**Table S6.** ClueGO analysis of the BeadArray analysis in CD45<sup>+</sup> cells isolated from *HBUS* polyps compared with unaffected proximal cecum

| GO term  | GO levels    | GO groups                         | Number of genes | % associated genes | Term p-value | Term p-value<br>corrected with<br>Benjamini and<br>Hochberg |
|--|--------------|-----------------------------------|-----------------|--------------------|--------------|---|
| cell activation                                    | [3]          | [Group3]                          | 28              | 4.3209877          | 2.20325E-15  | 8.51924E-14   |
| regulation of immune system process                | [2, 3]       | [Group3]                          | 31              | 4.1059604          | 2.39633E-16  | 1.38987E-14   |
| positive regulation of<br>immune system<br>process | [2, 3, 4]    | [Group3]                          | 24              | 5.084746           | 7.41507E-15  | 1.7203E-13  |
| regulation of<br>leukocyte activation              | [3, 4, 5]    | [Group2, Group3]                  | 18              | 5.4216866          | 6.73134E-12  | 1.11548E-10   |
| cellular protein<br>modification process           | [5, 6]       | [Group3]                          | 27              | 1.2162162          | 0.001421906  | 0.002390451   |
| orotein<br>ohosphorylation                         | [6, 7]       | [Group1, Group3]                  | 18              | 1.8218623          | 8.6142E-05   | 0.000212606   |
| phosphorus<br>metabolic process                    | [3]          | [Group3]                          | 28              | 1.3182675          | 0.00032174   | 0.00064348  |
| apoptotic process                                  | [5]          | [Group0, Group6]                  | 23              | 1.6511127          | 4.3055E-05   | 0.000128061   |
| esponse to stress                                  | [2]          | [Group11]                         | 41              | 1.663286           | 1.84774E-08  | 1.19076E-07   |
| lefense response                                   | [3]          | [Group11]                         | 27              | 2.9063509          | 7.93643E-11  | 9.20626E-10   |
| nflammatory<br>esponse                             | [4]          | [Group11]                         | 16              | 3.5874438          | 3.78664E-08  | 2.31184E-07   |
| mmune response                                     | [2]          | [Group3]                          | 39              | 4.785276           | 6.76247E-23  | 7.84447E-21   |
| ell communication                                  | [3]          | [Group3]                          | 53              | 1.0849539          | 8.99437E-05  | 0.000217364   |
| ell adhesion                                       | [2, 3]       | [None]                            | 19              | 2.183908           | 4.41252E-06  | 1.76501E-05   |
| signal transduction                                | [3, 4]       | [Group3]                          | 51              | 1.1713367          | 1.58363E-05  | 5.40296E-05   |
| ell surface receptor<br>signaling pathway          | [4, 5]       | [Group3]                          | 33              | 1.16649            | 0.000841894  | 0.001525932   |
| multicellular<br>organismal<br>development         | [2, 3]       | [Group4]                          | 49              | 1.2515965          | 3.89755E-06  | 1.6745E-05  |
| ell death  | [3]          | [Group6]                          | 24              | 1.6161616          | 4.10982E-05  | 0.000125458   |
| ell proliferation                                  | [2]          | [Group2]                          | 21              | 1.5261627          | 0.000277015  | 0.00056375  |
| esponse to<br>vounding                             | [3]          | [Group11]                         | 22              | 2.9490616          | 3.92457E-09  | 3.035E-08   |
| esponse to pacterium                               | [3, 4]       | [Group11]                         | 18              | 4.245283           | 3.71002E-10  | 3.58635E-09   |
| issue development                                  | [3]          | [None]                            | 17              | 1.1378849          | 0.018956411  | 0.026816387   |
| egulation of signal ransduction                    | [3, 4, 5]    | [Group0, Group3, Group8]          | 26              | 1.4985591          | 6.93715E-05  | 0.000178824   |
| positive regulation of<br>signal transduction      | [3, 4, 5, 6] | [Group0, Group10, Group3, Group6] | 15              | 1.7942584          | 0.000380566  | 0.000748232   |

