	Chr 22		Chr 2		Whole Genome	
	35.1 Mbases		238 Mbases		2.87 Gbases	
	Time	Speedup	Time	Speedup	Time	Speedup
Bowtie	8m:25s	-	11m:06s	-	22m:36s	-
Maq	8m:33s	1.0x	19m:55s	1.8x	13h:58m:40s	37.1x
Soap	22m:06s	2.6x	54m:30s	4.9x	-	-
	Virtual	Resident	Virtual	Resident	Virtual	Resident
Bowtie	33 MB	33 MB	128 MB	116 MB	1,174 MB	1,126 MB
Maq	767 MB	726 MB	796 MB	756 MB	804 MB	763 MB
Soap	767 MB	727 MB	796 MB	756 MB	-	-

2.4 GHz Intel Core 2 workstation with 2 GB of RAM

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 2.4 GHz Intel Core 2 Q6600 processor 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.