

**Figure S6.** Unplaced chr. Un contigs are enriched for LTR-gypsy retrotransposons, but not low complexity repeats or simple repeats. The total density of LTR-gypsy retrotransposons (A, D), Simple repeats (B, E), and low complexity repeats (C, F) were quantified in closed gaps (blue line) and the remaining contigs that could not be placed (chr. Un; black line). 10,000 10 Mb windows were randomly drawn across the genome to generate a null background distribution for the filled gaps and 10,000 15 Mb windows were randomly drawn across the genome to generate a null background distribution for the chr. Un contigs.