

Table S1 Primer sequences of target genes and internal reference gene for RT-qPCR

| Primer | Sequences |
|--------------------------|---------------------------|
| SPI1 | F: ATCCTGAGGGGCTCTGCATTG |
| SPI1 | R: ACGAGGGGAAACCCTTCCAT |
| FCER1G | F: CCAGCAGTGGTCTTGCTCTT |
| FCER1G | R: GGCCCGTGTAACACCATCT |
| ITGAX | F: ACCTTGGTCCAGCTCTTCTC |
| ITGAX | R: CCCAGGAGTTGGCATACTGG |
| NCF2 | F: ACGCTCCAACCTGTCTTCTC |
| NCF2 | R: TTCCAGTCCTTCTTGCCGC |
| Internal reference-GAPDH | F: CGAAGGTGGAGTCAACGGATTT |
| Internal reference-GAPDH | R: ATGGGTGGAATCATATTGGAAC |

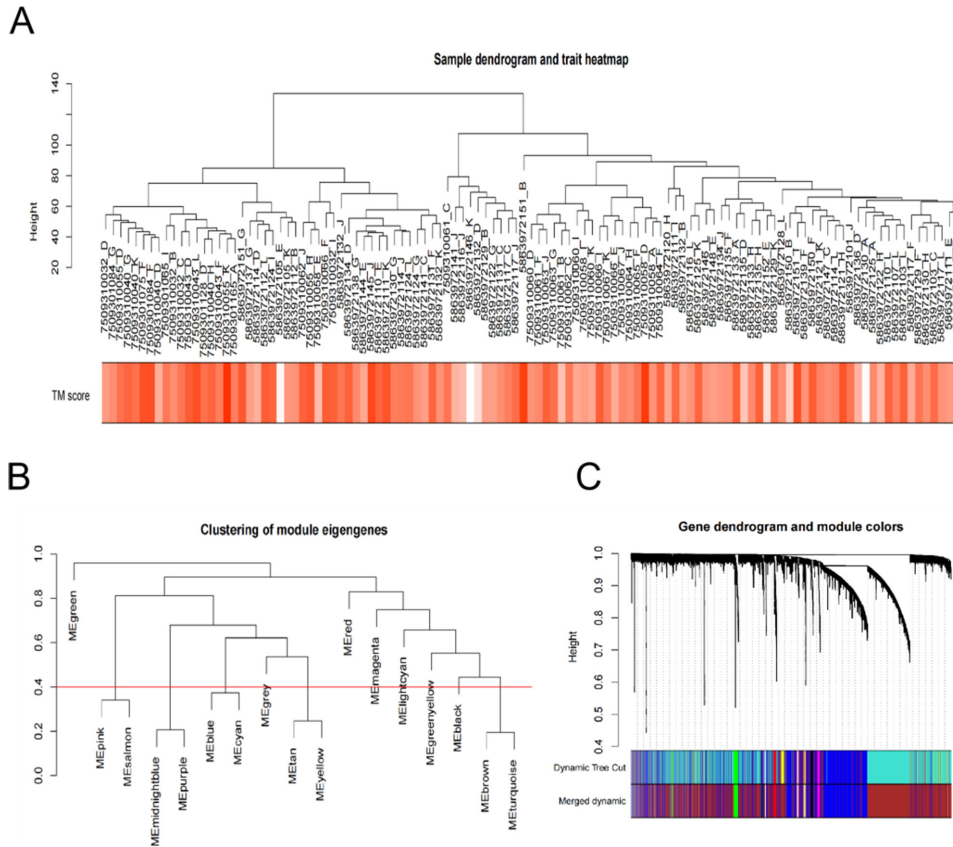


Figure S1 WGCNA. (A) Cluster dendrogram of all samples. (B) Dendrogram of the gene modules identified with scale-free fit index $R^2=0.9$ and mean connectivity threshold =6. (C) Merging of similar modules based on gene expression similarity. WGCNA, weighted gene co-expression network analysis.

