



**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 =  $\pm 0.049$ ).