	CPU Time	Wall clock time	Bowtie Speedup	Reads mapped Overall	w/r/t Bowtie
Bowtie	10m:39s	11m:11s	-	71.6%	-
Maq with -n 1	10h:52m:00s	10h:52m:52s	58.4x	70.3%	-1.9%
Maq	32h:56m:53s	32h:58m:39s	176.9x	73.8%	+3.0%

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.