

Additional File 1: Figure S1 to S8

Figure S1

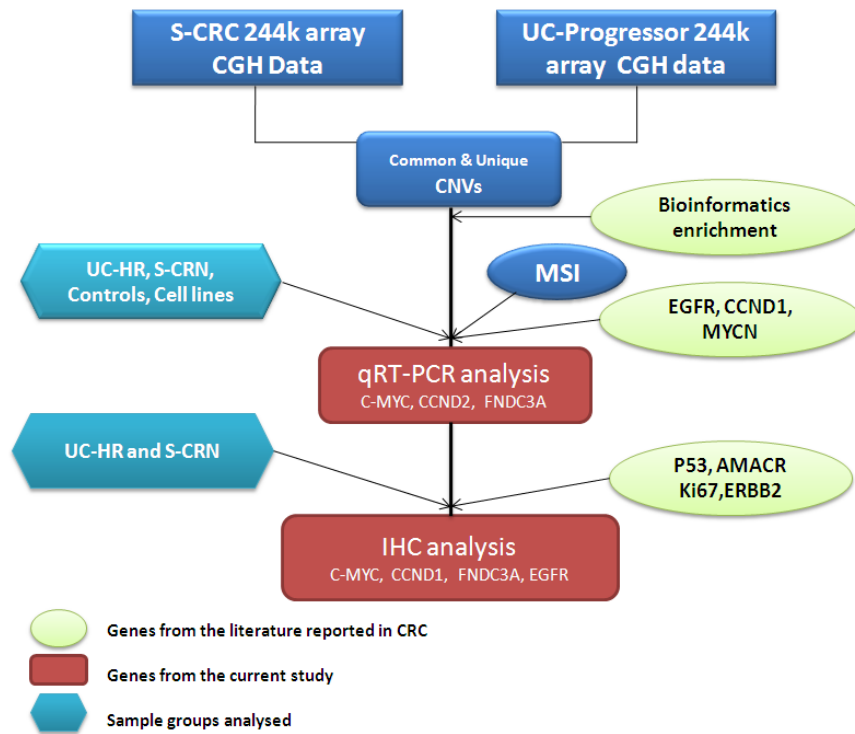


Figure S1: Overall workflow and design of the study.

Figure S2

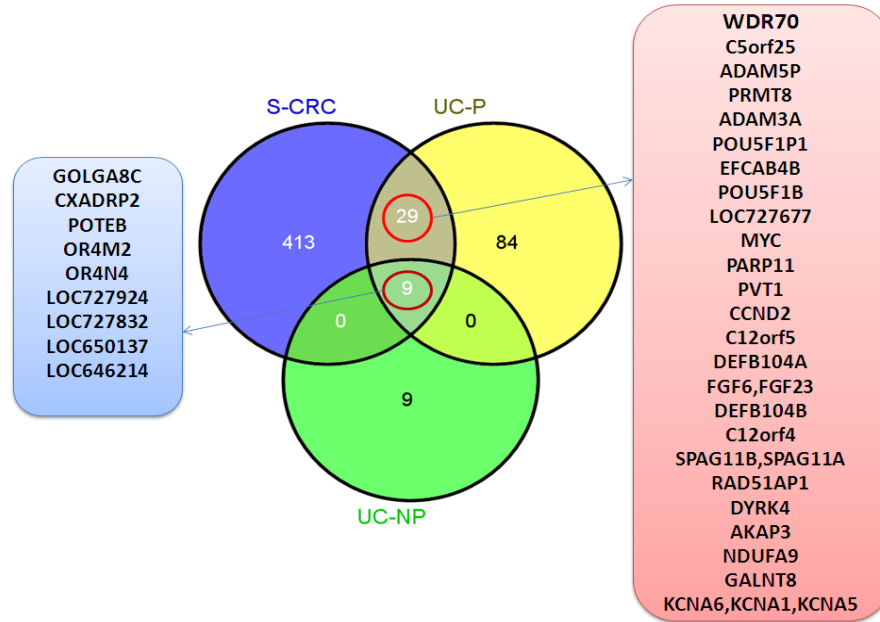


Figure S2: Common genes found associated with CNVs in three groups.

