

# Supplementary Figures

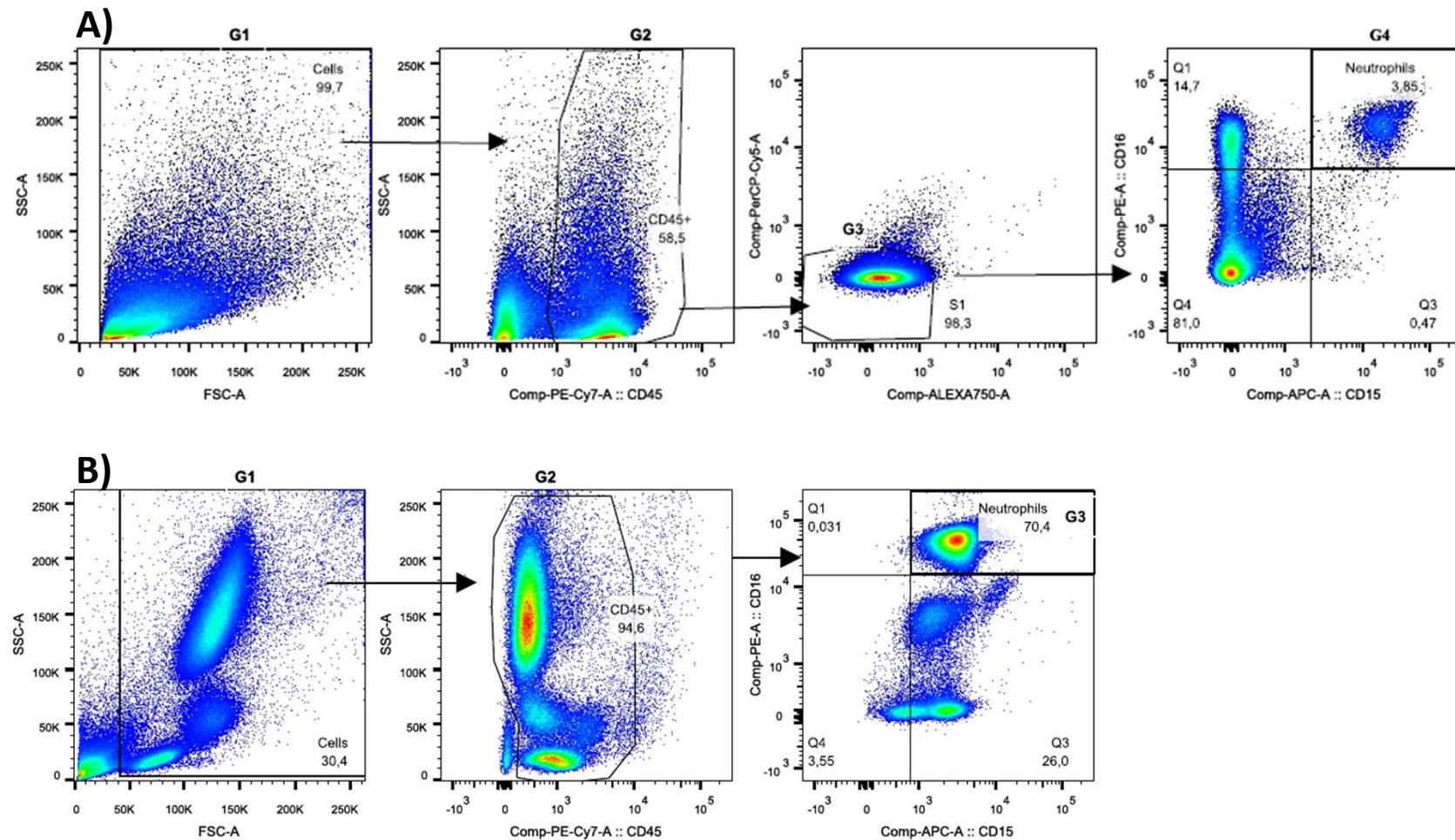
