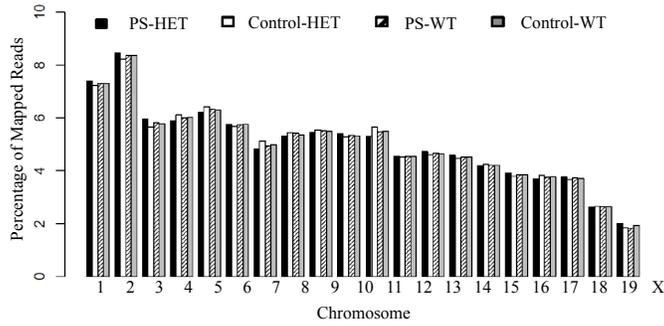
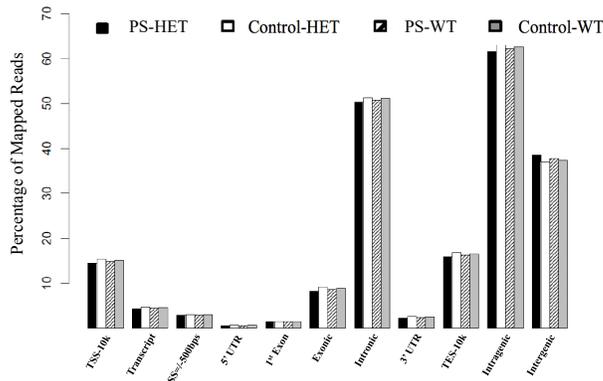


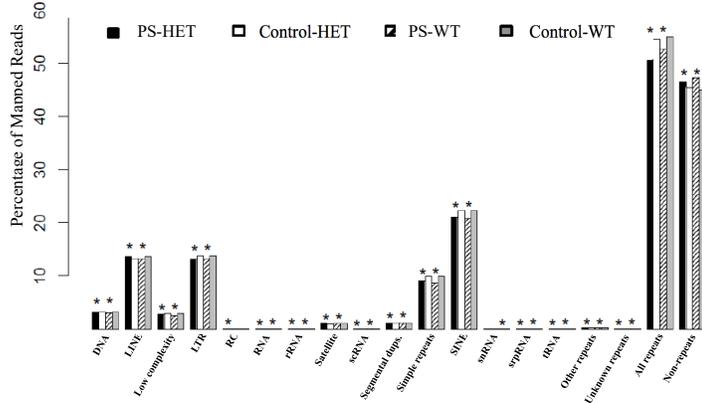
A



B



C



**Supplemental Figure 6:** Distribution and characterization of aligned reads derived from striatal tissue from the four experimental groups. (A) A bar plot depicts the percent of mapped reads (y-axis) relative to chromosomes (x-axis) for PS-HET (black bars), Control-HET (white bars), PS-WT (striped bars), and Control-WT (grey bars) mice. (B) A bar plot shows the percent of mapped reads (y-axis) as they relate to standard genomic structures (x-axis) for PS-HET (black bars), Control-HET (white bars), PS-WT (striped bars), and Control-WT (grey bars) mice. (C) A bar plot shows the proportion of mapped reads (y-axis) as they relate to repetitive elements across the genome (x-axis) for PS-HET (black bars), Control-HET (white bars), PS-WT (striped bars), and Control-WT (dark grey bars) mice. An asterisk (\*) represents a significant increase or decrease of 5hmC disruptions relative to the background regions, as determined by binomial testing ( $P$ -value  $< 0.05$ ).