### SUPPLEMENTARY TABLES

#### Supplementary Table 1. Top 10 GO terms enrichment analysis in the category molecular function of differentially expressed genes.

| Term ID     | Description                          | Observed gene count | Background gene count | FDR        |
|-------------|--------------------------------------|---------------------|-----------------------|------------|
| GO:0038023  | signaling receptor activity           | 197                 | 1429                  | 1.58E-21   |
| GO:0005102  | signaling receptor binding            | 199                 | 1513                  | 4.68E-20   |
| GO:0004888  | transmembrane signaling receptor activity | 163               | 1226                  | 1.91E-16   |
| GO:0005125  | cytokine activity                     | 59                  | 216                   | 1.91E-16   |
| GO:0008009  | chemokine activity                    | 31                  | 48                    | 3.05E-16   |
| GO:0042379  | chemokine receptor binding            | 33                  | 63                    | 2.34E-15   |
| GO:0048018  | receptor ligand activity              | 83                  | 458                   | 3.12E-14   |
| GO:0005126  | cytokine receptor binding              | 61                  | 272                   | 7.99E-14   |
| GO:0003823  | antigen binding                       | 29                  | 56                    | 1.73E-13   |

#### Supplementary Table 2. Top 10 GO terms enrichment analysis in the category biological process of differentially expressed genes.

| Term ID     | Description                          | Observed gene count | Background gene count | FDR        |
|-------------|--------------------------------------|---------------------|-----------------------|------------|
| GO:0002376  | immune system process                 | 483                 | 2370                  | 3.92E-120  |
| GO:0006955  | immune response                       | 388                 | 1560                  | 3.24E-115  |
| GO:0002682  | regulation of immune system process   | 338                 | 1391                  | 1.35E-95   |
| GO:0006952  | defense response                      | 302                 | 1234                  | 1.24E-84   |
| GO:0002684  | positive regulation of immune system process | 249              | 882                   | 8.15E-79   |
| GO:0050776  | regulation of immune response         | 237                 | 873                   | 7.77E-72   |
| GO:0050896  | response to stimulus                  | 785                 | 7824                  | 9.92E-65   |
| GO:0048583  | regulation of response to stimulus    | 500                 | 3882                  | 6.17E-60   |
| GO:0001775  | cell activation                       | 234                 | 1024                  | 6.76E-59   |
| GO:0007166  | cell surface receptor signaling pathway | 349               | 2198                  | 2.74E-56   |

#### Supplementary Table 3. Top 10 GO terms enrichment analysis in the category cellular component of differentially expressed genes.

| Term ID     | Description                          | Observed gene count | Background gene count | FDR        |
|-------------|--------------------------------------|---------------------|-----------------------|------------|
| GO:0071944  | cell periphery                        | 585                 | 5254                  | 6.64E-53   |
| GO:0005886  | plasma membrane                       | 577                 | 5159                  | 9.9E-53    |
| GO:0044459  | plasma membrane part                  | 370                 | 2651                  | 3.34E-48   |
| GO:0044425  | membrane part                         | 639                 | 6517                  | 1.35E-41   |
| GO:0031224  | intrinsic component of membrane       | 549                 | 5316                  | 5.93E-39   |
| GO:0005576  | extracellular region                  | 333                 | 2505                  | 1.51E-38   |
| GO:0016021  | integral component of membrane        | 529                 | 5155                  | 3.11E-36   |
| GO:0031226  | intrinsic component of plasma membrane | 250                | 1641                  | 4.94E-36   |
| GO:0016020  | membrane                              | 739                 | 8420                  | 4.57E-35   |
| GO:0005887  | integral component of plasma membrane | 238                | 1564                  | 4.25E-34   |
Supplementary Table 4. Top 10 KEGG enrichment results of differentially expressed genes.

| Term ID  | Description                             | Observed gene count | Background gene count | FDR      |
|----------|-----------------------------------------|---------------------|-----------------------|----------|
| hsa04060 | Cytokine-cytokine receptor interaction  | 87                  | 263                   | 8.54E-30 |
| hsa04640 | Hematopoietic cell lineage              | 45                  | 94                    | 3.85E-20 |
| hsa04062 | Chemokine signaling pathway             | 58                  | 181                   | 2.48E-19 |
| hsa04514 | Cell adhesion molecules (CAMs)          | 48                  | 139                   | 4.34E-17 |
| hsa05150 | Staphylococcus aureus infection         | 32                  | 51                    | 4.34E-17 |
| hsa05323 | Rheumatoid arthritis                    | 38                  | 84                    | 1.04E-16 |
| hsa04672 | Intestinal immune network for IgA production | 28             | 44                    | 3.6E-15  |
| hsa05332 | Graft-versus-host disease               | 25                  | 36                    | 3.21E-14 |
| hsa05140 | Leishmaniasis                           | 31                  | 70                    | 1.47E-13 |
| hsa05330 | Allograft rejection                     | 23                  | 35                    | 8.55E-13 |

Supplementary Table 5. Top 10 enriched GO terms in PPI network in the category molecular function of differentially expressed genes.

