

# Transcriptional Signatures That Define Ulcerative Colitis in Remission

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**Background:** This study addresses whether existing specific transcriptional profiles can improve and support the current status of the definition of ulcerative colitis (UC) remission apart from the existing endoscopic, histologic, and laboratory scoring systems. For that purpose, a well-stratified UC patient population in remission was compared to active UC and control patients and was investigated by applying the next-generation technology RNA-Seq.

**Methods:** Mucosal biopsies from patients in remission (n = 14), patients with active UC (n = 14), and healthy control patients (n = 16) underwent whole-transcriptome RNA-Seq. Principal component analysis, cell deconvolution methods, gene profile enrichment, and pathway enrichment methods were applied to define a specific transcriptional signature of UC in remission.

**Results:** Analyses revealed specific transcriptional signatures for UC in remission with increased expression of genes involved in O-glycosylation (*MUC17*, *MUC3A*, *MUC5AC*, *MUC12*, *SPON1*, *B3GNT3*), ephrin-mediated repulsion of cells (*EFNB2E*, *EFNA3*, *EPHA10*, *EPHA1*), GAP junction trafficking (*TUBA1C*, *TUBA4A*, *TUBB4B*, *GJB3*, *CLTB*), and decreased expression of several toll-like receptors (*TLR1*, *TLR3*, *TLR5*, *TLR6*).

**Conclusions:** This study reveals specific transcriptional signatures for remission. Partial restoration and improvement of homeostasis in the epithelial mucus layer and revival of immunological functions were observed. A clear role for bacterial gut flora composition can be implied. The results can be useful for the development of treatment strategies for UC in remission and may be useful targets for further investigations aiming to predict the outcome of UC in the future.

**Key Words:** ulcerative colitis, molecular signatures, remission

## INTRODUCTION

Ulcerative colitis (UC) is a chronic inflammatory disorder that requires long-term treatment to achieve remission.<sup>1</sup> The inflammation status of UC is usually determined by endoscopic, histologic, and laboratory parameters.<sup>2</sup> Current

management programs aim for induction and maintenance of clinical remission to prevent disease-related and treatment-induced complications.<sup>3, 4</sup> Different scoring systems for UC activity are used to evaluate endoscopic disease activity and activity status, but none have yet had all properties fully assessed.<sup>5, 6</sup> However, there is no consensus on how to define clinical remission as no validated definition exists. The last guidelines from the European Colitis and Crohn's Organization included clinical and endoscopic parameters where no mucosal lesions should appear (Mayo endoscopic grade 0).<sup>7</sup> Despite this instruction, in most clinical studies Mayo grade 1 is included in the definition of clinical remission.<sup>8, 9</sup> It is well known that clinical and endoscopic remission as defined above indeed may involve persisting microscopic inflammatory activity even in the absence of gastrointestinal symptoms.<sup>10-13</sup> This activity can result in progressive accumulation of bowel damage, such as dysmotility, fibrosis, and increased risk of colorectal neoplasia.<sup>10, 14-17</sup> There is a need for standardization of the assessment of remission and validation that gives a prognostic value.<sup>18</sup> Therefore, an urgent need to characterize the complex pathogenic and healing mechanisms in UC still exists.

It is believed that the elucidation of key inflammatory pathways and perturbations involved by integrated clinical and genomic analyses should provide insight into the molecular events and pathways that are involved during remission. Recently, attempts have been made to describe transcriptional

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levels in UC remission by using microarrays.<sup>19-21</sup> However, hybridization-based methods are restricted to predefined and often well-annotated species and RNA probe sets. Next-generation sequencing techniques have no such restrictions, which may lead to the discovery of potential new transcripts with a meaning for UC in remission. A transcriptomic study using RNA-Seq technology has been recently reported for the pediatric UC cohort PROTECT.<sup>22, 23</sup>

This study is the first to describe the entire transcriptomic landscape of adult UC in remission using next-generation sequencing technology with a focus on a clearly defined and representative group of UC patients in remission.

The establishment of robust and more specific biomarker groups and genomic signatures of UC remission may also lead to novel therapeutic approaches and is believed to pave the way for the development of personalized treatment options for UC patients in the future.

## METHODS

### Patient Material

A standardized sampling method was used to collect mucosal biopsies (N = 44) from patients in remission (n = 14), newly diagnosed treatment-naïve UC patients with mild to moderate disease (n = 14), and control patients (n = 16). Normal biopsies were taken from an earlier study.<sup>24</sup> Patients' UC was diagnosed based upon established clinical endoscopic and histological criteria as defined by the European Colitis and Crohn's Organization guidelines. The grade of inflammation was assessed during colonoscopy using the UC disease activity index endoscopic subscore of 3-10 for mild to moderate disease.<sup>7</sup> Tumor necrosis factor-alpha mRNA expression levels were measured by real-time quantitative polymerase

chain reaction (qPCR), thereby indicating the grade of UC activity.<sup>20</sup> Fecal calprotectin was measured in all patients representing remission and in 8 patients representing active UC with the Calprest ELISA kit (Eurospital). A total Geboes score was assessed for all biopsies representing remission and for 9 samples representing active UC.<sup>25</sup> Patients in the remission group remained in remission for more than 1.5 years after discontinuation of treatment. The samples were taken from an established biobank approved by the Norwegian Board of Health. Patient characteristics are depicted in Table 1.

### RNA Isolation

Total RNA was isolated using the Allprep DNA/RNA Mini Kit from Qiagen (catalog number 80204) and the QIAcube instrument (Qiagen), according to the manufacturer's protocol. The RNA quantity and purity were assessed by using the NanoDrop ND-1000 spectrophotometer (ThermoFisher Scientific, Wilmington, DE). The Experion Automated Electrophoresis System (Bio-Rad, Hercules, CA) and the RNA StdSens Analysis Kit (Bio-Rad, catalog number 700-7103) were used to evaluate RNA integrity, according to the instruction manual. The RNA samples were kept at  $-70^{\circ}\text{C}$  until further use. All RNA samples used for analyses had a RNA integrity number value of between 8.0 and 10.0.

### qPCR

The tumor necrosis factor-alpha levels in biopsies were measured by using qPCR. The RNA quantity was assessed with NanoVue Plus (GE Healthcare, United Kingdom). Synthesis of cDNA was performed using the QuantiTect Reverse Transcription Kit (Qiagen, catalog number 205314) and the QuantiNova Probe PCR Kit (Qiagen, catalog number 208256).

