

Figure S1. Data preprocessing. (A) PCA of original IBD datasets before bath-effect correction. (B) PCA of the integrated dataset after batch-effect correction. (C) A heatmap of the integrated dataset after batch-effect.

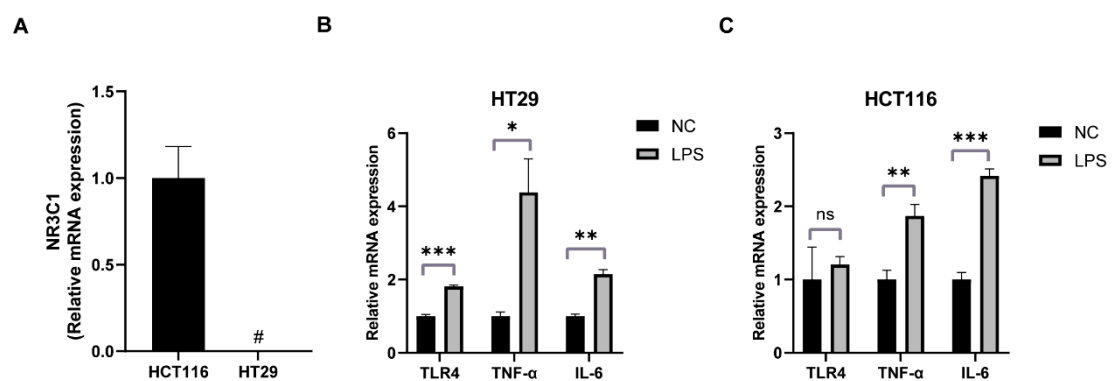


Figure S2. Construction of the *in vitro* inflammatory cell models. (A) Comparison of the baseline levels of GR expression between HT29 cells and HCT116 cells. # bare expression compared to the HCT116 cells. The expression of inflammatory factors TLR4, TNF- α , and IL-6 in (B) HT29 cells

and (C) HCT116 cells both treated with LPS for 24 h. Values are expressed as the means \pm SD, $n = 3$ in each group. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, and ns not significant.

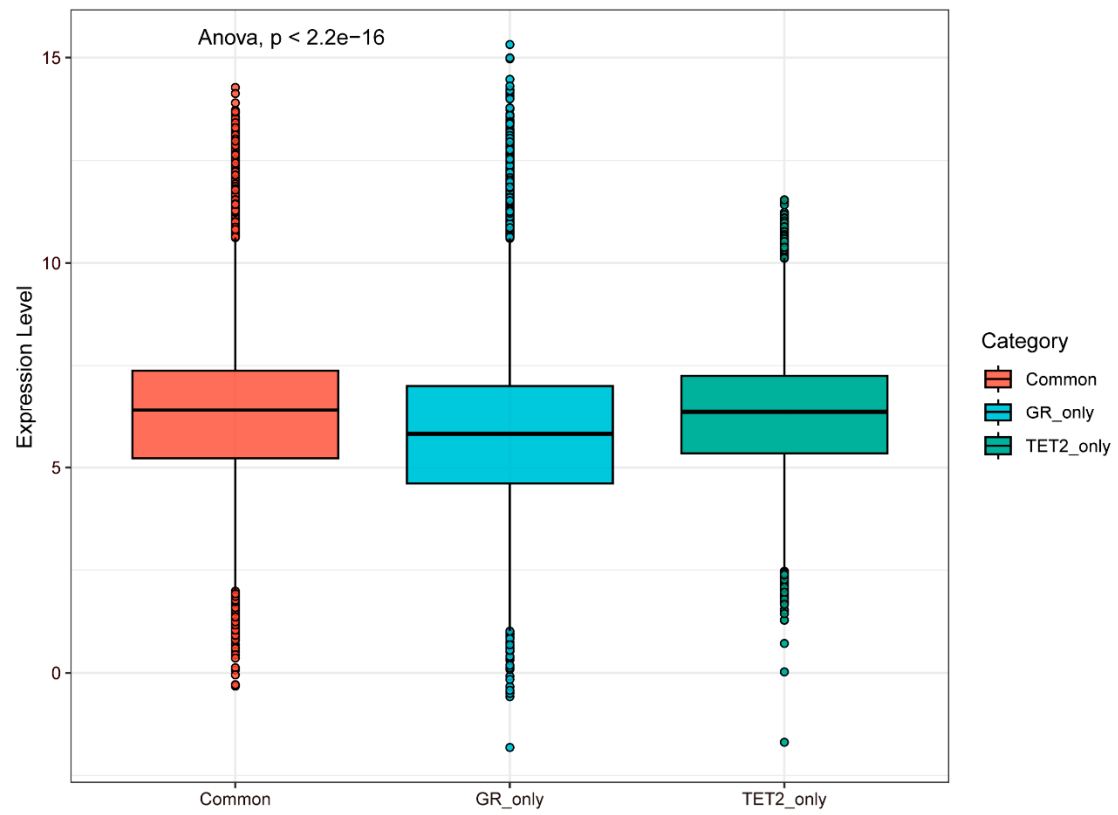


Figure S3. A one-way ANOVA analysis was performed to examine the differential impact of transcription factor regulation (GR only, TET2 only, and Common) on gene expression levels.