Supplementary Figure 10: Under expression of *BRINP3* is unlikely to be secondary to genetic inheritance. (A) Linkage disequilibrium plot demonstrating a non-significant single nucleotide polymorphism (SNP) (rs12402777, p=0.00691) post correction for multiple testing close to the *BRINP3* gene (1q31.1), using the SNP data from a recent UC meta-analysis. Dot plot created using SNP Annotation and Proxy (SNAP) Search (Version 2.2, Broad Institute). (B) Schematic diagram of *BRINP3* gene and promoter region. Primers for pyrosequencing were designed within a CpG island located in the promoter region of *BRINP3* (R1 and R2) in patients with UC (n=5) and HCs (n=4). Log$_2$ relative expression of *BRINP3* was determined by qPCR using primers downstream of the promoter in exon 7 (see Supplementary Figure 3B).