Supplemental Table 3. Bioinformatic tools and software versions used in data analysis pipeline

Package/Software	Version	Availability
Cytobank	7.0	https://www.cytobank.org
R	3.6.3	https://www.r-project.org
Python	3.8.2	https://www.python.org/downloads/
UMAP	0.5.1	https://pypi.org/project/umap-learn/
Sci-kit Learn	0.24.0	https://scikit-learn.org/stable/
Diffcyt	3.12	https://bioconductor.org/packages/release/bioc/html/diffcyt.html
PARC (phenotyping by accelerated refined community-partitioning)	0.33	https://github.com/ShobiStassen/PARC
ggplot	3.3.2	https://ggplot2.tidyverse.org/reference/ggplot.html
FlowCore	3.12	http://www.bioconductor.org/packages/release/bioc/html/flowCore.html

All packages and tools can be accessed using the links available in addition to the specific version of each tool used.