

Table S36. Runtime on HPC computer cluster for BioHansel and Snippy for 1 synthetic Illumina MiSeq dataset with 10X-1000X genome coverage (n=10).

Tool	Scheme	Runtime on 1 core for 1 synthetic FASTQ dataset with varying genome coverage (MM:SS)			
		10X (Std Dev)	50X (Std Dev)	100X (Std Dev)	1000X (Std Dev)
BioHansel	Typhi (136 k-mers)	00:13 (00:04)	00:19 (00:04)	00:31 (00:05)	03:20 (00:11)
	Heidelberg (404 k-mers)	00:11 (00:04)	00:20 (00:04)	00:31 (00:03)	03:37 (00:12)
	Enteritidis (634 k-mers)	00:12 (00:04)	00:23 (00:04)	00:34 (00:05)	03:48 (00:10)
	Typhimurium (860 k-mers)	00:14 (00:05)	00:25 (00:03)	00:35 (00:03)	04:13 (00:09)
Snippy	Typhi	01:10 (00:06)	04:32 (00:24)	09:26 (00:54)	50:10 (06:36)
	Heidelberg	01:06 (00:03)	04:44 (00:47)	09:15 (01:47)	48:10 (03:59)
	Enteritidis	01:05 (00:03)	04:20 (00:11)	08:26 (00:22)	46:16 (01:12)
	Typhimurium	01:12 (00:14)	04:28 (00:17)	08:43 (00:34)	49:39 (04:17)

The performance of BioHansel on genome assemblies and synthetic Illumina reads was measured on a desktop with the following specifications: CPU : Intel i5-6500 (4) @ 3.20GHz, GPU: Intel HD Graphics 530; RAM: 16Gb; OS: Ubuntu 18.04.2 LTS x86_64. BioHansel was run on either one core or 4 cores by specifying the number of threads (-t) at runtime, and with either only one output (Simple results) or all 3 outputs (Simple results, Results, and K-mer results). Each run consisted of 250-1000 genome assemblies of SE, SH, ST, and Typhi (supplementary Tables S13-S16).