Figure S3

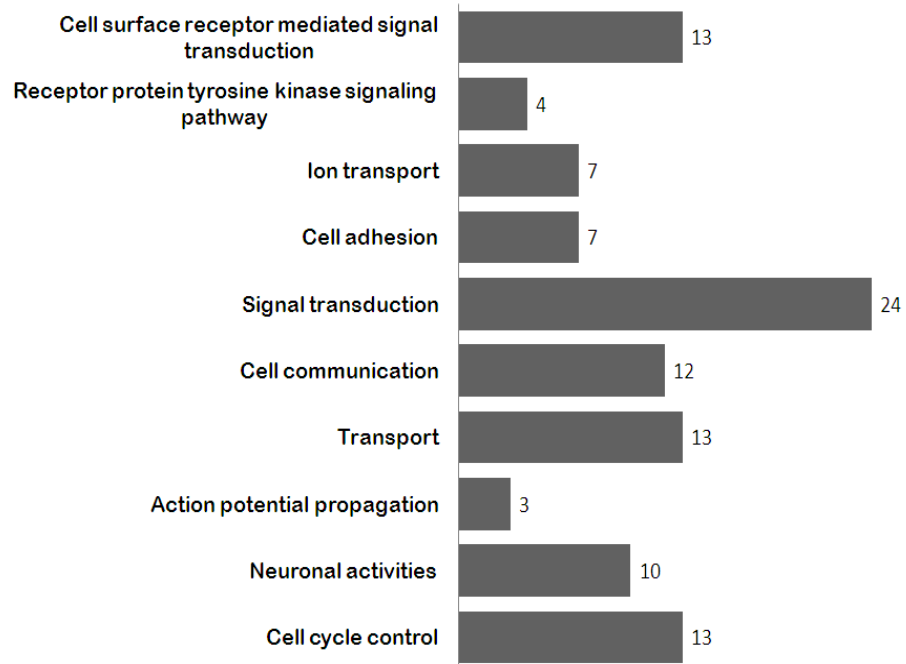


Figure S3: Enrichment in biological process (GO analysis) of the gene lists from S-CRC and UC-P samples 244k aCGH data. X-axis: number of genes involved in the given function and Y-axis: Biological function the genes are involved.

