

Workstation					
	CPU Time	Wall clock time	Bowtie Speedup	Peak VM Usage	Reads mapped
Bowtie -n 1	8m:15s	10m:05s	-	1,169 MB	71.6%
Maq -n 1	6h:36m:57s	6h:38m:53s	39.6x	804 MB	70.3%
Bowtie	16m:58s	19m:31s	-	1,169 MB	75.3%
Maq	17h:46m:35s	17h:53m:07s	55.0x	804 MB	73.8%

Server					
	CPU Time	Wall clock time	Bowtie Speedup	Peak VM Usage	Reads mapped
Bowtie -n 1	10m:24s	11m:06s	-	1,169 MB	71.6%
Maq -n 1	10h:52m:00s	10h:52m:52s	58.8x	804 MB	70.3%
Soap -v 1	61h:13m:03s	61h:02m:22s	329.9x	13,619 MB	64.5%
Bowtie	20m:48s	21m:16s	-	1,169 MB	75.3%
Maq	32h:56m:53s	32h:58m:39s	93.0x	804 MB	73.8%
Soap	107h:23m:44s	107h:12m:28s	302.5x	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 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. Reads are originally from the 1000-Genomes project pilot and were downloaded from 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. Soap v1.10 and Maq v0.6.6 were used.