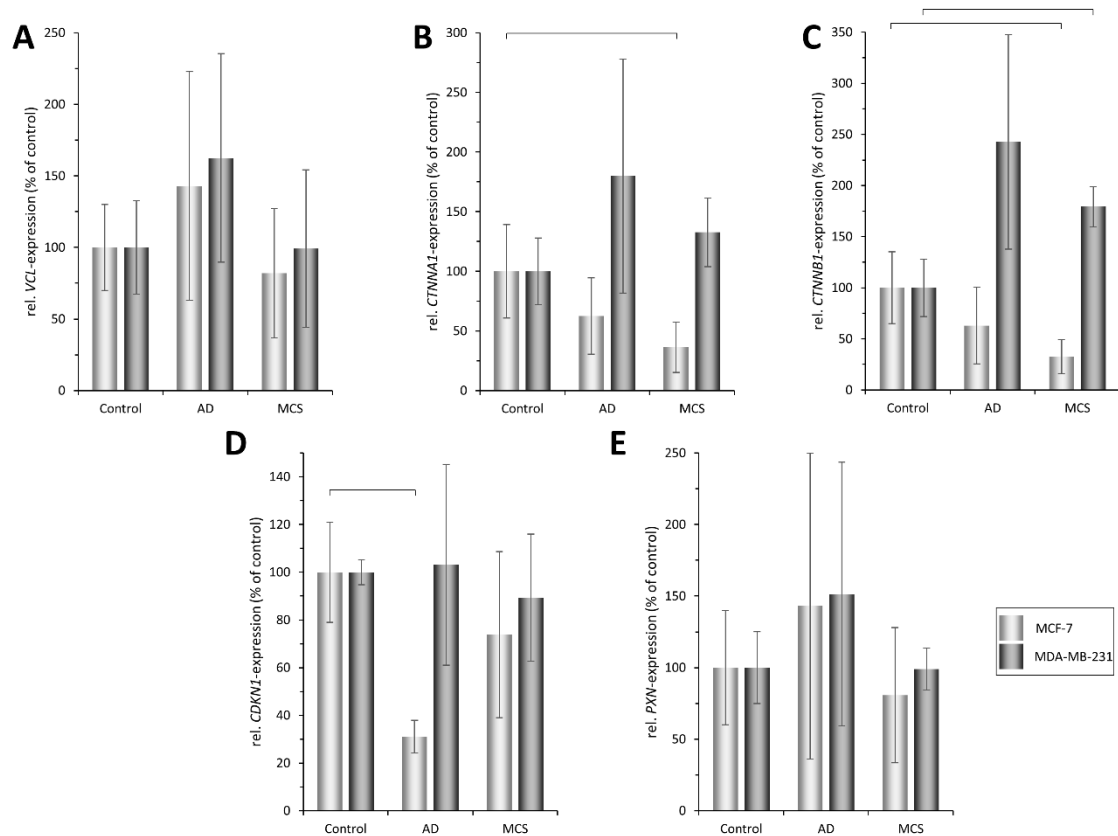


Figure S3: Gene expression of focal adhesion molecules

A: *VCL*, **B:** *CTNNA1*, **C:** *CTNNB1*, **D:** *CDKN1*, and **E:** *PXN* gene expression profiles of MCF-7 and MDA-MB-231 BCC exposed to the RPM for 14d. n=5. Brackets indicate statistically significant differences with $P < 0.05$.

