ICE integrated into contig in sample used for assembly

Mapping coverage in sample containing ICE:

Coverage remains constant thoughout the ICE
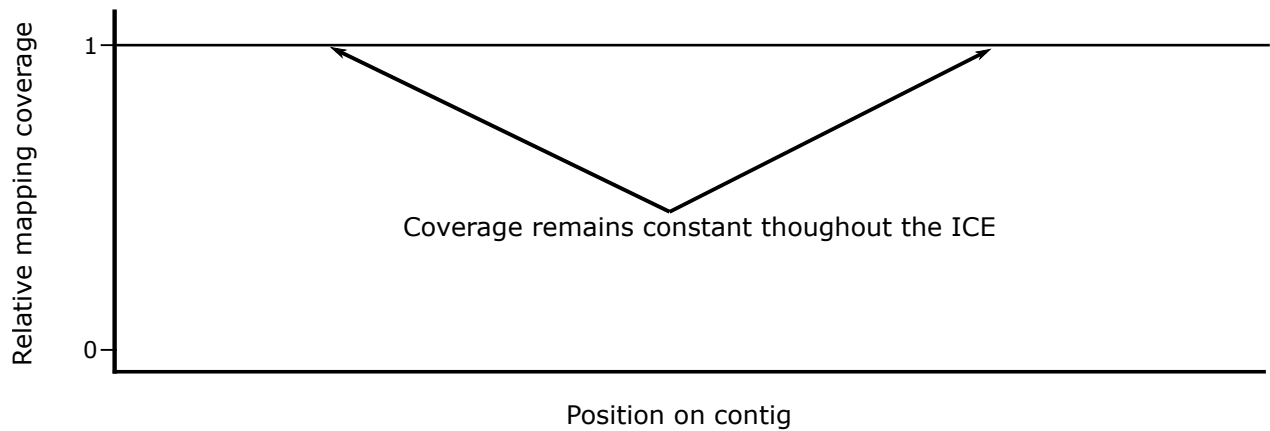
Mapping coverage in sample lacking ICE:

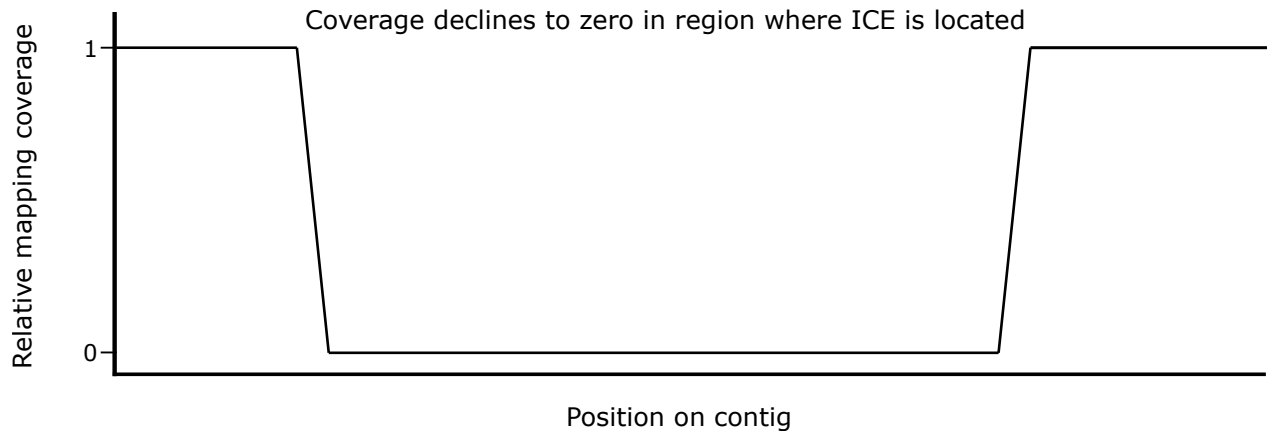Coverage declines to zero in region where ICE is located