**TABLE 1.** Patient Characteristics

Characteristics	Control Patients (n = 16)	Active UC (n = 14)	UC in Remission (n = 14)
Gender (male/female)	11/5	9/5	9/5
Age, y, mean $\pm$ SD	52.9 $\pm$ 16.9	40.7 $\pm$ 13.9	46.5 $\pm$ 16.0
Clinical score $\pm$ SD	0	7.78 $\pm$ 1.52	0.44 $\pm$ 1.01*
Endoscopy score mean $\pm$ SD	0	1.79 $\pm$ 0.43	0
Geboes score (total)	n.d.	6.53 $\pm$ 2.93	1.07 $\pm$ 1.73
TNF- $\alpha$ copies/ $\mu\text{g}$ RNA $\pm$ SD	3,663 $\pm$ 1,973	15,907 $\pm$ 9,623	4,645 $\pm$ 1,830
Calprotectin (mg/kg) mean $\pm$ SD	n.d.	587.5 $\pm$ 483.8 <sup>†</sup>	53.9 $\pm$ 41.1
Extension of disease <sup>‡</sup>	–	2/9/3	2/8/4
Medication <sup>§</sup>	–	–	14/4/5

\*Average score of 9 patients.

<sup>†</sup>Average calprotectin levels in 11 patients.

<sup>‡</sup>Proctitis/left-sided colitis/pancolitis.

<sup>§</sup>5-aminosalicylic acids/steroids/immunosuppressives.

n.d. indicates not determined; TNF- $\alpha$ , tumor necrosis factor-alpha.

Beta-actin was used as the housekeeping gene. For the detection, a CFX Connect Real Time PCR Detection System (BioRad) was used. The results were measured in copies/ $\mu$ g. Tissue samples with values  $<7,000$  copies/ $\mu$ g RNA were considered noninflamed tissues, and values  $>7,000$  copies/ $\mu$ g RNA were considered inflamed tissues as depicted in Table 1.<sup>26</sup>

## Library Preparation and Next-Generation Sequencing

Whole transcriptome libraries of UC in remission samples were prepared with the TruSeq Stranded Total RNA LT Sample Prep Kit from Illumina (catalog number RS-122–2203). The amount of input material was 1  $\mu$ g of total RNA. The Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA) and the Agilent DNA 1000 kit (cat number 5067-1504) were used to assess RNA library quality, according to the instruction manual. The RNA libraries comprised fragments with an average size of 307 base-pairs. The libraries were normalized to 10 nM and subsequently sequenced with the NextSeq 550 instrument (Illumina) according to the manufacturer's instructions. The average number of uniquely mapped reads per sequencing run were 88 million reads per sample.

## Data Analysis

Base calling and quality scoring were performed on the NextSeq 550 Illumina sequencer. Initial quality checks were performed by the NextSeq 550 on-board computer. The STAR-2.5.2b assembly algorithm and htseq-count were used for downstream analysis. Transcripts were aligned to human genome assembly GRCH38p.11 (<https://www.ncbi.nlm.nih.gov/grc/human/data>), and DESeq2 was used to compile and normalize from the individual raw htseq count matrixes. Transcripts with an average read count of  $<30$  after DESeq2 normalization were excluded from further analysis. The comparisons between the UC, remission (R), and normal (N) samples were made using the LIMMA package with EBayes to shrink probewise sample variances on the DESeq2 normalized data. Only transcripts with a log<sub>2</sub> fold change  $>0.5$  and a Benjamini-Hochberg adjusted  $P < 0.05$  in either UC-R or R-N comparisons were kept for further analysis.<sup>27</sup>

Profile analysis was conducted on the basis of the LIMMA results. The profile  $N < R > UC$  designated a situation where the log<sub>2</sub>(R)-log<sub>2</sub>(N) fold change was  $>0.5$  and where the log<sub>2</sub>(R)-log<sub>2</sub>(UC) fold change was greater than 0.5. Note that the comparison UC-N was not considered in the profiles, as this study focused on remission-specific profiles. Both comparisons had a  $P$  adjusted value  $<0.05$ . The profile  $N > R = UC$  designated a situation where log<sub>2</sub>(N)  $>$  log<sub>2</sub>(R) by more than 0.5 and was significant (adjusted  $P < 0.05$ ), but the absolute value of log<sub>2</sub>(UC)-log<sub>2</sub>(R) was  $<abs(0.5)$  and/or the comparison was not significant after the  $P$  value adjustment. Profiles included were  $N < R < UC$ ,  $N > R > UC$ ,  $N < R > UC$ ,  $N > R <$

$UC$ ,  $N > R = UC$ ,  $N < R = UC$ ,  $N = R > UC$ , and  $N = R < UC$ . The gene set overrepresentation test was conducted using the enrichPathway algorithm of the R Bioconductor ReactomePA package (<https://bioconductor.org/packages/release/bioc/html/ReactomePA.html>).<sup>28,29</sup> Genes for each profile were entered into the enrichPathway algorithm. Reactome pathways that had a significant (adjusted  $P < 0.05$ ) overrepresentation of genes were reported for all profiles.

For the estimation of specific cell populations in patient samples, an analysis was performed using the R/Bioconductor CellMix manual (<http://web.cbio.uct.ac.za/~renaud/CRAN/web/CellMix/>) with the immune response in silico (IRIS) weighted marker list characteristic for the different cell types.<sup>30</sup> The epithelial marker cadherin 1, the phosphatidylinositol glycan anchor biosynthesis class F, the epithelial cell adhesion molecule, the L1 cell adhesion molecule, and the laminin subunit alpha 1 were added to the IRIS marker list and weighted strongly to give an estimate of the presence of epithelial fractions in the patient samples.

Heat maps were generated using the pHeatmap R package (<https://CRAN.R-project.org/package=pheatmap>). Only genes that were present in one of the reactome overrepresented pathways were considered. Heat maps were drawn for genes found in an overrepresented reactome pathway for the following profiles:  $N < R < UC$ ,  $N > R > UC$ ,  $N < R > UC$ , and  $N > R < UC$ . Processed RNA-Seq data were deposited in the National Center for Biotechnology Information's Gene Expression Omnibus (<https://www.ncbi.nlm.nih.gov/geo/>) and are accessible through GEO series accession number GSE128682.

