



S10 Fig. Box plot of the number of reads in ER peaks with and without duplicate removal. Peaks were called with duplicate removal and the top 10% peaks with the smallest p values were shown. Number of raw reads in peaks was estimated from alignments both before and after duplicate removal. Y-axis indicates the input-subtracted number of reads per 10 million (RPK10M) on log2 scale. Only reads with a minimum mapping quality score of 20 and no mismatch at the first five bases were used.