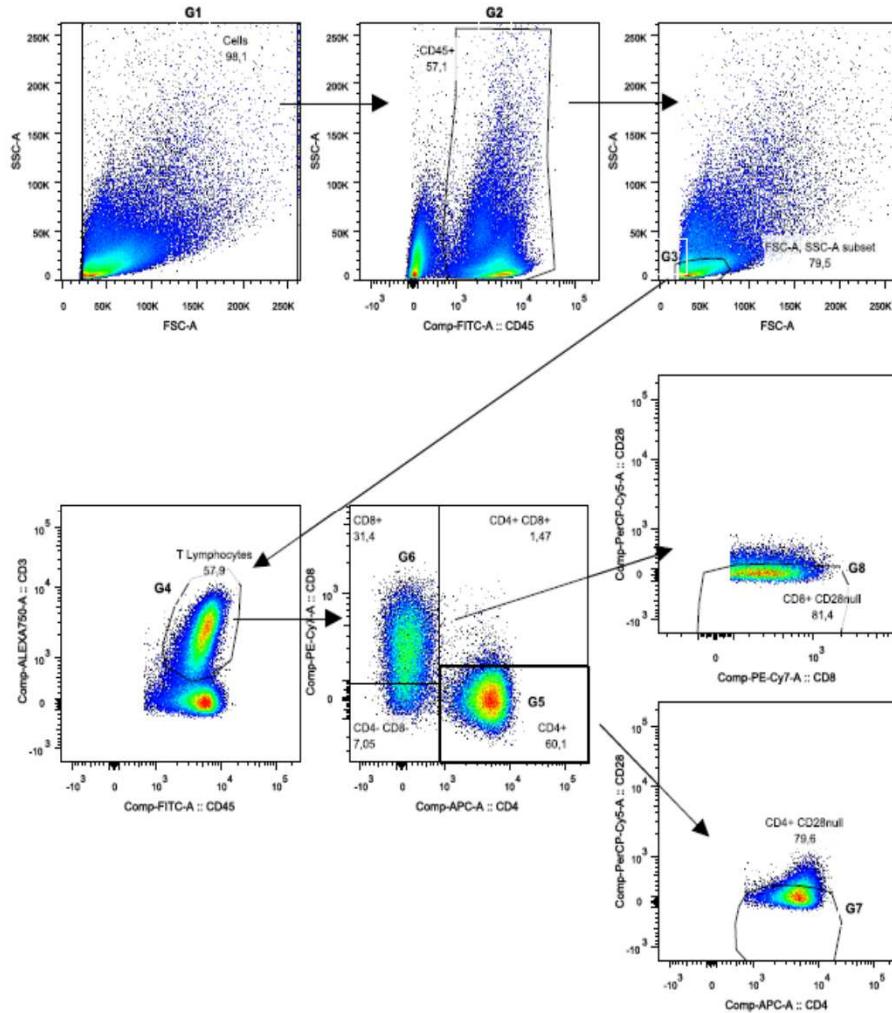
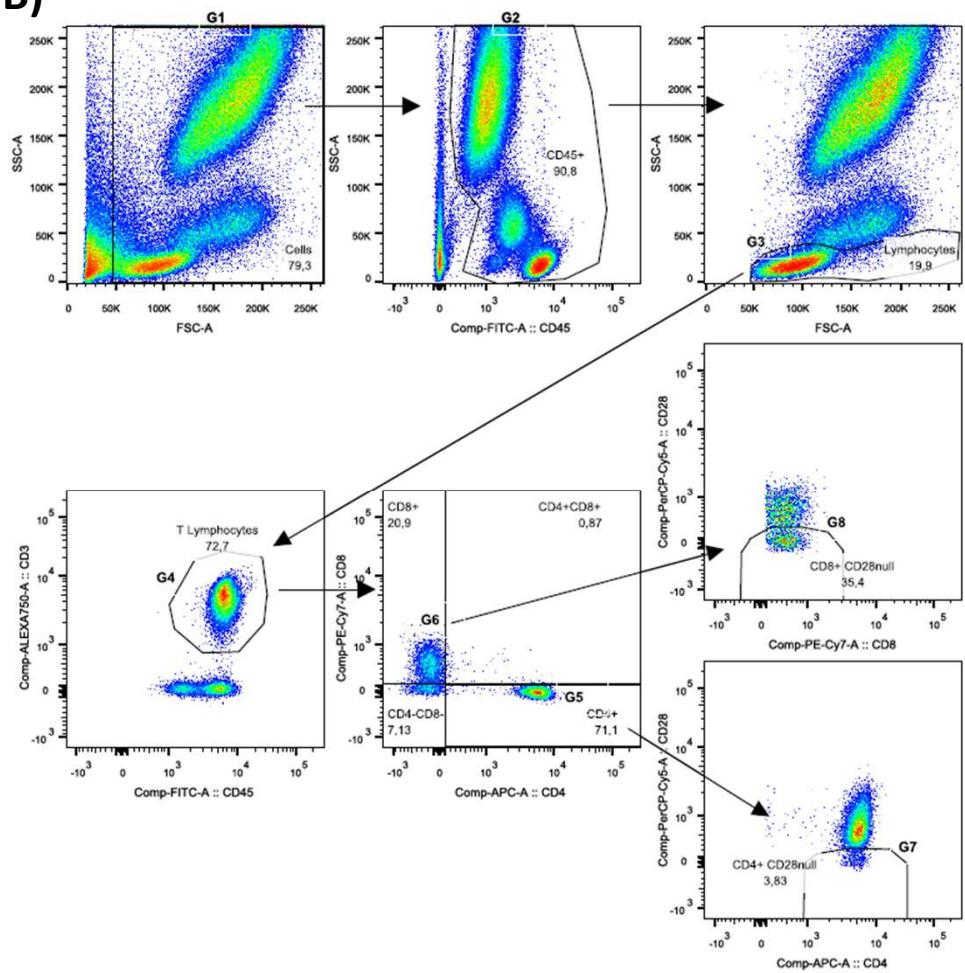
