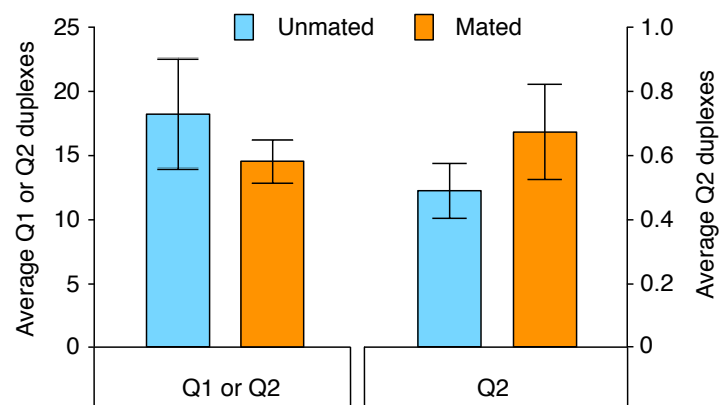




Supplemental Fig S2. Average number of Q1/Q2 or Q2 duplexes per genome position per sequenced sample (average computed across all mated or unmated MZs).