	CPU Time	Wall clock time	Bowtie Speedup	Peak VM Usage	Reads mapped
Bowtie -n 1	8m:15s	10m:05s	-	1,169 MB	71.6%
Maq -n 1	6h:36m:57s	6h:38m:53s	39.6x	804 MB	70.3%
Bowtie	16m:58s	19m:31s	-	1,169 MB	75.3%
Maq	17h:46m:35s	17h:53m:07s	55.0x	804 MB	73.8%

Table 1: Performance measurements for mapping 8.96M 35bp Illumina/Solexa reads against the whole human genome on a single CPU of a workstation with a 2.40GHz Intel Core 2 Q6600 processor and 2 GB of RAM. Bowtie speedup is calculated with respect to wall clock time. Reads are originally from the 1000-Genomes project pilot and were downloaded from the NCBI Short Read archive, accession #SRR001115, and trimmed to 35bps. Reference sequences were the contigs of Genbank human genome build 36.3. Soap was not run because its memory footprint would have exceeded the physical RAM of the workstation. For the Maq runs, the reads were first divided into chunks of 2M reads each, as per the Maq Manual. Maq v0.6.6 was used.