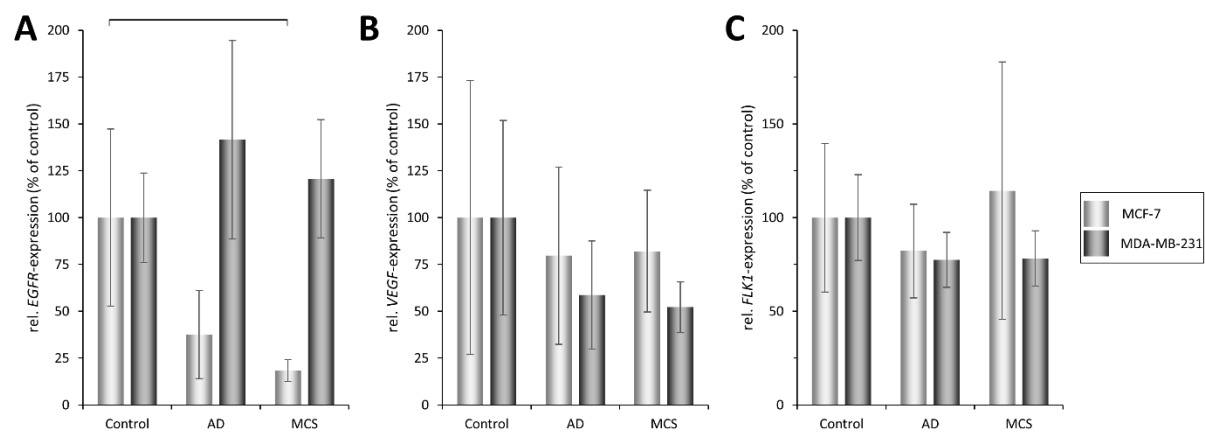


Figure S4: Gene expression of growth factors

A: *EGFR*, **B:** *VEGF*, and **C:** *FLK1* gene expression profiles of MCF-7 and MDA-MB-231 BCC exposed to the RPM for 14d. n=5. Brackets indicate statistically significant differences with $P < 0.05$.

