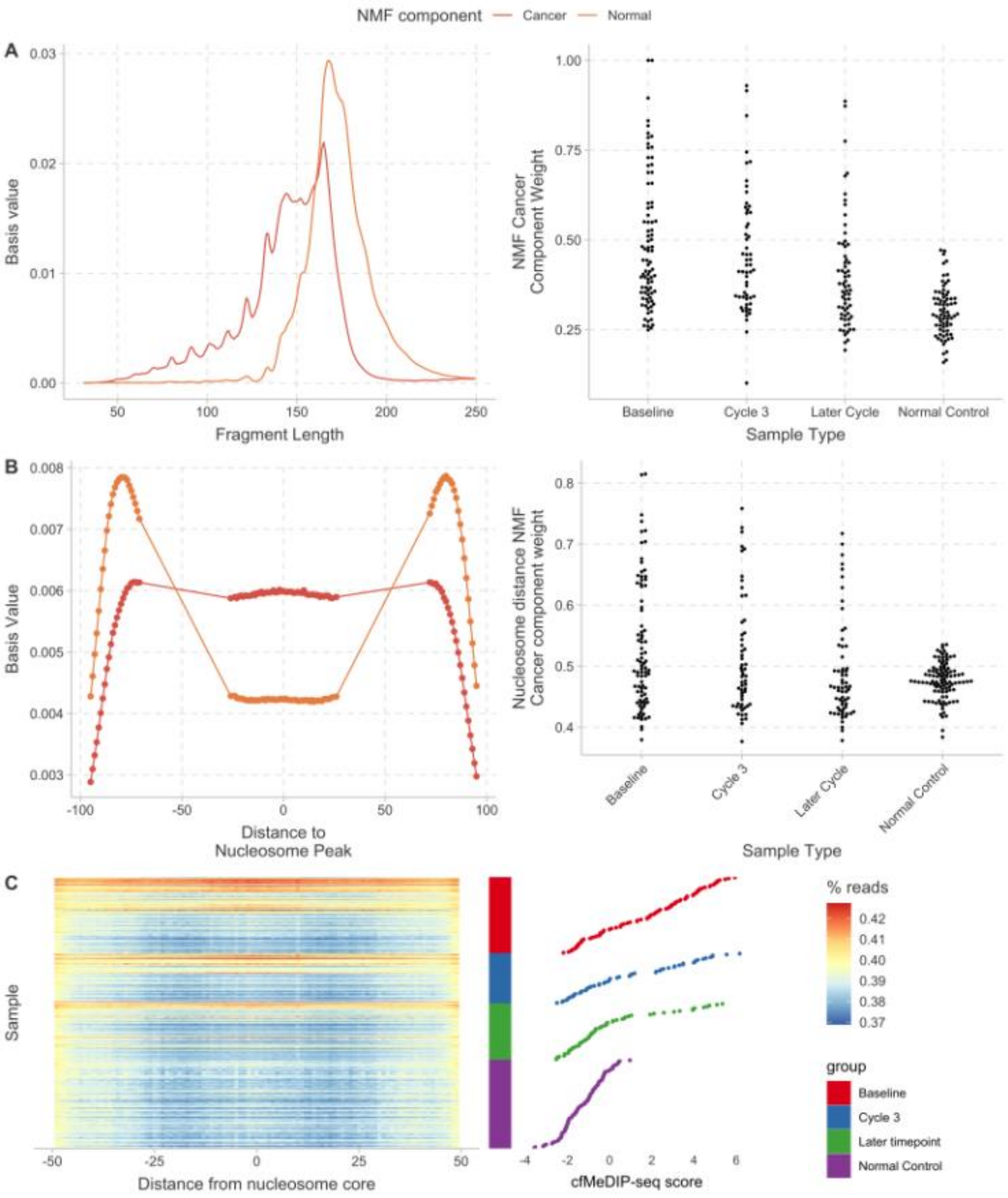
Supplementary Figure 6



Supplementary Figure 6. Non-negative matrix factorization identifies characteristic cancer-associated signatures of shorter fragment lengths and greater nucleosome core occupancy. (A) Genome-wide fragment lengths were used as features in a two-component non-negative matrix factorization analysis. This revealed a longer and a shorter component. The weight of the shorter was elevated in cell-free DNA of cancer patients relative to normal controls. (B) The distances of fragment ends to nucleosome centers were also used as features in two-component non-negative matrix factorization. This revealed two components with different proportions of intra-nucleosomal fragment ends. The signature with more intra-nucleosomal fragment ends was elevated in the cell-free DNA of cancer patients relative to normal controls. (C) A heatmap showing the localization of fragment ends within the nucleosome core, meaning within 50 bp of nucleosome peaks. Arranging by group and total cfMeDIP-seq score, we observe that those with higher estimated ctDNA levels demonstrated a higher fraction of read ends terminating within the nucleosome core.