| GO term   | GO levels     | GO groups                  | Number of genes | % associated genes | Term p-value   | Term p-value<br>corrected with<br>Benjamini and<br>Hochberg |
|---|---------------|----------------------------|-----------------|--------------------|----------------|---|
| response to organic substance                       | [3]           | [Group10]                  | 29              | 1.609323           | 6.51873E-06    | 2.43927E-05   |
| regulation of cell communication                    | [3, 4]        | [Group0, Group3<br>Group8] | 3, 28           | 1.4155713          | 9.68949E-05    | 0.000220388   |
| regulation of cell death                            | [3, 4]        | [Group6]                   | 17              | 1.5260323          | 0.001029729    | 0.001782814   |
| regulation of phosphate metabolic process           | [5, 6]        | [Group3, Group8]           | 19              | 1.6964285          | 0.000141304    | 0.000298023   |
| regulation of metabolic process                     | [2, 3]        | [Group3]                   | 47              | 1.0322864          | 0.000889362    | 0.001587169   |
| protein metabolic process                           | [3, 4]        | [Group3]                   | 37              | 1                  | 0.006308821    | 0.009382349   |
| regulation of signaling                             | [2, 3]        | [Group0, Group3<br>Group8] | 3, 28           | 1.4205986          | 9.11282E-05    | 0.000215732   |
| regulation of cellular metabolic process            | [3, 4]        | [Group3]                   | 41              | 0.9982956          | 0.004012414    | 0.006205867   |
| regulation of cellular protein metabolic process    | [4, 5, 6]     | [Group1, Group3]           | 16              | 1.4096916          | 0.00316694     | 0.005102292   |
| regulation of localization                          | [2, 3]        | [Group1, Group3]           | 19              | 1.3798112          | 0.001770293    | 0.00289231  |
| intracellular signal transduction                   | [4, 5]        | [Group0, Group3]           | 27              | 1.489              | 0.000          | 0.000   |
| T cell activation                                   | [4, 6]        | [Group3]                   | 21              | 6.442              | 0.000          | 0.000   |
| regulation of cell proliferation                    | [3, 4]        | [Group2, Group3]           | 17              | 1.540              | 0.001          | 0.002   |
| response to chemical stimulus                       | [2]           | [Group10]                  | 41              | 1.197              | 0.000          | 0.000   |
| homeostatic process regulation of apoptotic process | [3]<br>[5, 6] | [Group7]<br>[Group6]       | 17<br>16        | 1.324<br>1.505     | 0.005<br>0.002 | 0.007<br>0.003  |
| positive regulation of molecular function           | [3]           | [Group8]                   | 17              | 1.974              | 0.000          | 0.000   |
| cellular metabolic process                          | [2]           | [Group3]                   | 66              | 0.837              | 0.016          | 0.023   |
| cellular catabolic process                          | [3]           | [None]                     | 15              | 1.125              | 0.028          | 0.039   |
| cellular protein<br>metabolic process               | [4, 5]        | [Group3]                   | 30              | 1.024              | 0.010          | 0.015   |
| small molecule<br>metabolic process                 | [3]           | [Group9]                   | 19              | 1.094              | 0.020          | 0.028   |

| GO term   | GO levels    | GO groups        | Number of genes | % associated genes | Term p-value | Term p-value<br>corrected with<br>Benjamini and<br>Hochberg |
|---|--------------|------------------|-----------------|--------------------|--------------|---|
| single organism<br>signaling                      | [2]          | [Group3]         | 53              | 1.111              | 0.000        | 0.000   |
| single-multicellular organism process             | [2]          | [Group4]         | 64              | 1.067              | 0.000        | 0.000   |
| single-organism cellular process                  | [2]          | [Group3]         | 94              | 0.971              | 0.000        | 0.000   |
| single-organism<br>transport                      | [2, 3, 4]    | [Group1]         | 27              | 1.149              | 0.003        | 0.005   |
| single-organism<br>developmental<br>process       | [2]          | [Group4, Group5] | 43              | 1.165              | 0.000        | 0.000   |
| lymphocyte activation                             | [3, 5]       | [Group3]         | 23              | 4.782              | 0.000        | 0.000   |
| organ development                                 | [3, 4, 5]    | [Group4]         | 39              | 1.501              | 0.000        | 0.000   |
| positive regulation of biological process         | [1, 2, 3]    | [Group3]         | 51              | 1.514              | 0.000        | 0.000   |
| negative regulation of biological process         | [1, 2, 3]    | [Group3, Group5] | 39              | 1.278              | 0.000        | 0.000   |
| positive regulation of cellular process           | [2, 3, 4]    | [Group3]         | 43              | 1.431              | 0.000        | 0.000   |
| negative regulation of cellular process           | [2, 3, 4]    | [Group3, Group5] | 35              | 1.265              | 0.000        | 0.000   |
| hematopoietic or<br>lymphoid organ<br>development | [3, 4, 5, 6] | [Group3]         | 15              | 2.396              | 0.000        | 0.000   |
| regulation of response to stimulus                | [2, 3]       | [Group3]         | 41              | 1.854              | 0.000        | 0.000   |
| positive regulation of response to stimulus       | [2, 3, 4]    | [Group0, Group3] | 27              | 2.379              | 0.000        | 0.000   |
| negative regulation of response to stimulus       | [2, 3, 4]    | [Group3]         | 18              | 2.267              | 0.000        | 0.000   |
| system development                                | [3, 4]       | [Group4]         | 45              | 1.325              | 0.000        | 0.000   |
| anatomical structure development                  | [2]          | [Group4]         | 51              | 1.287              | 0.000        | 0.000   |
| cellular<br>developmental<br>process              | [2, 3]       | [Group4]         | 38              | 1.277              | 0.000        | 0.000   |
| cell motility                                     | [2, 3, 4]    | [None]           | 17              | 1.912              | 0.000        | 0.000   |
| regulation of immune response                     | [3, 4]       | [Group3]         | 18              | 4.545              | 0.000        | 0.000   |
| positive regulation of immune response            | [3, 4, 5]    | [Group3]         | 16              | 5.517              | 0.000        | 0.000   |

