|  |  |  |  |
| --- | --- | --- | --- |
| **Gene symbol** | **CC-Patchy, n=5** | **Pooled CC-diffuse, n=8/****pooled normal controls, n=8** | **Function** |
| **Patient****1** | **Patient****2** | **Patient****3** | **Patient****4** | **Patient****5** |
|  | I/U | I/P | I/U | I/P | I/U | I/P | I/U | I/P | I/U | I/P |  |  |
| **CCL16** | 1.03 | -2.61 | 1.49 | 1.09 | 1.14 | -1.38 | -3.06 | -3.19 | 1.05 | -1.17 | -1.59 | Chemotaxis |
| **CCL18** | -1.01 | 2.60 | -4.41 | -1.54 | 2.14 | 2.06 | 2.21 | 3.36 | -1.14 | 1.64 | 3.37 | Chemotaxis |
| **CCL2** | 1.03 | 2.00 | 1.12 | 2.56 | 1.28 | 1.17 | 1.70 | 2.79 | -1.24 | 2.40 | 2.23 | Chemotaxis |
| **CCL22** | 1.29 | 2.02 | -5.73 | -1.71 | -1.43 | 1.58 | 3.65 | 4.09 | 1.16 | 3.26 | 2.72 | Chemotaxis |
| **CCL23** | 1.76 | -3.77 | -3.59 | 1.53 | 1.02 | 1.41 | 3.08 | 3.10 | 4.66 | 4.83 | 1.55 | Chemotaxis |
| **CCL26** | 1.03 | -2.39 | -1.22 | -1.58 | 1.05 | -2.28 | 1.21 | -2.04 | -2.84 | -2.74 | 3.22 | Chemotaxis |
| **CCL3** | 1.05 | 1.22 | 1.28 | 1.92 | 1.36 | 1.67 | 1.53 | 1.89 | 1.23 | 1.78 | 1.64 | Chemotaxis |
| **CCL4** | 1.30 | 1.94 | 1.06 | 2.55 | 1.25 | 3.41 | 2.21 | 2.71 | 1.06 | 2.54 | 2.62 | Chemotaxis |
| **CCL5** | -1.24 | 1.62 | -1.50 | 1.12 | 1.20 | 3.54 | 2.01 | 1.52 | 1.20 | 2.00 | 1.84 | Chemotaxis |
| **CCL7** | -1.89 | -2.92 | 1.45 | -2.05 | 2.85 | -1.17 | -1.72 | -2.97 | 1.54 | -2.08 | -1.97 | Chemotaxis |
| **CCL8** | -1.29 | -1.00 | -1.06 | -4.63 | 1.25 | -1.78 | -2.05 | -1.30 | -1.58 | -4.19 | -1.59 | Chemotaxis |
| **CCR10** | 1.42 | 1.87 | -1.72 | 1.49 | 1.71 | 3.45 | -1.80 | -1.36 | -1.16 | 3.58 | 2.07 | Chemotaxis |
| **CCR3** | 1.46 | 1.17 | 1.01 | 2.05 | 1.39 | 2.76 | 2.11 | 3.82 | -1.79 | 1.51 | 2.37 | Chemotaxis |
| **CCR5** | 1.02 | 1.54 | -1.44 | -1.03 | -1.04 | 1.19 | 2.40 | 2.10 | -1.19 | 1.32 | 1.63 | Chemotaxis |
| **CCR7** | -1.64 | 1.27 | -5.40 | -1.06 | -1.32 | 2.84 | 4.30 | 3.32 | 2.73 | 3.84 | 1.85 | Chemotaxis |
| **CCR8** | 2.35 | 8.36 | -1.08 | 6.11 | 1.25 | 9.36 | 109 | 17.81 | -1.89 | 4.89 | 11.05 | Chemotaxis |
| **CXCL1** | 1.39 | 7.25 | 1.23 | 2.77 | 1.21 | 3.11 | 3.56 | 4.71 | 1.33 | 12.10 | 5.65 | Chemotaxis |
| **CXCL10** | 1.12 | 8.29 | 1.29 | 6.39 | 1.29 | 6.96 | 10.67 | 14.85 | -2.13 | 3.01 | 7.88 | Chemotaxis |
| **CXCL2** | 1.21 | 4.86 | 1.42 | 1.91 | 1.20 | 1.68 | 2.41 | 2.97 | 3.37 | 12.79 | 4.83 | Chemotaxis |
| **CXCL3** | 1.47 | 7.51 | 1.28 | 2.65 | 1.00 | 1.27 | 6.41 | 4.74 | 2.52 | 17.79 | 6.08 | Chemotaxis |
