**Supplemental material for Häsler *et al* „A functional methylome map of ulcerative colitis”**

**Supplemental methods**

*Substratification analysis*

To validate the impact of potentially confounding factors on the observed differential mRNA expression and epigenetic modification a substratification analysis was performed. Patients from validation panel I and validation panel II (supplemental table 2) were categorized according to potentially confounding factors. As only one confirmed smoker was included in the study, smoking was excluded from the substratification analysis. The resulting substratification criteria were: age (all individuals younger than 30 years were excluded), gender (females only and males only), biopsy position (all non-sigmoidal biopsies excluded), immunosuppressant medication (all individuals with immunosuppressant therapy removed) and steroid medication (all individuals with steroid therapy removed). Each of the 10 candidate transcripts (mRNA) and candidate loci (methylation) was analyzed separately in the substratified validation panel. Differences between the groups were determined using the Mann-Whitney U-test, while p-values were corrected for multiple testing using the Benjamini-Hochberg method.

**Supplemental figure legends:**

**Supplementary figure 1:** Genome-wide profiles of DNAm and transcription (enlarged). The x-axis represents the genomic location. The significance of the differences between ulcerative colitis patients and healthy individuals is displayed as –log(*p*) for the mRNA and as log(p) for the epigenetic modifications. Effect size (induction/fold change) is encoded by colors (methylation: upregulated = black, not regulated = blue, downregulated = purple; mRNA-expression: upregulated = red, no regulation = yellow, downregulated = green). Grey arrows indicate transcription start sites of candidate genes, labeled with the corresponding gene-symbol, while a star next to the gene symbol indicates that this transcript was part of the candidates selected for validation. Each chromosome is displayed on a separate panel (1A: Chr1; 1B: Chr2; 1C: Chr3; 1D: Chr4; 1E: Chr5; 1F: Chr6; 1G: Chr7; 1H: Chr8; 1I: Chr9; 1J: Chr10; 1K: Chr11; 1L: Chr12; 1M: Chr13; 1N: Chr14; 1O: Chr15; 1P: Chr16; 1Q: Chr17; 1R: Chr18; 1S: Chr19; 1T: Chr20; 1U: Chr21; 1V: Chr22; 1W: ChrX; 1X: ChrY).

**Supplemental Figure 2:** Bimodal distribution of CpG methylation, as analyzed by pyrosequencing (validation panel). The y-axis displays the count of the binned values (0-100%, x-axis).

**Supplemental Figure 3:** Distribution of significant MVPs/DMRs in different genomic regions (promoters, exons, introns and others, as analyzed in the genome-wide screen). A: Distribution of significantly hypomethlated CpGs when comparing ulcerative colitis patients to healthy controls, B: Distribution of significantly hypermethlated CpGs when comparing ulcerative colitis patients to healthy controls.

**Supplemental Figure 4:** Intra Class Correlation for all three levels of the genome-wide functional epigenetic map (screening approach). A: mRNA levels (n=1400 transcripts); B: MVPs (n=27.000 signals);C: DMRs (n= 400.000 signals). Red areas indicate where differentially regulated items are found. Intra class correlation coefficient was calculated based on the variance within twins compared to the variance between unrelated individuals

**Supplemental Figure 5:** Principal component analysis of differential transcription and DNAm in UC, based on genome wide data (screening approach). A: the two strongest components separating the samples based on all significantly differentially expressed mRNA transcripts (n=361) are displayed. B: the two strongest components separating the samples based on all significantly differentially methylated MVPs (n=731) are displayed. Arrows indicate the connection from the healthy twin to its diseased sibling. Grey areas represent the healthy group, while one outlier (pair 12) was not located within the healthy group in either of the two approaches.

**Supplemental Figure 6:** A:Cluster analysis of mRNA expression signals; B: cluster analysis of DNAm signals (B) for 61 selected candidate transcripts/loci (listed in supplemental table 2, originiating from genome wide data, screening approach).. Transcripts/loci are displayed in rows, labeled with gene symbol and DNAm-ID (prefix MVP for Illumina, DMR for Nimblegen), while each patient is displayed in a column. Row dendograms display similarities between candidate genes/loci, column dendograms display similarities between samples. Corresponding twin pair samples are labeled with a/b. Expression and methylation levels are color coded (green = low; black = median, red = high). For better readability, expression and methylation values were z-score normalized. Healthy individuals are indicated by light grey, diseased individuals by dark grey.

**Supplemental Figure 7**: Correlation analysis of mRNA expression and epigenetic modification. Each box-plot represents an individual loci/transcript correlation set based on a Spearman-Rho correlation, displaying the 25th, 50th and 75th percentile. Whiskers correspond to the 5th and 95th percentile while outliers are plotted separately. P-values describe the differences between the individual sets of r-values, calculated by a Mann-Whitney U-test. For better readability r-values were transformed to absolute values.

**Supplemental Figure 8:** Biological processes affected by differential DNAm or gene expression in UC patients as analyzed by Gene-Ontology analysis, based on genome-wide mRNA/DNAm data (screening approach). The 30 most significantly enriched biological processes are displayed for three different categories: i) all MVPs and DMRs, ii) all mRNA transcripts and iii) all mRNA transcripts associated with at least one MVP and/or DMR. Significance of the enrichment (observed vs. expected) is displayed as –log10(p).

**Supplemental Figure 9**: Frequencies of validated effects. Frequencies describe the probability at which a random individual will follow the presented regulatory pattern of DNAm-mRNA pair. Frequencies of the methylation effects (black bars) and the transcript effects (grey bars) are displayed separately for each of the 10 selected candidate loci. SLC7A7 represents a control loci where regulated DNAm and no differential expression was observed, while IGHG1 represents a control loci where differential mRNA expression without corresponding altered DNAM levels is observed. Control loci are labeled with a star (\*). Not-significant findings are indicated by shaded bars.

**Supplemental Figure 10**: Impact of potential confounding factors on the differential mRNA expression in selected candidate loci (validation approach). Each originally selected candidate transcript is represented in a separate panel (A-J). Each panel shows 7 color coded sets of analysis from validation panel I, split into healthy individuals (HN) and ulcerative colitis patients (UC): 1) no substratification (all samples included)2); substratified by age (all individuals younger than 30 years were excluded); 3) substratified by gender (females only); 4) substratified by gender (males only); 5) substratified by biopsy position (all non-sigmoidal biopsies excluded); 6) substratified by immunosuppressant therapy (all individuals with immunosuppressant therapy removed) and 7) substratified by steroid medication (all individuals with steroid therapy removed). Box plots represent the 20th, 50th and 75th percentile, while whispers illustrate the 5th and 95th percentile. Control transcripts are labeled: 1) negative control candidate for differential expression without epigenetic modification; 2) negative control candidate for epigenetic modification without differential mRNA expression.

