	CPU Time	Wall clock time	Bowtie Speedup	Reads mapped	
				Overall	w/r/t Bowtie
Bowtie	10m:29s	11m:30s	-	64.0%	-
Maq with -n 1	6h:36m:57s	6h:38m:53s	34.7x	71.8%	+12.1%
Maq	17h:46m:35s	17h:53m:07s	93.3x	73.8%	+15.3%

Table 1: CPU time for mapping 8.96M 35bp Illumina/Solexa reads (1 lane's worth) against the whole human genome on a workstation with a 2.40GHz Intel Core 2 Q6600 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.