2.4 GHz AMD Opteron 850 server with 32 GB of RAM						
	Chr 22 35.1 Mbases		Chr 2 238 Mbases		Whole Genome 2.87 Gbases	
	Time	Speedup	Time	Speedup	Time	Speedup
Bowtie	10m:06s	-	14m:57s	-	26m:57s	-
Maq	33m:01s	3.3x	1h:26m:25s	5.8x	24h:25m:16s	54.4x
Soap	53m:53s	5.3x	4h:13m:13s	16.9x	70h:07m:53s	156.1x
	Virtual	Resident	Virtual	Resident	Virtual	Resident
Bowtie	33 MB	33 MB	128 MB	115 MB	1,174 MB	1,126 MB
Maq	767 MB	727 MB	796 MB	756 MB	804 MB	763 MB
Soap	392 MB	379 MB	1,418 MB	1,331 MB	13,619 MB	13,312 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 server with a 2.4 GHz AMD Opteron 850 processor and 32 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.