## Ethical Considerations

The participants signed an informed and written consent form. The study was approved by the Regional Ethics Committee of North Norway and the Norwegian Social Science Data Services (REK Nord 2012/1349).

## RESULTS

### Whole Transcriptional Profile Characterization of UC in Remission

The entire transcriptome representing UC in remission was established by RNA-Seq, which revealed 13,927 differentially expressed genes (DEGs). Initial principal component analysis (PCA) of the entire DESeq2 log-normalized count matrix revealed a clear distinction between UC in remission, normal, and active UC samples along the first principal component with 46.9% and the second principal component with 9.8% of the total variance (Fig. 1). There were no differences in the UC remission sample profile that indicated any gender separation.

To further describe and analyze the transcriptome, the differentially expressed transcripts were adjusted to  $P < 0.05$

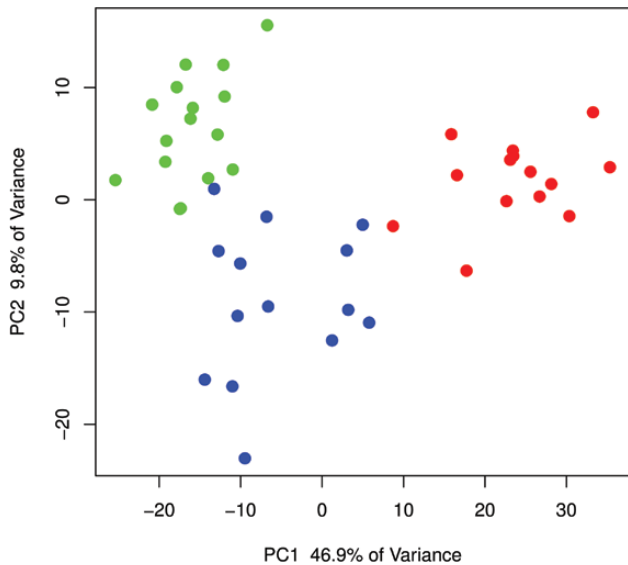


FIGURE 1. PCA showing the difference between active UC (red), UC remission (blue), and normal control (green) samples of the top 5,000 most variable transcripts after DESeq2 rlog normalization. Principal component 1 explained 46.9 % of the total variance, and principal component 2 explained 9.8 % of the total variance.

and a  $\log_2$  fold change  $> 0.5$ . The resulting number of significant DEGs ( $n = 5,407$ ; [Supplementary Data 1](#)) was used for further downstream analyses. [Fig. 2](#) depicts the assignment of significantly DEGs of normal (green), UC (red), and remission (blue) groups to clusters specific for all possible matching profiles. The number of genes found in each profile, the number of overrepresented reactome pathways, the total number of genes found in overrepresented reactome pathways, and a sample box plot for 3 genes from each profile are shown. For further interpretation of the results, we describe 4 of the 8 possible profiles, indicated by an asterisk in the figure, in detail. They represent genes ( $n = 924$ ) in an intermediate state in remission ( $N < R < UC$ ;  $N > R > UC$ ) and genes specific for remission ( $N < R > UC$ ;  $N > R < UC$ ; [Fig. 2](#)). The gene clusters of each profile underwent reactome pathway enrichment as described in detail in “Methods” above, which resulted in a total of 50 annotated pathways representative for these profiles ([Supplementary Data 2](#)). Genes in the remaining profiles have been published in previous research.<sup>24</sup> All genes and pathways matching any of the profiles can be found in [Supplementary Data 1](#).

A comparison of the data obtained for UC vs normal samples with recent published transcriptomic data for the pediatric UC cohort PROTECT showed a strong correlation of 0.94, indicating that the datasets are comparable ([Supplementary Data 3](#)).<sup>22</sup> Therefore, we used a remission dataset from the PROTECT cohort including a 115 glucocorticoid response gene signature and compared it with a remission dataset containing 4 glucocorticoid patient samples from this study. Four significantly regulated genes—*PHLDA3*, *DSG3*, *ABCA12*,

and *XKR9*—overlapped with the PROTECT glucocorticoid response gene signature. In addition, the 4 patient samples with glucocorticoid treatment did not separate from the remaining remission samples in the PCA ([Fig. 1](#)). All the results regarding the comparison with the datasets from the PROTECT study are shown and summarized in [Supplementary Data 3](#).

### Genes in an Intermediate State in UC Remission

The different expression profile patterns with the number of genes ( $n = 78$ ) including the 3 groups—N, R, and active UC for the intermediate state of remission ( $N < R < UC$ ;  $N > R > UC$ )—are shown in [Fig. 3](#). Genes that have been previously shown to have an increased expression in active UC<sup>24</sup> showed increased expression but to a lesser extent during remission ( $n = 43$ ) ([Fig. 3A](#)). Functional annotation ([Table 2](#)) revealed involvement in neutrophil degranulation (*CHI3L1*, *CD55*, *TCIRG1*, *OLFM4*, *UNC13D*, *LRG1*, *PLAUR*, *CXCR1*, *SIRPB1*, *LPCAT1*, *TMEM173*, *FRMPD3*, *CXCL1*) and degradation of the extracellular matrix, represented by members of the collagen family (*COL4A1*, *COL1A1*, *COL5A3*, *COL18A1*, *COL7A1*) and several matrix metalloproteinases (*MMP3*, *MMP7*, *MMP10*). Further, genes were annotated for interleukin signaling (*NFKB2*, *CASP1*, *SAAI*, *SOCS1* and *SOCS3*, *IGTAX*, *CCL22*, *JAK3*, *IL-1B*, *LCN2*, *IL-13RA2*) and amino acid transport across the plasma membrane, represented by several members of the solute carrier family (*SLC7A5*, *SLC6A20*, *SLC7A11*, *SLC6A14*).

Genes that were downregulated in remission to a lesser extent than in active UC ( $n = 35$ ) are depicted in [Fig. 3B](#). Those genes could be functionally annotated to pathways ([Table 2](#)) including biological oxidation, in particular glucuronidation (represented by 8 different UDP glucuronosyltransferase family members: *UGT1A3*, *UGT1A4*, *UGT1A5*, *UGT1A6*, *UGT1A7*, *UGT1A9*, *UGT1A10*, *UGT2B7*; and 2 cytochrome members: *CYP27A1* and *CYP3A4*), solute carrier-mediated transmembrane transport and related disorders (represented by 10 solute carrier family members), synthesis of bile acids (*ABCB11* and *AMACR*), metallothioneins (*MT1E*, *MT1M*, *MT1F*), and digestion (*GUCA2B* and *GUCA2A*; *ALPI*). All genes representing these regulatory profiles can be found in [Supplementary Data 2](#).

