

RNA Sequencing Data

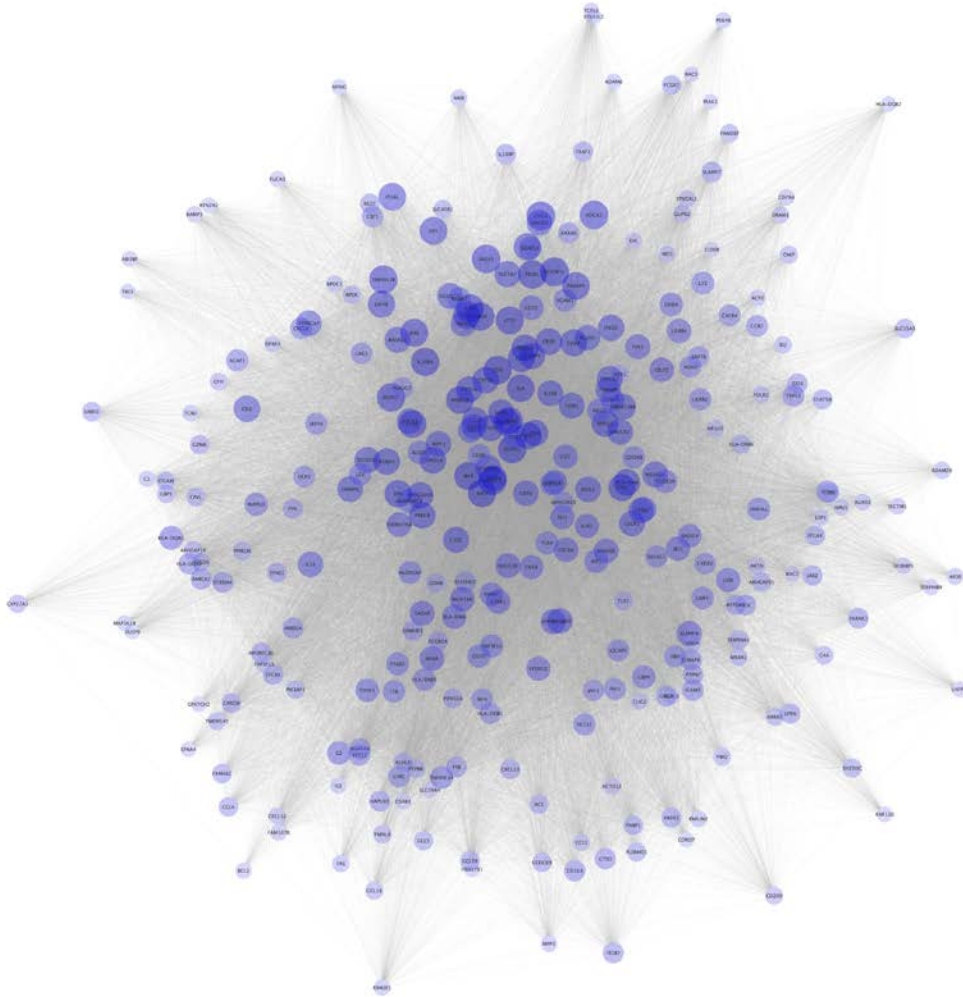
We used RNA-seq data publicly available in The Cancer Genome Atlas (TCGA) (1). Using ‘TCGABiolinks’ R/Bioconductor package (2), we downloaded the level three RNA-seq data of head and neck squamous cell carcinoma from TCGA data portal (<https://portal.gdc.cancer.gov/>), which consisted of 21022 genes from 520 samples obtained with Illumina HiSeq RNASeqV2 (Illumina, San Diego, CA, USA). Clinical information, including vital status, follow-up time, and time of death was also collected as the same manner.

