

Table 1: Detailed event count numbers per cohort with the maximum event number in the given cutoff written in brackets.

	i= 20000	i= 30000	i= 40000	i= 50000
AML	0 (max 0)	0 (max 0)	7 (max 37756)	124 (max 50000)
CLL	2 (max 16153)	291 (max 29999)	1249 (max 39988)	3356 (max 50000)
FL	0 (max 0)	2 (max 29795)	7 (max 38991)	216 (max 50000)
HCL	0 (max 0)	0 (max 0)	3 (max 35901)	187 (max 50000)
HCLv	0 (max 0)	0 (max 0)	3 (max 37997)	54 (max 50000)
LPL	1 (max 19693)	5 (max 29814)	22 (max 39318)	622 (max 50000)
MBL	0 (max 0)	1 (max 29588)	11 (max 39441)	1458 (max 50000)
MCL	2 (max 15545)	12 (max 29887)	62 (max 39702)	415 (max 50000)
MM	0 (max 0)	1 (max 26217)	2 (max 38324)	101 (max 50000)
MZL	0 (max 0)	4 (max 28871)	50 (max 39812)	968 (max 50000)
normal	1 (max 14598)	1 (max 14598)	19 (max 39860)	8434 (max 50000)
PL	1 (max 12301)	20 (max 29810)	132 (max 39995)	597 (max 50000)

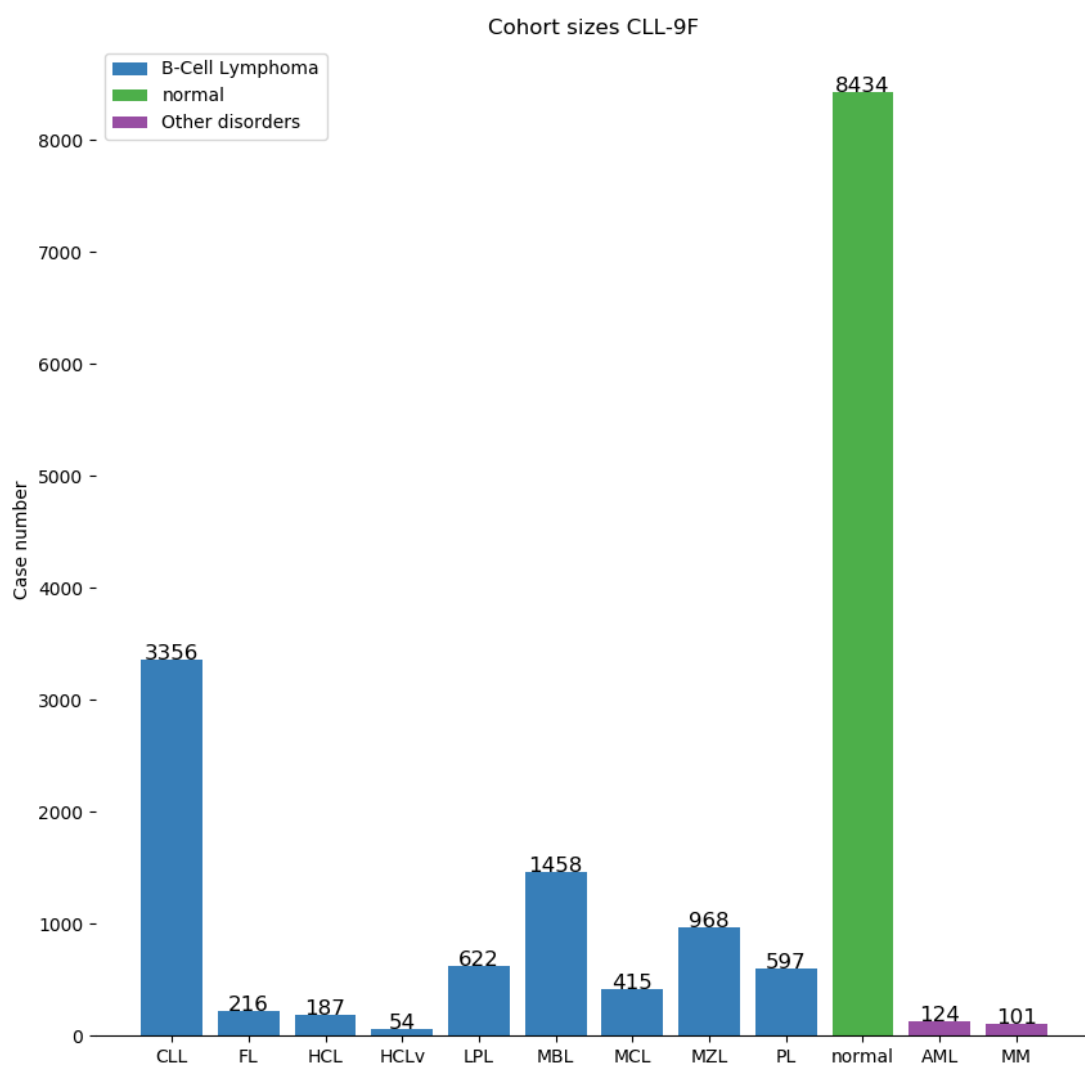


Figure 1: Overview of cohort sizes using the CLL 9F panel. These numbers include only cases with at least tube 1 and 2 of the same material and each fcs file having more than 10,000 events.