| **CXCL6** | 2.02 | 3.41 | 1.16 | 2.01 | 1.30 | 4.44 | 3.10 | 3.60 | -1.19 | 3.14 | 5.25 | Chemotaxis |
| **CXCL11** | 1.36 | 13.61 | 1.97 | 12.61 | 1.14 | 18.39 | 41.86 | 32.87 | -2.09 | 7.70 | 16.78 | Chemotaxis |
| **CXCL12** | -1.25 | -1.96 | -1.29 | 1.55 | -1.08 | -1.62 | -2.67 | -1.35 | -1.06 | -1.19 | -1.76 | Chemotaxis |
| **CXCL13** | 1.02 | -2.66 | -17.3 | -5.26 | -1.95 | -1.33 | 2.92 | -1.52 | 2.27 | 4.93 | -1.92 | Chemotaxis |
| **CXCR2** | 1.47 | 2.88 | -1.66 | 3.10 | -1.10 | 1.41 | 1.66 | 4.56 | -2.00 | 2.53 | 5.71 | Chemotaxis |
| **CXCR3** | 1.54 | 3.28 | -1.42 | 2.14 | 1.09 | 2.10 | 2.93 | 3.74 | -1.11 | 2.80 | 2.54 | Chemotaxis |
| **CXCR6** | 1.05 | 2.64 | -1.49 | 1.31 | -1.04 | 3.90 | 3.38 | 4.15 | 1.221 | 3.53 | 2.79 | Chemotaxis |
| **CX3CR1** | -1.24 | -1.10 | -3.69 | -2.11 | 1.28 | -1.07 | -1.21 | 1.79 | -1.02 | -1.04 | -1.93 | Chemotaxis |
| **XCL1** | 2.97 | 7.54 | -1.60 | 5.55 | 1.73 | 4.53 | 26.14 | 7.72 | -1.19 | 2.52 | 5.16 | Chemotaxis |
| **BST2** | 1.13 | 1.43 | -1.15 | 1.08 | -1.07 | 1.74 | 1.30 | 1.66 | -1.59 | 1.13 | 1.74 | IFNG regulated genes |
| **GBP1** | 1.21 | 5.92 | 1.32 | 3.32 | 1.02 | 4.89 | 6.87 | 6.53 | -1.31 | 3.77 | 4.95 | IFNG regulated genes |
| **GBP5** | 1.07 | 4.35 | -1.42 | 2.31 | 1.28 | 6.43 | 5.72 | 5.30 | -1.12 | 5.32 | 5.25 | IFNG regulated genes |
| **ICAM1** | 1.14 | 2.54 | -1.23 | 1.52 | 1.05 | 1.87 | 2.31 | 3.21 | 1.01 | 2.11 | 2.52 | IFNG regulated genes |
| **IFITM1** | 1.02 | 2.57 | 1.07 | 1.30 | -1.07 | 1.77 | 2.44 | 2.69 | -1.63 | 1.15 | 2.00 | IFNG regulated genes |
| **IFIT3** | -1.12 | 3.12 | 1.29 | 2.88 | -1.12 | 2.02 | 4.76 | 3.43 | -1.78 | 2.38 | 3.81 | IFNG regulated genes |
| **IFI44** | 1.10 | 1.69 | -1.71 | 1.26 | 1.05 | 1.20 | 1.71 | 1.89 | 1.05 | 1.85 | 2.51 | IFNG regulated genes |
| **IFI35** | 1.02 | 1.88 | 1.07 | 1.30 | -1.07 | 1.77 | 2.44 | 2.69 | -1.63 | 1.15 | 2.00 | IFNG regulated genes |
| **IL6** | 3.42 | 17.27 | 2.14 | 6.30 | 1.27 | 1.31 | 9.77 | 16.48 | -1.29 | 8.55 | 7.95 | IFNG regulated genes |
| **IRF1** | 1.06 | 3.02 | 1.34 | 1.97 | 1.01 | 2.94 | 3.28 | 2.88 | -1.19 | 2.05 | 2.63 | IFNG regulated factor |
| **IRF4** | 2.00 | 1.47 | 1.19 | 2.74 | 1.05 | 1.94 | -1.03 | 1.47 | -1.57 | 1.38 | 1.86 | IFNG regulated factor |
| **IRF7** | 1.24 | 1.33 | 1.24 | 1.63 | -1.00 | 1.39 | 1.09 | 1.01 | -1.12 | 1.28 | 1.78 | IFNG regulated factor |
| **PML** | 1.17 | 1.83 | 1.11 | 1.91 | -1.05 | 1.69 | 1.53 | 1.78 | -1.22 | 1.41 | 1.86 | IFNG regulated genes |
