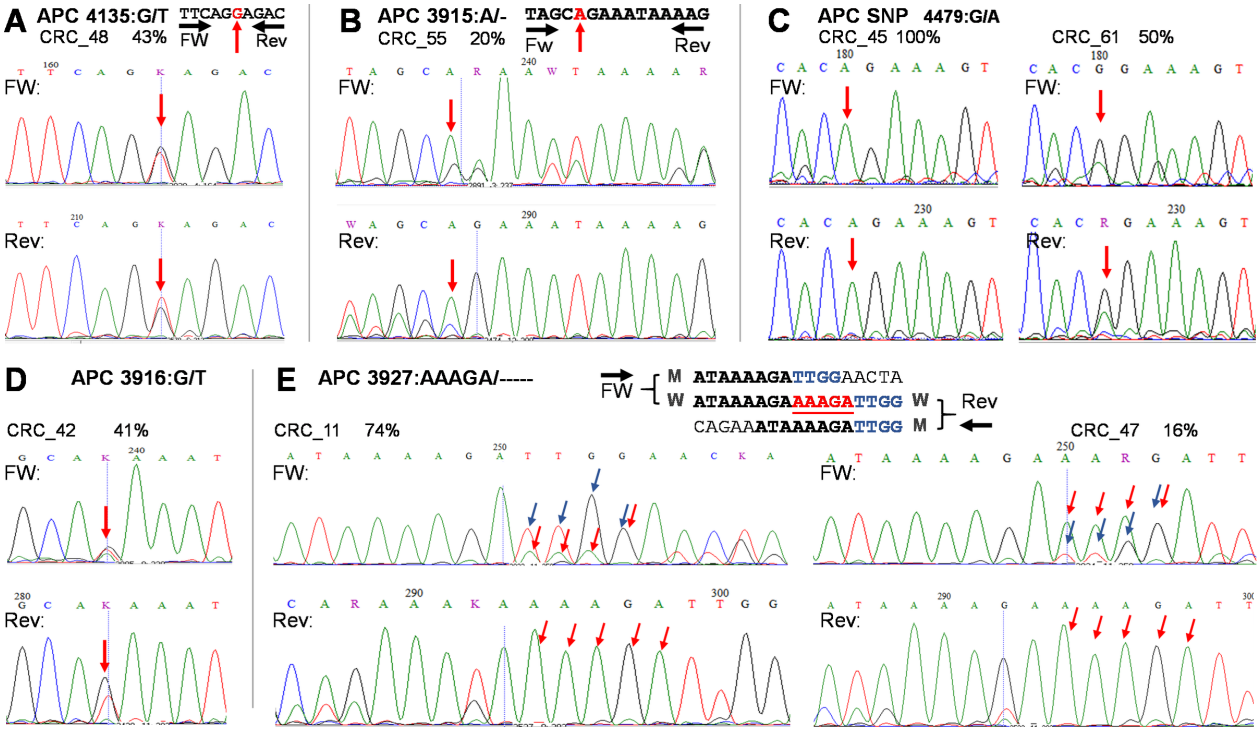

Figure S1 - Re-sequencing of *APC* variants by Sanger protocol.

APC point mutations (A, B, D), an SNP (C) and a 5 nucleotide deletion mutation (E), of CRC samples were re-sequenced by Sanger sequencing protocol. The name of the variant and sample and the allele frequency obtained by the GS Junior instrument, together with the short sequence around the variant analyzed is illustrated. Variable positions are marked with red arrows. A guide material is given in case of the 5 nucleotide deletion (E) to help the interpretation of the electropherograms. This guide shows the expected nucleotide peaks from the wild type (W) and the mutant (M) alleles obtained by the forward (FW) or reverse (Rev) sequencing primers. Deleted nucleotides are highlighted with underlined red letters in the W sequence, and red arrows on the electropherogram.

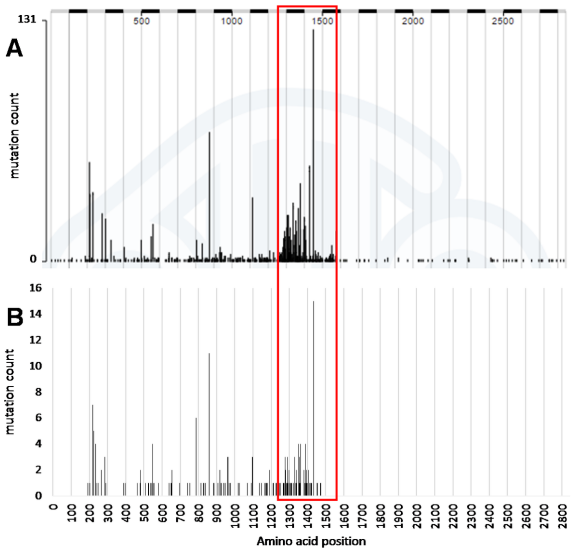

Figure S2 - Distribution of *APC* mutations by TCGA and COSMIC data.

Histograms show the number and position of mutations on *APC* cDNA by COSMIC (A), and TCGA (B) data. The target area of the colon PCR panel on the *APC* gene is marked with a red frame.