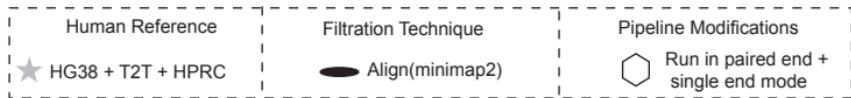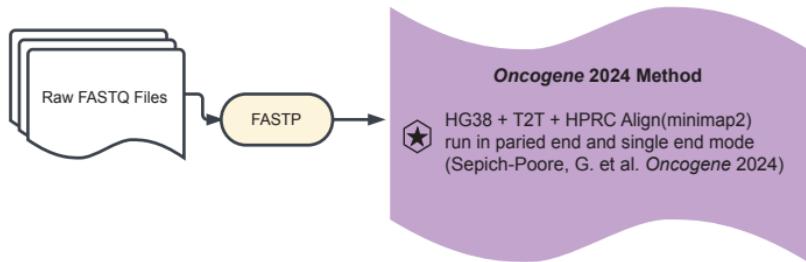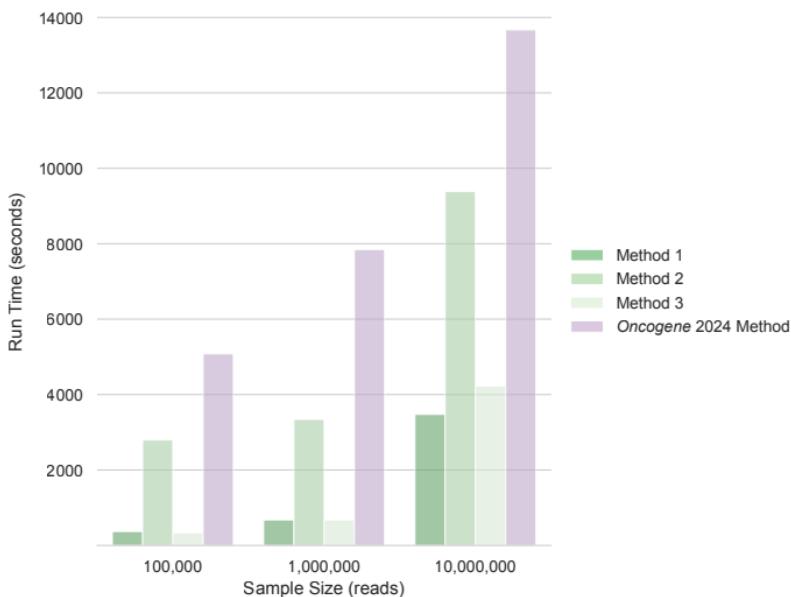**Supplementary Figure 2. Host filtration pipeline runtime evaluation** (a) Pipeline of prior host filtration methods. (b) Using simulated data with a 50/50 mix of human data from HPRC[20] and microbial data from FDA-ARGOS[16], we ran the 3 host filtration methods displayed in the paper along with the prior method as outlined in (a) with 3 different sample sizes. Runtimes were averaged across 10 runs per sample size. HG38 : GRCH38.p14, T2T: T2T-CHM13v2.0, HPRC: Human Pangenome Reference Consortium 2024 release.