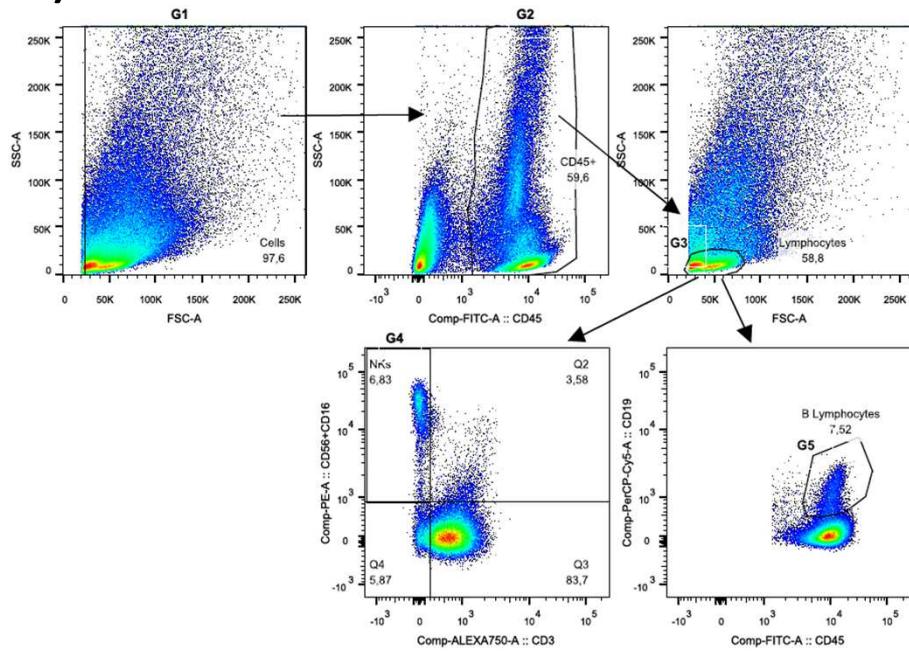
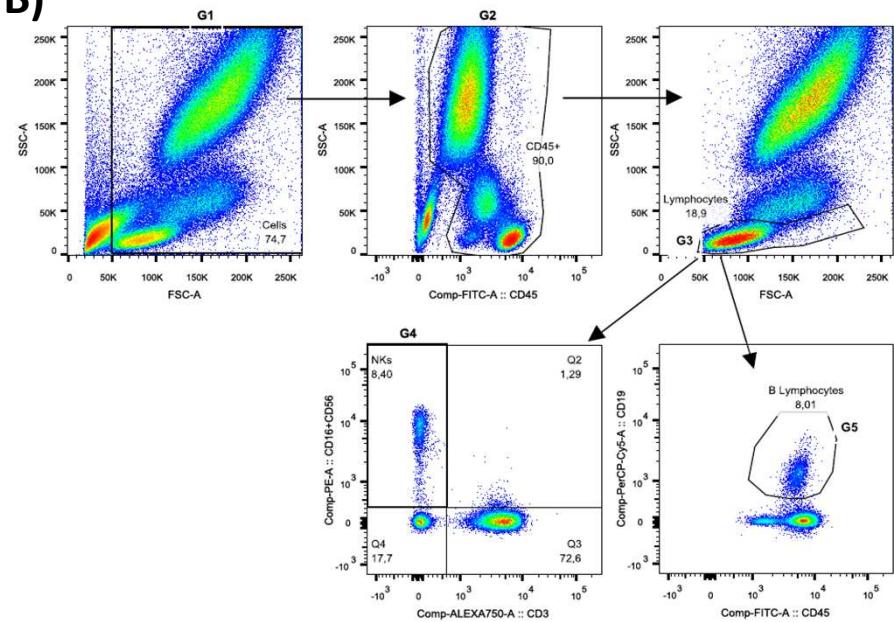