### Genes Specific for UC Remission

Specific expression profile patterns with the number of genes ( $n = 25$ ) including samples for the N, R, and active UC ( $N < R > UC$ ;  $N > R < UC$ ) groups are shown in [Fig. 4](#). Overrepresented pathways of genes ([Table 2](#) and [Supplementary Data 4](#)) with increased expression ( $n = 20$ ) during remission ([Fig. 4A](#)) are mainly involved in diseases of glycosylation, represented by different mucins (*MUC5AC*, *MUC3A*, *MUC12*, *MUC17*), *BCAN*, *SPON1*, *CSPG4*, *ADAMTSL5*, *GNE*, and *B3GNT3*. Others could be annotated to GAP junction




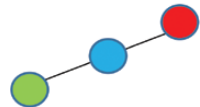
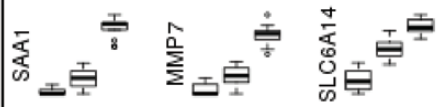
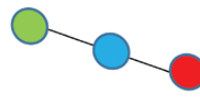
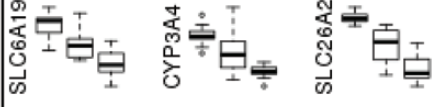
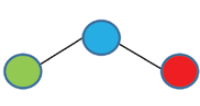



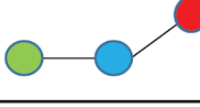
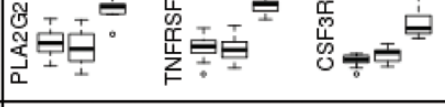
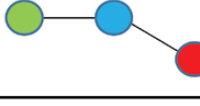

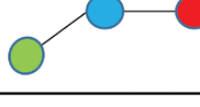

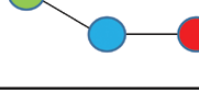

 N R UC	Profile	#Genes	#Enriched Pathways	#Genes in enriched pathways	Sample Profiles
 *	N<R<UC	165	16	43	
 *	N>R>UC	213	14	35	
 *	N<R>UC	273	16	20	
 *	N>R<UC	273	4	5	
	N=R<UC	1624	76	554	
	N=R>UC	1061	17	114	
	N<R=UC	896	12	106	
	N>R=UC	902	0	0	

FIGURE 2. Overview of transcriptional profiles found for UC in remission. Assignment of significantly DEGs of normal (green), UC (red), and remission (blue) groups to clusters specific for all possible matching profiles. Transcripts with a minimum fold change difference of 0.5, an adjusted  $P < 0.05$ , and a minimum of 30 reads are depicted as # genes. Genes left after pathway enrichment of the different profiles are indicated. The first column is a pictorial representation of profiles. The number of genes found in each profile, the number of enriched reactome pathways, the total number of genes found in enriched reactome pathways, and sample box plots for 3 genes from each profile are shown. Profiles indicated with (\*) are considered and discussed in this study.

trafficking, such as tubulins (*TUBA1C*, *TUBA4A*, *TUBB4B*), *CLTB*, and *GJB3*, and in the ephrin-mediated repulsion of cells represented by ephrins (*EFNA3* and *EFNB2*), and ephrin type A receptors (*EPHA10* and *EPHA1*) (Fig. 4A). Only 5 genes with decreased expression during remission could be enriched and annotated to overrepresented pathways for diseases of the immune system, in particular diseases associated with the

toll-like receptor (TLR) signaling cascade including *TLR1*, *TLR3*, *TLR5*, and *TLR6* and the innate immune signal transduction adaptor MyD88 and interleukin-1 IRAK4 deficiency (Fig. 4B). All genes representing these regulatory profiles can be found in Supplementary Data 2, and all remaining genes after gene set enrichment representing these regulatory profiles can be found in Table 2 and Supplementary Data 3.