TCGA Data Preprocessing

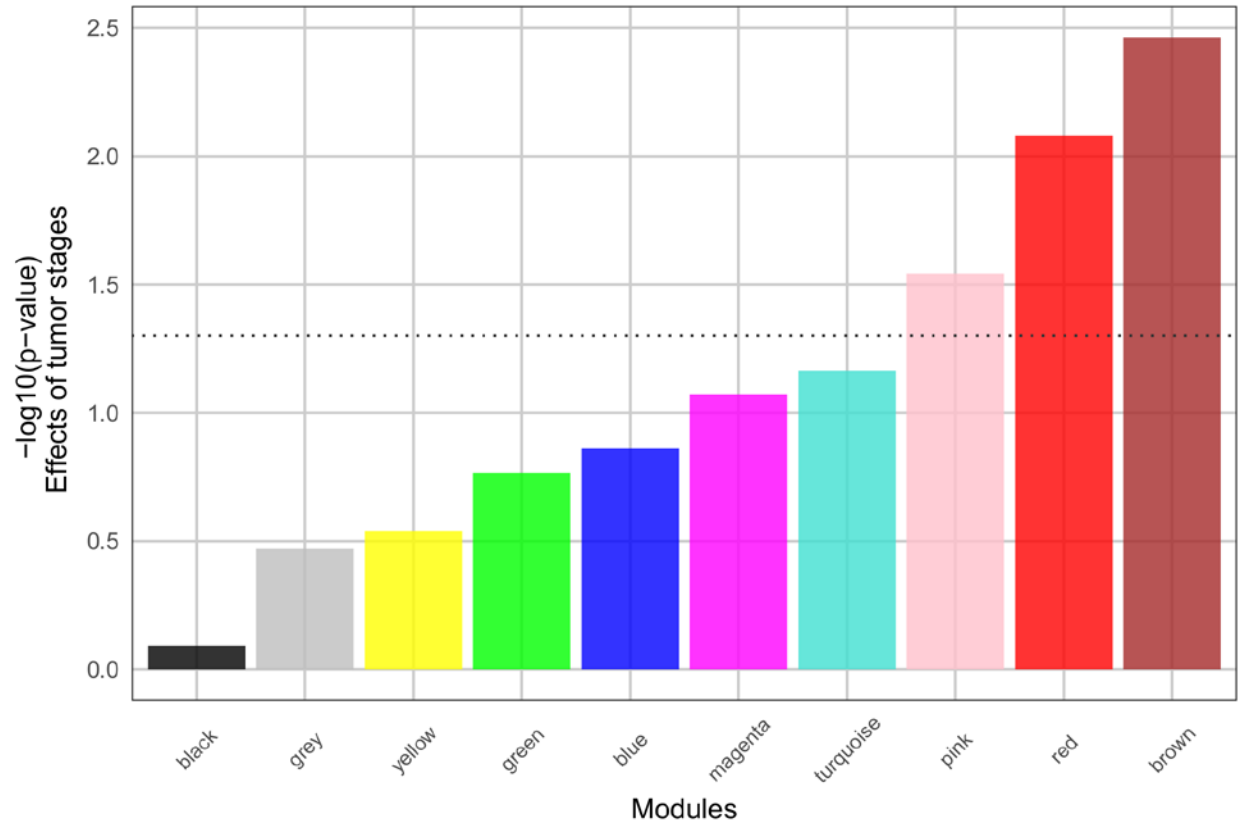
We searched for possible outlier samples from the raw expression data by calculating array-array intensity correlation based on the Pearson’s correlation coefficient for all samples; consequently, thirty outliers were removed from the raw expression data. We normalized mRNA transcripts using ‘TCGAAalyze_Normalization’ function and filtered out mRNAs with low signals across samples using ‘TCGAAalyze_Filtering’ function in ‘TCGABiolinks’ package (2). Consequently, the expression data of 5827 genes from 490 samples were included in coexpression network analysis.

Visualization and Functional Annotation of Significantly Correlated Network Modules

The gene network of significantly correlated module was visualized with Cytoscape Software 3.4.0 (3). The enrichment of the gene ontology biologic process terms in significantly correlated module was evaluated based on the hypergeometric test using ‘clusterProfiler’ R package (4). The gene ontology terms at false discovery rate under < 0.05 were regarded as significantly enriched terms.



Supplemental Figure 1. High-resolution image for Figure 3D. The coexpression network of blue module, a module significantly correlated with FDG uptake parameters, was visualized.



Supplemental Figure 2. Effect of tumor stage on gene network modules. Three modules (brown, red and pin) were significantly associated with tumor stage. Note that blue module, a module significantly correlated with PET parameters, did not associated with tumor stage.

SUPPLEMENTAL REFERENCES

1. Cancer Genome Atlas N. Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*. 2015;517:576-582.
2. Costa A, Scholer-Dahirel A, Mehta-Grigoriou F. The role of reactive oxygen species and metabolism on cancer cells and their microenvironment. *Semin Cancer Biol*. 2014;25:23-32.
3. Cline MS, Smoot M, Cerami E, et al. Integration of biological networks and gene expression data using Cytoscape. *Nat Protoc*. 2007;2:2366-2382.
4. Yu G, Wang L-G, Han Y, He Q-Y. clusterProfiler: an R package for comparing biological themes among gene clusters. *OMICS*. 2012;16:284-287