Figure S1

**A)****B)****Figure S2**

**A)****B)****Figure S3**

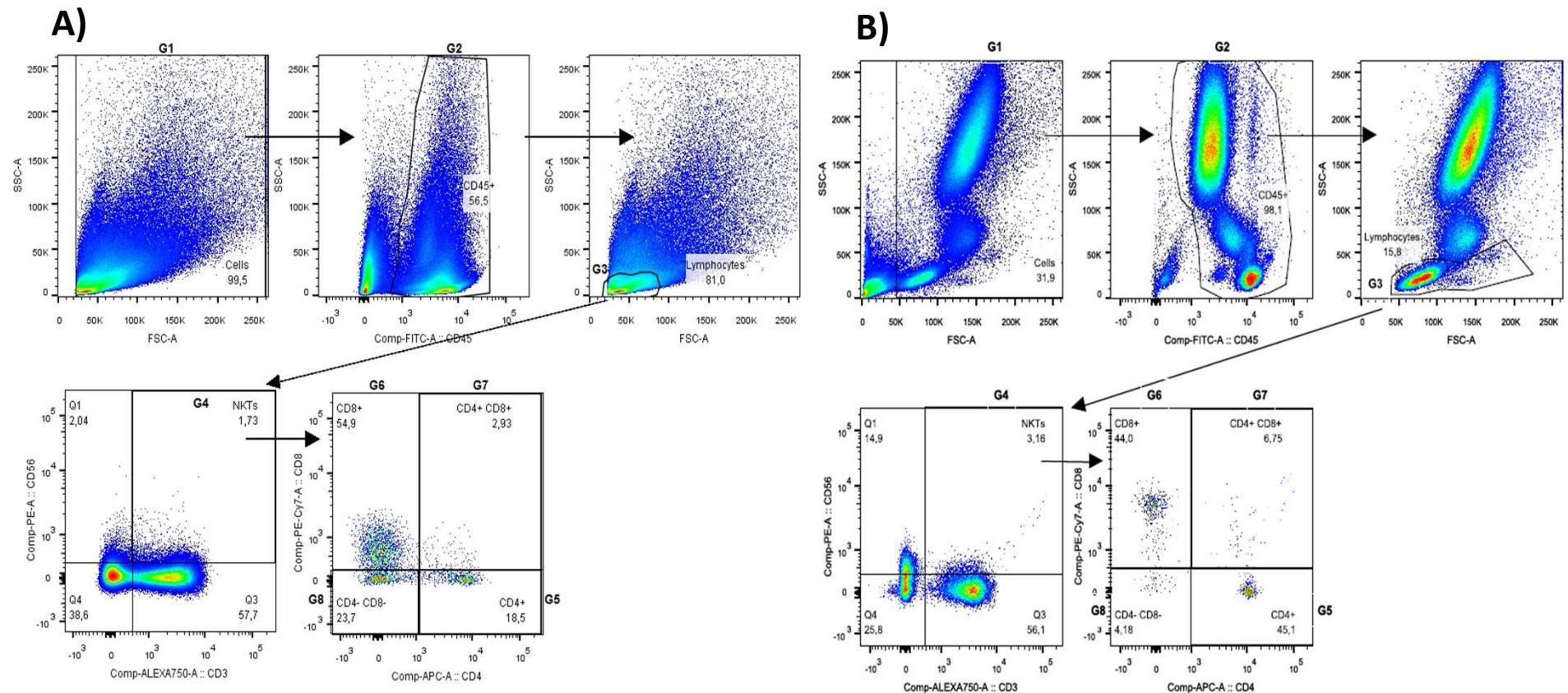


Figure S4

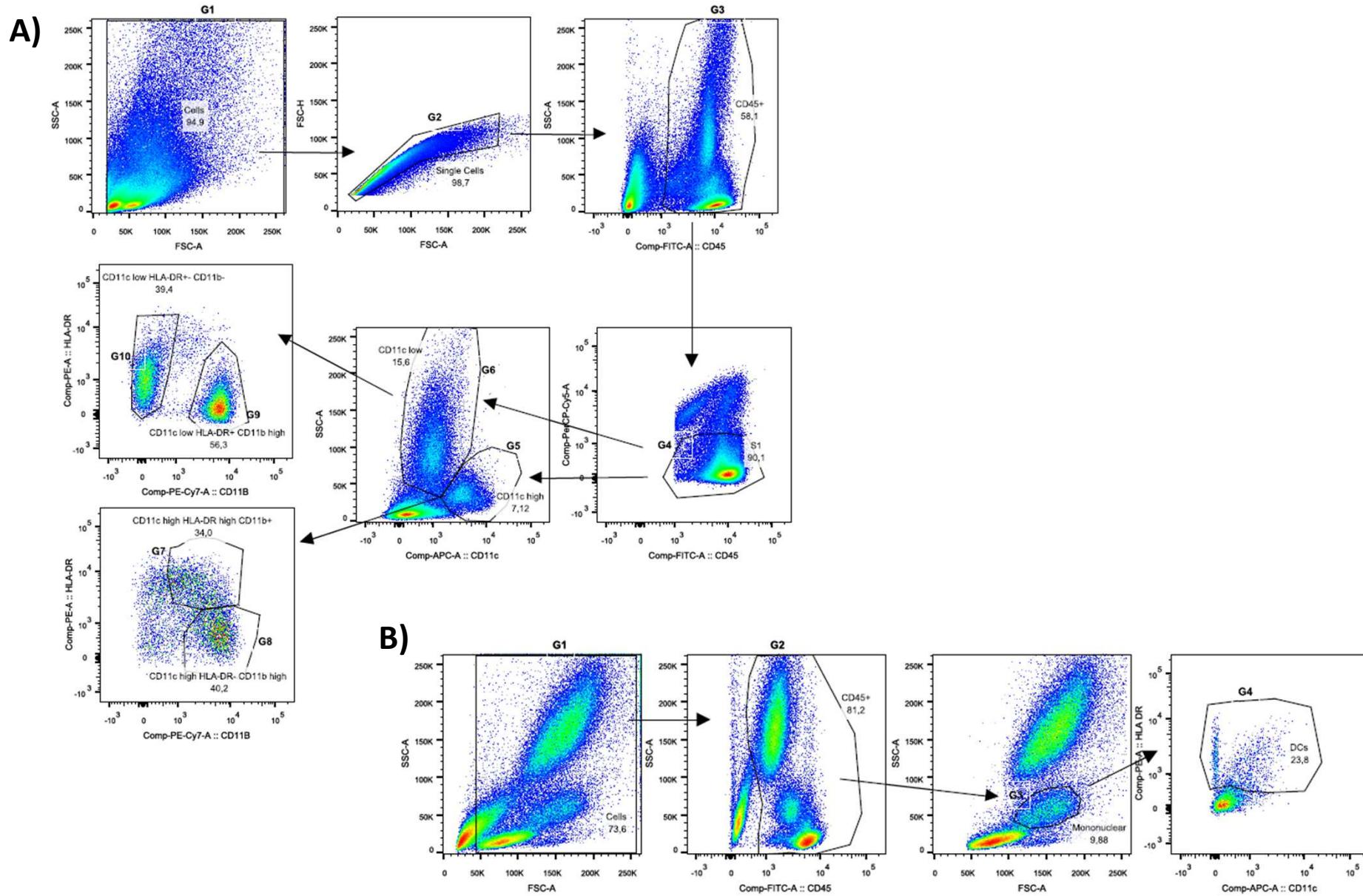


Figure S5

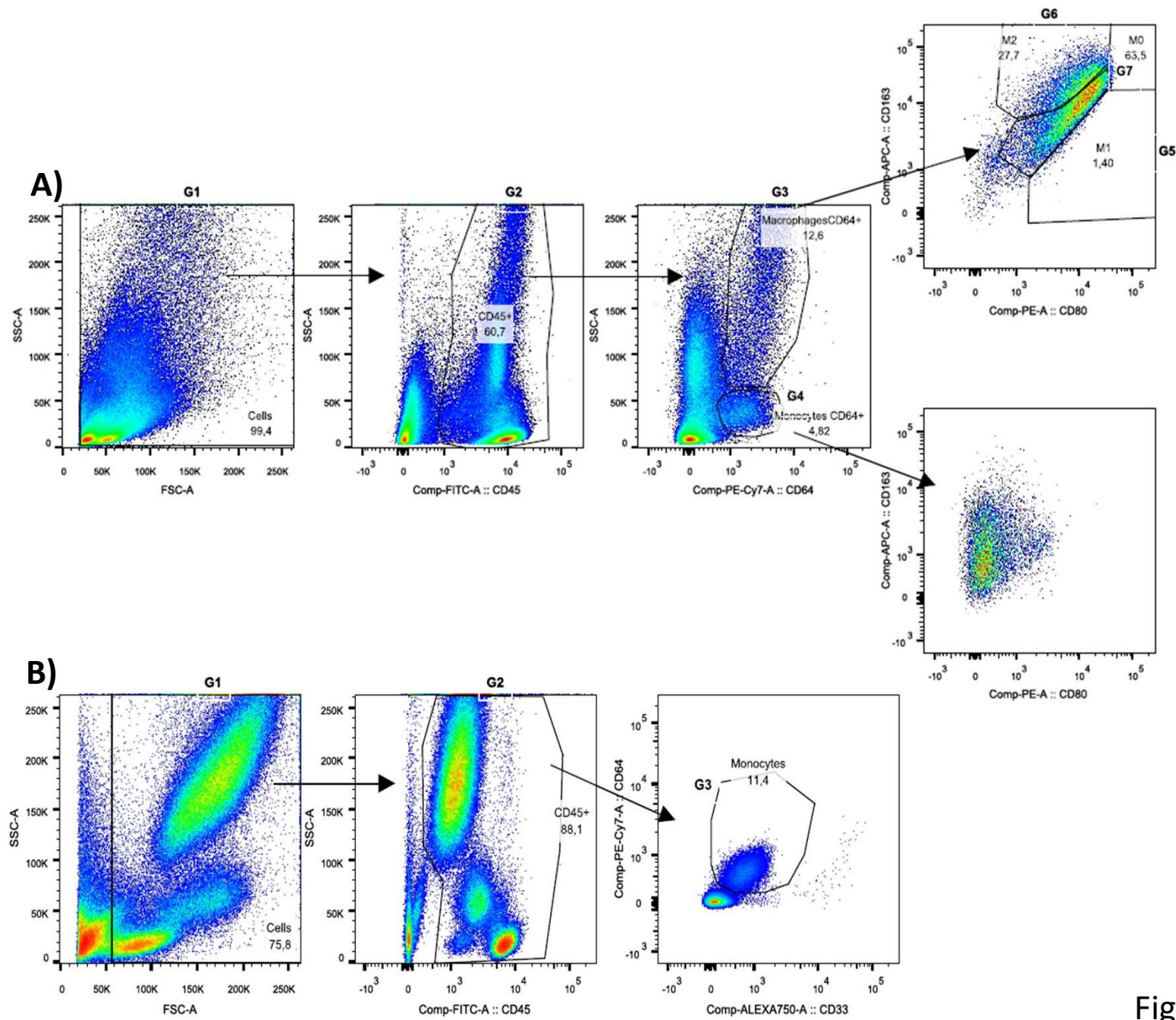


Figure S6

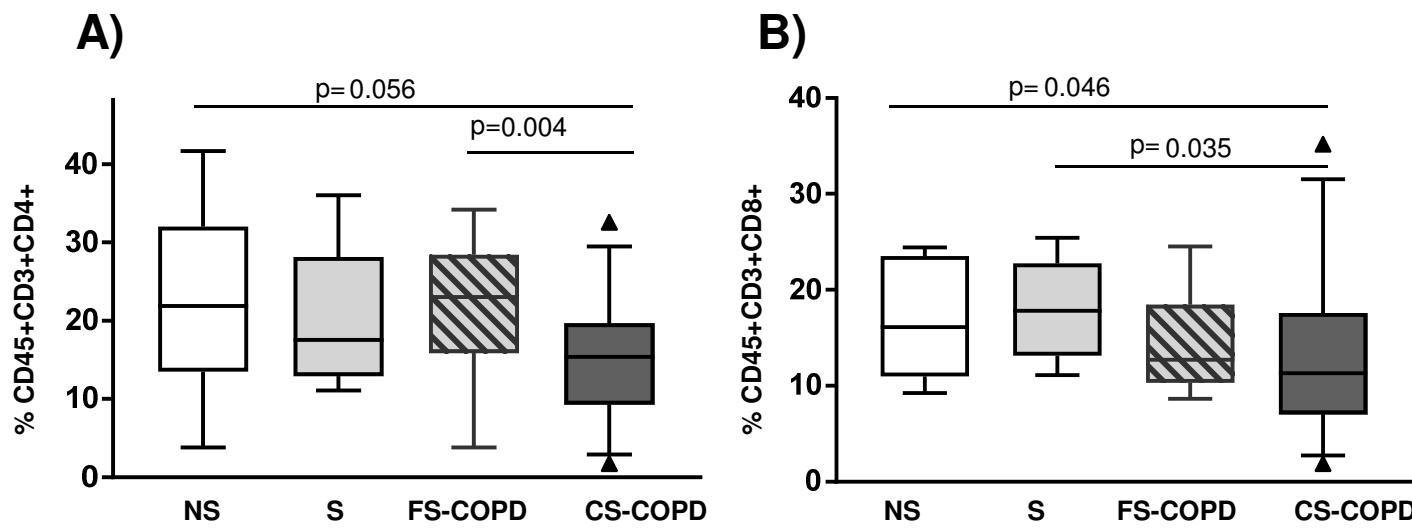


