



Figure S5: The nucleosome pattern is largely unchanged when the dataset is partitioned according to local repeat content, although the A and T curves shift upwards relative to the C and G curves. (a) 70% of the nucleosome positions are at least 30 bases away from a repeat; (b) 19% are in a repeat that extends at least 30 bases to both sides; and (c) 11% are near the edge of a repeat. The Pearson correlation between local AT content and local repeat fraction is +0.23 (although Alu repeats are only 45-50% AT, other repeats generally have higher AT content, particularly LINE1 repeats which are approximately 65% AT). The increased noise in the patterns in (b) and (c) is due to the smaller number of sequences used to create these two patterns.