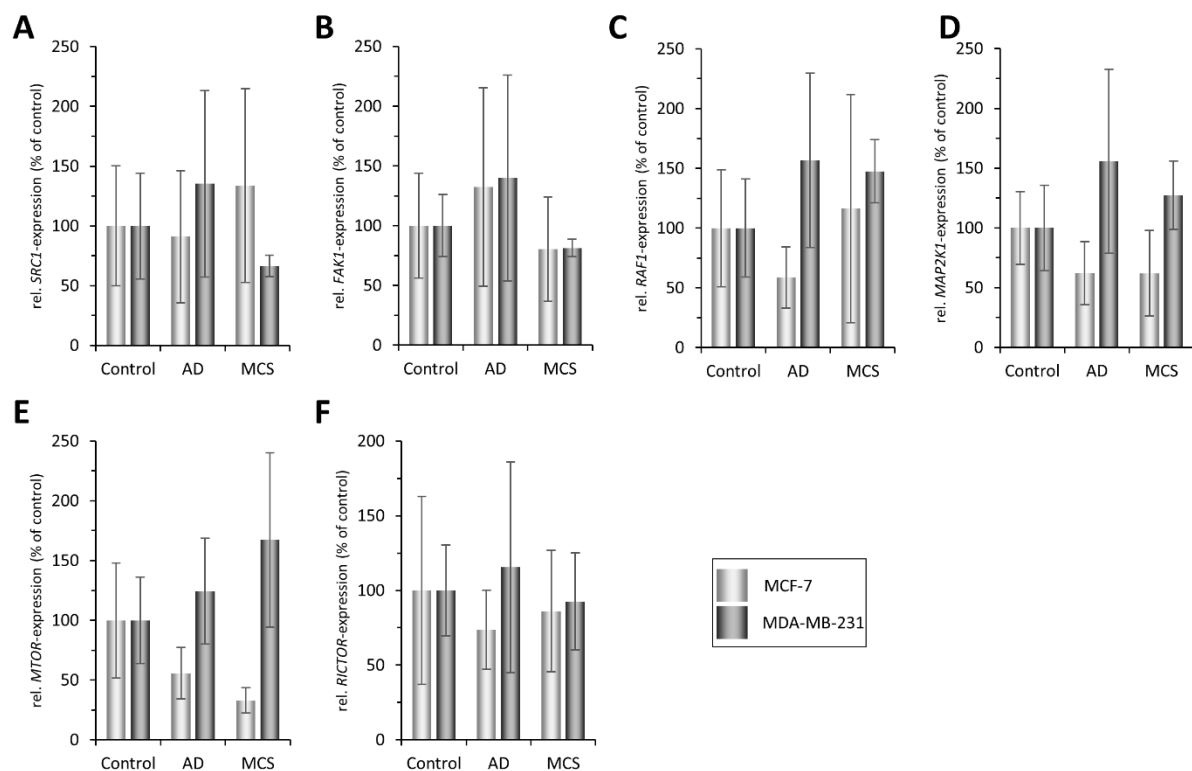


Figure S5: Gene expression of signaling factors

A: *SRC1*, **B:** *FAK1*, **C:** *RAF1*, **D:** *MAP2K1(MEK)*, **E:** *MTOR* and **F:** *RICTOR* gene expression profiles of MCF-7 and MDA-MB-231 BCC exposed to the RPM for 14d. n=5. Brackets indicate statistically significant differences with $P < 0.05$.

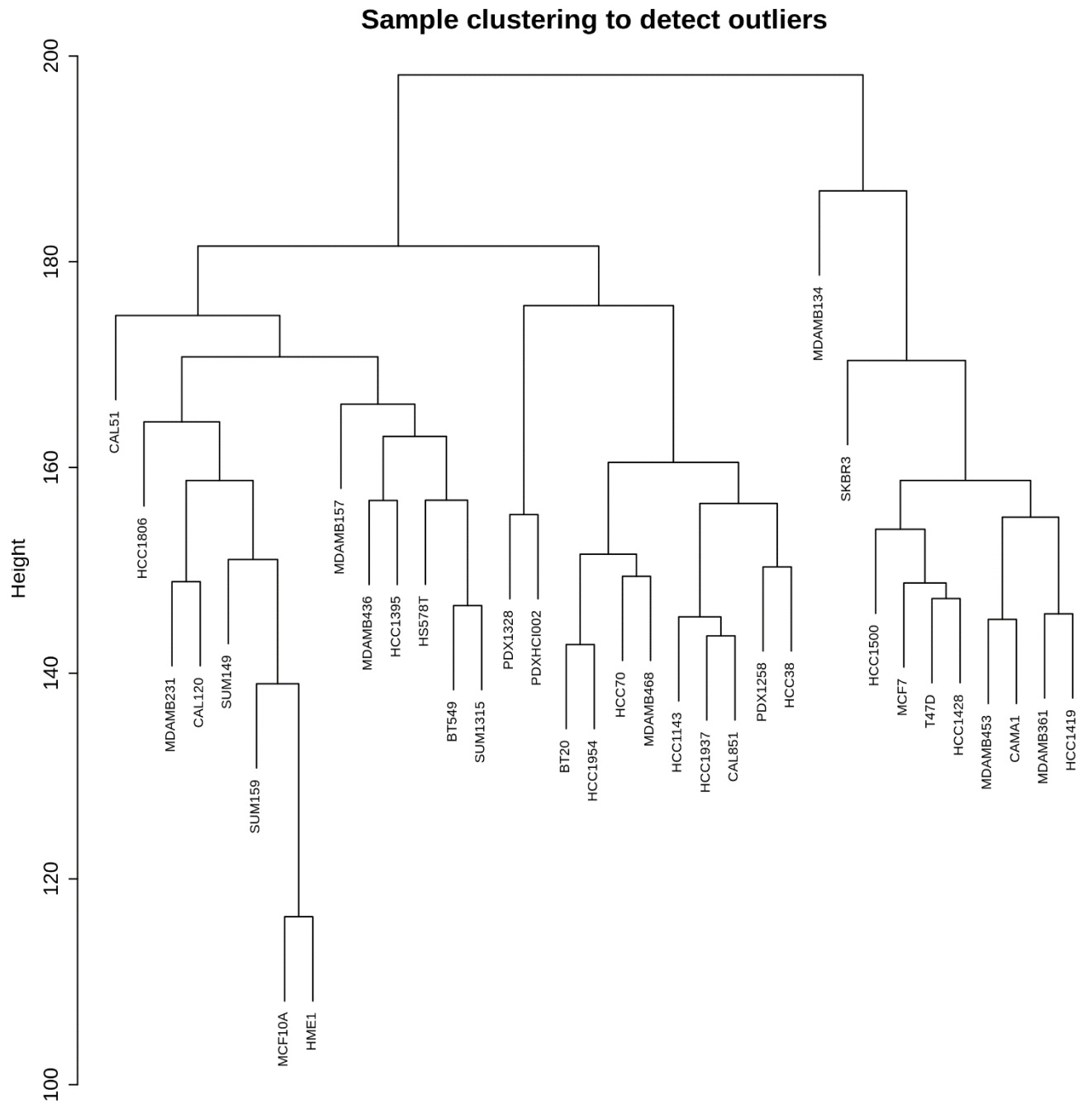


Figure S6: The sample cluster of the cancer cell lines.

