

2.4 GHz Intel Core 2 workstation with 2 GB of RAM

| | Chr 22 35.1 Mbases | | Chr 2 238 Mbases | | Whole Genome 2.87 Gbases | |
|--------|-----------------------|----------|---------------------|----------|-----------------------------|----------|
| | Time | Speedup | Time | Speedup | Time | Speedup |
| Bowtie | 8m:25s | - | 11m:06s | - | 22m:36s | - |
| Maq | 22m:06s | 2.6x | 54m:30s | 4.9x | 13h:58m:40s | 37.1x |
| Soap | 36m:22s | 4.3x | 3h:06m:29s | 16.8x | - | - |
| | Virtual | Resident | Virtual | Resident | Virtual | Resident |
| | | | | | | |
| Bowtie | 33 MB | 33 MB | 128 MB | 116 MB | 1,174 MB | 1,126 MB |
| Maq | 767 MB | 727 MB | 796 MB | 756 MB | 804 MB | 763 MB |
| Soap | 393 MB | 380 MB | 1,417 MB | 1,331 MB | - | - |

Table 1: Wall clock time and peak virtual/resident memory usage for mapping 8M simulated 35bp reads against human chromosomes 22 and 2 and the whole human genome on a single CPU of a workstation with a 2.4 GHz Intel Core 2 Q6600 processor and 2 GB of RAM. Simulated reads were extracted only from the relevant region using a read simulator that attempts to recreate the error profile of typical Illumina/Solexa reads. Reference sequences were taken from 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. Soap v1.10 and Maq v0.6.6 were used.