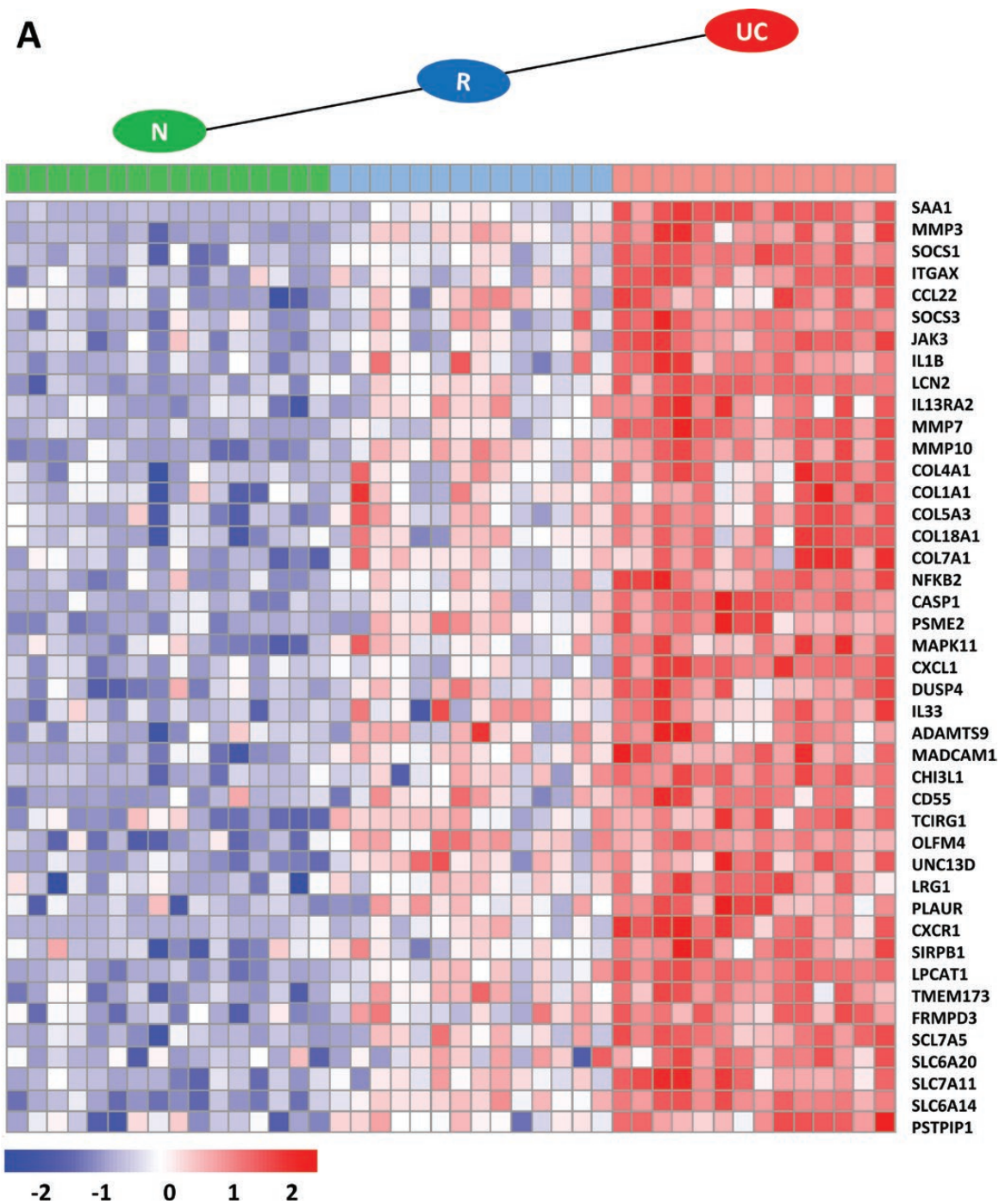


FIGURE 3. Heatmap of genes found in enriched reactome pathway profiles in an intermediate state in remission with indicated profile patterns. A, Transcripts with significantly higher expression in remission (R; blue) than in normal (N; green) samples, and transcripts with significantly higher expression in UC (red) than in R samples (N < R < UC). B, Transcripts with significantly lower expression in R (blue) than in N (green) samples, and transcripts with significantly lower expression in UC (red) than in R samples (N > R > UC). Only transcripts with an absolute fold change >0.5, an adjusted *P* <0.05, and a minimum of 30 reads are depicted. Transcripts were normalized from raw count to log<sub>2</sub> values by using DESeq2. Fold change and *P* values were calculated with LIMMA.

### Changes in Fractions of Cell Populations

To estimate specific cell populations in the UC remission samples compared with the control and active UC tissue

samples, a cell deconvolution method was applied as described in “Methods” above. The deconvolutions were restricted to the following cell types: epithelial cells, monocytes, T-cells, neutrophils, B

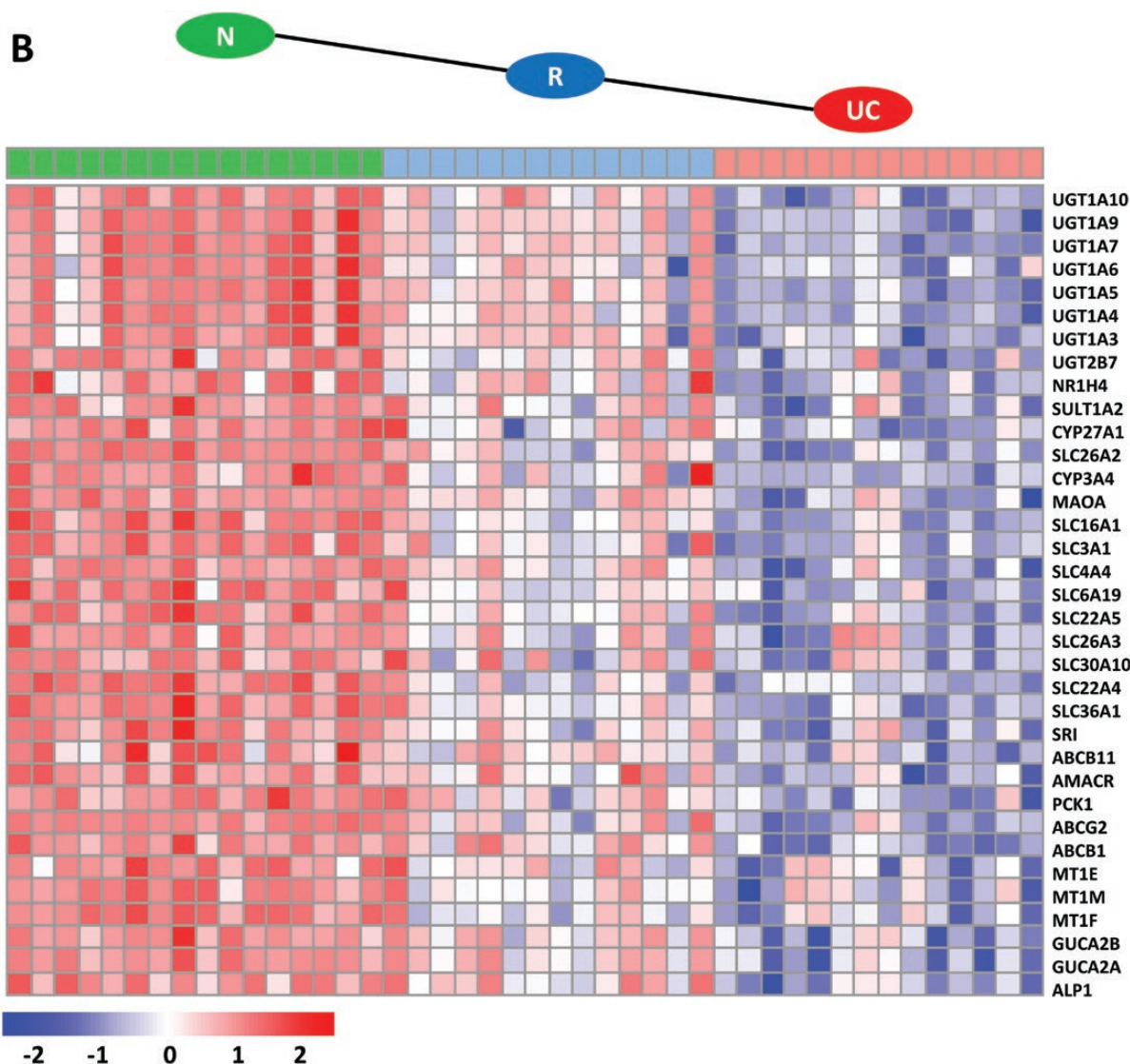


FIGURE 3. Continued.

cells/lymphoid cells, and myeloid cells. The results showed a clear difference of cell fractions present in the UC remission samples when they were compared with the active UC and control samples (Fig. 5). The epithelial cell fraction showed intermediate levels in the remission samples when they were compared with the normal samples and active UC samples. A decrease in fractions of monocytes, T-cells, and B cells/lymphoid cells was observed for the remission samples when they were compared with the active UC samples. High fractions of neutrophils observed for active UC samples were almost reduced to levels of normal samples in remission. The fractions of myeloid cells remained unchanged in the remission samples compared with those in the normal samples and active UC samples. The results of the deconvolution experiments are summarized in Fig. 5.

