Supplementary Material

**Additional file 1: Figure S1. The paired plot of the samples in GEO.** CD8+T cells and plasma cells, resting Mast cells were lower in tumor group. On the contrary, activated Dendritic cells and follicular helper T cells, macrophages M0 were higher in tumor group. \*P<0.05 is considered statistically significant.

S1

**Additional file 2: Figure S2. Barplot of the 18 genes.** 18 genes were up-regulated in tumor group. All of them were statistically different. Type N represents normal group, type T represents tumor group.

S2

**Additional file 3: Figure S3. Heat map of 18 genes.** The 18 genes were up-regulated in tumor tissues.

S3

**Additional file 4: Figure S4. The verification of hub genes on protein level by THPA and GEPIA.** (A) In GEPIA the expression level of CD86, CYBB and C3AR1 was showed on the left. Translational level of GC and normal tissues were demonstrated on the upper side and the lower side in THPA. (B) Violin plot of CD86, CYBB and C3AR1 in different stages. (C-E) Co-expression of every two genes.

Fig S4

**Additional file 5: Table S1. Other GO-Biological Process enrichment analysis of DEGs in GC samples.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Ontology | Term | Description | Count | p.adjust |
| BP | GO:0060263 | regulation of respiratory burst | 2 | 3.49E-03 |
| BP | GO:0045076 | regulation of interleukin-2 biosynthetic process | 2 | 4.18E-03 |
| BP | GO:0042535 | positive regulation of tumor necrosis factor biosynthetic process | 2 | 4.19E-03 |
| BP | GO:0002688 | regulation of leukocyte chemotaxis | 3 | 4.19E-03 |
| BP | GO:0042035 | regulation of cytokine biosynthetic process | 3 | 4.19E-03 |
| BP | GO:0042094 | interleukin-2 biosynthetic process | 2 | 4.58E-03 |
| BP | GO:0042089 | cytokine biosynthetic process | 3 | 4.58E-03 |
| BP | GO:0042107 | cytokine metabolic process | 3 | 4.58E-03 |
| BP | GO:0032753 | positive regulation of interleukin-4 production | 2 | 4.58E-03 |
| BP | GO:0032103 | positive regulation of response to external stimulus | 4 | 4.58E-03 |
| BP | GO:0051251 | positive regulation of lymphocyte activation | 4 | 5.03E-03 |
| BP | GO:0090025 | regulation of monocyte chemotaxis | 2 | 5.03E-03 |
| BP | GO:0010758 | regulation of macrophage chemotaxis | 2 | 5.28E-03 |
| BP | GO:0032673 | regulation of interleukin-4 production | 2 | 5.53E-03 |
| BP | GO:0006909 | phagocytosis | 4 | 6.46E-03 |
| BP | GO:0032743 | positive regulation of interleukin-2 production | 2 | 6.46E-03 |
| BP | GO:0002696 | positive regulation of leukocyte activation | 4 | 6.90E-03 |
| BP | GO:0032633 | interleukin-4 production | 2 | 6.97E-03 |
| BP | GO:0032680 | regulation of tumor necrosis factor production | 3 | 6.97E-03 |
| BP | GO:0050867 | positive regulation of cell activation | 4 | 6.97E-03 |
| BP | GO:0042533 | tumor necrosis factor biosynthetic process | 2 | 6.97E-03 |
| BP | GO:0042534 | regulation of tumor necrosis factor biosynthetic process | 2 | 6.97E-03 |
| BP | GO:0032640 | tumor necrosis factor production | 3 | 6.97E-03 |
| BP | GO:0045619 | regulation of lymphocyte differentiation | 3 | 7.46E-03 |
| BP | GO:1902622 | regulation of neutrophil migration | 2 | 7.46E-03 |
| BP | GO:0002478 | antigen processing and presentation of exogenous peptide antigen | 3 | 7.80E-03 |
| BP | GO:0002695 | negative regulation of leukocyte activation | 3 | 7.80E-03 |
| BP | GO:0048246 | macrophage chemotaxis | 2 | 7.80E-03 |
| BP | GO:1905521 | regulation of macrophage migration | 2 | 8.05E-03 |
| BP | GO:0019884 | antigen processing and presentation of exogenous antigen | 3 | 8.26E-03 |
| BP | GO:0048002 | antigen processing and presentation of peptide antigen | 3 | 9.04E-03 |
| BP | GO:0045088 | regulation of innate immune response | 4 | 9.43E-03 |
| BP | GO:0002685 | regulation of leukocyte migration | 3 | 9.45E-03 |
| BP | GO:0002697 | regulation of immune effector process | 4 | 9.45E-03 |
| BP | GO:0002221 | pattern recognition receptor signaling pathway | 3 | 9.45E-03 |
| BP | GO:0050866 | negative regulation of cell activation | 3 | 9.49E-03 |
| BP | GO:0042110 | T cell activation | 4 | 9.49E-03 |
| BP | GO:0050870 | positive regulation of T cell activation | 3 | 9.64E-03 |
| BP | GO:0002429 | immune response-activating cell surface receptor signaling pathway | 4 | 9.85E-03 |
| BP | GO:0060263 | regulation of respiratory burst | 2 | 3.49E-03 |

P<0.01 is considered statistically significant.