Workstation

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie -n 1	9m:07s	11m:21s	-	1,169 MB	71.6%
Maq -n 1	6h:36m:57s	6h:38m:53s	35.1x	804 MB	70.3%
Bowtie	25m:11s	27m:17s	-	1,169 MB	76.5%
Maq	17h:46m:35s	17h:53m:07s	39.3x	804 MB	73.8%

Server

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie -n 1	9m:05s	10m:11s	-	1,169 MB	71.6%
Maq -n 1	10h:52m:00s	10h:52m:52s	64.1x	804 MB	70.3%
Soap -v 1	60h:49m:26s	61h:02m:22s	359.6x	13,619 MB	64.5%
Bowtie	26m:38s	29m:11s	-	1,169 MB	76.7%
Maq	32h:56m:53s	32h:58m:39s	67.8x	804 MB	73.8%
Soap	106h:57m:37s	107h:12m:28s	220.4x	13,619 MB	70.6%

Table 1: Performance measurements for mapping 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 on the system. Note that Maq indexes the reads as it maps them, whereas Bowtie requires that an index of the genome be pre-built. 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. Soap was not run on the workstation because its memory footprint would have exceeded the physical RAM of the workstation. 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.