Table1 Module analysis of the protein–protein interaction network.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Category** | | **Pathway description** | **FDR** | | | **Nodes** | | | **Genes** |
| **Hypomethylation and high expression** | | |  |  | | |  | |  |
|  | TNF signaling pathway | | 1.62E-07 | | | | 4 | CCL2,SOCS3,CXCL2,  TNFAIP3 | |
|  | IL-17 signaling pathway | | 1.76E-05 | | | | 3 | CCL2,CXCL2,TNFAIP3 | |
|  | NOD-like receptor signaling pathway | | 6.66E-05 | | | | 3 | CCL2,CXCL2,TNFAIP3 | |
|  | Legionellosis | | 0.00064 | | | | 2 | CXCL2,TLR5 | |
|  | NF-kappaB signaling pathway | | 0.0012 | | | | 2 | CXCL2,TNFAIP3 | |
| **Hypermethylation and low expression** | | |  | |  | |  | |  |
|  | DNA replication | | 7.92E-07 | | | | 4 | POLE2,MCM2,FEN1,  RFC3 | |
|  | Pyrimidine metabolism | | 0.0009 | | | | 3 | POLE2,TK1,TYMS | |
|  | Base excision repair | | 0.0024 | | | | 2 | POLE2,FEN1 | |
|  | Nucleotide excision repair | | 0.0034 | | | | 2 | POLE2,RFC3 | |