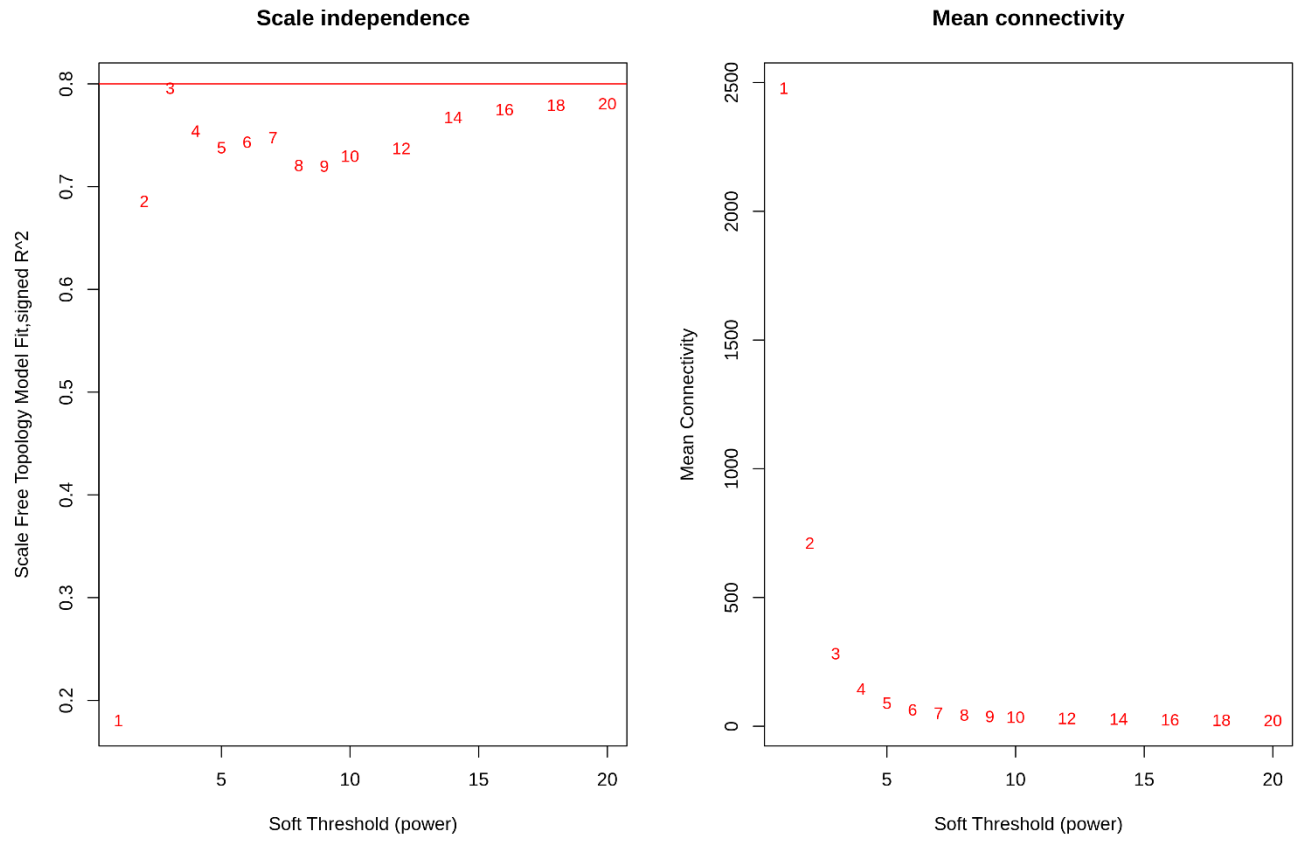


Figure S7: WGCNA network and module detection. Selection of the soft-thresholding powers. The left panel showed the scale-free fit index versus soft-thresholding power. The right panel displayed the mean connectivity versus soft-thresholding power.

