Supplementary Figure 1. Comparison of old and new oligonucleotide array CGH protocols. Genome-wide profiles are shown that were obtained from hybridisation of BT474 DNA with human male reference DNA. A shows the data as previously published using the old protocol on a 19K human oligonucleotide array (6). B shows the data obtained with the optimised protocol on a 29K human oligonucleotide array and is the same as shown in Figure 1A allowing easy comparison of both protocols. Log2ratios were calculated with a weighted moving average as described(11) using a window of 250 kb and are displayed as a function of their position in the genome. Log2ratios of the odd and even chromosomes are shown in aqua blue and black, respectively. Chromosome numbers are indicated. Smoothed values of the log2ratios were calculated using a dedicated smoothing algorithm(14) (red).