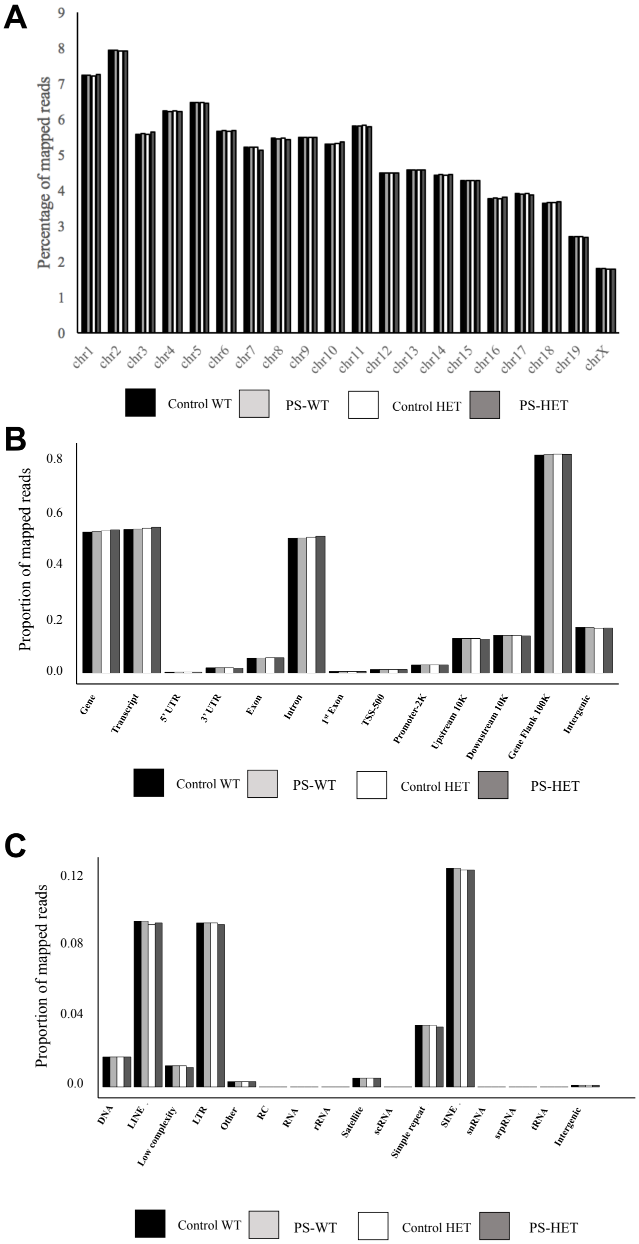

Supplemental Figure 2: Distribution and characterization of aligned reads derived from hippocampal tissue from the four experimental groups. (A) A bar plot depicts the percent of mapped reads (y-axis) relative to chromosomes (x-axis) for Control-WT (black bars), PS-WT (light grey bars), Control-HET (white bars), and PS-HET (dark grey bars) mice. (B) A bar plot shows the proportion of mapped reads (y-axis) as they relate to standard genomic structures (x-axis) for Control-WT (black bars), PS-WT (light grey bars), Control-HET (white bars), and PS-HET (dark 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 Control-WT (black bars), PS-WT (light grey bars), Control-HET (white bars), and PS-HET (dark grey bars) mice.