Figure S7

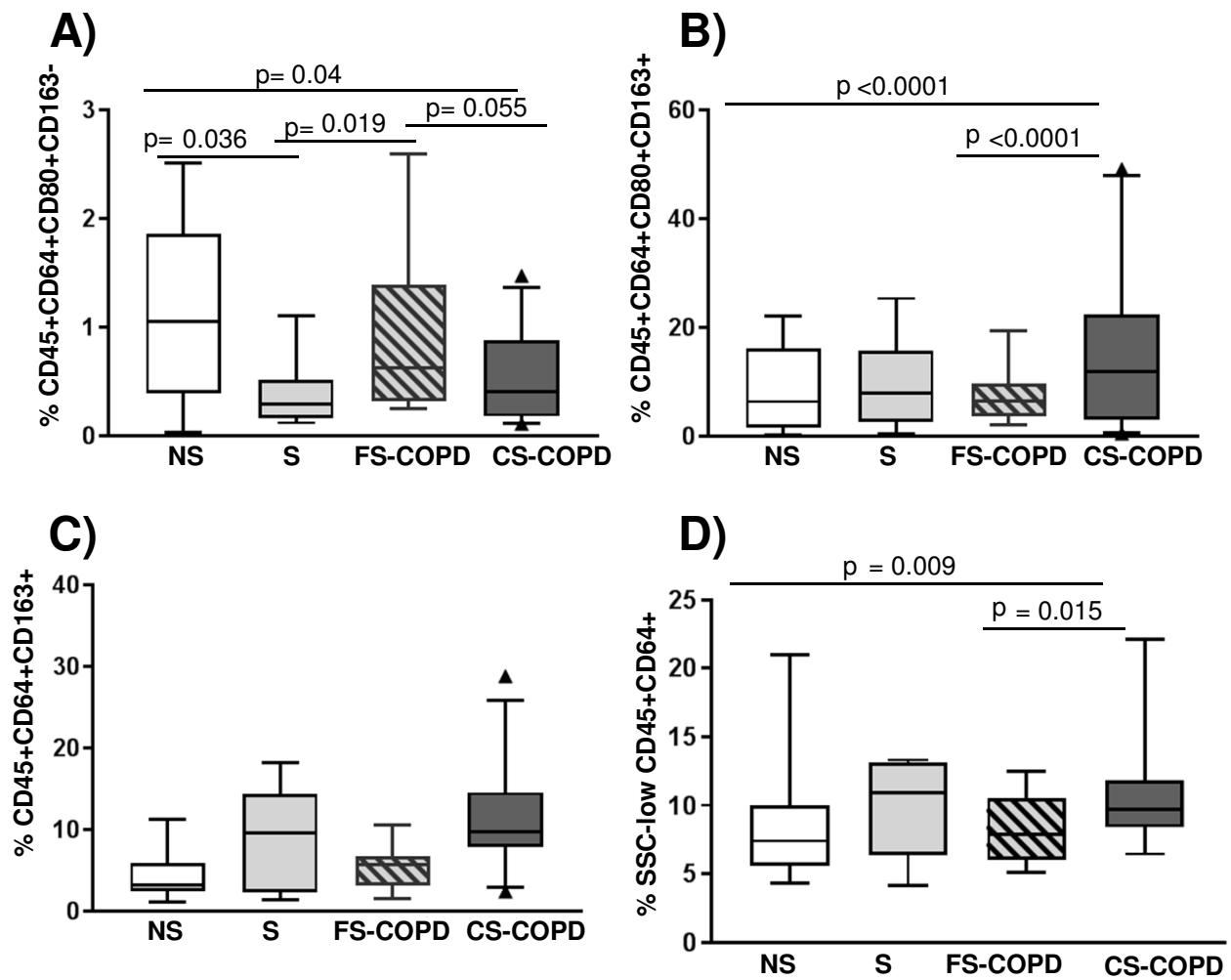


Figure S8

MODULE	MAIN GENE ONTOLOGIES				
Tan	0.00282 (0.0303)	0.02831 (0.4627)	0.00288 (0.0628)	0.00478 (0.2075)	- Phospholipid catabolism - Iron ion transport
Greenyellow	0.00230 (0.1169)	-0.04444 (0.2990)	0.00178 (0.3087)	0.00853 (0.0403)	- Collagen metabolism - Extracellular matrix organization
Yellow	-0.00112 (0.4047)	-0.00724 (0.8531)	-0.00098 (0.5358)	-0.00326 (0.3973)	- Cilium organization
Royalblue	-0.00162 (0.2068)	-0.01804 (0.6296)	-0.00184 (0.2257)	-0.00232 (0.5308)	- T cell activation
Lightcyan	0.00376 (0.0074)	-0.00896 (0.8321)	0.00498 (0.0024)	0.00168 (0.6874)	- mRNA processing
Blue	0.00264 (0.0757)	0.01240 (0.7765)	0.00400 (0.0207)	-0.00104 (0.8092)	- Regulation of translation - ER to Golgi ves-med transport
Lightcyan	-0.00232 (0.1039)	0.01705 (0.6840)	-0.00308 (0.0663)	-0.00262 (0.5274)	- Proteasomal protein catabolism
Salmon	-0.00183 (0.1936)	0.03392 (0.4085)	-0.00216 (0.1936)	-0.00321 (0.4298)	- Negative Regulation of translation
	MΦ	MΦ CD80+	MΦ CD163+	MΦ CD80+CD163+	

Figure S9