	Chr 22 35.1 Mbases		Chr 2 238 Mbases		Whole Genome 2.87 Gbases	
	Time	Speedup	Time	Speedup	Time	Speedup
Bowtie	7m:46s	-	9m:25s	-	12m:36s	-
Maq with -n 1	33m:32s	4.3x	1h:21m:56s	8.7x	8h:21m:55s	39.8x
Maq	12m:46s	1.6x	29m:02s	3.1x	22h:09m:29s	105.5x
Soap with -v 1	12m:49s	1.7x	30m:46s	3.3x	8h:33m:07s	40.7x
Soap	33m:01s	4.3x	1h:26m:25s	9.2x	24h:25m:16s	116.3x
	Virtual	Resident	Virtual	Resident	Virtual	Resident
Bowtie	29 MB	29 MB	128 MB	109 MB	1,169 MB	1,126 MB
Maq with -n 1	3,008 MB	2,867 MB	3,008 MB	2,867 MB	3,008 MB	2,867 MB
Maq	3,008 MB	2,867 MB	3,008 MB	2,867 MB	3,008 MB	2,867 MB
Soap with -v 1	767 MB	726 MB	796 MB	756 MB	804 MB	763 MB
Soap	767 MB	727 MB	796 MB	756 MB	804 MB	763 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 workstation with a 2.40GHz Intel Core 2 Q6600 and 2 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.