**Supplementary Information**

**qPCR internal controls and reference genes**

The PCR-array included positive controls, reverse transcriptase controls, five reference genes and a human genomic control. All samples were subjected to DNAse treatment prior to qPCR analysis (RNeasy MinElute Cleanup Kit, Catalog nr 74204, Qiagen).

Standardized CT thresholds were set across plates. CT cut off for lower limit of detection was set at 40. The Normfinder software identified endoglin (ENG) and transforming growth factor beta receptor 1 (TGFBR1) as the best combination for normalization of the qPCR data with a stability value of 0.002. The five reference genes provided (ACTB, B2M, GAPDH, HPRT1 RPLP0) showed significant differences (≥1 CT value) in expression across groups alone or in combinations, and were thus not selected for normalisation. No outliers were excluded. All samples past quality control checks of PCR efficiency, reproducibility and no human genomic contamination detected. qPCR-array 96-well plate set up is shown in supplemental figure 1.

**Supplementary Table 1. Geboes score**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |   | Patient 1 | Patient 2 | Patient 3 | Patient 4 | Patient 5 | Patient 6 | Patient 7 |
| 0 | Structural changes | 0 | 0 | 1 | 1 | 0 | 1 | 1 |
| 1 | Chronic inflammatory infiltrate | 1 | 0 | 0 | 0 | 0 | 1 | 1 |
| 2a | Lamina propria neutrophils | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2b | Lamina propria eosinophils | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | Neutrophils in epithelium | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | Crypt destruction | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | Erosion or ulceration | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
|  | **Grade** | **3.1** | **0** | **0.1** | **0.1** | **0** | **2.1** | **2.1** |

