

| 2.4 GHz AMD Opteron 850 server with 32 GB of RAM | | | | |
|--|--------------|--------------------|-------------------|-----------------|
| | CPU Time | Wall clock time | Bowtie Speedup | Reads mapped |
| Bowtie -n 1 | 10m:24s | 11m:06s | - | 71.6% |
| Maq -n 1 | 10h:52m:00s | 10h:52m:52s | 58.8x | 70.3% |
| Soap -v 1 | 61h:13m:03s | 61h:02m:22s | 329.9x | 64.5% |
| Bowtie | 20m:48s | 21m:16s | - | 75.3% |
| Maq | 32h:56m:53s | 32h:58m:39s | 93.0x | 73.8% |
| Soap | 107h:23m:44s | 107h:12m:28s | 302.5x | 70.6% |

Table 1: CPU time for mapping 8.96M 35bp Illumina/Solexa reads against the whole human genome on a server with a 2.4 GHz AMD Opteron 850 processor and 32 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.