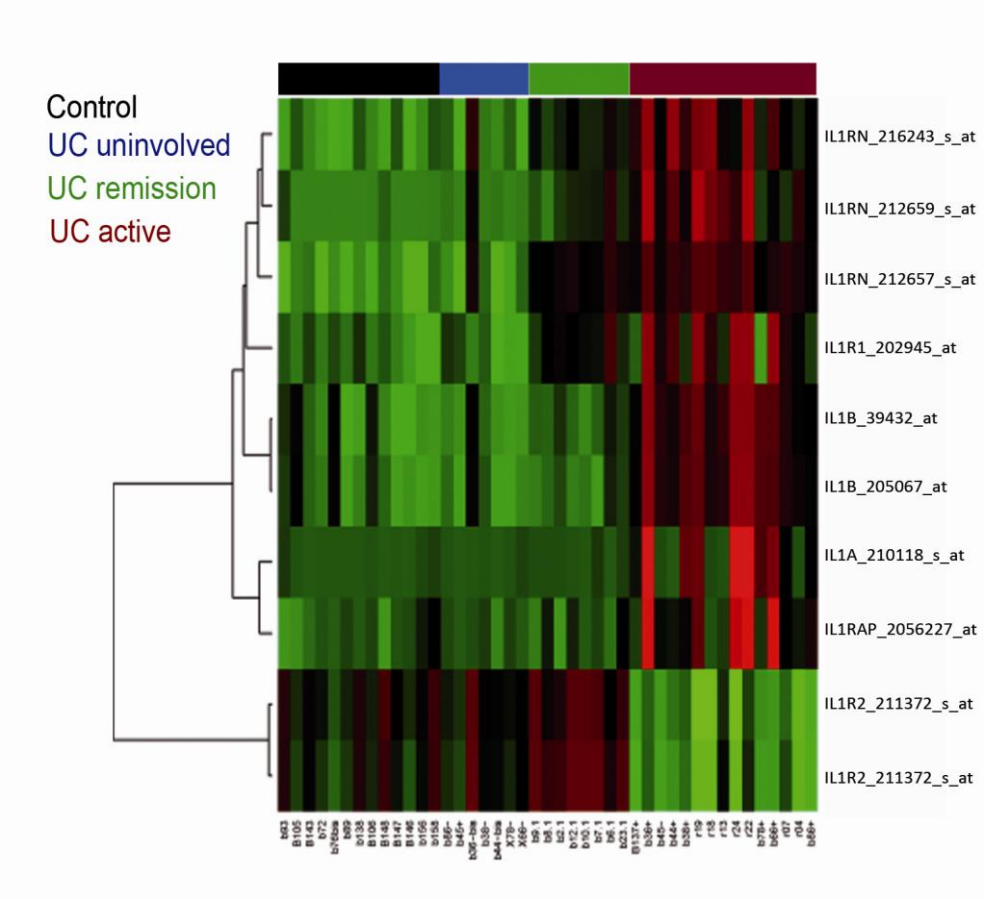
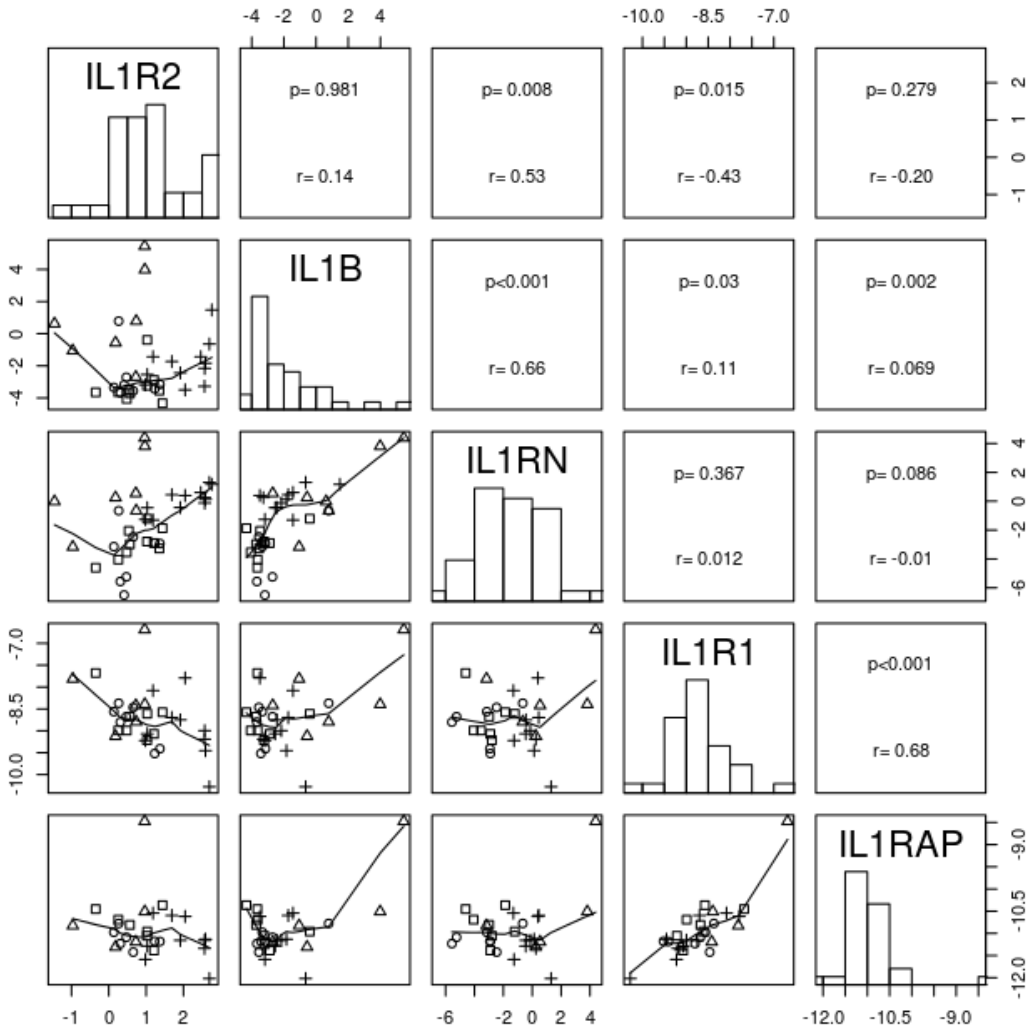
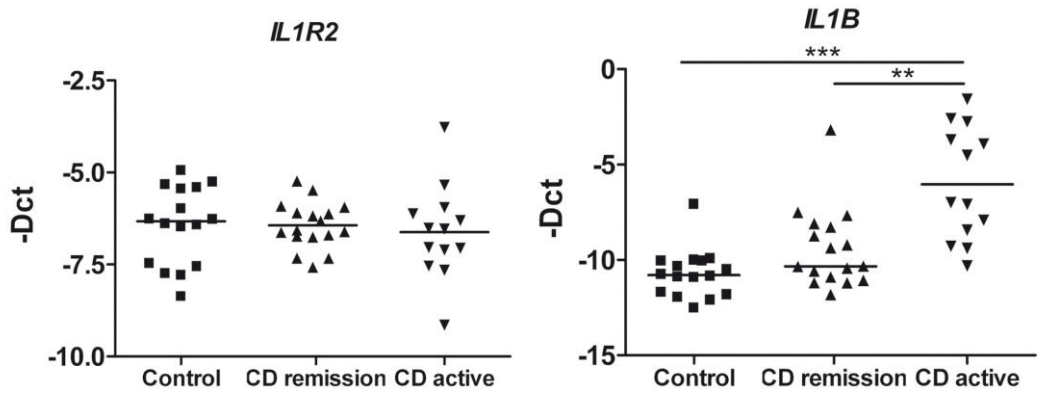


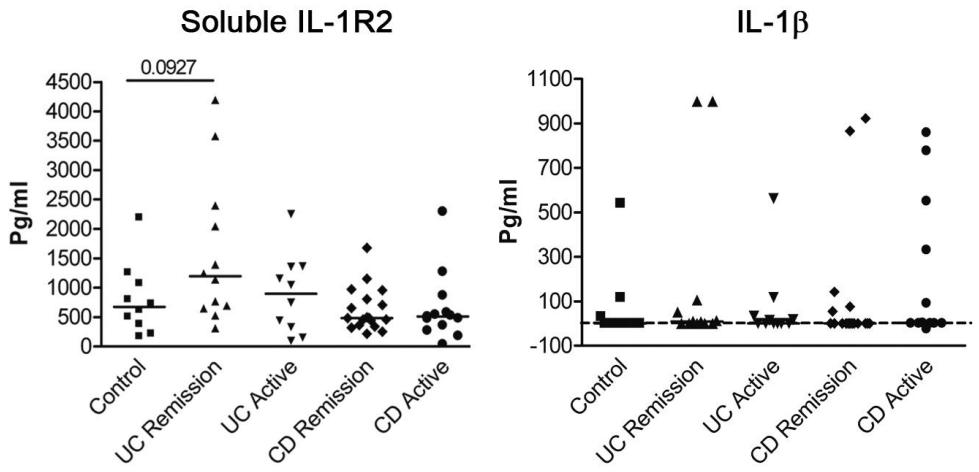
Supplementary Figure S1. Heatmap representation of microarray expression of IL-1 family genes. Each row shows one individual probe (representing 6 selected genes) and each column an experimental sample. High expression levels are shown in red and low expression levels in green. An unsupervised hierarchical cluster method, using a Pearson distance