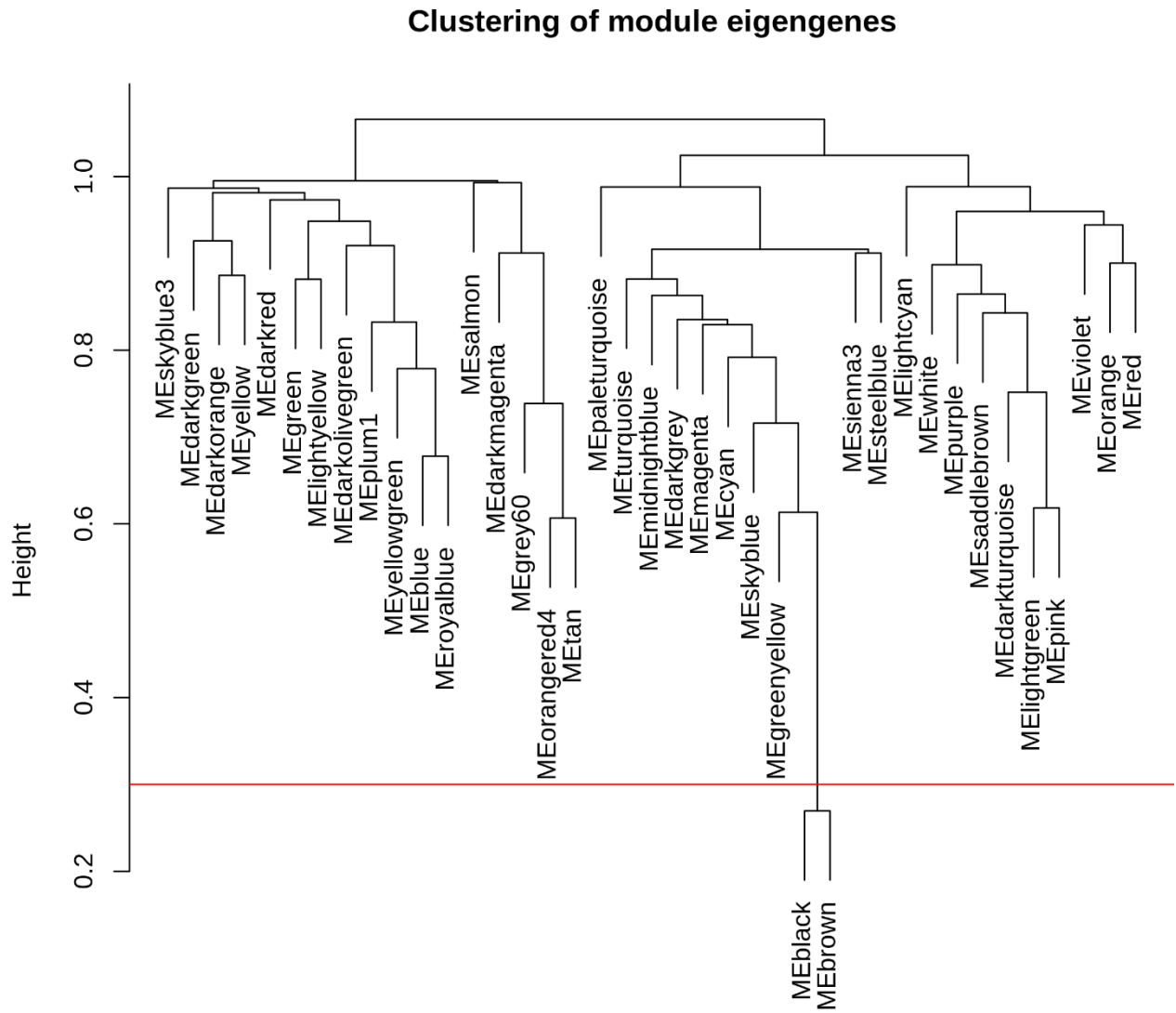


Figure S8: Clustering dendrogram of genes, with dissimilarity based on topological overlap, the red line indicates the cut height of 0.3, corresponding to merge correlation with 0.7.