| GO term  | GO levels | GO groups         | Number of genes | % associated genes | Term p-value | Term p-value<br>corrected with<br>Benjamini and<br>Hochberg |
|--|-----------|-------------------|-----------------|--------------------|--------------|---|
| regulation of biological process                     | [1, 2]    | [Group3]          | 84              | 0.987              | 0.000        | 0.000   |
| regulation of catalytic activity                     | [3, 4]    | [Group3, Group8]  | 18              | 1.564              | 0.001        | 0.001   |
| regulation of developmental process                  | [2, 3]    | [Group4, Group5]  | 23              | 1.492              | 0.000        | 0.000   |
| regulation of cellular<br>process                    | [2, 3]    | [Group3]          | 76              | 0.945              | 0.000        | 0.000   |
| establishment of localization                        | [1, 2]    | [Group1]          | 32              | 1.060              | 0.005        | 0.007   |
| regulation of<br>multicellular<br>organismal process | [2, 3]    | [Group3, Group5]  | 32              | 1.642              | 0.000        | 0.000   |
| regulation of protein metabolic process              | [4, 5]    | [Group3]          | 20              | 1.484              | 0.001        | 0.001   |
| regulation of<br>lymphocyte<br>activation            | [4, 5, 6] | [Group3]          | 16              | 5.654              | 0.000        | 0.000   |
| response to other organism                           | [2, 3]    | [Group11]         | 21              | 3.344              | 0.000        | 0.000   |
| cellular response to stimulus                        | [2, 3]    | [Group3]          | 62              | 1.177              | 0.000        | 0.000   |
| regulation of macromolecule metabolic process        | [3, 4]    | [Group3]          | 36              | 0.907              | 0.030        | 0.041   |
| regulation of biological quality                     | [2]       | [Group7]          | 28              | 1.212              | 0.001        | 0.002   |
| regulation of molecular function                     | [2]       | [Group3, Group8]  | 22              | 1.429              | 0.000        | 0.001   |
| cellular response to chemical stimulus               | [3, 4]    | [Group10]         | 23              | 1.704              | 0.000        | 0.000   |
| regulation of primary metabolic process              | [3, 4]    | [Group3]          | 41              | 1.006              | 0.003        | 0.005   |
| regulation of response to stress                     | [3, 4]    | [Group11]         | 15              | 2.304              | 0.000        | 0.000   |
| organonitrogen compound metabolic process            | [3]       | [Group9]          | 16              | 1.200              | 0.014        | 0.020   |
| response to oxygen-<br>containing<br>compound        | [3]       | [Group0, Group10] | 16              | 1.633              | 0.001        | 0.001   |

| GO term  | GO levels | GO groups | Number of genes | % associated genes | Term p-value | Term p-value<br>corrected with<br>Benjamini and<br>Hochberg |
|--|-----------|-----------|-----------------|--------------------|--------------|---|
| regulation of multicellular organismal development | [3, 4]    | [Group5]  | 21              | 1.724              | 0.000        | 0.000   |