and average linkage method, was applied for each gene classification. Samples belonged to one of the following groups: non-IBD controls (shown in black, n=13), non-involved mucosa segments from patients with active UC (UC uninvolved; in blue, n=7), involved mucosa segments from patients with active UC (UC active; in red n=15) and endoscopically and histologically inactive UC (UC remission; in green, n=8).



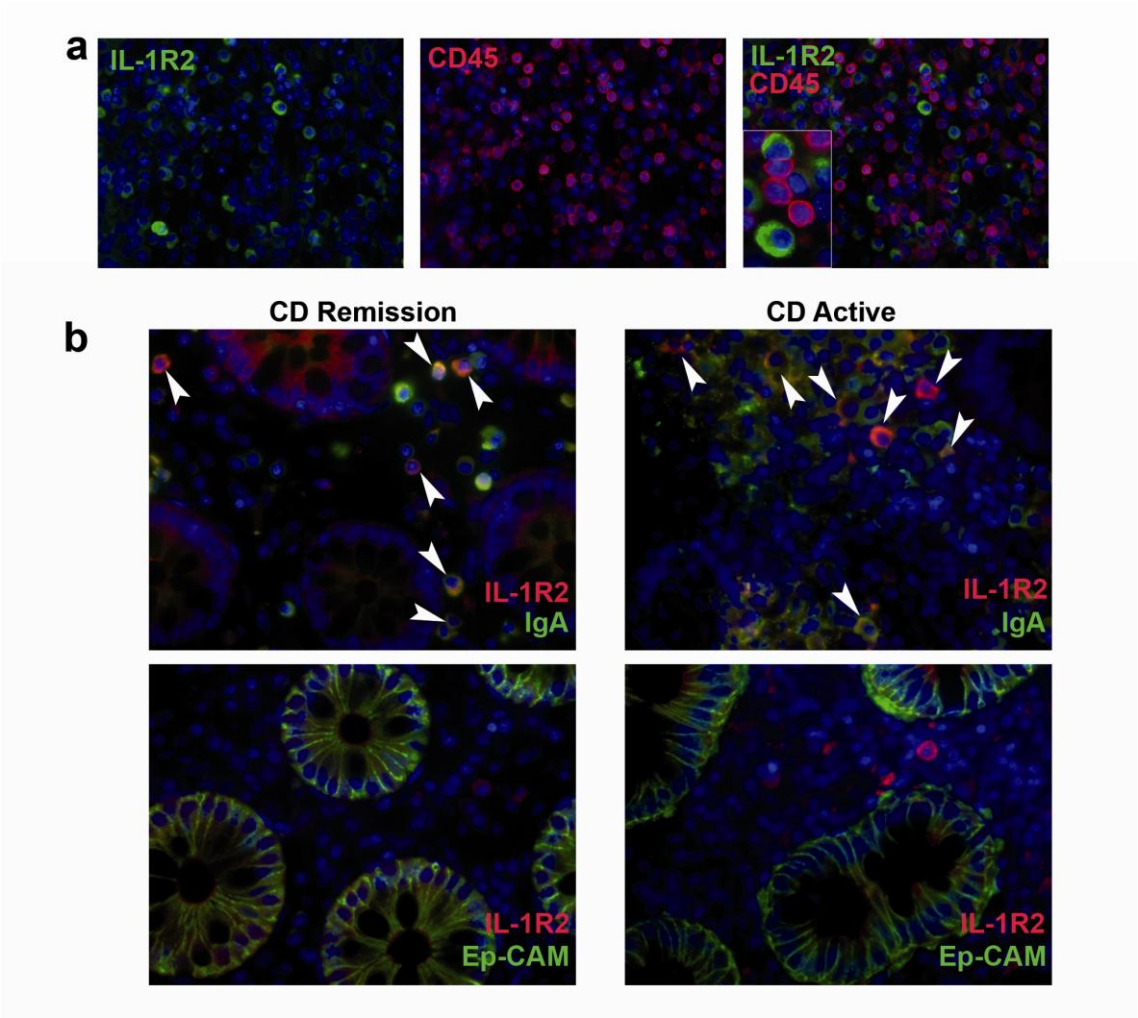