| **PSMB10** | -1.00 | 2.28 | 1.25 | 1.51 | -1.01 | 1.75 | 2.11 | 1.87 | 1.00 | 1.88 | 1.85 | IFNG regulated genes |
| **PSMB8** | 1.01 | 2.10 | 1.21 | 1.50 | -1.04 | 1.90 | 2.53 | 1.79 | -1.11 | 1.55 | 1.86 | IFNG regulated genes |
| **PSMB9** | -1.01 | 3.60 | 1.33 | 2.46 | 1.01 | 3.66 | 5.43 | 3.82 | -1.27 | 3.12 | 3.53 | IFNG regulated genes |
| **TAP1** | 1.01 | 3.60 | 1.34 | 2.80 | 1.02 | 3.93 | 5.00 | 3.60 | -1.18 | 2.36 | 3.16 | IFNG regulated genes |
| **LILRA2** | -1.07 | -1.19 | 9.01 | -1.53 | 2.39 | -1.63 | -4.12 | -7.25 | -4.15 | -2.51 | -2.83 | Leukocyte Ig-like receptor |
| **LILRA4** | 1.03 | -10.4 | 1.49 | 6.88 | 1.05 | -9.94 | -9.11 | -8.89 | 1.00 | -10.7 | -10.74 | Leukocyte Ig-like receptor |
| **LILRA5** | -1.10 | 3.32 | 1.06 | 1.33 | 1.55 | 2.19 | -1.07 | 2.00 | -2.27 | 1.33 | 3.32 | Leukocyte Ig-like receptor |
| **LILRA6** | -1.12 | 2.61 | 9.40 | 1.06 | 2.03 | 1.80 | -1.27 | 2.09 | -1.10 | -1.18 | 2.07 | Leukocyte Ig-like receptor |
| **LILRB4** | 1.04 | 2.23 | -2.03 | -1.04 | 1.23 | 2.41 | 2.19 | 3.02 | -1.37 | 1.51 | 2.83 | Leukocyte Ig-like receptor |
| **TBX21** | -1.2 | 1.99 | -3.13 | -1.04 | 1.02 | 2.80 | 2.03 | 2.68 | -1.15 | 2.37 | 1.73 | Th1 pathway |
| **TIGIT** | 1.31 | 2.91 | -1.68 | 1.81 | 1.09 | 3.76 | 4.56 | 4.16 | 1.04 | 3.45 | 2.98 | Th1 pathway |
| **IL12A** | 1.58 | 2.00 | -1.13 | 1.32 | -1.03 | 1.98 | 1.29 | 1.72 | 1.20 | 1.87 | 2.03 | Th1 pathway |
| **IL12B** | 1.03 | 1.03 | 1.49 | 1.56 | 11.76 | 12.11 | 1.21 | 1.21 | 1.00 | 1.00 | 4.14 | Th1 pathway |
| **IL12RB1** | 1.04 | 1.95 | 1.03 | 2.04 | 1.00 | 2.23 | 1.30 | 2.13 | -1.05 | 2.07 | 1.95 | Th1 pathway |
| **FOXP3** | 1.51 | 5.80 | 1.22 | 5.18 | 1.10 | 5.64 | 7.96 | 10.46 | -1.12 | 5.37 | 6.53 | Regulatory T cells |

**Supplemental Table 4.** **Genes differentially expressed (up- or down-regulated greater than 1.5 fold) in collagenous colitis by NanoString nCounter gene expression assay. The gene expression was not confirmed by qRT-PCR.** Data represent the fold changes (FC) of gene expression in involved mucosa or pooled CC samples compared with pooled normal colonic controls. The corresponding FC between histologically involved and uninvolved mucosa from 5 CC patients are listed for comparison. I/U, involved mucosa vs. uninvolved mucosa; I/P, involved mucosa vs. pooled normal colonic controls. Positive FC indicates upregulation and negative FC indicates downregulation. Positive FC indicates upregulation and negative FC indicates downregulation.