**Supplemental Figure 11**: Impact of potential confounding factors on the differential DNA methylation in selected candidate loci (validation approach). Each originally selected candidate transcript is represented in a separate panel (A-J). Each panel shows 7 color coded sets of analysis from validation panel I, split into healthy individuals (HN) and ulcerative colitis patients (UC): 1) no substratification (all samples included)2); substratified by age (all individuals younger than 30 years were excluded); 3) substratified by gender (females only); 4) substratified by gender (males only); 5) substratified by biopsy position (all non-sigmoidal biopsies excluded); 6) substratified by immunosuppressant therapy (all individuals with immunosuppressant therapy removed) and 7) substratified by steroid medication (all individuals with steroid therapy removed). Box plots represent the 20th, 50th and 75th percentile, while whispers illustrate the 5th and 95th percentile. Control transcripts are labeled: 1) negative control candidate for differential expression without epigenetic modification; 2) negative control candidate for epigenetic modification without differential mRNA expression.

**Supplemental Tables**

**Supplemental Table 1A**: Identified methylation/transcription pairs, based on differentially methylated regions (DMRs) in monozygotic twins.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene Symbol | Methylation ID,Type | ProbeSetID | Alignment start chromosome, position, length | DMR position relative to transcript | DMRp Value | mRNA [fold change] p value |
| GOT1 | 10\_752, DMR | 208813\_at | 10, 101180897, 45 | +TSS | ↑ 4.2E-02 | ↓ -1.4/4.1\*10-2 |
| CFI | 114\_722, DMR | 203854\_at | 4, 110969215, 57 | +TSS | ↑ 1.1E-02 | ↑ 4.9/3.6\*10-2 |
| IRS2 | 12\_446, DMR | 209185\_s\_at | 13, 109236885, 45 | -TSS, SGB | ↑ 4.2E-02 | ↑ 1.5/3.6\*10-2 |
| PRDX5 | 160\_742, DMR | 1560587\_s\_at | 11, 63815385, 45 | -TSS | ↑ 4.2E-02 | ↓ -1.6/2.8\*10-3 |
| PRDX5 | 160\_742, DMR | 222994\_at | 11, 63815385, 45 | -TSS | ↑ 4.2E-02 | ↓ -1.6/4.7\*10-3 |
| SIRT6 | 235\_323, DMR | 219613\_s\_at | 19, 4075291, 45 | -TSS | ↓ 2.0E-02 | ↓ -1.5/2.9\*10-2 |
| HIST2H2 | 285\_661, DMR | 214290\_s\_at | 1, 148088565, 45 | -TSS | ↓ 2.0E-02 | ↑ 1.5/5.0\*10-2 |
| PSME2 | 343\_375, DMR | 201762\_s\_at | 14, 23675013, 45 | -TSS | ↓ 3.1E-02 | ↑ 1.7/2.4\*10-2 |
| DUSP28 | 362\_276, DMR | 229211\_at | 2, 241156651, 45 | +TSS | ↓ 4.2E-02 | ↓ -1.6/4.1\*10-2 |
| ARV1 | 43\_731, DMR | 223223\_at | 1, 229193399, 60 | +TSS, SGB | ↑ 4.2E-02 | ↓ -2.1/5.0\*10-2 |
| PTN | 455\_711, DMR | 209465\_x\_at | 7, 136679601, 57 | +TSS | ↑ 3.1E-02 | ↓ -1.9/2.8\*10-3 |
| PTN | 455\_711, DMR | 211737\_x\_at | 7, 136679601, 57 | +TSS | ↑ 3.1E-02 | ↓ -3.2/2.9\*10-2 |
| PTN | 455\_711, DMR | 209466\_x\_at | 7, 136679601, 57 | +TSS | ↑ 3.1E-02 | ↓ -1.9/2.9\*10-2 |
| FLNA | 527\_875, DMR | 214752\_x\_at | 23, 153241374, 45 | -TSS, SGB | ↓ 2.7E-02 | ↑ 2.2/3.6\*10-2 |
| FLNA | 527\_875, DMR | 213746\_s\_at | 23, 153241374, 45 | -TSS, SGB | ↓ 2.7E-02 | ↑ 2.1/4.1\*10-2 |
| CDK6 | 576\_808, DMR | 224848\_at | 7, 92057717, 45 | -TSS | ↓ 1.5E-02 | ↓ -1.9/5.0\*10-2 |
| DCI | 613\_959, DMR | 209759\_s\_at | 16, 2226310, 45 | -TSS | ↓ 4.2E-02 | ↓ -1.5/5.0\*10-2 |
| NRARP | 626\_776, DMR | 226499\_at | 9, 139265392, 45 | -TSS | ↓ 6.3E-03 | ↓-2.1/1.2\*10-2 |
| TMEM216 | 639\_701, DMR | 223305\_at | 11, 60886245, 45 | -TSS | ↓ 2.7E-02 | ↓ -1.6/2.9\*10-2 |
| VIPR1 | 667\_713, DMR | 205019\_s\_at | 3, 42518005, 45 | -TSS | ↓ 6.3E-03 | ↓ -2.7/4.1\*10-2 |
| GMDS | 674\_12, DMR | 214106\_s\_at | 6, 1555156, 45 | -TSS | ↓ 6.3E-03 | ↑ 1.5/3.6\*10-2 |
| REPIN1 | 689\_467, DMR | 219041\_s\_at | 7, 149707167, 45 | +TSS | ↓ 4.2E-02 | ↓ -1.6/3.6\*10-2 |
| IGHG1 | 719\_773, DMR | 215118\_s\_at | 14, 105139221, 45 | -TSS | ↓ 1.5E-02 | ↓ -1.9/7.9\*10-3 |
| IGH@ | 719\_773, DMR | 211430\_s\_at | 14, 105139221, 45 | -TSS | ↓ 1.5E-02 | ↑ 2.9/3.6\*10-2 |
| AACS | 722\_978, DMR | 218434\_s\_at | 12, 124237597, 45 | +TSS | ↓ 1.5E-02 | ↓ -1.4/5.0\*10-2 |
| ABHD2 | 87\_71, DMR | 225337\_at | 15, 87542094, 57 | +TSS, SGB | ↑ 3.1E-02 | ↑ 1.5/1.0\*10-2 |

-TSS: pre Transcription start site; +TSS post transcription start site; SGB: Spanning into gene body, ↑ upregulated, ↓ downregulated, (-) not significantly regulated, DMR: differentially methylated region (based on Nimblegen 385k tiling array data); mRNA data is based on genome wide screening.