Supplementary Figure S2. Correlation analysis between IL1-family genes. The distribution of each gene is shown in the diagonal of the matrix. The right side panels show the results of the Spearman correlation test for each combination; rho and p-values are shown. The left side panels show the dot plot (-Delta Ct) of each combination highlighting the sample; non-IBD control samples are represented with squares, non-affected active UC samples with circles, affected active UC samples with triangles and inactive UC samples with plus symbol (+). In addition, the lowess non-parametric regression curve is represented in each case.



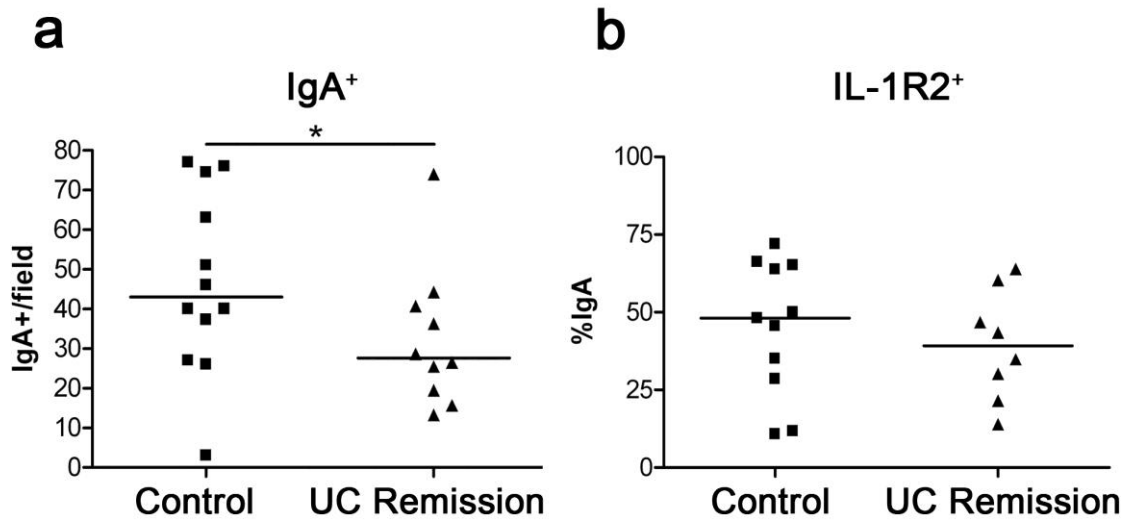
Supplementary Figure S3. ***IL1R2*** **and** ***IL1B*** **expression in colonic mucosa from Crohn's Disease (CD) patients**. mRNA expression determined by qPCR (-Delta Ct) in controls (n=16), CD patients in remission (n=16), and CD patients with active disease (n=13). Gene expression data is analyzed by a Kruskal-Wallis test, followed by a Benjamini-Hochberb post-hoc correction test. $^{**}P<.005$, $^{***}P<.0005$.



