

ONLINE SUPPLEMENT

Timing of blood sample processing affects the transcriptomic and epigenomic profiles in CD4⁺ T-cells of atopic subjects

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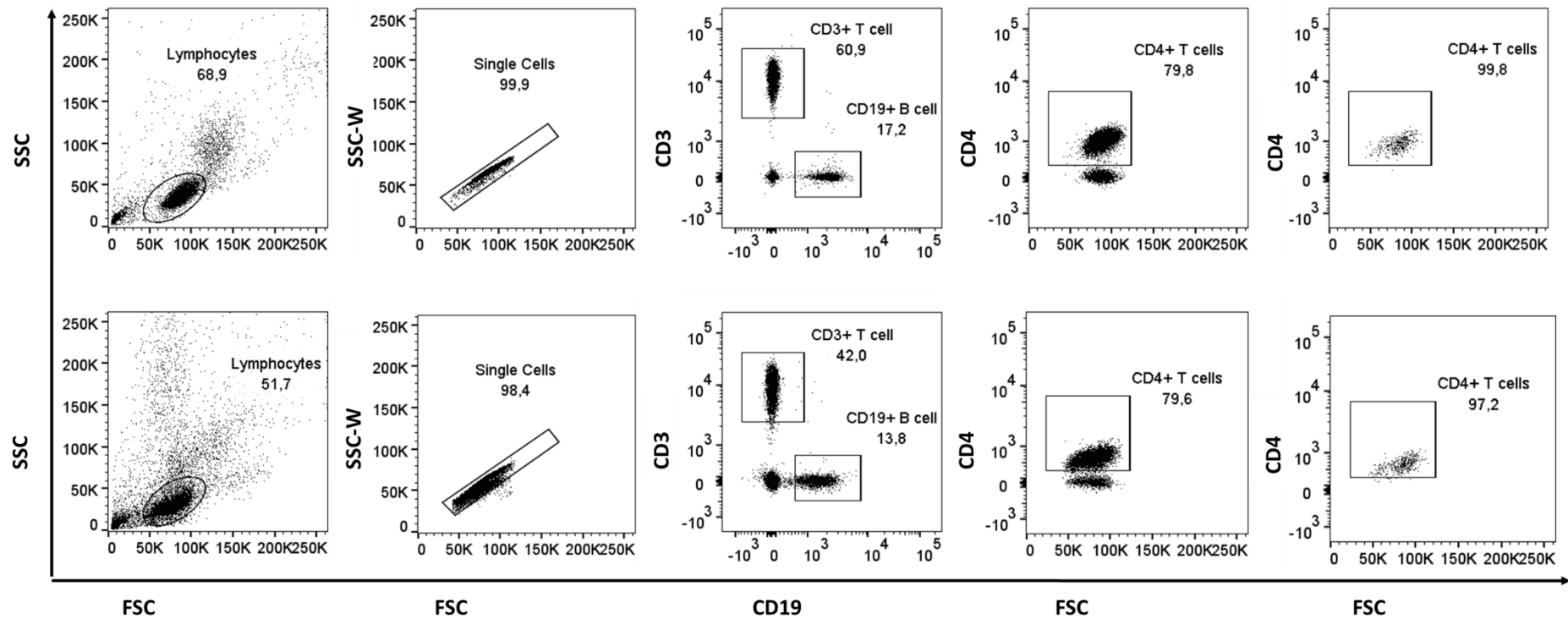
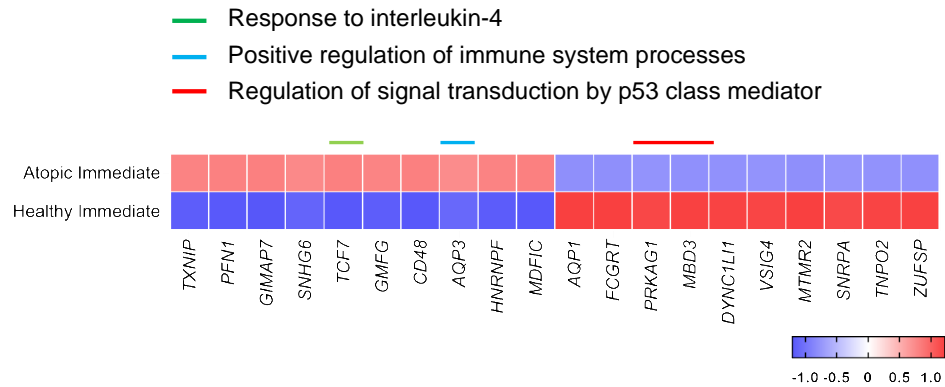
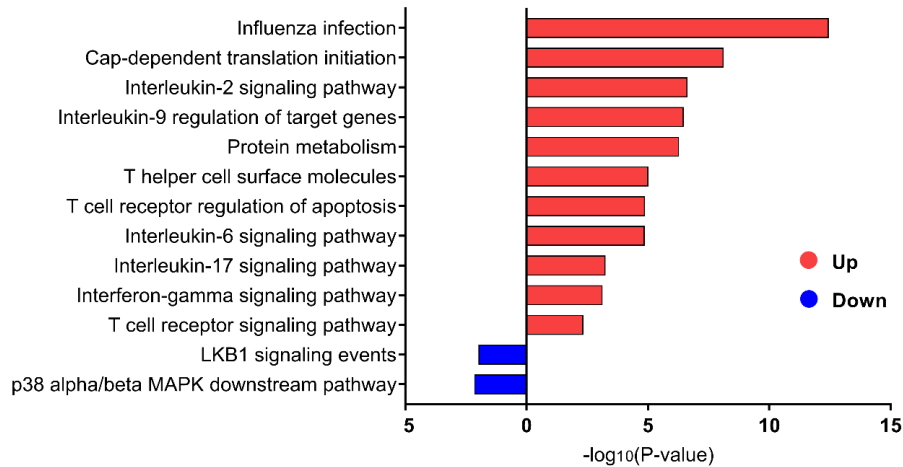