Figure S4

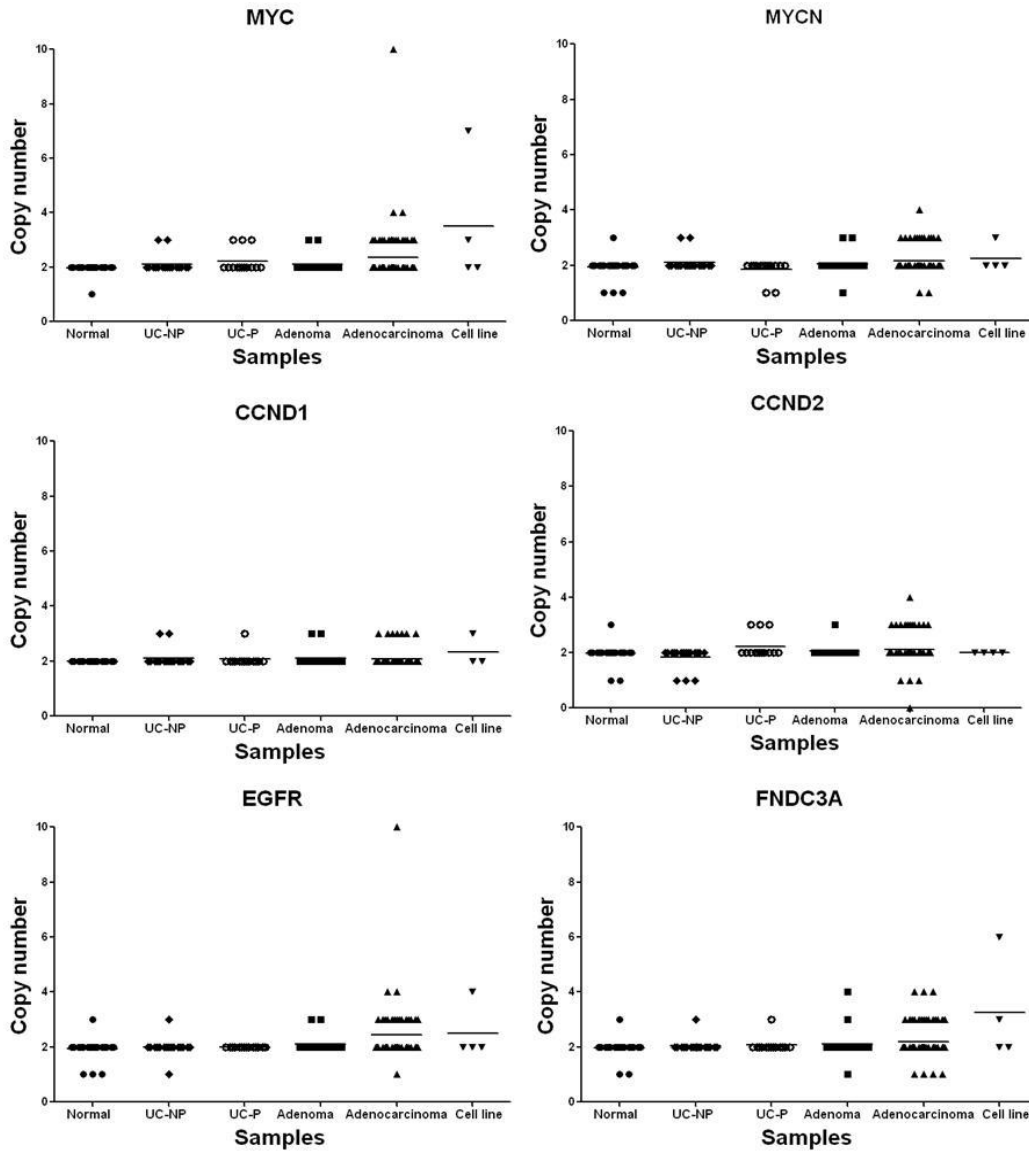


Figure S4: Results from the screening of gene alterations (amplification and deletion) in subgroups of sporadic and ulcerative colorectal neoplasm samples in our validation panel of markers by qRT-PCR method. (Abbreviations used are as given earlier)

Figure S5

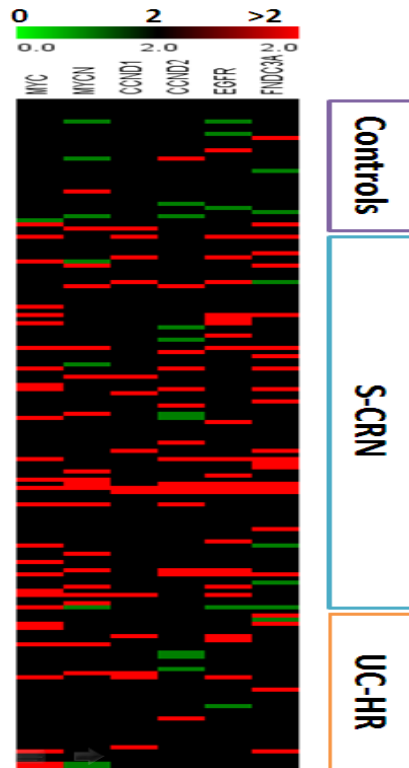


Figure S5: Clustering of qRT-PCR data using 6 genes and 163 samples of different groups. The relative copy number for each gene was plotted against different sample groups in the current study.

Figure S6

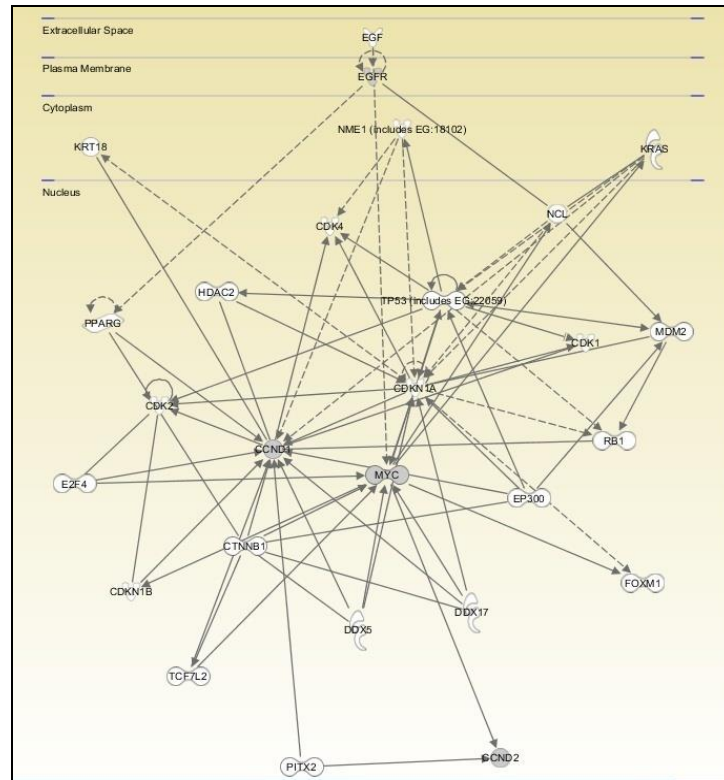


Figure S6: Summary of Ingenuity Pathways Analysis (IPA) for the role and interaction of the 6 genes of the markers panel

