Figure S1: **Interspecies rates of divergence around nucleosome dyads in the human lineage**. Coloured solid lines correspond to 25bp sliding averages. Dotted vertical lines represent the estimated dyad position. Transversions are plotted on the secondary y axis due to their substantially lower rates. Nucleosome positioning data were derived from the Barski et al. dataset.

Figure S2: **Intraspecies rates of divergence around nucleosome dyads in the human lineage**. Coloured solid lines correspond to 25bp sliding averages. Dotted vertical lines represent the estimated dyad position. Transversions are plotted on the secondary y axis due to their substantially lower rates. Nucleosome positioning data were derived from the Barski et al. dataset.

Figure S3: **Rates of selection in and around nucleosome dyads.** Ratios of background corrected inter and intraspecies divergence rates plotted against position from nucleosomal dyad ($S_{x->y}$ scores). Dotted horizontal lines correspond to an uncorrected p value of 0.004 (corrected p value of 0.05). Nucleosome positioning data were derived from the Barski et al. dataset.

Figure S4: **Rates of selection in and around nucleosome dyads having excluded rare variants.** Ratios of background corrected inter and intraspecies divergence rates plotted against position from nucleosomal dyad ($S_{x->y}$ scores). Intraspecies single nucleotide polymorphisms with a minor allele frequency less than 15% were excluded. Dotted horizontal lines correspond to an uncorrected p value of 0.004 (corrected p value of 0.05). Nucleosome positioning data were derived from the Schones et al. dataset.

Figure S5: **Rates of selection in and around non-coding nucleosome dyads.** Ratios of background corrected inter and intraspecies divergence rates plotted against position from nucleosomal dyad ($S_{x->y}$ scores). All nucleosomes within 500bp of an exon were excluded. Dotted horizontal lines correspond to an uncorrected p value of 0.004. Nucleosome positioning data were derived from the Barski et al. dataset.

Figure S6: **Selected 5mer frequencies in and around nucleosome dyads**. (A) Frequency of 5mers of different dinucleotide composition in and around the nucleosome dyad. (B) Stepwise change from low to high nucleosome occupancy via introduction of AT base pairs.

Figure S7: **Mononucleotide frequencies in and around nucleosomes with different flanking GC percentages (1).** Flanking GC percentages were measured at +/-250-500bp from nucleosome dyad. Nucleosome positioning data were derived from the Schones et al. dataset.

Figure S8: **Mononucleotide frequencies in and around nucleosomes with different flanking GC percentages (2).** Flanking GC percentages were measured at +/-250-500bp from nucleosome dyad. Nucleosome positioning data were derived from the Barski et al. dataset.

Figure S9: **Deviation of interspecies divergence rates from flanking rates in and around nucleosomes and at different flanking GC compositions.** The percent enrichment (or depletion) of background corrected interspecies rates of changes with respect to corresponding observed rates of intraspecies change. Significantly elevated or depleted levels are indicated by * (uncorrected p value of 0.05) and ** (uncorrected p value of 0.00046, corrected p value of 0.05). Nucleosome positioning data were derived from the Barski et al. dataset.

Table S1: **Counts of inter and intraspecies base changes by position from the dyad**