***Expanding epigenomics to archived FFPE tissues: An evaluation of DNA repair methodologies*** *Siegel, EM et al*

**Supplementary Figure**

**Supplementary Figure 1.** **Representative density correlation plot between FF-FFPE pairs using the minfi-Illumina normalization.** Plots shown for (a) Restore (RES1 vs. FF) and (b) REPLI-g Ligase (LIG3 vs. FF) across patient samples processed using the minfi-Illumina normalization method.

**Supplementary Figure 2.** Distribution of mean Δβ for each experimental condition by normalization: (a) DASEN and (a) minfi-Illumina. Normal distribution of mean Δβ peaked approximately at 0 for DASEN and <0 for minfi-Illumina.

**Supplementary Figure 3: The distribution of β-values across all CpG loci measured on the Illumina 450K array for (a) the FFPE colon tumors and (b) the 121 FFPE samples from RTOG compared to FF** tissues. All samples, regardless of storage type, had β-value peaks at 0.2 and 0.8 and variability between β-values of 0.3 and 0.6.