Figure S7

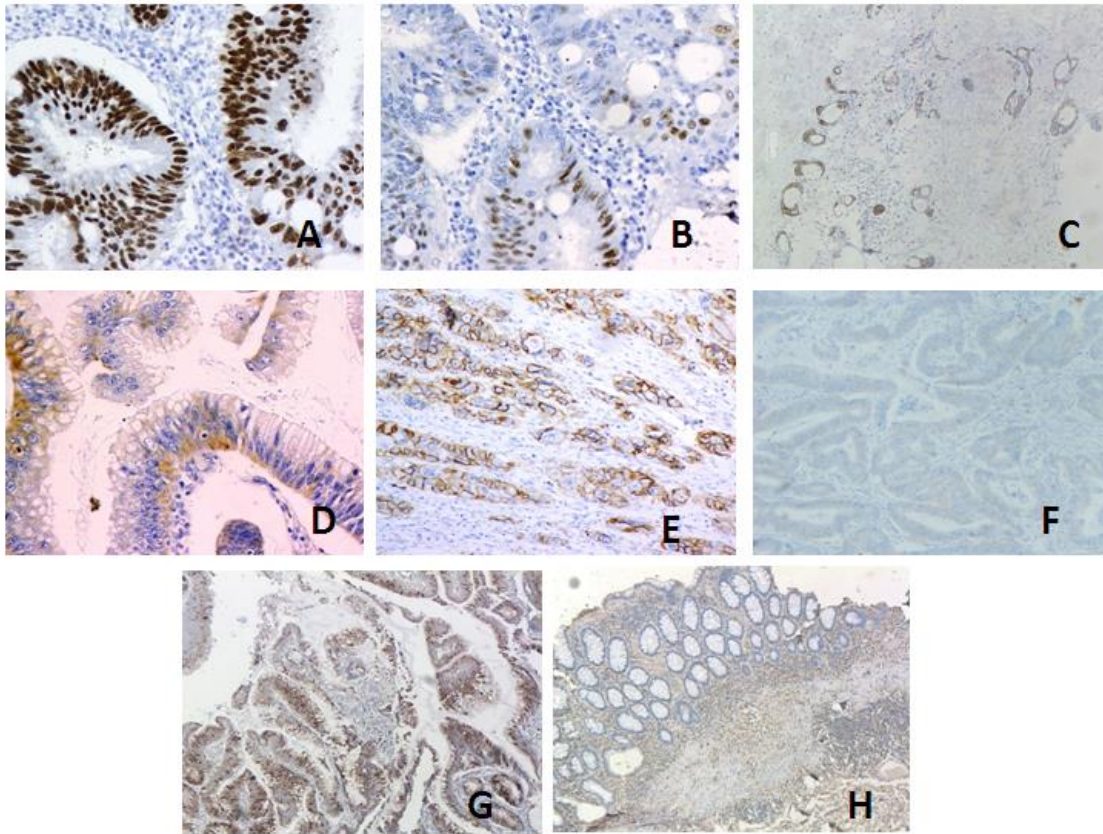


Figure S7: Results of immunohistochemistry analysis carried out on UC associated and sporadic colorectal cancer samples for various proteins; images in order **A:** p53 **B:** Cyclin D1; **C:** AMACR; **D:** EGFR; **E:** C-MYC; **F:** ERBB2; **G:** Ki67; **H:** FNDC3A.

Figure S8

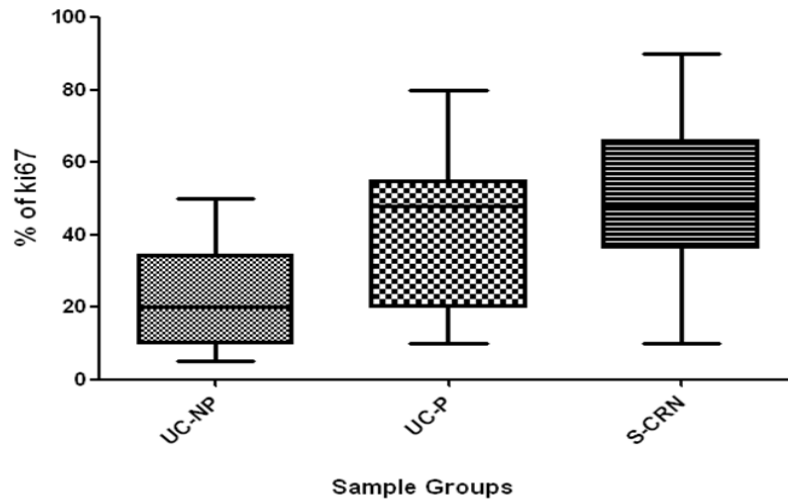


Figure S8: Box plot illustrating percentage of Ki-67 positive cells in different sample groups of the current study: ulcerative colitis-non progressor (UC-NP) group, ulcerative colitis- progressor (UC-P) group and sporadic colorectal neoplasia (S-CRN) group.