## DISCUSSION

This study provides a unique, comprehensive, and quantitative record of high-resolution gene expression in UC patients in remission using next-generation RNA-Seq technology and provides for the first time well-defined transcriptional signature patterns for UC in remission obtained by pathway enrichments. A clearly defined patient sample group representing UC in remission was used to characterize the representative transcriptional signature of UC in remission (Table 1). Initial PCA revealed a quite complex pathology of remission (Fig. 1). Some remission samples clustered close to UC and others close to N, demonstrating the variability within remission and the challenge of defining remission-specific profiles statistically. The assignment of genes to different expression profiles (Fig. 2) and gene set enrichment (Table 2) made it possible



**TABLE 2.** Reactome-Enriched Pathways and Genes of Indicated UC Remission Profiles for N, UC, and R

Pathway	Gene Symbol
Enriched pathways for N < R < UC (adjusted $P < 0.05$ )	
Interleukin-4 and interleukin-13 signaling	<i>SAA1, MMP3, SOCS1, ITGAX, CCL22, SOCS3, JAK3, IL-1B, LCN2, IL-12RA2</i>
Collagen degradation	<i>MMP7, MMP10, COL4A1, COL1A1, COL5A3, COL18A1, COL7A1</i>
Signaling by interleukins	<i>PSME2, MAPK11, CXCL1, DUSP4, IL-33</i>
Extracellular matrix organization	<i>ADAMTS9, MADCAM1</i>
Neutrophil degradation	<i>CHI3L3, CD55, TCIRG1, OLFM4, UNC13D, LRG1, PLAUR, CXCR1, SIRPB1, LPCAT1, TMEM173, FRMPD3</i>
Amino acid transport across plasma membrane	<i>SLC7A5, SLC6A20, SLC7A11, SLC6A14</i>
<i>NLRP3</i> inflammasome	<i>PSTPIP1, CASP1, NFKB2</i>
Enriched pathways for N > R > UC (adjusted $P < 0.05$ )	
Glucuronidation	<i>UGT1A10, UGT1A9, UGT1A7, UGT1A6, UGT1A5, UGT1A4, UGT2B7, UGT2B7</i>
Biological oxidations	<i>NRIH4, SULT1A2, CYP27A1, SLC26A2, CYP3A4, MAOA</i>
Solute carrier-mediated transport	<i>SLC16A1, SLC3A1, SLC4A4, SLC6A19, SLC22A5, SLC26A3, SLC30A10, SLC22A4, SLC36A1, SRI</i>
Bile acids and bile salt metabolism	<i>ABCB11, AMACR</i>
Abacavir transport and metabolism	<i>ABCG2, ABCB1, PCK1</i>
Metallothioneins (binding metals)	<i>MT1E, MT1M, MT1F</i>
Digestion	<i>GUCA2B, GUCA2A, ALPI</i>
Enriched pathways for N < R > UC (adjusted $P < 0.05$ )	
O-linked glycosylation; O-linked-glycosylation of mucins	<i>MUC5AC, MUC3A, MUC12, MUC17, B3GNT3</i>
O-linked glycosylation	<i>SPON1, ADAMTSL5</i>
Diseases of glycosylation	<i>GNE</i>
Chondroitin sulfate and dermatan sulfate degradation	<i>CSPG4, BCAN, HYAL</i>
GAP junction trafficking	<i>GJB3, TUBA1C, TUBA4A, CLTB, TUBB4B</i>
EPH-ephrin-mediated repulsion of cells	<i>EPHA10, EFNA3, EFNB2, EPHA1</i>
Enriched pathways for N > R < UC (adjusted $P < 0.05$ )	
TLR signaling cascade; MyD88 deficiency ( <i>TRL2/4</i> ); <i>IRAK4</i> deficiency ( <i>TRL2/4</i> )	<i>TLR1, TLR6, LY96</i>
TLR signaling cascade	<i>TLR3, TLR5</i>

to show that genes found in an intermediate state in remission showed reduced but not completely diminished levels of inflammatory signatures when compared with active UC (Fig. 3). This decrease may represent the remaining quiescent microscopic disease activities during remission as suggested by others.<sup>7,10,11,13</sup> Examples of considerable downregulated transcripts in remission for previously reported top upregulated transcripts in active UC are genes involved in the degradation of the extracellular matrix, collagen degradation, neutrophil degranulation, and signaling by interleukins (Table 2 and Supplementary Data 3). The downregulation of the 2 inflammatory bowel disease (IBD) susceptibility genes *CXCL1* and *CXCR1* (Fig. 3) involved in neutrophil degranulation was in agreement with almost absent fractions of neutrophils present during remission (Fig. 5). These results concurred with a recent transcriptomic cohort study including pediatric UC patients.<sup>22</sup> Note also that a downregulation of transcripts for *MMP3*, *MMP10*,

*CHI3L1*, and *CXCL1* during remission has been reported by using real-time qPCR.<sup>21</sup>

The involvement of the microflora and their importance in the onset, development, and preservation of UC has been implied.<sup>31–34</sup> During remission, several genes involved in patient antibacterial response showed reduced expression, like the transporter *SLC6A14*; the IBD disease marker *LCNC2*; *SAA1*, which represents an important link between mucosal T-cells and microbial communities; and *CHI3L1*, which lessens bacterial adhesion and invasion on/into colonic epithelial cells.<sup>35–38</sup> These observations are in concordance with the results obtained by cell deconvolutions, which revealed an improvement of the mucus layer in the remission samples when compared with the active UC samples by showing decreased fractions of monocytes, T-cells, and B cells/lymphoid cells and enhanced fractions of epithelial cells (Fig. 5).