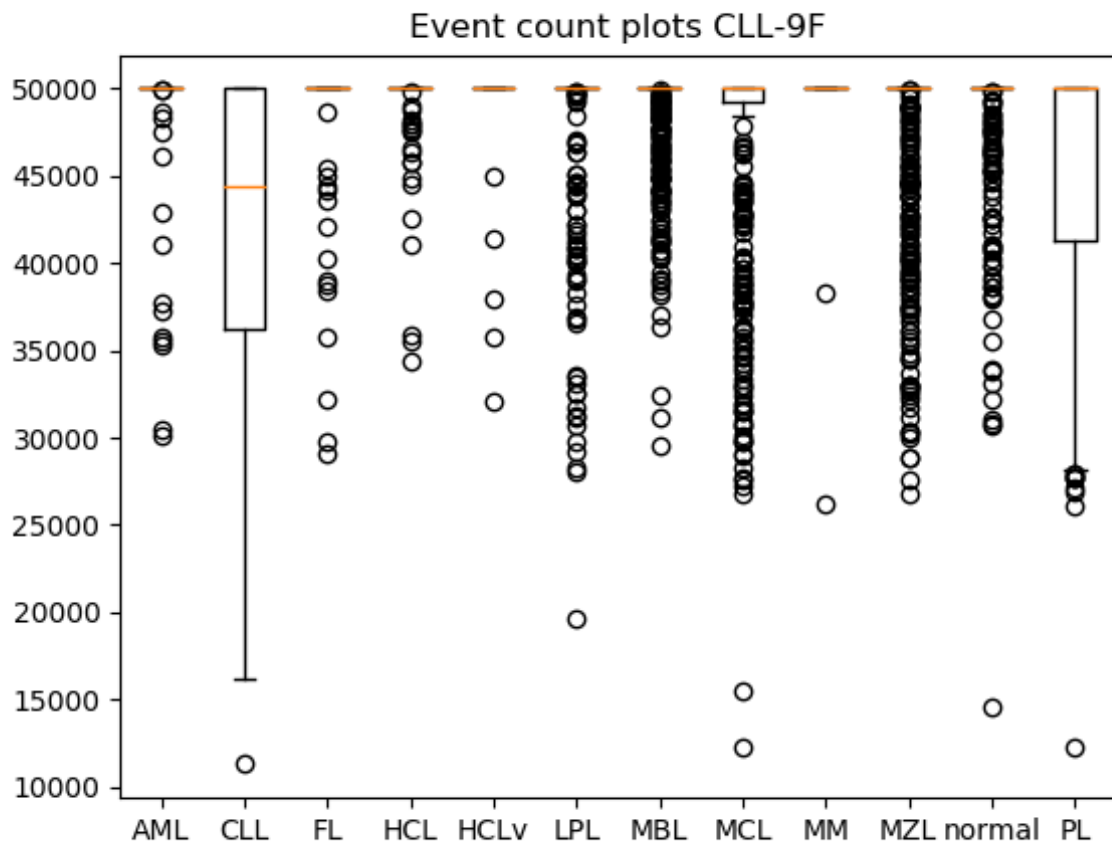


Figure 2: Number of events in each fcs file in tube 1 for each cohort. The whiskers represent 25th and 75th percentile. Numbers outside these ranges are represented as individual dots.

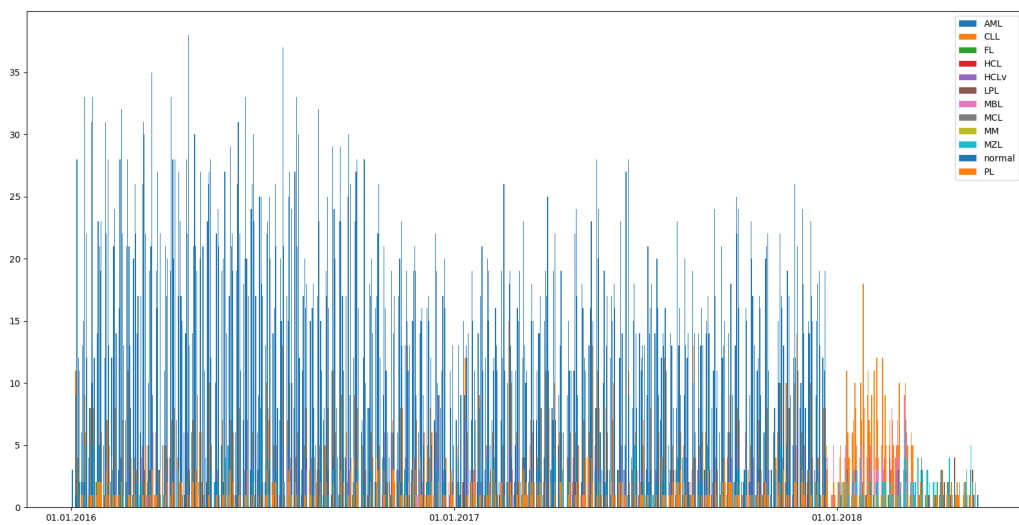


Figure 3: Time-histogram of case date over time. This visualization can be used to spot skewed distributions in individual cohorts.