Mapping time: workstation

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie	21m:32s	23m:27s	-	1,169 MB	76.5%
Maq	17h:46m:35s	17h:53m:07s	45.8x	804 MB	73.8%

Mapping time: server

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie	24m:28s	25m:26s	-	1,169 MB	76.5%
Maq	32h:56m:53s	32h:58m:39s	77.8x	804 MB	73.8%

Reads mapped

By Maq or Bowtie or both	By both Maq and Bowtie	By Bowtie but not Maq	By Maq but not Bowtie
7,053,875	6,404,715 (90.8%)	446,917 (6.3%)	202,243 (2.9%)

Table 1: Performance and sensitivity measurements for mapping an unfiltered set of 8.96M 35bp Illumina/Solexa reads against 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, and on a server with a 2.4 GHz AMD Opteron 850 processor and 32 GB of RAM. Bowtie speedup is calculated with respect to wall clock time. Both CPU time and wall clock times are included to demonstrate that no one tool suffers disproportionately from I/O pauses or contention with other processes. Maq and Soap create their indexes while mapping, whereas Bowtie is provided with a pre-built index of the genome. The cost of building the Bowtie index is not included in these timings since we expect that in practice that cost will be rapidly amortized across multiple mapping jobs. Reads are taken from the 1000-Genomes project pilot via the NCBI Short Read archive, accession #SRR001115 and trimmed to 35bps. Reference sequences were the contigs of Genbank human genome build 36.3. For the Maq runs, the reads were first divided into chunks of 2M reads each, as per the Maq Manual. Maq v0.6.6 was used.