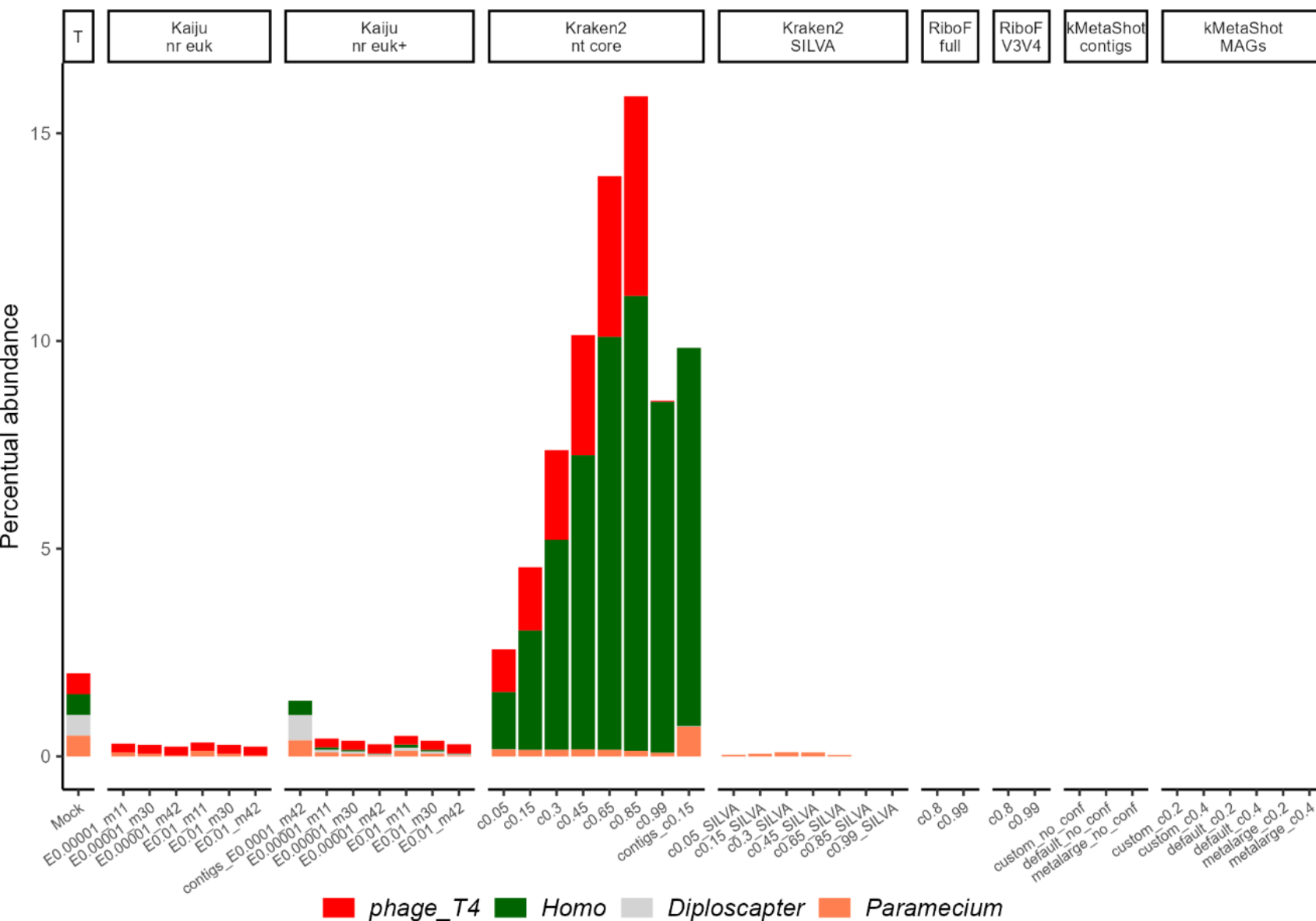




Supplementary figure 3: Bar plots depicting the relative abundances of the T4 phage, *Homo*, *Diploscapter* and *Paramecium* present in the mock community as estimated by various programs and parameter settings. The column “T” displays the true abundances of the clades in the mock. Genera inferred but not actually included in the mock are categorized as “misclassified”. The x-axis represents the classification types: “E” denotes the E-value threshold, “m” indicates the coverage threshold, and “c” represents the confidence level of the classification, depending on the classifier available options. The prefix “contigs” specifies classifications based on contigs rather than individual reads in case of Kaiju and Kraken2. The prefixes “default”, “metalarge” and “custom” refer to the different MEGAHIT assembly settings.