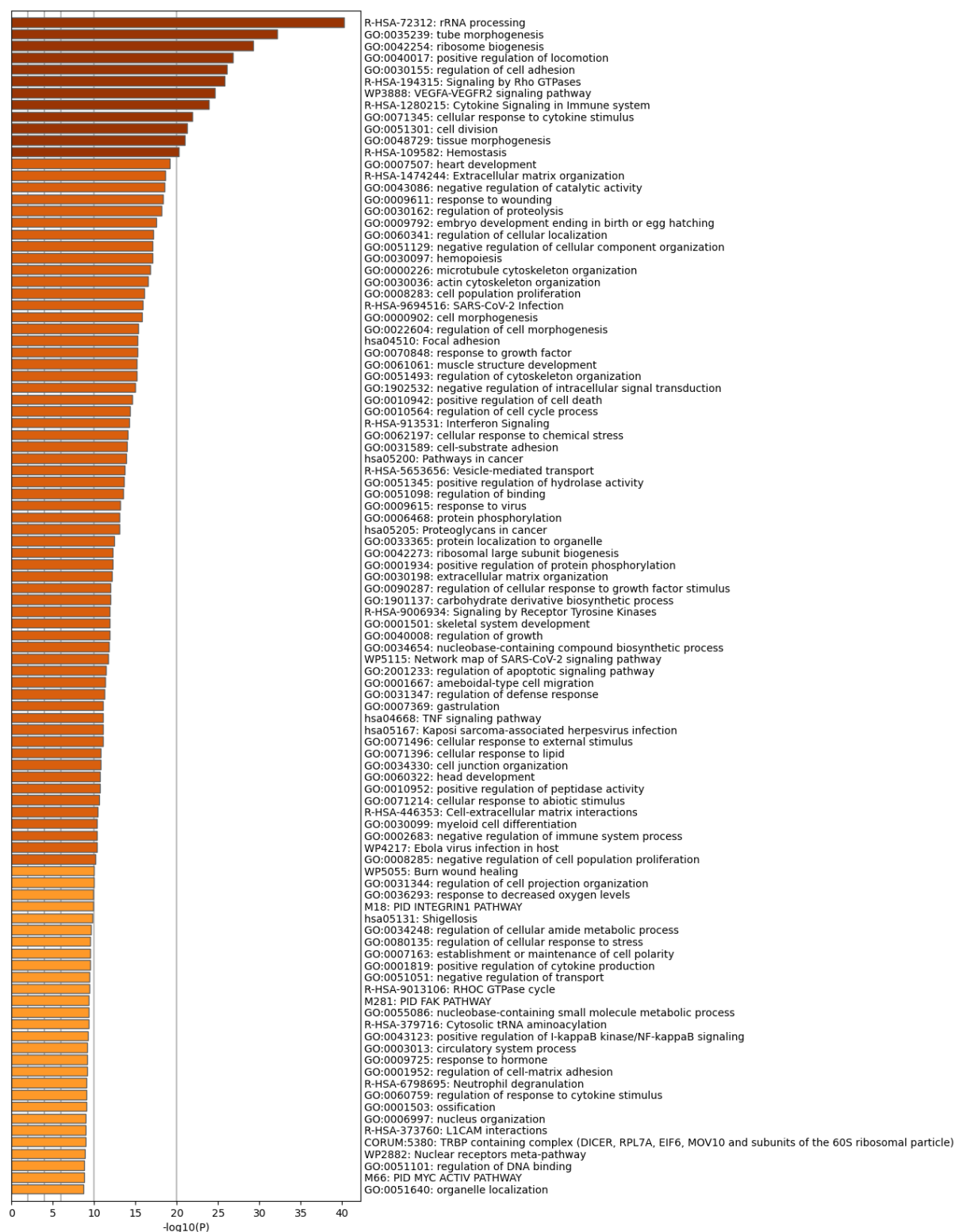


Figure S9: Bar graph of top 100 enriched terms across input gene lists, colored by p-values

