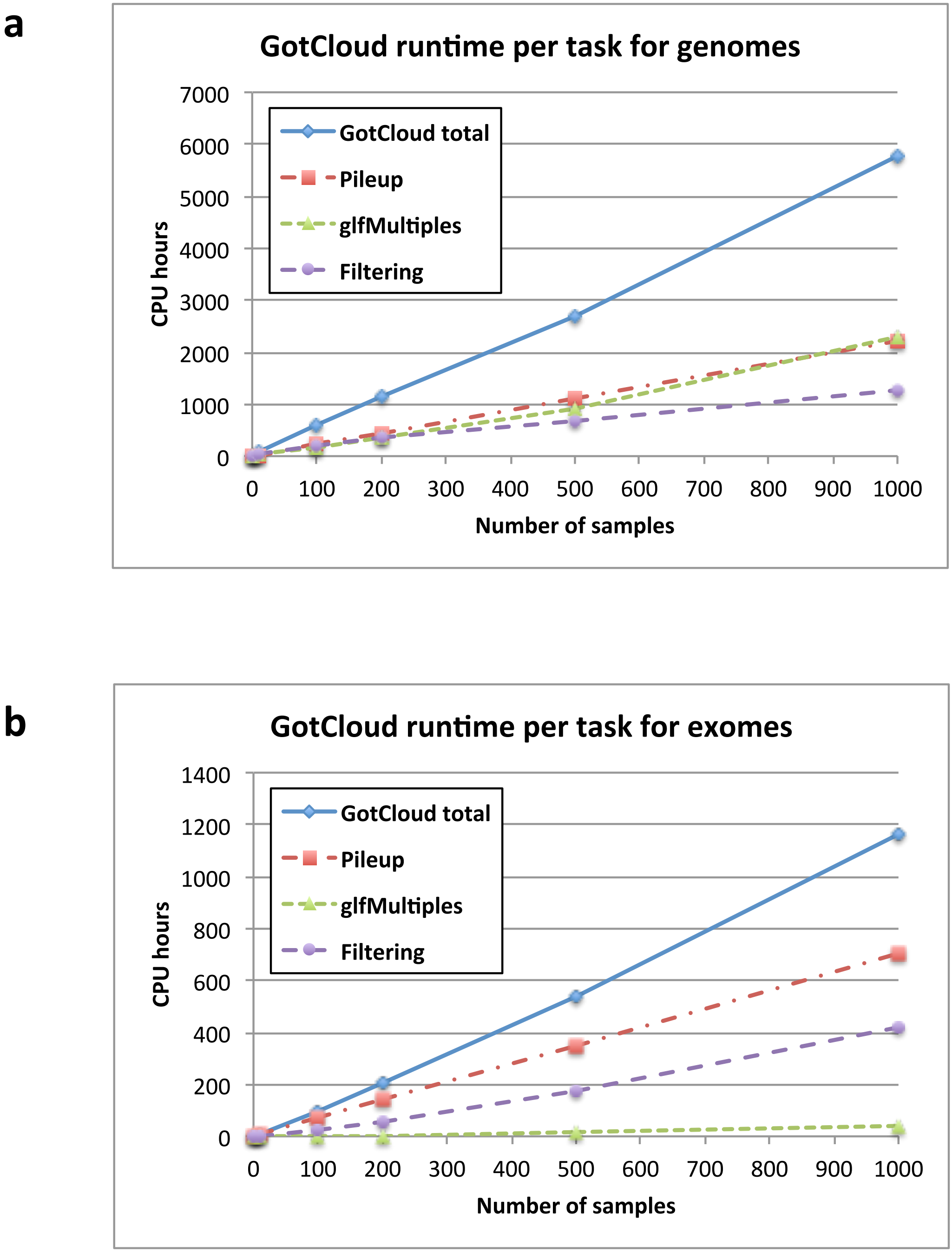

Supplementary Figure S1. a) GotCloud runtime broken down into sub-tasks for low-pass genome. b) Sub-task runtime estimates for deep exomes. Runtimes were measured using a single 5 mega-base genomic region of chromosome 20, and scaled by 600 to estimate the time required for processing the whole genome.