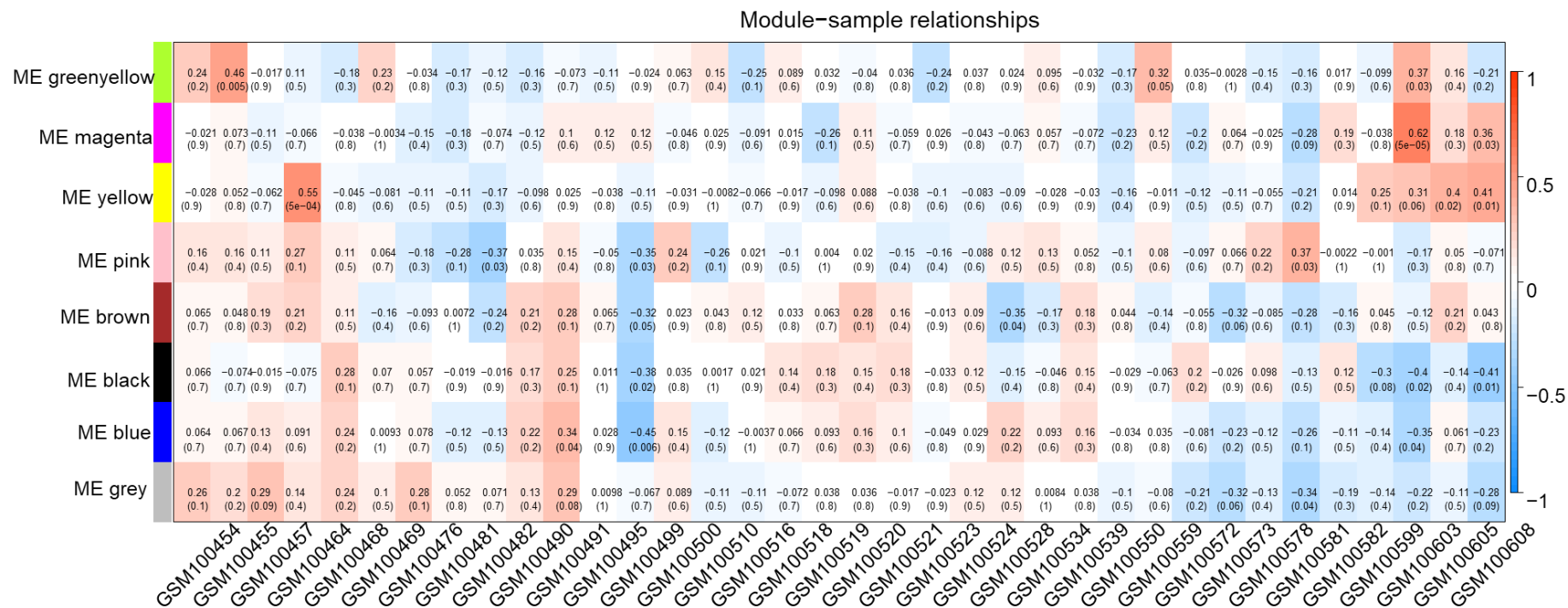


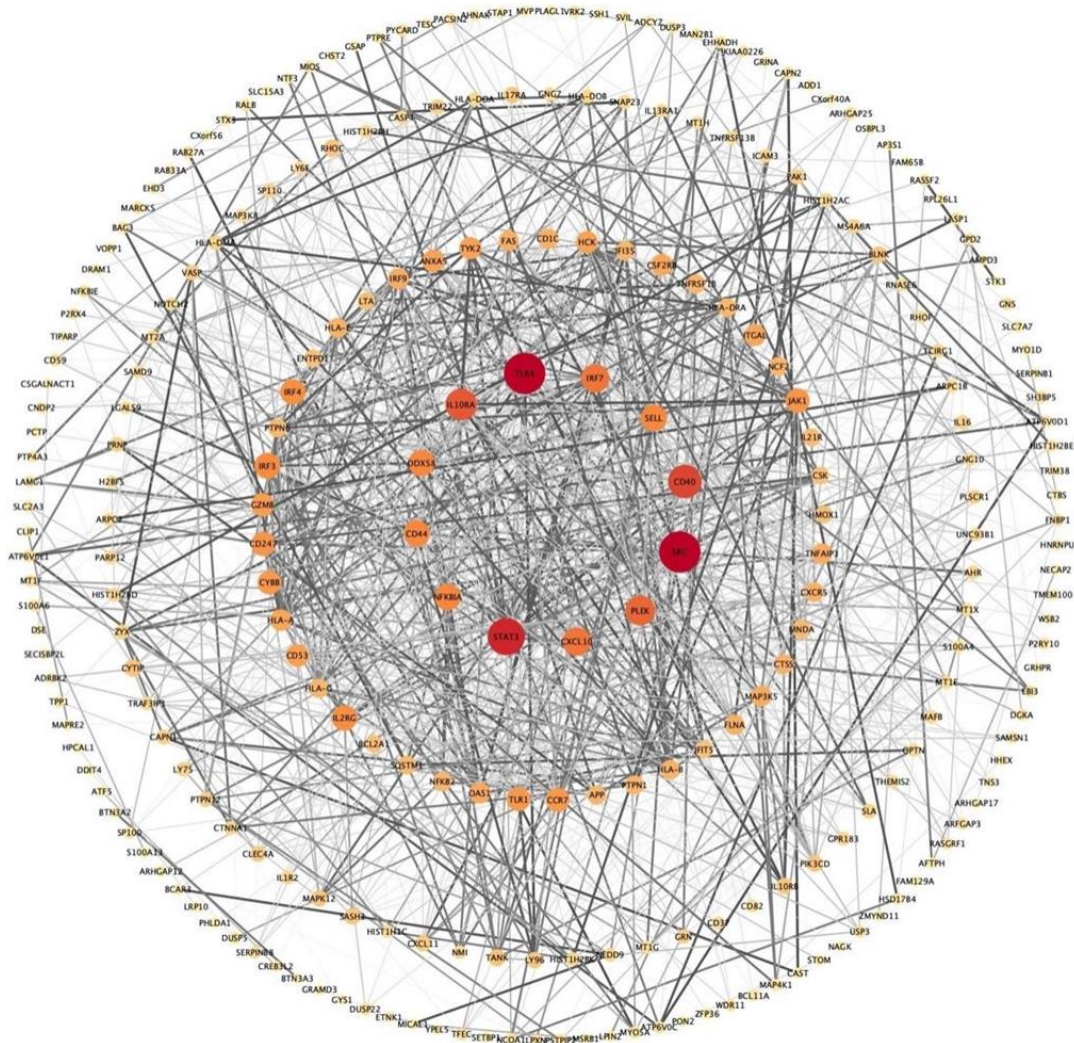
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Supplementary Figure 1 Network topology analysis with different soft threshold power. A: The scale-free fitting index as a function of the soft threshold power; B: The average connectivity as a function of the soft threshold power.



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Supplementary Figure 2 Module-sample association. Correlation thermography between modular feature genes and samples of Burkitt lymphoma. Each row corresponds to a module feature, and the column corresponds to a sample. Each cell contains the correlation and the corresponding *P* value.



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Supplementary Figure 3 The Protein-Protein Interaction network ranked by the weighted degree in the yellow co-expression module. Nodes were ordered and sized according to their degree and edges were sized according to their weight.

Supplementary Table 1 Gene Ontology analysis of the hub genes

Category	Term	Description	Count	P value
BP	GO: 0006954	Inflammatory response	7	7.29E-09
BP	GO: 0071222	Cellular response to lipopolysaccharide	4	7.87E-05
BP	GO: 0032735	Positive regulation of interleukin-12 production	3	1.80E-04
BP	GO: 0043406	Positive regulation of MAP kinase activity	3	5.97E-04

