	Time	Speedup	% reads mapped	% more reads mapped
Bowtie	10m:29s	1.0x	64.0	0.0%
Maq with -n 1	6h:36m:57s	37.9x	70.3	9.9%
Maq	17h:46m:35s	101.7x	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.