

Mapping time: server					
	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie	24m:28s	25m:26s	-	1,169 MB	76.5%
Soap	106h:57m:37s	107h:12m:28s	252.9x	13,619 MB	70.6%

  

Reads mapped				
By Soap or Bowtie or both	By both Soap and Bowtie	By Bowtie but not Soap	By Soap but not Bowtie	
6,332,570	6,268,551 (99.0%)	6,957 (0.1%)	57,062 (0.9%)	

Table 1: Performance and sensitivity measurements for mapping an unfiltered set of 8.96M 35bp Illumina/Solexa reads against 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, and on a server with a 2.4 GHz AMD Opteron 850 processor and 32 GB of RAM. Bowtie speedup is calculated with respect to wall clock time. Both CPU time and wall clock times are included to demonstrate that no one tool suffers disproportionately from I/O pauses or contention with other processes. Soap indexes its inputs as it maps, whereas Bowtie must be provided with a pre-built index of the genome. The cost of building the Bowtie index is not included in these timings since we expect that in practice that cost will be rapidly amortized across multiple mapping jobs. Reads are taken from the 1000-Genomes project pilot via the NCBI Short Read archive, accession #SRR001115 and trimmed to 35bps. Reference sequences were the contigs of Genbank human genome build 36.3. Soap was not run on the workstation because its memory footprint would have exceeded the physical RAM of the workstation. Soap v1.10 was used.