

Supplementary data for “Fast multiclonal clusterization of V(D)J recombination from high-throughput sequencing”

October 9, 2013

	reads	40-windows detected	unique 40-windows	clones with ≥ 100 reads
Diagnosis (Diag)	191 095	62 461 (32.7 %)	13 074 (20.9%)	18
Scale- 10^{-2}	85 903	27 734 (32.3 %)	12 430 (44.8%)	3
Scale- 10^{-3}	292 535	100 990 (34.5 %)	34 056 (33.7%)	17
Scale- 10^{-4}	437 490	142 230 (32.5 %)	44 499 (31.3%)	32
Scale- 10^{-5}	969 026	315 011 (32.5 %)	80 548 (25.6%)	302
Follow-up 1 (Fu-1, 35 days)	624 078	161 458 (25.9 %)	66 435 (41.1%)	13
Follow-up 2 (Fu-2, 122 days)	1 360 656	406 606 (29.9 %)	95 862 (23.6%)	807
Follow-up 4 (Fu-4, 207 days)	375 510	66 361 (17.7 %)	29 633 (44.6%)	6

Table 1: Statistics on the eight samples sequenced for a patient with ALL and on the results of Vidjil. On each dataset, starting from some number of reads, Vidjil detects 40-windows overlapping the CDR3. The count of unique 40-windows is smaller as clones gather several reads. The last columns shows the number of clones with at least 100 reads. All percentages are computed with respect to the number of reads of each dataset.