

	Chr 22 35.1 Mbases		Chr 2 238 Mbases		Whole Genome 2.87 Gbases	
	Time	Speedup	Time	Speedup	Time	Speedup
Bowtie	5m:50s	-	7m:05s	-	11m:26s	-
Maq with -n 1	8m:33s	1.5x	19m:55s	2.8x	4h:53m:18s	25.7x
Maq	22m:06s	3.8x	54m:30s	7.7x	13h:58m:40s	73.4x
Soap with -v 1	28m:12s	4.8x	2h:24m:31s	20.4x	-	-
Soap	36m:22s	6.2x	3h:06m:29s	26.3x	-	-
	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	767 MB	726 MB	796 MB	756 MB	804 MB	763 MB
Maq	767 MB	727 MB	796 MB	756 MB	804 MB	763 MB
Soap with -v 1	391 MB	380 MB	1,416 MB	1,331 MB	-	-
Soap	393 MB	380 MB	1,417 MB	1,331 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.