Figure S1. Gating strategy for sorting of CD3⁺CD4⁺ T-cells. Stepwise gating is exemplarily indicated from left to right showing plots of related samples from one atopic subject with immediate and delayed processing. The purity of the sorted CD3⁺CD4⁺ T-cells used for the analyses is shown in the last plot to the right.

A GO terms of the 10 top significant up- and down-regulated genes of Atopic vs. Healthy (Immediate)



B Biological pathways affected by differentially expressed genes of Atopic vs. Healthy (Immediate)



C Associated genes of 3 selected pathways

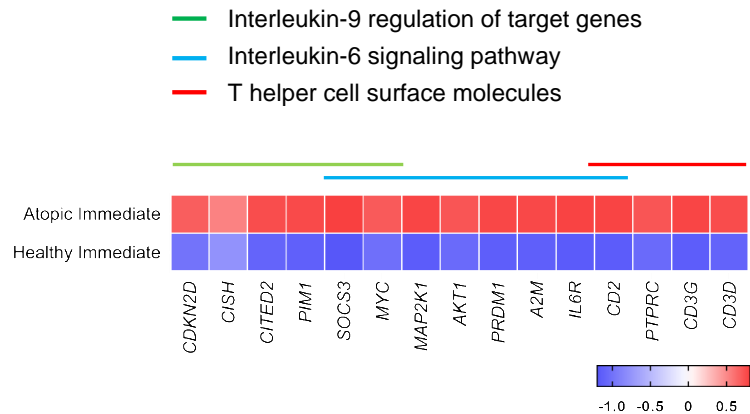


Figure S2. Biological processes and pathways affected by the differentially expressed genes in immediately processed CD4⁺ T-cells in atopic versus healthy. (A) Heatmap depicting the top 10 significant up- and down-regulated genes of immediately processed CD4⁺ T-cells in atopic versus healthy subjects alongside with their associated biological processes (GO Terms). **(B)** Biological pathways affected by up- and down-regulated genes of the previous comparison using a significance cut-off of $p < 0.05$, and **(C)** heatmap showing three selected biological pathways (indicated by colored lines) and their associated genes.

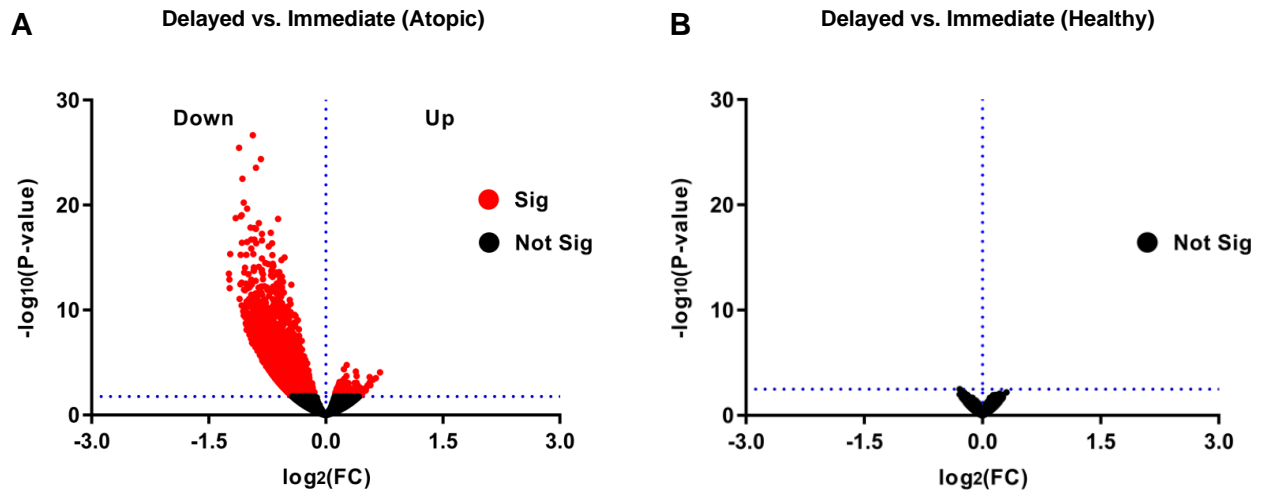


Figure S3. Differential gene analysis of H3K27ac ChIP-Seq analysis in delayed versus immediately processed blood-derived CD4⁺ T-cells. Volcano plots depicting genes associated with differential H3K27 acetylation identified by ChIP-Seq analyses (significance cut-off at FDR < 0.1) of delayed versus immediately processed blood-derived CD4⁺ T-cells from **(A)** atopic and **(B)** healthy subjects.