**Supplemental Table 1B**: Identified methylation/transcription pairs, based on individual CpG positions in monozygotic twins.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene Symbol | Methylation ID,Type | ProbeSetID | Alignment start chromosome, position, length | MVPposition relative to transcript | MVPp Value | mRNA (fold change)p value |
| ELOVL5 | cg00024396, CpG | 208788\_at | 6, 53321967, 1 | +TSS | ↑ 3.7\*10-2 | ↑ 2.3/5.0\*10-2 |
| COL6A3 | cg00573606, CpG | 201438\_at | 2, 237987419, 1 | -TSS | ↑ 2.1\*10-2 | ↑ 4.1/1.0\*10-2 |
| IGH@ | cg02507952, CpG | 211430\_s\_at | 14, 105461686, 1 | -TSS, SGB | ↓ 1.4\*10-2 | ↑ 2.9/3.6\*10-2 |
| RSAD1 | cg02593766, CpG | 218307\_at | 17, 45963676, 1 | +TSS | ↓ 3.0\*10-2 | ↓ -1.5/2.4\*10-2 |
| PID1 | cg02799466, CpG | 219093\_at | 2, 229844655, 1 | +TSS | ↓ 3.0\*10-2 | ↓ -1.6/3.6\*10-2 |
| BAG1 | cg04103317, CpG | 229720\_at | 9, 33230960, 1 | -TSS | ↓ 8.3\*10-3 | ↓ -1.6/1.9\*10-2 |
| SPINK4 | cg04103317, CpG | 207214\_at | 9, 33230960, 1 | +TSS, SGB | ↓ 8.3\*10-3 | ↑ 6.9/4.1\*10-2 |
| HSD11B2 | cg06810461, CpG | 204130\_at | 16, 66075645, 1 | +TSS | ↓ 6.4\*10-3 | ↓ -2.2/7.9\*10-3 |
| ABHD2 | cg10173075, CpG | 225337\_at | 15, 87565840, 1 | +TSS | ↓ 1.4\*10-2 | ↑ 1.5/1.0\*10-2 |
| OLFM4 | cg10246520, CpG | 212768\_s\_at | 13, 52499945, 1 | -TSS | ↓ 3.7\*10-2 | ↑ 58.4/4.7\*10-3 |
| ALKBH7 | cg10280342, CpG | 227878\_s\_at | 19, 6327576, 1 | +TSS | ↓ 2.1\*10-2 | ↓ -1.7/5.0\*10-2 |
| HKDC1 | cg11639651, CpG | 227614\_at | 10, 70649817, 1 | -TSS | ↓ 1.7\*10-2 | ↑ 5.3/7.9\*10-3 |
| SUPV3L1 | cg11639651, CpG | 212894\_at | 10, 70649817, 1 | +TSS | ↓ 1.7\*10-2 | ↓ -1.6/3.6\*10-2 |
| HKDC1 | cg11762346, CpG | 227614\_at | 10, 70650118, 1 | +TSS, SGB | ↓ 4.9\*10-3 | ↑ 5.3/7.9\*10-3 |
| SUPV3L1 | cg11762346, CpG | 212894\_at | 10, 70650118, 1 | +TSS | ↓ 4.9\*10-3 | ↓ -1.6/3.6\*10-2 |
| TMEM141 | cg11873854, CpG | 225568\_at | 9, 138762696, 1 | -TSS | ↓ 3.7\*10-2 | ↓ -1.8/4.1\*10-2 |
| CFI | cg12243271, CpG | 203854\_at | 4, 110942151, 1 | -TSS, SGB | ↓ 2.5\*10-2 | ↑ 4.9/3.6\*10-2 |
| PPP1R1B | cg12894984, CpG | 225165\_at | 17, 35077157, 1 | +TSS | ↓ 3.7\*10-2 | ↓ -2.1/7.9\*10-3 |
| PRDX5 | cg13412615, CpG | 1560587\_s\_at | 11, 63814383, 1 | -TSS | ↓ 8.3\*10-3 | ↓ -1.6/2.8\*10-3 |
| PRDX5 | cg13412615, CpG | 222994\_at | 11, 63814383, 1 | -TSS | ↓ 8.3\*10-3 | ↓ 1.6/4.7\*10-3 |
| CES3 | cg14221831, CpG | 220335\_x\_at | 16, 65510215, 1 | -TSS | ↓ 1.7\*10-2 | ↓ -1.8/2.9\*10-2 |
| USP21 | cg14448116, CpG | 232219\_x\_at | 1, 159436734, 1 | +TSS | ↓ 4.5\*10-2 | ↓ -1.6/5.0\*10-2 |
| TMEM141 | cg14611112, CpG | 225568\_at | 9, 138763172, 1 | -TSS | ↓ 1.4\*10-2 | ↓ -1.8/4.1\*10-2 |
| CES3 | cg14792480, CpG | 220335\_x\_at | 16, 65511758, 1 | -TSS | ↓ 3.7\*10-2 | ↓ -1.8/2.9\*10-2 |
| C11orf1 | cg15227610, CpG | 231530\_s\_at | 11, 111287226, 1 | +TSS | ↓ 1.7\*10-2 | ↓ -1.5/2.9\*10-2 |
| MMP12 | cg16466334, CpG | 204580\_at | 11, 102219568, 1 | -TSS | ↓ 1.7\*10-2 | ↑ 6.0/3.6\*10-2 |
| SLC7A7 | cg18960218, CpG | 204588\_s\_at | 14, 22355205, 1 | +TSS | ↓ 8.8\*10-4 | ↑ 1.7/5.0\*10-2 |
| MACROD1 | cg21111471, CpG | 219188\_s\_at | 11, 63627576, 1 | -TSS, SGB | ↓ 3.7\*10-3 | ↓ -1.6/1.0\*10-2 |
| THY1 | cg21633698, CpG | 213869\_x\_at | 11, 118799744, 1 | +TSS | ↓ 2.1\*10-2 | ↑ 1.8/1.5\*10-2 |
| ALKBH7 | cg25221254, CpG | 227878\_s\_at | 19, 6284547, 1 | -TSS | ↓ 3.0\*10-2 | ↓ -1.7/5.0\*10-2 |
| KLK1 | cg26149550, CpG | 216699\_s\_at | 19, 56026308, 1 | +TSS | ↓ 4.5\*10-2 | ↓ -2.0/3.6\*10-2 |
| NUMA1 | cg26149678, CpG | 200747\_s\_at | 11, 71387565, 1 | -TSS | ↓ 3.7\*10-2 | ↓ -1.5/3.6\*10-2 |
| COL5A1 | cg26164184, CpG | 212488\_at | 9, 136911327, 1 | +TSS | ↓ 1.7\*10-2 | ↑ 1.5/2.4\*10-2 |
| TMEM139 | cg26756862, CpG | 227753\_at | 7, 142723082, 1 | +TSS | ↓ 1.7\*10-2 | ↑ 2.2/4.1\*10-2 |
| RHOQ | cg27485921, CpG | 212119\_at | 2, 46600883, 1 | -TSS | ↓ 3.7\*10-3 | ↑ 1.7/5.0\*10-2 |