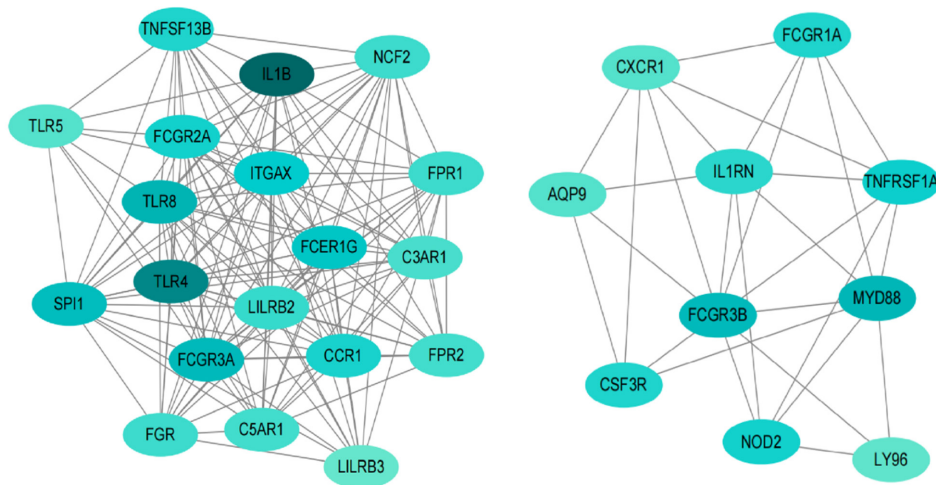


Figure S2 Most significant modules identified by MCODE analysis of the PPI network; key genes highlighted. PPI, protein-protein interaction.

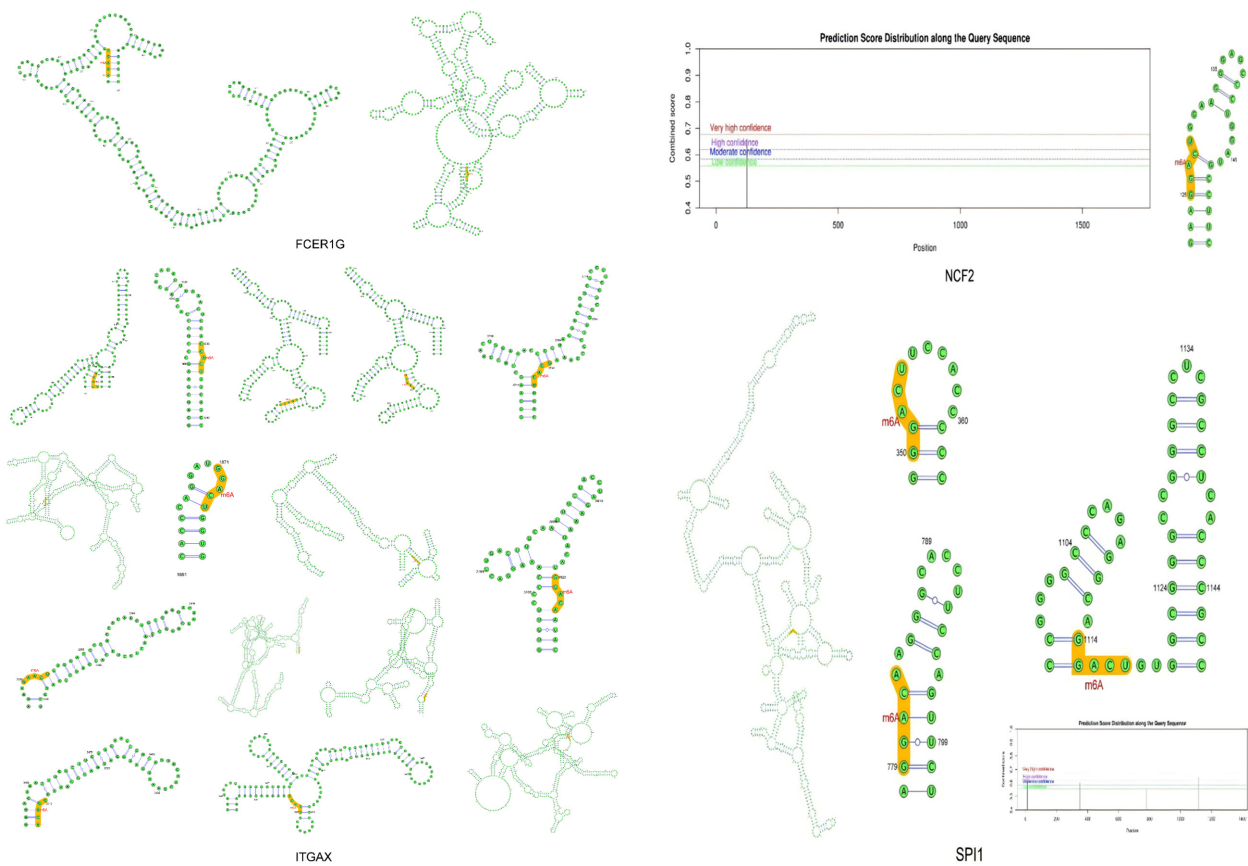


Figure S3 m⁶A modification site of biomarkers. m⁶A, N⁶-methyladenosine.