Additional file 1: Feature definition and fragment length separation under CUTAC conditions. (a) Fragments were mapped to hg19, and 3.2 million fragments were randomly sampled from each dataset and used to make bedgraph tracks. A representative region is shown. To compare peaks with very different signal-to-noise levels, samples were group-autoscaled with ranges indicated to the left of each set of tracks. Pol2S5p CUTAC of K562 cells with linear pre-amplification using only P5 primers for 12 cycles was followed by addition of P7 primers and PCR for various numbers of cycles. (**b**) Size distributions were not affected by differences in the number of PCR cycles following linear amplification. (**c**) Fragment length distributions for K562 cells (left) and H1 ES cells (right) are shown for linear pre-amplified fragments after tagmentations in 10 mM TAPS + 5 mM MgCl$_2$ ± 1,6-hexanediol or 300 mM NaCl + 10 mM MgCl$_2$ plotted as fractions of the total mapped fragments for linear pre-amplified datasets. Percentages of total fragments ≤120 bp iare shown. Tagmentation in 1,6-hexanediol generally results in a smaller fragment distribution, especially conspicuous for H1 cell nucleosomes. The higher recovery of nucleosome-sized fragments from K562 cells than H1 ES cells reflects the much lower abundance of Polycomb domains in H1 cells.