-TSS: pre Transcription start site; +TSS post transcription start site; SGB: Spanning to gene body, ↑ upregulated, ↓ downregulated, (-) not significantly regulated, MVP: methylation variable position (based on Illumina Infinium 27K array data); mRNA data is based on genome wide screening.

**Supplemental Table 2:** Epigenetic modification and transcript regulation of previously published loci associated to ulcerative collitis

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **dbSNP** | **Chr** | **MVP in proximity** | **MVP distance [bp]** | **MVP p‑value** | **MVP fold change** | **DMR in proximity** | **DMR distance [bp]** | **DMR p‑value** | **DMR fold change** | **Associated genes/transcripts (p-value / fold change)** |
| rs254560 | 5 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 2) |
| rs267939 | 5 | cg21046940 | 8544 | 0.789 | 1.24 | 4\_750 | 3442 | 0.974 | 1.08 | *DAP* (0.517 / 1.08) |
| rs678170 | 11 | cg27227156 | 1670 | 1) | 1) | 97\_557 | 1049 | 0.955 | 1.08 | 2) |
| rs734999 | 1 | cg05610148 | 4210 | 0.525 | 1.23 | 388\_658 | 4183 | 1.031 | -1.08 | *TNFRSF14* (0.971 / -1.02); *MMEL1* (0.390 / -1.13); *PLCH2*3) |
| rs798502 | 7 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | *GNA12* (0.199 / 1.05) |
| rs907611 | 11 | cg26158194 | 249 | 0.496 | -1.16 | 584\_700 | 13 | 1.031 | 1.02 | *LSP1* (0.937 / 1.16) |
| rs941823 | 13 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 2) |
| rs943072 | 6 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 2) |
| rs1297265 | 21 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 2) |
| rs1801274 | 1 | cg27470554 | 4504 | 0.315 | -1.12 | 358\_172 | 3917 | 0.974 | -1.01 | *FCGR2B* (0.679 / 1.15) |
| rs2155219 | 11 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 2) |
| rs2297441 | 20 | cg18611245 | 10654 | 0.853 | -1.26 | 159\_97 | 433 | 0.955 | 1.07 | *SLC2A4RG*3); *STMN3*3); *ZBTB46*3); *ZGPAT* (0.945 / -1.00); *RTEL1*3) |
| rs2310173 | 2 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | *IL1R2* (0.065 / -2.31) |
| rs2836878 | 21 | 1) | 1) | 1) | 1) | 741\_343 | 33734 | 0.955 | -1.01 | 2) |
| rs2838519 | 21 | 1) | 1) | 1) | 1) | 517\_389 | 20907 | 0.974 | -1.06 | *ICOSLG*3) |
| rs2872507 | 17 | cg14914852 | 15965 | 0.525 | 1.08 | 600\_252 | 15642 | 0.955 | -1.06 | *IKZF3*3); *ORMDL3* (0.937 / -1.03); *IKZF3*3); *PNMT*3); *ZPBP2*3) |
| rs3024505 | 1 | cg17067005 | 5443 | 0.315 | -1.08 | 143\_227 | 22 | 0.974 | -1.09 | *IL10*3); *IL19*3) |
| rs3194051 | 5 | cg04312209 | 19143 | 1) | 1) | 105\_1001 | 18996 | 0.974 | 1.27 | *IL7R*3) |
| rs4246905 | 9 | cg11809085 | 14508 | 1) | 1) | 643\_137 | 14915 | 1.031 | 1.03 | *TNFSF8*3); *TNFSF15*3) |
| rs4510766 | 7 | cg01025762 | 38575 | 1) | 1) | 207\_929 | 38617 | 0.955 | 1.19 | 2) |
| rs4676406 | 2 | cg07432969 | 9550 | 0.525 | -1.02 | 218\_140 | 11648 | 0.955 | -1.07 | *GPR35* (0.846 / 1.02) |
| rs4728142 | 7 | cg26616347 | 3786 | 0.912 | 1.25 | 168\_892 | 3779 | 1.031 | -1.02 | *IRF5*3); *TNPO3* (0.954 / -1.00) |
| rs5771069 | 22 | 1) | 1) | 1) | 1) | 195\_653 | 2214 | 1.031 | -1 | *PIM3* (0.837 / 1.70); *IL17REL*3) |
| rs6017342 | 20 | cg00431114 | 39000 | 1) | 1) | 645\_453 | 28952 | 1.031 | -1.02 | *SERINC3* (0.199 / -1.16) |
| rs6426833 | 1 | cg09195271 | 29362 | 0.525 | 1.08 | 53\_167 | 29661 | 0.955 | 1.14 | 2) |
| rs6451493 | 5 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | *PTGER4* (0.670 / -1.05) |
| rs6499188 | 16 | cg19034028 | 2577 | 1) | 1) | 693\_223 | 3875 | 0.974 | -1.11 | *ZFP90* (0.945 / -1.00) |
| rs6584283 | 10 | 1) | 1) | 1) | 1) | 39\_119 | 326 | 1.031 | -1.08 | 2) |
| rs6871626 | 5 | 1) | 1) | 1) | 1) | 18\_750 | 46859 | 0.974 | -1.01 | *IL12B*3) |
| rs6911490 | 6 | cg19464016 | 11932 | 0.789 | 1.38 | 736\_824 | 11920 | 1 | 1.03 | *PRDM1*3) |
| rs6920220 | 6 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 3) |
| rs7134599 | 12 | 1) | 1) | 1) | 1) | 521\_873 | 43646 | 1.031 | 1.15 | *IFNG*3); *IL26*3) |
| rs7524102 | 1 | 1) | 1) | 1) | 1) | 440\_344 | 47983 | 1.031 | -1.06 | 2) |
| rs7554511 | 1 | cg15250507 | 17196 | 0.525 | 1.14 | 248\_116 | 3033 | 0.955 | -1.17 | *C1orf106* (0.945 / -1.02) |
| rs7608910 | 2 | cg09469394 | 39133 | 0.853 | 1.17 | 200\_246 | 39766 | 1.031 | 1.03 | *PUS10*3) |