| Term ID       | Description                             | Observed gene count | Background gene count | FDR      |
|---------------|-----------------------------------------|---------------------|-----------------------|----------|
| GO:0038023    | signaling receptor activity             | 46                  | 1429                  | 7.63E-14 |
| GO:0004888    | transmembrane signaling receptor activity | 37                 | 1226                  | 2.30E-10 |
| GO:0004896    | cytokine receptor activity              | 13                  | 91                    | 2.30E-10 |
| GO:0042287    | MHC protein binding                     | 7                   | 31                    | 1.27E-06 |
| GO:003823     | antigen binding                         | 8                   | 56                    | 2.29E-06 |
| GO:0005102    | signaling receptor binding              | 34                  | 1513                  | 2.29E-06 |
| GO:0019956    | chemokine binding                       | 6                   | 22                    | 3.32E-06 |
| GO:0015026    | coreceptor activity                     | 7                   | 42                    | 4.47E-06 |
| GO:0004950    | chemokine receptor activity             | 6                   | 27                    | 7.06E-06 |
| GO:0019955    | cytokine binding                        | 9                   | 99                    | 7.06E-06 |

Supplementary Table 6. Top 10 enriched GO terms in PPI network in the category biological process of differentially expressed genes.

| Term ID       | Description                             | Observed gene count | Background gene count | FDR      |
|---------------|-----------------------------------------|---------------------|-----------------------|----------|
| GO:0002376    | immune system process                   | 90                  | 2370                  | 5.10E-38 |
| GO:0006955    | immune response                         | 73                  | 1560                  | 1.34E-34 |
| GO:0002682    | regulation of immune system process     | 65                  | 1391                  | 5.24E-30 |
| GO:0046649    | lymphocyte activation                   | 39                  | 358                   | 7.23E-29 |
| GO:0050776    | regulation of immune response           | 51                  | 873                   | 8.34E-27 |
| GO:0002250    | adaptive immune response                | 34                  | 280                   | 2.22E-26 |
| GO:0002684    | positive regulation of immune system process | 49             | 882                   | 8.66E-25 |
| GO:0006952    | defense response                        | 55                  | 1234                  | 7.00E-24 |
| GO:0045321    | leukocyte activation                    | 48                  | 894                   | 1.09E-23 |
| GO:0001775    | cell activation                         | 50                  | 1024                  | 4.19E-23 |
Supplementary Table 7. Top 10 enriched GO terms in PPI network in the category cellular component of differentially expressed genes.

| Term ID   | Description                          | Observed gene count | Background gene count | FDR      |
|-----------|--------------------------------------|---------------------|-----------------------|----------|
| GO:0071944 | cell periphery                       | 101                 | 5254                  | 2.62E-20 |
| GO:0005886 | plasma membrane                      | 99                  | 5159                  | 7.33E-20 |
| GO:0044459 | plasma membrane part                 | 69                  | 2651                  | 1.67E-18 |
| GO:0044425 | membrane part                        | 107                 | 6517                  | 2.66E-17 |
| GO:0009897 | external side of plasma membrane    | 22                  | 223                   | 2.07E-15 |
| GO:0098552 | side of membrane                     | 28                  | 436                   | 2.21E-15 |
| GO:0031224 | intrinsic component of membrane      | 91                  | 5316                  | 1.86E-14 |
| GO:0016021 | integral component of membrane       | 88                  | 5155                  | 1.09E-13 |
| GO:0031226 | intrinsic component of plasma membrane | 47                | 1641                  | 2.24E-13 |
| GO:0016020 | membrane                             | 115                 | 8420                  | 2.89E-13 |

Supplementary Table 8. Top 10 KEGG results in PPI network of differentially expressed genes.

| Term ID   | Description                              | Observed gene count | Background gene count | FDR      |
|-----------|------------------------------------------|---------------------|-----------------------|----------|
| hsa05340  | Primary immunodeficiency                 | 10                  | 37                    | 3.78E-10 |
| hsa04060  | Cytokine-cytokine receptor interaction   | 17                  | 263                   | 5.16E-09 |
| hsa04659  | Th17 cell differentiation                | 12                  | 102                   | 5.16E-09 |
| hsa04660  | T cell receptor signaling pathway        | 12                  | 99                    | 5.16E-09 |
| hsa04658  | Th1 and Th2 cell differentiation         | 11                  | 88                    | 9.63E-09 |
| hsa04640  | Hematopoietic cell lineage               | 11                  | 94                    | 1.53E-08 |
| hsa04514  | Cell adhesion molecules (CAMs)           | 12                  | 139                   | 5.34E-08 |
| hsa04612  | Antigen processing and presentation      | 8                   | 66                    | 2.03E-06 |
| hsa05321  | Inflammatory bowel disease (IBD)         | 7                   | 62                    | 1.76E-05 |
| hsa04650  | Natural killer cell mediated cytotoxicity| 8                   | 124                   | 0.00013  |

Supplementary Table 9. Literature supports five genes associated with the prognosis of hepatocellular carcinoma.

| Gene Symbol | Publication                                                                 |
|-------------|-----------------------------------------------------------------------------|
| GZMA        | Cytolytic Activity (CYT) Score Is a Prognostic Biomarker Reflecting Host Immune Status in Hepatocellular Carcinoma (HCC). |
| CD79A       | Hepatosplenic Gamma Delta T-Cell Lymphoma (HSGDTCL): Two Rare Case Reports from Western India. |
| IGJ         | Prediction of Response to Sorafenib in Hepatocellular Carcinoma: A Putative Marker Panel by Multiple Reaction Monitoring-Mass Spectrometry (MRM-MS). |
| CYP3A4      | CYP3A4 Gene Is a Novel Biomarker for Predicting a Poor Prognosis in Hepatocellular Carcinoma. |
| SPP1        | A four-gene-based prognostic model predicts overall survival in patients with hepatocellular carcinoma. |