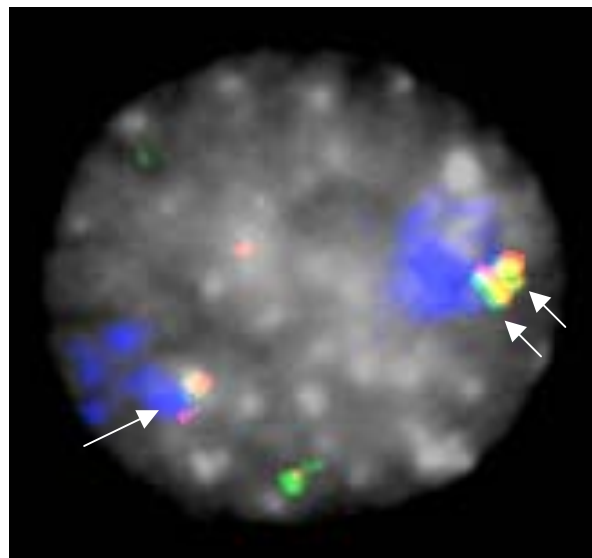


**Figure 1a** Array CGH for 8p in T47D. The ability of the array to detect copy number variation was evaluated by hybridising it to the T47D breast cancer cell line for which copy number changes on 8p had been extensively characterised by FISH (Pole *et al.*, 2006). A copy number change from two to four in T47D (vertical dashed line) was reflected by a shift in  $\log_2$  ratio from  $-0.18 \pm 0.12$  S.D. to  $0.37 \pm 0.14$  S.D. In addition, a 110kb deletion of two out of four copies at 38.1Mb (black arrow), a region for which the average  $\log_2$  ratio was 0.37, was detected by the array as a single clone with a  $\log_2$  ratio of -0.22 and two flanking clones with intermediate  $\log_2$  ratios. Black diamonds, hybridisation ratios plotted at BAC midpoints; Open squares, rejected data points; Grey arrows, polymorphism or segmental duplication.



**Figure 1b** A normal polymorphism in 8p23. A normal lymphoblastoid cell line (m62) interphase nucleus showing a tandem duplication of BAC probes on one copy of chromosome 8 (two arrows) and a single copy of each on the other chromosome 8 (single arrow). Blue, chromosome 8 paint; Red, RP11-43B8 (7.76 Mb); Green, RP11-185K20 (7.80 Mb).