**Supplementary Table 2:** Significantly differentially expressed genes (adjusted p-value < 0.05)

|  |  |  |
| --- | --- | --- |
| **AvsN** | **AvsR** | **RvsN** |
| Gene | Log2FC | Gene | Log2FC | Gene | Log2FC |
| **MMP3** | 5.94  | **MMP3** | 2.76 | **MMP3** | 3.19 |
| **MMP1** | 4.01 | **AGT** | 2.32 | **MMP1** | 2.29 |
| **IL13RAa** | 3.74 | **MMP9** | 2.24 | **IL13RAa** | 1.73 |
| **SERPINE1** | 3.38 | **CCL3** | 2.08 | **GREM1** | 1.65 |
| **IL1B** | 3.11 | **IL13RAa** | 2.01 | **SERPINE1** | 1.46 |
| **MMP9** | 2.34 | **SERPINE1** | 1.92 | **IL1B** | 1.36 |
| **IL10** | 2.20 | **IL1B** | 1.75 | **IL10** | 1.24 |
| **PLAU** | 2.17 | **MMP1** | 1.72 | **THBS2** | 1.08 |
| **GREM1** | 2.07 | **PLAU** | 1.51 | **SNAI1** | 1.02 |
| **CCL3** | 1.93 | **IL1A** | 1.47 | **TIMP1** | 0.93 |
| **TIMP1** | 1.91 | **IFNG** | 1.43 | **TNF** | 0.92 |
| **IL1A** | 1.89 | **TIMP1** | 0.98 | **BMP7** | 0.90 |
| **IFNG** | 1.84 | **IL10** | 0.96 | **ACTA2** | 0.89 |
| **THBS2** | 1.62 | **STAT1** | 0.88 | **CCL2** | 0.80 |
| **SNAI1** | 1.53 | **ITGB6** | 0.76 | **HGF** | 0.75 |
| **AGT** | 1.51 | **CCR2** | 0.60 | **PLAU** | 0.66 |
| **TNF** | 1.41 | **FASLG** | 0.56 | **CAV1** | 0.62 |
| **CCL11** | 1.14 | **THBS2** | 0.54 | **TIMP3** | 0.61 |
| **MMP13** | 1.09 | **SNAI1** | 0.51 | **COL3A1** | 0.49 |
| **TGFB2** | 0.99 | **TGFB2** | 0.51 | **CXCR4** | 0.46 |
| **CCL2** | 0.92 | **CEBPB** | 0.50 | **LOX** | 0.39 |
| **STAT1** | 0.91 | **TNF** | 0.49 | **SMAD2** | -0.37 |
| **HGF** | 0.87 | **ITGA2** | 0.43 | **ILK** | -0.39 |
| **BMP7** | 0.76 | **ENG** | 0.42 | **TGIF1** | -0.46 |
| **COL1A2** | 0.76 | **GREM1** | 0.42 | **PLAT** | -0.47 |
| **CXCR4** | 0.73 | **COL1A2** | 0.29 | **VEGFA** | -0.49 |
| **ENG** | 0.49 | **MMP14** | 0.28 | **AKT1** | -0.51 |
| **SERPINA1** | 0.42 | **TGFB1** | 0.19 | **ITGA3** | -0.54 |
| **TGFB3** | 0.32 | **TIMP2** | -0.25 | **NFKB1** | -0.54 |
| **TIMP2** | -0.27 | **JUN** | -0.26 | **SMAD4** | -0.58 |
| **TGFBR2** | -0.42 | **ITGB8** | -0.27 | **ITGB5** | -0.60 |
| **VEGFA** | -0.45 | **COL3A1** | -0.28 | **SMAD6** | -0.70 |
| **TGFBR1** | -0.49 | **ITGB1** | -0.30 | **PLG** | -0.74 |
| **ITGB8** | -0.50 | **STAT6** | -0.35 | **INHBE** | -0.78 |
| **LTBP1** | -0.64 | **NFKB1** | -0.38 | **SMAD3** | -0.80 |
| **ITGB1** | -0.77 | **EDN1** | -0.40 | **AGT** | -0.81 |
| **ILK** | -0.87 | **TGFBR1** | -0.42 | **SP1** | -0.84 |
| **MYC** | -0.88 | **ITGA3** | -0.42 | **PDGFA** | -0.87 |
| **PLG** | -0.88 | **TGFBR2** | -0.43 | **BCL2** | -0.87 |
| **NFKB1** | -0.92 | **CAV1** | -0.46 | **ITGB6** | -1.07 |
| **ITGA3** | -0.96 | **ILK** | -0.48 | **SMAD7** | -1.25 |
| **THBS1** | -1.00 | **TIMP3** | -0.50 | **JUN** | -1.71 |
| **TGIF1** | -1.02 | **SMAD6** | -0.53 | **EDN1** | -2.10 |
| **SP1** | -1.03 | **SMAD7** | -0.56 |  |  |
| **SMAD3** | -1.06 | **TGIF1** | -0.57 |  |  |
| **SMAD2** | -1.06 | **ITGB5** | -0.57 |  |  |
| **PLAT** | -1.11 | **EGF** | -0.59 |  |  |
| **STAT6** | -1.13 | **LTBP1** | -0.60 |  |  |
| **AKT1** | -1.16 | **SMAD4** | -0.61 |  |  |
| **INHBE** | -1.18 | **AKT1** | -0.65 |  |  |
| **ITGB5** | -1.18 | **PLAT** | -0.66 |  |  |
| **SMAD4** | -1.20 | **IL5** | -0.66 |  |  |
| **SMAD6** | -1.23 | **THBS1** | -0.68 |  |  |
| **TIMP4** | -1.26 | **BCL2** | -0.68 |  |  |
| **BCL2** | -1.55 | **SMAD2** | -0.70 |  |  |
| **PDGFA** | -1.63 | **PDGFA** | -0.76 |  |  |
| **SMAD7** | -1.81 | **MYC** | -0.81 |  |  |
| **JUN** | -1.97 | **TIMP4** | -1.03 |  |  |
| **EDN1** | -2.50 | **ACTA2** | -1.09 |  |  |

Abbreviations: AvsN = Acute UC versus Normal control group, AvsR = Acute UC versus Remission UC, RvsN= Remission UC versus Normal control group.

**Supplemental Table 3.** Antibody details

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**Supplementary figure 1.** PCR-array set up.