**Supplemental Table 3** (continued): Epigenetic modification and transcript regulation of previously published loci associated to ulcerative collitis

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **dbSNP** | **Chr** | **MVP in proximity** | **MVP distance [bp]** | **MVP p‑value** | **MVP fold change** | **DMR in proximity** | **DMR distance [bp]** | **DMR p‑value** | **DMR fold change** | **Associated genes/transcripts (p-value / fold change)** |
| rs9268853 | 6 | cg19248557 | 21804 | 0.912 | 1.09 | 328\_1008 | 450 | 0.955 | 1.04 | *HLA-DRB5*3); *HLA-DQA1* (0.856 / 1.02); *HLA-DRB1* (0.517 / 1.61); *HLA-DRA* (0.517 / 1.68) |
| rs9822268 | 3 | cg21958034 | 6112 | 0.315 | -1.07 | 374\_156 | 3416 | 0.955 | 1.19 | *UBA7*3); *MST1*3); *APEH* (0.665 / -1.30); *AMIGO3*3); *GMPPB* (0.937 / 1.19) |
| rs10758669 | 9 | cg20394284 | 2605 | 0.853 | 1.02 | 20\_920 | 2943 | 1.031 | -1.05 | *JAK2* (0.517 / 1.06) |
| rs10781499 | 9 | cg02516189 | 1688 | 0.525 | -1.11 | 480\_724 | 672 | 1.031 | -1.02 | *CARD9*3); *INPP5E* (0.962 / -1.00); *SDCCAG3* (0.665 / -1.12); *SEC16A*3) |
| rs11209026 | 1 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | *IL23R*3) |
| rs11676348 | 2 | cg14150666 | 18835 | 0.496 | -1.07 | 188\_388 | 19018 | 1.031 | 1.04 | *IL8RA*3); *SLC11A1*3); *IL8RB*3); *AAMP* (0.856 / -1.07) |
| rs11739663 | 5 | cg19108785 | 17929 | 0.853 | 1.42 | 467\_749 | 8145 | 0.974 | -1.08 | *EXOC3* (0.040 / -1.36) |
| rs12261843 | 10 | cg23218877 | 18043 | 0.912 | 1.02 | 1) | 1) | 1) | 1) | *CCNY*3) |
| rs16940202 | 16 | 1) | 1) | 1) | 1) | 700\_466 | 23 | 0.955 | -1.16 | 2) |
| rs17085007 | 13 | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 1) | 2) |
| rs17388568 | 4 | cg17850932 | 48539 | 0.789 | -1.08 | 3\_485 | 28543 | 1.031 | -1.04 | *IL21*3) |
| rs35675666 | 1 | cg25007680 | 151 | 0.496 | 1.16 | 509\_517 | 40 | 0.955 | -1.08 | *TNFRSF9*3); *ERFFI1*3); *UTS2*3) |

dbSNP: previously published loci, associated to ulcerative colitis (Anderson et al. 2011); MVP: methylation variable positions (listed with its ID); DMR: differentially methylated region; distance describes the distance between the SNP and MVP/DMR position in bp; associated genes/transcripts are listed with their gene symbol, p-value and fold change; 1) no MVP/DMR within proximity of SNP analyzed; 2) no gene/transcript within proximity of SNP analyzed; 3) associated gene/transcript was categorized as not expressed in the tissue.

**Supplemental Table 3**

Clinical characteristics of ulcerative colitis patients and control individuals

**Patient Groups**: 1: healthy discordant twin; 2: diseased discordant twin; 3: diseased control inflamed; 4: disease control non-inflamed; 5 healthy individual; 6: ulcerative colitis patient inflamed; 7: ulcerative colitis patient non-inflamed; **Gender**: F: female; M: male; **Disease status**: DC: diseased control; DH: discrodant healthy; HN: hospitalized normal control; UC: ulcerative colitis; **Position of biopsy**: C.DES: descending colon; C.TRANS: transverse colon; COE: coecum; ILE: ileum; JEJ: jejunum; SIG: sigmoindal colon; STE: sigmoidal stenosis; T.ILE: terminal ileum; **Tissue status / inflammation**: I: moderate and/or high inflammation; NI: no inflammation; Disease duration: U: unknown; **Smoking status**: NS: non-smoker; S: smoker; U: smoking status unknown; **CAI (clinical activity index)**: 0: healthy individuals; U: unkown; **Medication**: NM: no medication; St: Steroids; Is: Immunosuppressant; AB: antibiotics; Bi: biologics; CS: cytostatics; NS: NSAID; BB: beta blocker; NR: no current medication recorded; OM: other medication.