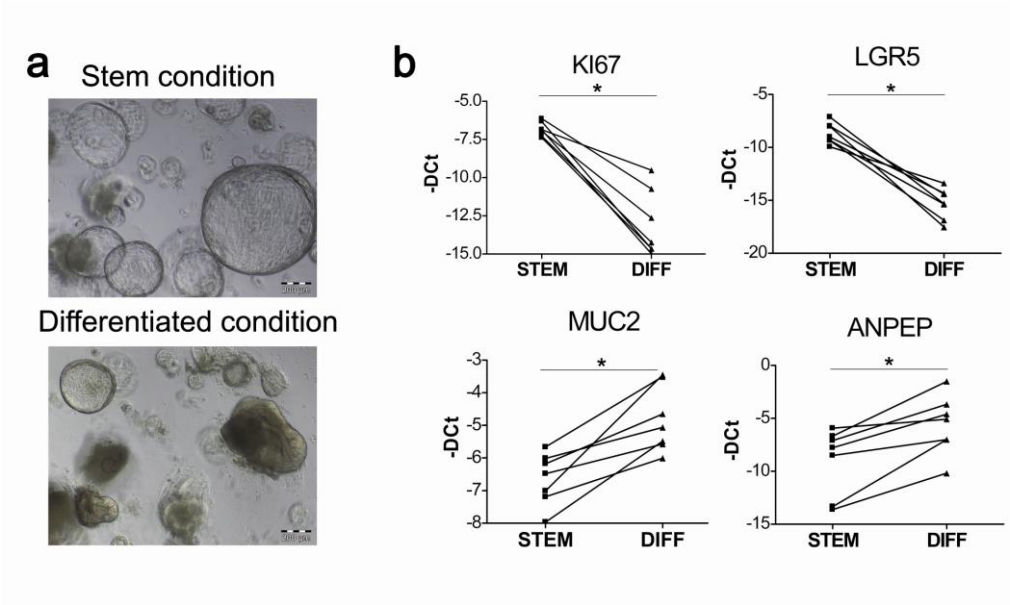
Supplementary Figure S4. Concentration of serum soluble IL-1 receptor type 2 and IL-1β. Samples from non-IBD control subjects (n=10), patients with ulcerative colitis (UC) disease in remission (n=12), active UC patients (n=10), Crohn's Disease (CD) patients in remission (n=18) and patients with active disease (n=13). A Mann-Whitney p value from control vs. UC remission is shown.



Supplementary Figure S5. IL-1R2 immunofluorescent staining in colonic mucosa. Representative two-color immunofluorescent staining of fixed paraffin-embedded colonic tissue. (a) Fixed paraffin-embedded healthy colonic tissue. Samples were co-stained with IL-1R2 (green) and CD45 (red). (b) Mucosal sections of Crohn's disease (CD) patients in remission and with active disease. Samples were co-stained with IL-1R2 (red) and IgA (green). White arrows show IL-1R2 expression by IgA-positive cells. Samples were co-stained with IL-1R2 (red) and Ep-CAM (green). Sections were counterstained with DAPI (blue). Images were taken with a 40X objective lens.



Supplementary Figure S6. Immunofluorescence quantification. (a) Immunostaining quantification of IgA^+ cells per field under a 20X objective lens. (b) Percentage of IL-$1R2^+$ among IgA^+ cells in healthy control mucosa (n=12) and in UC in remission mucosa (n=10).. Data is analyzed using a Mann-Whitney test. $^*P<.05$.



Supplementary Figure S7. *In vitro* organoid culture of colonic epithelial stem cells. (a) Representative picture of stem and differentiated organoids. (b) *KI67*, *LGR5*, *MUC2* and *ANPEP* gene expression by qPCR (-Delta Ct) of stem and differentiated organoids. (n=7) Gene expression data was analyzed using a Wilcoxon matched paired test. $^{*}P<.05$.