|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene symbol** | **CC-Patchy, n=5** | **CC-diffuse,****Pooled CC/pooled N, n=8** | **q-PCR, *p* values** | **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 |  |  |  |
| **MMP3** | 3.49 | 3.44 | -1.01 | 1.45 | -1.44 | -1.1 | 57.19 | 2.46 | -2.35 | 1.85 | 7.84 | 0.008 | Fibrolysis |
| **MMP9** | 1.06 | 2.29 | -2.04 | 2.42 | 1.04 | 2.61 | 2.65 | 7.37 | 1.15 | 3.65 | 3.50 | 0.029 | Fibrolysis |
| **TIMP1** | NT | NT | NT | NT | NT | NT | NT | NT | NT | NT | NT | 0.027 | Fibrogenesis |
| **TGFβ1** | -1.09 | 1.11 | 1.18 | 1.39 | 1.08 | 1.42 | 3.61 | 1.51 | 1.07 | 1.36 | 1.33 | 0.664 | Fibrogenesis |
| **IL22** | 1.03 | 1.03 | 1.49 | 1.56 | 1.05 | 1.08 | 1.21 | 1.21 | 1.00 | 1.00 | 3.19 | 0.377 | Inflammatory and immunologic regulation |
| **IL22RA2** | -2.31 | -11.3 | -57.5 | -7.47 | -1.41 | 1.22 | 4.88 | 2.66 | 6.64 | 2.66 | 5.66 | 0.194 | Inflammatory and immunologic regulation |
| **TNFα** | 1.10 | 1.45 | -2.69 | -1.43 | -1.17 | -1.04 | 1.74 | 2.67 | 1.19 | 1.46 | 1.28 | 0.377 | TNF family \* |
| **MAPK1** | -1.11 | -1.35 | -1.14 | -1.09 | -1.06 | -1.05 | -1.33 | -1.13 | -1.00 | -1.30 | -1.27 | 0.657 | MAPK \* signaling |
| **NOD2** | 1.02 | 1.78 | -1.28 | 1.34 | 1.23 | 1.42 | 2.00 | 1.73 | -1.35 | 1.40 | 1.51 | 0.499 | NOD2\* signaling |
| **CCL11** | 1.58 | 2.77 | 1.58 | 5.79 | 1.29 | 2.65 | 2.06 | 6.68 | -3.66 | 1.81 | 3.38 | 0.031 | Chemotaxis |
| **CCL20** | 1.26 | 2.64 | -1.12 | 8.06 | 1.49 | 4.60 | 4.07 | 4.79 | 2.05 | 14.59 | 3.65 | 0.061 | Chemotaxis |
| **CXCL5** | 12.77 | 479.8 | 1.5 | 2.04 | 1 | 1.00 | 14.48 | 15.06 | 4.59 | 1252 | 43.39 | 0.042 | Chemotaxis |
| **CXCL8****(IL8)** | 1.5 | 24.11 | 1.43 | 4.68 | 1.06 | 8.43 | 5.28 | 18.52 | -1.31 | 25.46 | 30.52 | 0.049 | Chemotaxis |
| **CXCL9** | -1.06 | 9.40 | 1.18 | 6.63 | 1.06 | 12.77 | 13.96 | 13.28 | -1.83 | 8.20 | 10.97 | 0.011 | Chemotaxis |
| **LILRA3** | -2.14 | 15.2 | 1.11 | 17.23 | 1.39 | 38.04 | 3.95 | 17.69 | -4.11 | 11.35 | 26.99 | 0.031 | Inflammatory and immunologic regulation |
| **LILRB2** | -1.09 | 1.6 | 1.28 | 1.54 | 1.05 | 1.82 | 1.08 | 1.82 | -1.29 | 1.46 | 2.06 | 0.032 | Inflammatory and immunologic regulation |
| **LILRB3** | -1.04 | 2.16 | -4.57 | -12.77 | 1.22 | -1.65 | 1.29 | 1.67 | -1.6 | -1.24 | 2.02 | 0.031 | Inflammatory and immunologic regulation |
| **IFNG** | 1.19 | 37.13 | -1.63 | 6.98 | 1.25 | 42.58 | 50.28 | 20.38 | 1.04 | 25.08 | 31.00 | 0.007 | Th1 pathway |
| **STAT1** | -1.09 | 3.71 | 1.18 | 2.8 | 1.08 | 4.27 | 3.61 | 3.99 | 1.07 | 3.98 | 3.98 | 0.012 | IFNG regulated transcription factor |
| **IFIT3** | -1.12 | 3.33 | 1.29 | 2.98 | -1.13 | 2.1 | 5.78 | 3.66 | -1.21 | 2.46 | 3.84 | 0.001 | IFNG-induced antiviral protein |
| **NOS2** | 1.8 | 20.94 | 1.67 | 5.77 | -1.1 | 3.00 | 10.46 | 9.37 | -1.26 | 14.94 | 7.48 | 0.049 | Nitric oxide synthesis |

**Supplemental Table 3.** **Representative genes differentially expressed in collagenous colitis, confirmed by quantitative RT-PCR (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. The expression levels of these genes in pooled CC and pooled normal colonic controls are further confirmed by quantitative PCR and the p values (unpaired t tests) are shown.

\* Expression of other members of TNF family, MAPK and NOD1/2 signaling is summarized in Table 3.