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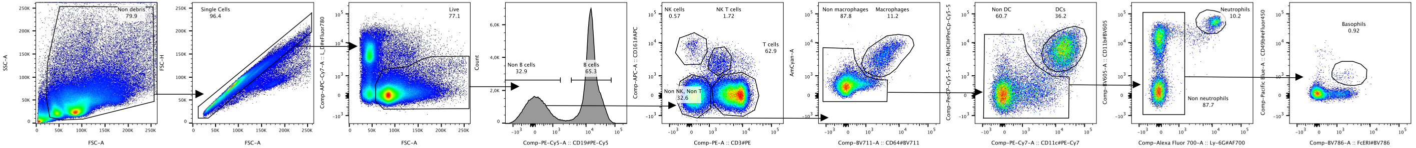
Supplementary information

Analyzing high-dimensional cytometry data using FlowSOM

In the format provided by the
authors and unedited



Supplementary Figure 1 | An overview of the gating strategy to obtain the manual labels that will be mapped on the FlowSOM tree.

```
R version 4.0.3 (2020-10-10)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Big Sur 10.16

Matrix products: default
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/
libRlapack.dylib

locale:
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attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] ggplot2_3.3.3  FlowSOM_2.1.10 igraph_1.2.6   flowCore_2.2.0

loaded via a namespace (and not attached):
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colorspace_2.0-0            ggsignif_0.6.1
  [5] rjson_0.2.20                ellipsis_0.3.1
rio_0.5.16                  colorRamps_2.3
  [9] rprojroot_2.0.2             circlize_0.4.12
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CytoML_2.2.1                ggrepel_0.9.1
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knitr_1.31                  polyclip_1.10-0
 [25] jsonlite_1.7.2              Cairo_1.5-12.2
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