



Figure S6 Differential Hi-C efficiency rates by species for the M-Y sample. For each species, the Hi-C efficiency rate was

calculated as $E_{species} = \frac{f_{species}^{(Hi-C)}}{f_{species}^{(shotgun)}}$, where $f_{species}^{(library)}$ is the fraction of reads from a sequencing library that align to the given species' reference genome. These efficiency rates were log-scaled and then normalized to create an average of 0 over all species.