	Chr 22 35.1 Mbases		Chr 2 238 Mbases		Whole Genome 2.91 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: Running time and peak virtual/resident memory usage for mapping 8M simulated reads against human chromosomes 22 and 2 and the whole human genome on a workstation with 2 GB of RAM. Soap is omitted from Whole Human because its memory footprint exceeds physical RAM. Simulated reads were exacted only from the relevant region. For the Maq runs, the reads were first divided into chunks of 2M reads each, as per the Maq Manual.