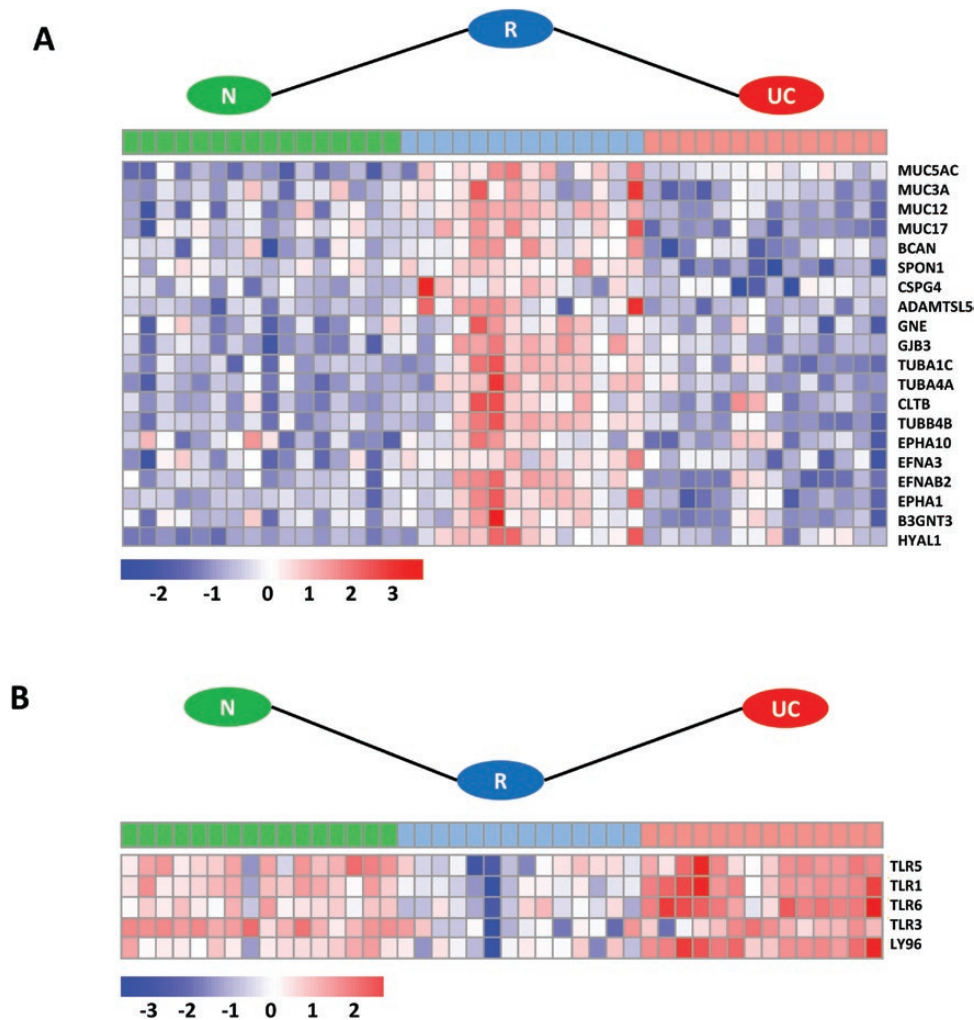


FIGURE 4. Heatmap of specific genes for UC in remission with indicated profile patterns. A, Transcripts with significantly higher expression in remission (R; blue) than in normal (N; green) and UC (red) samples;  $N < R > UC$ . B, Transcripts with significantly lower expression in R (blue) than in N (green) and UC (red) samples;  $N > R < UC$ . Transcripts with a minimum fold change difference of 0.5, an adjusted  $P < 0.05$ , and a minimum of 30 reads are depicted. Transcripts were normalized from raw count to log2 values by using DESeq2. Fold change and  $P$  values were calculated with LIMMA.

However, the main focus of this study was to determine more specific transcriptional signatures involved in remission. By assigning transcripts to different expression profiles and using gene set enrichment methods, we were able to uncover transcripts in the remission samples that were differentially up- or downregulated as compared to the UC and N samples (Fig. 4). Surprisingly, enriched pathways for upregulated genes in the remission samples were found for pathways such as O-glycosylation, GAP junction trafficking, and ephrin-mediated repulsion of cells (Table 2). It is well acknowledged that gastrointestinal O-glycosylated mucins are constituents of luminal barrier function and are the first line of host defense against invading pathogens.<sup>39</sup> The observed increased expression of the mucin *MUC17* and its paralog *MUC3A* during remission (Fig. 4A) may prevent bacterial invasion through

barrier function by maintaining the integrity of the surface epithelial layer and homeostasis on the mucus surface.<sup>39-41</sup> In addition, *MUC17* has been shown to be instrumental in limiting the epithelial adhesion and invasion of enteroinvasive *Escherichia coli*.<sup>42, 43</sup> In concordance with these results was the observation of a partial restoration of the epithelial mucus layer (Fig. 5). However, epithelial cell fractions did not reach levels as seen in the normal samples, which indicates that mucosal healing in UC remission was not fully accomplished. Epithelial cells are tightly coupled together through specialized intercellular junctions, including tight junctions and gap junctions,<sup>44</sup> and the increased expression of genes annotated for GAP junctions in this study (*TUBA1C*, *TUBA4A*, *TUBB4B*, *CLTB*, *GNE*, *GJB3*) confirm this notion. In addition, the observed increased expression of *MUC12* may support protection of the epithelial cells in the

