Figure S14. Percent GC Bias for Aligned ATAC-Seq reads.
A. Barplot of the total number of reads per sample per sequencing run. We performed two sequencing runs on the pooled samples; each sequencing run yielded approximately 200 million paired-end reads (yielding >400 million paired-end reads in total). **B.** Boxplot comparing the read depth per sample between females and males. There is no significant difference in the mean read depth between females and males (28.9M versus 27.3M; t-test p-value = 0.41), and there is no significant difference in the variance of read depth between females and males (standard deviation of 4.5M versus 6.0M; F-test p-value = 0.49). **C.** Barplot illustrating read depth per sample, grouped by gender. **D.** Boxplot comparing the %GC bias per sample between females and males. There is no significant difference in the mean %GC between females and males (42.1% versus 41.9%; t-test p-value = 0.51), and there is no significant difference in the variance of %GC between females and males (standard deviation of 0.57% versus 0.74%; F-test p-value = 0.45). **E.** Barplot illustrating %GC bias per sample, grouped by gender.