Workstation

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie -n 1	8m:29s	10m:26s	-	1,169 MB	71.6%
Maq -n 1	6h:36m:57s	6h:38m:53s	38.2x	804 MB	70.3%
Bowtie	21m:32s	23m:27s	-	1,169 MB	76.5%
Maq	17h:46m:35s	17h:53m:07s	45.8x	804 MB	73.8%

Server

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie -n 1	9m:55s	10m:26s	-	1,169 MB	71.6%
Maq -n 1	10h:52m:00s	10h:52m:52s	62.6x	804 MB	70.3%
Soap -v 1	60h:49m:26s	61h:02m:22s	351.0x	13,619 MB	64.5%
Bowtie	24m:28s	25m:26s	-	1,169 MB	76.5%
Maq	32h:56m:53s	32h:58m:39s	77.8x	804 MB	73.8%
Soap	106h:57m:37s	107h:12m:28s	252.9x	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. Note that Maq and Soap create their indexes while mapping, whereas Bowtie must be 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. 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. Soap v1.10 and Maq v0.6.6 were used.