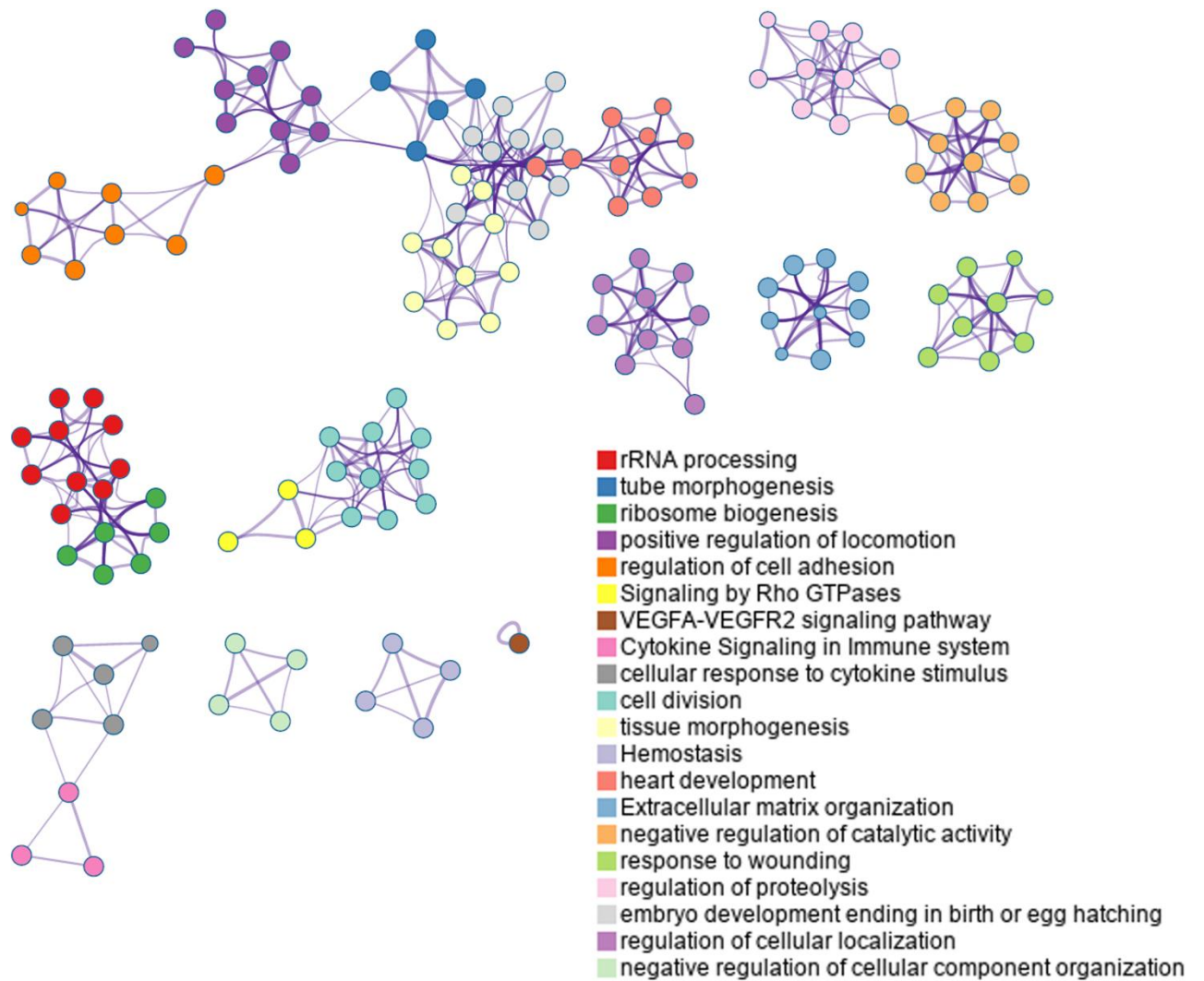


Figure S10: Network of enriched terms colored by cluster ID, where nodes that share the same cluster ID are typically close to each other.