**Supplemental Table 3A**

Sceening panel for genome-wide transcriptome analysis, genome-wide MVP quantification and genome-wide DMR quantification

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient ID** | **Patient Group** | **Age [a]** | **Gender** | **Disease status** | **Position of biopsy** | **TIssue status / InflammatIon** | **Disease duration [a]** | **Smoking status** | **CAI** | **Medication** |
| H-T\_01A | 1 | 52 | M | H | SIG | NI | 0 | NS | 0 | OM |
| UC-T\_01B | 2 | 52 | M | UC | SIG | NI | 15 | NS | 4 | St IS |
| H-T\_02A | 1 | 70 | M | H | SIG | NI | 0 | U | 0 | NM |
| UC-T\_02B | 2 | 70 | M | UC | SIG | NI | U | U | U | St IS |
| H-T\_03A | 1 | 18 | F | H | SIG | NI | 0 | U | 0 | NM |
| UC-T\_03B | 2 | 18 | F | UC | SIG | NI | U | U | U | St IS |
| H-T\_04A | 1 | 26 | F | H | SIG | NI | 0 | NS | 0 | NM |
| UC-T\_04B | 2 | 26 | F | UC | SIG | NI | 5 | NS | 2 | IS |
| H-T\_06A | 1 | 42 | M | H | SIG | NI | 0 | S | 0 | NM |
| UC-T\_06B | 2 | 42 | M | UC | ILE | NI | 14 | NS | 3 | NM |
| H-T\_07A | 1 | 18 | F | H | SIG | NI | 0 | NS | 0 | NM |
| UC-T\_07B | 2 | 18 | F | UC | SIG | NI | 3 | NS | 3 | NM |
| H-T\_08A | 1 | 21 | F | H | SIG | NI | 0 | NS | 0 | NM |
| UC-T\_08B | 2 | 21 | F | UC | SIG | NI | 4 | NS | 7 | IS |
| H-T\_09A | 1 | 23 | M | H | SIG | NI | 0 | NS | 0 | NM |
| UC-T\_09B | 2 | 23 | M | UC | SIG | NI | 4 | NS | 7 | St IS |
| H-T\_10A | 1 | 49 | F | H | SIG | NI | 0 | NS | 0 | NM |
| UC-T\_10B | 2 | 49 | F | UC | SIG | NI | 6 | NS | 6 | IS |
| H-T\_12A | 1 | 21 | M | H | SIG | NI | 0 | NS | 0 | NM |
| UC-T12B | 2 | 21 | M | UC | SIG | NI | 5 | NS | 7 | St IS |

**Supplemental Table 3B**

Validation panel I for selected candidate transcripts

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient ID** | **Patient Group** | **Age [a]** | **Gender** | **Disease status** | **Position of biopsy** | **TIssue status / InflammatIon** | **Medication** |
| DCinfl\_01 | 3 | 68 | M | DC | SIG | I | NR |
| DCinfl\_02 | 3 | 41 | F | DC | JEJ | I | NR |
| DCinfl\_03 | 3 | 70 | M | DC | C.DES | I | NR |
| DCinfl\_04 | 3 | 58 | F | DC | C.TRANS | I | NM  |
| DCinfl\_05 | 3 | 18 | F | DC | SIG | I | AB  |
| DCinfl\_06 | 3 | 64 | M | DC | SIG | I | AB BB NS OM  |
| DCinfl\_07 | 3 | 19 | M | DC | COE | I | NM  |
| DCinfl\_08 | 3 | 36 | M | DC | SIG | I | NR |
| DCinfl\_09 | 3 | 43 | F | DC | SIG | I | NM  |
| DCinfl\_10 | 3 | 41 | F | DC | C.TRANS | I | NR |
| DCinfl\_11 | 3 | 34 | F | DC | SIG | I | IS  |
| DCinfl\_12 | 3 | 24 | F | DC | C.TRANS | I | NM  |
| DCinfl\_13 | 3 | 65 | M | DC | SIG | I | IS  |
| DCinfl\_14 | 3 | 72 | F | DC | SIG | I | NM  |
| DCinfl\_15 | 3 | 52 | M | DC | SIG | I | NR |
| DCn-infl\_01 | 4 | 71 | M | DC | SIG | NI | NR |
| DCn-infl\_02 | 4 | 44 | F | DC | COE | NI | NR |
| DCn-infl\_03 | 4 | 35 | M | DC | COE | NI | NR |
| DCn-infl\_04 | 4 | 60 | M | DC | COE | NI | NR |
| DCn-infl\_05 | 4 | 27 | M | DC | COE | NI | NR |
| DCn-infl\_06 | 4 | 53 | M | DC | SIG | NI | NR |
| DCn-infl\_07 | 4 | 67 | M | DC | T.ILE | NI | NR |
| DCn-infl\_08 | 4 | 71 | F | DC | COE | NI | NR |
| DCn-infl\_09 | 4 | 67 | M | DC | SIG | NI | IS  |
| DCn-infl\_10 | 4 | 54 | F | DC | SIG | NI | AB  |
| DCn-infl\_11 | 4 | 52 | F | DC | SIG | NI | NM  |
| DCn-infl\_12 | 4 | 71 | M | DC | SIG | NI | NR |
| DCn-infl\_13 | 4 | 18 | F | DC | COE | NI | NR |
| DCn-infl\_14 | 4 | 69 | F | DC | SIG | NI | NR |
| DCn-infl\_15 | 4 | 26 | M | DC | SIG | NI | IS  |
| DCn-infl\_16 | 4 | 42 | F | DC | Sig | NI | IS  |
| DCn-infl\_17 | 4 | 40 | M | DC | SIG | NI | NM  |
| DCn-infl\_18 | 4 | 64 | F | DC | SIG | NI | NM  |
| DCn-infl\_19 | 4 | 24 | F | DC | SIG | NI | NR |
| DCn-infl\_20 | 4 | 76 | M | DC | SIG | NI | NR |
| DCn-infl\_21 | 4 | 29 | F | DC | T.ILE | NI | NR |
| DCn-infl\_22 | 4 | 49 | M | DC | SIG | NI | NR |
| DCn-infl\_23 | 4 | 66 | F | DC | COE | NI | NR |
| DCn-infl\_24 | 4 | 39 | F | DC | SIG | NI | OM  |
| DCn-infl\_25 | 4 | 63 | F | DC | SIG | NI | CS  |
| DCn-infl\_26 | 4 | 34 | F | DC | SIG | NI | NR |
| DCn-infl\_27 | 4 | 67 | M | DC | SIG | NI | NM  |
| DCn-infl\_28 | 4 | 40 | F | DC | SIG | NI | NR |
| DCn-infl\_29 | 4 | 75 | M | DC | SIG | NI | NM  |
| DCn-infl\_30 | 4 | 27 | M | DC | COE | NI | NR |

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**Supplemental Table 3B continued (page 2 of 3)**

