2.4 GHz Intel Core 2 workstation with 2 GB of RAM				
	CPU Time	Wall clock time	Bowtie Speedup	Reads mapped
Bowtie -n 1	8m:15s	10m:05s	-	71.6%
Maq -n 1	6h:36m:57s	6h:38m:53s	39.6x	70.3%
Bowtie	16m:58s	19m:31s	-	75.3%
Maq	17h:46m:35s	17h:53m:07s	55.0x	73.8%

Table 1: CPU time for mapping 8.96M 35bp Illumina/Solexa reads against the whole human genome on a workstation with a 2.40GHz Intel Core 2 Q6600 processor and 2 GB of RAM. Reads were originally extracted as part of the 1000-Genomes project pilot. They were downloaded from the NCBI Short Read archive, accession #SRR001115. Reference sequences were the contigs of Genbank human genome build 36.3. Soap was not run against the whole-human reference because its memory footprint exceeds physical RAM. For the Maq runs, the reads were first divided into chunks of 2M reads each, as per the Maq Manual.