Supplementary Figure 5S: Hierarchical cluster analysis of 67 gene expression profiles in the 8 HCT116 cell lines. We used Agilent long (60bp) oligonucleotide microarrays and the dual color analysis method in which probes from specimens and from the reference are differentially labeled with Cyanine 5 and Cyanine 3. We performed two independent sets of dye swap experiments to compare RNAs obtained, in each case, from 4 tetraploid and 4 diploid HCT116 cell lines. In each set of experiments the reference was the equimolar mix of the 8 RNAs from diploid and tetraploid cells. Probes were obtained from 500 ng total RNA in two steps: double stranded cDNA using MMLV reverse transcriptase followed by T7 RNA polymerase linear amplification and labeling. One μg of purified cRNA was mixed with the same amount of reference cRNA. Mixed cRNAs were hybridized to a human whole genome 44k oligonucleotide array (Agilent G4112A) for 17 hours at 60°C, then washed with 0.6X and 0.01X SSC buffers containing triton, and dried with a nitrogen gun. Microarrays were scanned using the Agilent scanner. Data analysis was performed with the Feature Extraction software (Agilent) and Rosetta Resolver® (Rosetta Biosoftware). The final ratio (i.e., fold change) is the average of the two individual ratios from dye swap experiments. An ANOVA test is performed on the 41059 probes of the chips with a threshold p-value of 10-5. These genes were subjected to a hierarchical cluster analysis using a calculation based on cosine correlation and agglomerative method on the average link. Each row represents the combination of two dye-swap experimental samples and each column represents a single accession number. The clones C1 and C2 and N1 and N2 are tetraploid, generated upon cytochalasine D or nocodazole treatment, respectively. Clones Co1-4 are diploid.