Validation panel I for selected candidate transcripts

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient ID** | **Patient Group** | **Age [a]** | **Gender** | **Disease status** | **Position of biopsy** | **TIssue status / InflammatIon** | **Medication** |
| HN\_01 | 5 | 58 | F | HN | SIG | NI | NR |
| HN\_02 | 5 | 52 | F | HN | SIG | NI | NR |
| HN\_03 | 5 | 46 | M | HN | SIG | NI | NM  |
| HN\_04 | 5 | 61 | M | HN | SIG | NI | NM  |
| HN\_05 | 5 | 57 | M | HN | SIG | NI | NS OM  |
| HN\_06 | 5 | 34 | F | HN | SIG | NI | NM  |
| HN\_07 | 5 | 26 | F | HN | SIG | NI | NR |
| HN\_08 | 5 | 59 | M | HN | SIG | NI | NR |
| HN\_09 | 5 | 34 | F | HN | SIG | NI | NM  |
| HN\_10 | 5 | 62 | F | HN | SIG | NI | NR |
| HN\_11 | 5 | 28 | F | HN | SIG | NI | NR |
| HN\_12 | 5 | 39 | F | HN | SIG | NI | NR |
| HN\_13 | 5 | 38 | M | HN | SIG | NI | NM  |
| HN\_14 | 5 | 49 | F | HN | SIG | NI | NR |
| HN\_15 | 5 | 66 | M | HN | SIG | NI | OM  |
| HN\_16 | 5 | 62 | M | HN | SIG | NI | NM  |
| HN\_17 | 5 | 61 | M | HN | SIG | NI | BB  |
| HN\_18 | 5 | 58 | M | HN | SIG | NI | BB NS  |
| HN\_19 | 5 | 41 | F | HN | SIG | NI | NM  |
| HN\_20 | 5 | 73 | F | HN | SIG | NI | AB  |
| HN\_21 | 5 | 67 | F | HN | SIG | NI | NM  |
| HN\_22 | 5 | 67 | M | HN | SIG | NI | St  |
| HN\_23 | 5 | 39 | F | HN | SIG | NI | OM  |
| HN\_24 | 5 | 56 | M | HN | SIG | NI | NR |
| HN\_25 | 5 | 70 | M | HN | SIG | NI | NM  |
| HN\_26 | 5 | 32 | F | HN | SIG | NI | NM  |
| HN\_27 | 5 | 30 | M | HN | SIG | NI | NM  |
| HN\_28 | 5 | 58 | M | HN | SIG | NI | NM  |
| HN\_29 | 5 | 47 | F | HN | SIG | NI | NM  |
| HN\_30 | 5 | 41 | F | HN | C.DES | NI | NR |
| UCinfl\_01 | 6 | 31 | M | UC | SIG | I | NR |
| UCinfl\_02 | 6 | 30 | M | UC | SIG | I | NM  |
| UCinfl\_03 | 6 | 29 | M | UC | SIG | I | NR |
| UCinfl\_04 | 6 | 26 | F | UC | SIG | I | NM  |
| UCinfl\_05 | 6 | 32 | M | UC | SIG | I | IS  |
| UCinfl\_06 | 6 | 19 | F | UC | SIG | I | IS  |
| UCinfl\_07 | 6 | 21 | M | UC | SIG | I | NR |
| UCinfl\_08 | 6 | 57 | M | UC | T.ILE | I | NR |
| UCinfl\_09 | 6 | 29 | M | UC | SIG | I | IS AB Bi  |
| UCinfl\_10 | 6 | 29 | F | UC | COE | I | OM  |
| UCinfl\_11 | 6 | 40 | F | UC | SIG | I | NR |
| UCinfl\_12 | 6 | 40 | F | UC | SIG | I | NR |
| UCinfl\_13 | 6 | 31 | M | UC | SIG | I | IS  |
| UCinfl\_14 | 6 | 22 | M | UC | COE | I | NR |
| UCinfl\_15 | 6 | 36 | F | UC | SIG | I | NR |

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**Supplemental Table 3B continued (page 3 of 3)**

Validation panel I for selected candidate transcripts

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient ID** | **Patient Group** | **Age [a]** | **Gender** | **Disease status** | **Position of biopsy** | **TIssue status / InflammatIon** | **Medication** |
| UCinfl\_16 | 6 | 40 | F | UC | SIG | I | IS  |
| UCinfl\_17 | 6 | 39 | F | UC | SIG | I | OM  |
| UCinfl\_18 | 6 | 28 | M | UC | SIG | I | IS  |
| UCinfl\_19 | 6 | 27 | M | UC | SIG | I | NR |
| UCinfl\_20 | 6 | 26 | F | UC | SIG | I | NR |
| UCinfl\_21 | 6 | 34 | M | UC | SIG | I | IS  |
| UCinfl\_22 | 6 | 61 | F | UC | SIG | I | St  |
| UCinfl\_23 | 6 | 40 | M | UC | C.DES | I | NR |
| UCinfl\_24 | 6 | 47 | M | UC | SIG | I | IS  |
| UCinfl\_25 | 6 | 35 | F | UC | SIG | I | St CS  |
| UCinfl\_26 | 6 | 46 | F | UC | SIG | I | IS Bi  |
| UCinfl\_27 | 6 | 40 | M | UC | SIG | I | NM  |
| UCinfl\_28 | 6 | 30 | F | UC | SIG | I | NR |
| UCinfl\_29 | 6 | 30 | F | UC | SIG | I | St IS CS  |
| UCinfl\_30 | 6 | 50 | F | UC | SIG | I | St  |
| UCn-infl\_01 | 7 | 52 | F | UC | SIG | nI | NM  |
| UCn-infl\_02 | 7 | 36 | M | UC | SIG | NI | IS  |
| UCn-infl\_03 | 7 | 70 | M | UC | SIG | NI | St  |
| UCn-infl\_04 | 7 | 42 | M | UC | SIG | NI | St IS  |
| UCn-infl\_05 | 7 | 30 | M | UC | SIG | NI | NR |
| UCn-infl\_06 | 7 | 32 | F | UC | SIG | NI | IS  |
| UCn-infl\_07 | 7 | 42 | F | UC | SIG | NI | NR |
| UCn-infl\_08 | 7 | 32 | M | UC | SIG | NI | IS  |
| UCn-infl\_09 | 7 | 42 | F | UC | SIG | NI | NM  |
| UCn-infl\_10 | 7 | 18 | M | UC | SIG | NI | NR |
| UCn-infl\_11 | 7 | 38 | M | UC | SIG | NI | NR |
| UCn-infl\_12 | 7 | 47 | M | UC | SIG | NI | NR |
| UCn-infl\_13 | 7 | 32 | F | UC | SIG | NI | NR |
| UCn-infl\_14 | 7 | 64 | F | UC | SIG | NI | NR |
| UCn-infl\_15 | 7 | 35 | M | UC | SIG | NI | IS  |
| UCn-infl\_16 | 7 | 40 | F | UC | SIG | NI | OM  |
| UCn-infl\_17 | 7 | 64 | F | UC | COE | NI | NR |
| UCn-infl\_18 | 7 | 56 | M | UC | SIG | NI | NM  |
| UCn-infl\_19 | 7 | 44 | M | UC | SIG | NI | IS  |
| UCn-infl\_20 | 7 | 55 | M | UC | SIG | NI | IS  |
| UCn-infl\_21 | 7 | 35 | F | UC | SIG | NI | IS  |
| UCn-infl\_22 | 7 | 37 | F | UC | SIG | NI | NR |
| UCn-infl\_23 | 7 | 33 | F | UC | SIG | NI | NR |
| UCn-infl\_24 | 7 | 29 | M | UC | SIG | NI | IS  |
| UCn-infl\_25 | 7 | 37 | F | UC | SIG | NI | St  |
| UCn-infl\_26 | 7 | 58 | F | UC | SIG | NI | IS  |
| UCn-infl\_27 | 7 | 37 | F | UC | SIG | NI | NR |
| UCn-infl\_28 | 7 | 62 | F | UC | SIG | NI | NR |
| UCn-infl\_29 | 7 | 40 | M | UC | SIG | NI | St IS  |
| UCn-infl\_30 | 7 | 34 | M | UC | SIG | NI | NR |

