



Figure S7: A subset of the nucleosome patterns derived from the training set of  $\sim 200,000$  nucleosome dyad positions. The pattern for T is a reflection of the A pattern across the (vertical) dyad axis, and similarly the TT pattern is a mirror image of the AA pattern. (The same holds for C/G and CC/GG.) The patterns for dinucleotides which are their own reverse complements are symmetrical about the dyad axis. Intriguingly, the normalized patterns for CG and GC are nearly identical to one another, suggesting that these dinucleotides play the same role in positioning nucleosomes despite their dramatically different occurrence rates.