Skew values between the frequency of Potential Overlaps in Phase 1 and Phase 2

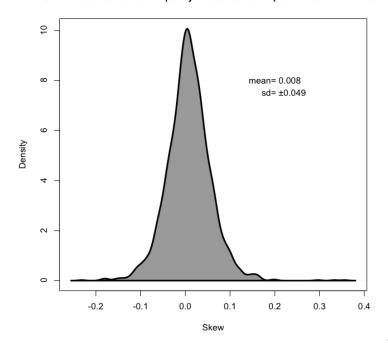


Figure S17 Distribution of the skew values for the pairwise differences between potential phase 1 and potential phase 2 overlaps. Skew values were calculated for each genome as followed: (fpp1 - fpp2)/(fpp1 + fpp2), where fpp1: frequency of potential phase 1 overlaps and fpp2: frequency of potential phase 1 overlaps. Skew values can vary between -1 (no potential phase 2 overlaps) and 1 (no potential phase 1 overlaps). If skew equals to zero, then no biased distribution is found. Our results show a small mean skewed distribution towards potential phase 1 overlaps (mean = 0.008, sd = \pm 0.049).