**Supplemental Table 3C**

Validation panel II for selected candidate MVPs and DMRs

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient ID** | **Patient Group** | **Age [a]** | **Gender** | **Disease status** | **Position of biopsy** | **TIssue status / InflammatIon** | **Medication** |
| DCinfl\_01 | 4 | 68 | M | DC | SIG | I | NR |
| DCinfl\_02 | 4 | 41 | F | DC | JEJ | I | NR |
| DCinfl\_06 | 4 | 64 | M | DC | SIG | I | AB BB NS OM  |
| DCinfl\_08 | 4 | 36 | M | DC | SIG | I | NR |
| DCinfl\_09 | 4 | 43 | F | DC | SIG | I | NM  |
| DCinfl\_10 | 4 | 41 | F | DC | STE | I | NR |
| DCinfl\_12 | 4 | 24 | F | DC | C.TRANS | I | NM  |
| DCinfl\_13 | 4 | 65 | M | DC | SIG | I | IS  |
| DCinfl\_15 | 4 | 52 | M | DC | SIG | I | NR |
| DCinfl\_16 | 4 | 52 | F | DC | SIG | I | NM  |
| HN\_04 | 5 | 61 | M | DC | SIG | NI | NM  |
| HN\_06 | 5 | 34 | F | DC | SIG | NI | NM  |
| HN\_08 | 5 | 59 | M | DC | SIG | NI | NR |
| HN\_10 | 5 | 62 | F | DC | SIG | NI | NR |
| HN\_11 | 5 | 28 | F | DC | SIG | NI | NR |
| HN\_12 | 5 | 39 | F | DC | SIG | NI | NR |
| HN\_13 | 5 | 38 | M | DC | SIG | NI | NM  |
| HN\_14 | 5 | 49 | F | DC | SIG | NI | NR |
| HN\_15 | 5 | 66 | M | DC | SIG | NI | OM  |
| HN\_16 | 5 | 62 | M | DC | SIG | NI | NM  |
| HN\_17 | 5 | 61 | M | DC | SIG | NI | BB  |
| HN\_18 | 5 | 58 | M | DC | SIG | NI | BB NS  |
| HN\_19 | 5 | 41 | F | DC | SIG | NI | NM  |
| HN\_20 | 5 | 73 | F | DC | SIG | NI | AB  |
| HN\_21 | 5 | 67 | F | DC | SIG | NI | NM  |
| HN\_22 | 5 | 67 | M | DC | SIG | NI | St  |
| HN\_23 | 5 | 39 | F | DC | SIG | NI | OM  |
| HN\_24 | 5 | 56 | M | DC | SIG | NI | NR |
| HN\_26 | 5 | 32 | F | DC | SIG | NI | NM  |
| HN\_27 | 5 | 30 | M | DC | SIG | NI | NM  |
| UCinfl\_02 | 6 | 30 | M | DC | SIG | I | NM  |
| UCinfl\_03 | 6 | 29 | M | DC | SIG | I | NR |
| UCinfl\_09 | 6 | 29 | M | DC | SIG | I | IS AB Bi  |
| UCinfl\_12 | 6 | 40 | F | DC | SIG | I | NR |
| UCinfl\_13 | 6 | 31 | M | DC | SIG | I | IS  |
| UCinfl\_15 | 6 | 36 | F | DC | SIG | I | NR |
| UCinfl\_17 | 6 | 39 | F | DC | SIG | I | OM  |
| UCinfl\_19 | 6 | 27 | M | DC | SIG | I | NR |
| UCinfl\_22 | 6 | 61 | F | DC | SIG | I | St  |
| UCinfl\_25 | 6 | 35 | F | DC | SIG | I | St CS  |
| UCinfl\_27 | 6 | 40 | M | DC | SIG | I | NM  |
| UCinfl\_28 | 6 | 30 | F | DC | SIG | I | NR |
| UCinfl\_31 | 6 | 41 | F | DC | SIG | I | NR |
| UCinfl\_32 | 6 | 30 | M | DC | SIG | I | NR |
| UCinfl\_33 | 6 | 25 | F | DC | SIG | I | OM  |

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**Supplemental Table 3C continued (page 2 of 2)**

Validation panel II for selected candidate MVPs and DMRs

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient ID** | **Patient Group** | **Age [a]** | **Gender** | **Disease status** | **Position of biopsy** | **TIssue status / InflammatIon** | **Medication** |
| UCinfl\_34 | 6 | 29 | M | DC | SIG | I | IS  |
| UCinfl\_35 | 6 | 20 | F | DC | SIG | I | NR |
| UCinfl\_36 | 6 | 18 | M | DC | SIG | I | NR |
| UCinfl\_37 | 6 | 54 | M | DC | SIG | I | IS NS OM  |
| UCinfl\_38 | 6 | 29 | F | DC | SIG | I | St NS |