FIGURE S4.—The determination of DNA sequences bound by yKu70p using the median percentile rank method that involves plotting the number (Frequency) of genomic segments (probes) falling into each percentile (Lieb et al., 2001). We performed a total of eight individual IP’s and NoAb (Mock IP) controls on three separate MEM4 (YKU70-Myc) cultures, generically PCR-amplified the enriched DNA and competitively hybridized it to our tiling arrays covering chromosomes III, VII and XI. Each probe was given a percentile rank according to the normalized median ratio intensities calculated from their relative enrichment to genomic DNA. We then calculated the median percentile rank for each probe and plotted the number of DNA segments falling into each percentile (1 percentile bins). A unimodal distribution is usually seen in the NoAb mock IP’s indicating no strong selection of any particular probes, whereas a bimodal distribution is expected for the IP’s indicating a subset of DNA segments that are consistently enriched (Lieb et al., 2001). The use of this method shows (A) a distinct group of genomic segments in our chromatin IP data above the 96 percentile, which (B) are not apparent in the data for the NoAb controls (Mock IP). A black smoothing line is shown for both datasets.