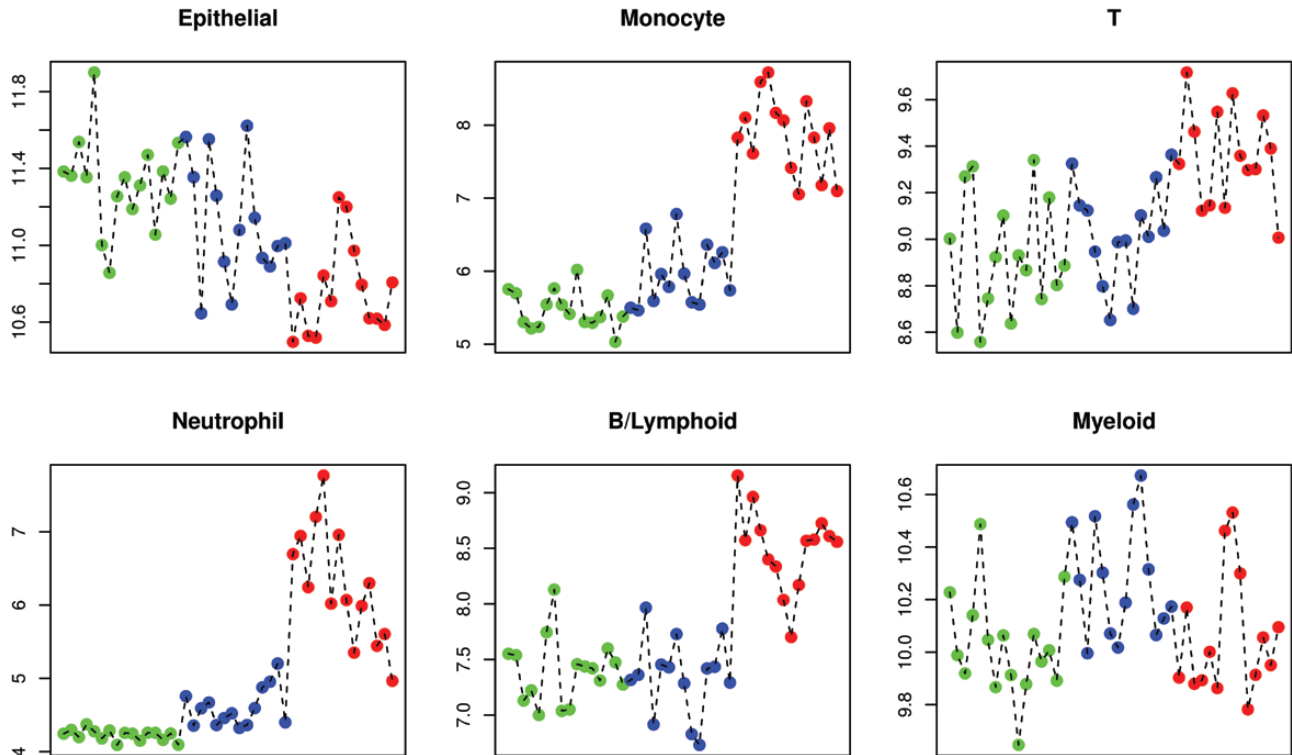


FIGURE 5. Estimation of cell fractions in patient samples using the Bioconductor CellMix package and the IRIS marker set as described in “Methods.” The blue dots indicate normal control samples, the red dots indicate active UC samples from a former study,<sup>24</sup> and the green dots indicate UC in remission. The y axis depicts the mean weighted expression of IRIS marker genes within each cell type set.

mucosa: previous findings showed a significant downregulation of *MUC12* in the colon and ileum in patients with Crohn disease.<sup>45, 46</sup>

In addition to the mucins, other genes involved in O-linked glycosylation such as *B3GNT3* (lymphocyte homing and lymphocyte trafficking), *SPONI*, and *ADAMTSL5* (metalloendopeptidase activity) showed increased expression (Fig. 4A). In particular, *SPONI* has been shown to regulate macrophage microbicidal activity by effectively phagocytizing the bacteria *Salmonella typhimurium* and *E. coli*.<sup>47-50</sup>

An increasing body of evidence suggests that epithelial cells also directly exchange information at cell-cell contacts via the ephrin family of receptor tyrosine kinases and their membrane-associated ephrin ligands.<sup>51, 52</sup> It has been reported that impaired intestinal epithelial barrier and abnormal T-cell responses are evident during IBD.<sup>53, 54</sup> This implies that the observed increased levels of *EFNB2* in the remission samples may be directly involved in the activation of T-cell development,<sup>54, 55</sup> in the organization of stem cell compartments, and in the ordered migration of epithelial cells along the intestinal villus axis.<sup>44</sup> Increased expression of *EFNB2* has been also found to enhance intestinal wound healing in patients with Crohn disease and may play a potential role in the EphB/ephrin-B system as a pharmacological target in intestinal inflammatory disorders.<sup>56, 57</sup>

In addition, some of the differentially regulated genes have been reported to be associated with the development of colorectal cancer such as *MUC5AC*, the ephrin receptors *EPHA10* and *EPHA2*, and *OLFM4*.<sup>58-60</sup> However, the value of these genes as reliable predictors for disease outcome remains to be elucidated.

Gene pathway enrichment revealed downregulation of several TLRs in the remission samples (Fig. 4B). It has been suggested that UC may be associated with specific alterations in selective TLR expression in the intestinal epithelium.<sup>61, 62</sup> A recent report also implies a role for mucin and TLRs in patient defense against intestinal parasites.<sup>42</sup> In this study, TLRs were expressed higher in normal mucosa and active UC samples than in the remission samples. These observations are most likely a result of different treatment strategies applied for this patient group and may be used to establish therapeutic options for UC to obtain better clinical outcomes.<sup>63-65</sup>

A limitation of this work is the amount of patient samples, with  $n = 14$ . The low sample size made it difficult to define molecular remission patterns caused by different treatments. However the number of patients included in this study is still larger than reported for other studies, and PCA (Fig. 1) revealed sufficient separation of the different patient groups.<sup>21</sup> It is also possible that the remission signature seen here reflects a response to treatment or natural recovery after initial disease presentation. Such a response could have been evaluated

with follow-up for active UC samples, which was not available during this study.

## CONCLUSIONS

The data demonstrate that remission is a permanently altered state of UC characterized by a unique transcriptional signature in the mucosa, which is different from that in UC and normal samples. The analysis revealed new and more specific molecular signatures for UC in remission compared with earlier studies conducted with microarrays.<sup>19,21</sup> Partial restoration of the epithelial mucus layer and revival of immunological functions in the mucus layer were supported by the expression of protective genes. In addition, a clear role for bacterial gut flora composition can be implied. Some expressed genes have been associated with the development of colorectal cancer, but a role for these genes as reliable predictors for disease outcome remains uncertain. Further studies will tell whether transcriptomic, epigenetic, metagenomic, and meta-transcriptomic signatures together can reveal biomarkers and/or biomarker groups of valuable character to be used for the prognosis of relapse and for the definition of new criteria for de-escalating treatment.

## SUPPLEMENTARY DATA

Supplementary data are available at *Inflammatory Bowel Diseases* online.

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