Figure 1: Conceptual diagram of the mapping coverage of an assembled integrative and conjugative element. The mapping coverage in the first plot shows an even mapping coverage across the contig because the ICE is present in the sample and the average mapping coverage of the contig would be an accurate metric. In the second plot, the ICE is missing in the sample and the mapping coverage falls to zero where the ICE is located on the contig. As a way to quantify the presence of the ICE, the average mapping coverage for the entire contig would be artificially high. Limiting the mapping to only the region containing the conjugative proteins solves this issue.
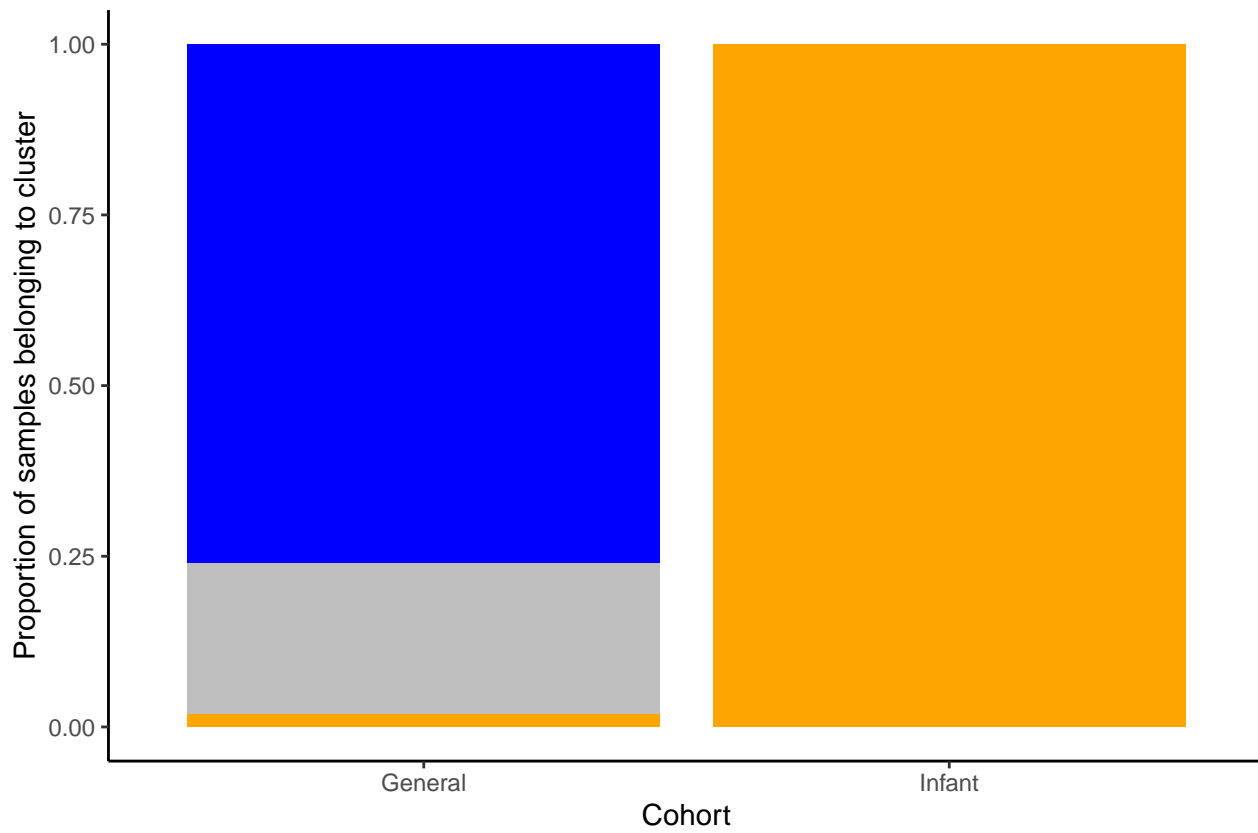
Figure 2: Stacked bar plot of the proportions of samples belonging to the hdbscan clusters from each cohort.
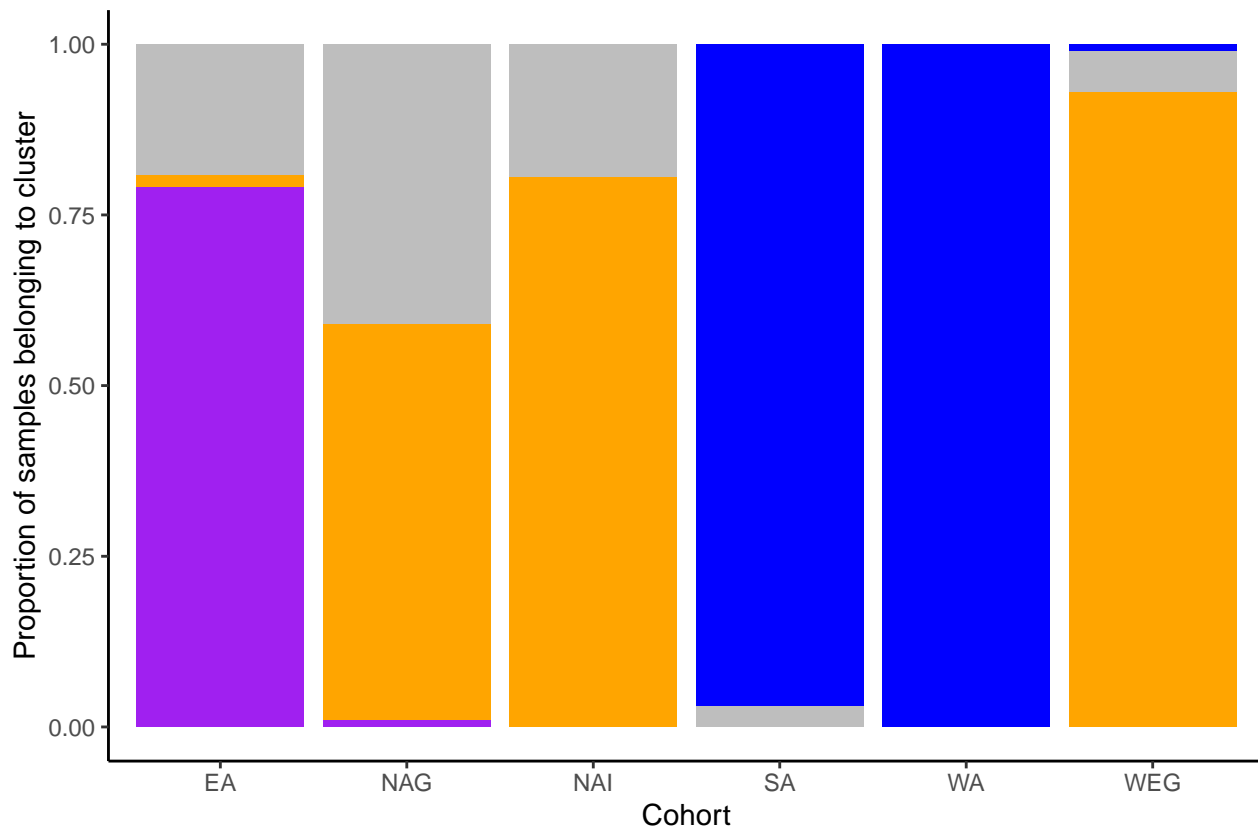
Figure 3: Stacked bar plot of the proportions of samples belonging to the hdbscan clusters from each cohort.