

	Chr 22 35.1 Mbases		Chr 2 238 Mbases		Whole Genome 2.87 Gbases	
	Time	Speedup	Time	Speedup	Time	Speedup
Bowtie	11m:54s	1.0x	12m:26s	1.0x	16m:42s	1.0x
Maq with -n 1	8m:18s	0.7x	19m:40s	1.6x	4h:51m:45s	17.5x
Maq	21m:23s	1.8x	54m:22s	4.4x	13h:53m:20s	49.9x
Soap with -v 1	27m:55s	2.3x	2h:23m:27s	11.5x	-	-
Soap	36m:04s	3.0x	3h:04m:26s	14.8x	-	-
	Virtual	Resident	Virtual	Resident	Virtual	Resident
Bowtie	23 MB	23 MB	110 MB	103 MB	1,152 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: CPU 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 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.