BP	GO: 0046330	Positive regulation of JNK cascade	3	8.95E-04
BP	GO: 0006955	Immune response	4	0.00122726
BP	GO: 0002922	Positive regulation of humoral immune response	2	0.00186095
BP	GO: 0097398	Cellular response to interleukin-17	2	0.00186095
BP	GO: 0032496	Response to lipopolysaccharide	3	0.00230099
BP	GO: 0051092	Positive regulation of NF-kappaB transcription factor activity	3	0.00238775
BP	GO: 0035666	TRIF-dependent toll-like receptor signaling pathway	2	0.00325463
BP	GO: 0043123	Positive regulation of I-kappaB kinase/NF-kappaB signaling	3	0.00337383
BP	GO: 0070374	Positive regulation of ERK1 and ERK2 cascade	3	0.00476072
BP	GO: 0070102	Interleukin-6-mediated signaling pathway	2	0.00649985
BP	GO: 0007166	Vell surface receptor signaling pathway	3	0.00830022
BP	GO: 0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2	0.00973567
BP	GO: 0014911	Positive regulation of smooth muscle cell migration	2	0.01111958
BP	GO: 0036120	Cellular response to platelet-derived growth factor stimulus	2	0.01250177
BP	GO: 1900017	Positive regulation of cytokine production involved in inflammatory response	2	0.01342227
BP	GO: 0050900	Leukocyte migration	2	0.01388224
BP	GO: 0043552	Positive regulation of phosphatidylinositol 3-kinase activity	2	0.0148016
BP	GO: 0045944	Positive regulation of transcription from RNA polymerase II promoter	4	0.01544529
BP	GO: 0007165	Signal transduction	4	0.01753065

BP	GO: 0032733	Positive regulation of interleukin-10 production	2	0.01892931
BP	GO: 0050776	Regulation of immune response	2	0.01984449
BP	GO: 0045747	Positive regulation of Notch signaling pathway	2	0.02075891
BP	GO: 0030890	Positive regulation of B cell proliferation	2	0.02121583
BP	GO: 1904646	Cellular response to beta-amyloid	2	0.02167257
BP	GO: 0010507	Negative regulation of autophagy	2	0.02531964
BP	GO: 0030168	Platelet activation	2	0.02940814
BP	GO: 0032757	Positive regulation of interleukin-8 production	2	0.02986147
BP	GO: 0032731	Positive regulation of interleukin-1 beta production	2	0.02986147
BP	GO: 0006952	Defense response	2	0.03618844
BP	GO: 0071260	Cellular response to mechanical stimulus	2	0.03978736
BP	GO: 0007179	Transforming growth factor beta receptor signaling pathway	2	0.04605674
BP	GO: 0032755	Positive regulation of interleukin-6 production	2	0.04739543
BP	GO: 0032760	Positive regulation of tumor necrosis factor production	2	0.04917776
CC	GO: 0009897	External side of plasma membrane	6	7.72E-07
CC	GO: 0005886	Plasma membrane	9	1.36E-04
CC	GO: 0016021	Integral component of membrane	7	0.01284043
CC	GO: 0005887	Integral component of plasma membrane	4	0.0203224
CC	GO: 0009986	Cell surface	3	0.03024391
MF	GO: 0005102	Receptor binding	4	7.02E-04
MF	GO: 0038023	Signaling receptor activity	3	0.0050559
MF	GO: 0001540	Beta-amyloid binding	2	0.04020651

BP: Biological processes; CC: Cellular components; GO: Gene ontology; MF: Molecular functions.

Supplementary Table 2 Kyoto Encyclopedia of Genes and Genomes analysis of the hub genes

Term	Description	Count	P value
hsa04061	Viral protein interaction with cytokine and cytokine receptor	4	1.40E-04
hsa04060	Cytokine-cytokine receptor interaction	5	1.79E-04
hsa05145	Toxoplasmosis	4	1.96E-04
hsa05162	Measles	4	3.71E-04
hsa05152	Tuberculosis	4	7.91E-04
hsa04062	Chemokine signaling pathway	4	9.55E-04
hsa05417	Lipid and atherosclerosis	4	0.00132612
hsa04620	Toll-like receptor signaling pathway	3	0.0054055
hsa05161	Hepatitis B	3	0.01273318
hsa04630	JAK-STAT signaling pathway	3	0.01334125
hsa05169	Epstein-Barr virus infection	3	0.01937427
hsa05205	Proteoglycans in cancer	3	0.01992131
hsa05163	Human cytomegalovirus infection	3	0.02373574
hsa05171	Coronavirus disease-COVID-19	3	0.02513826