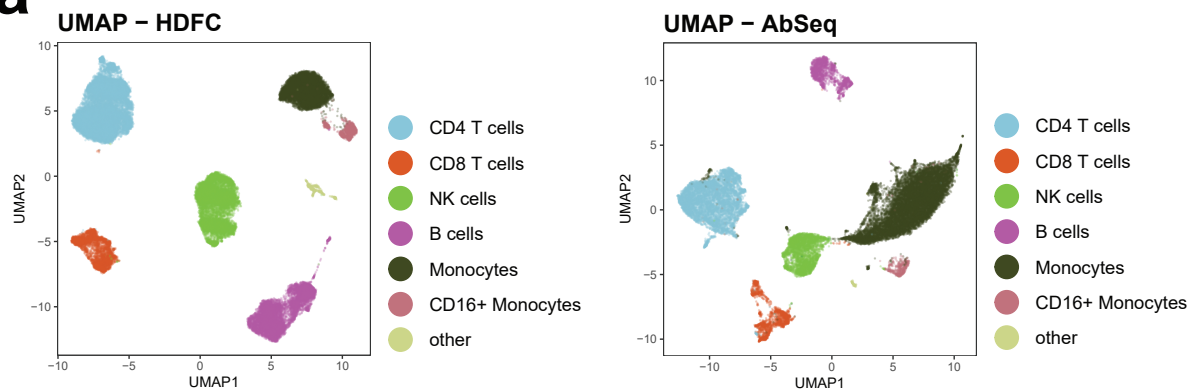
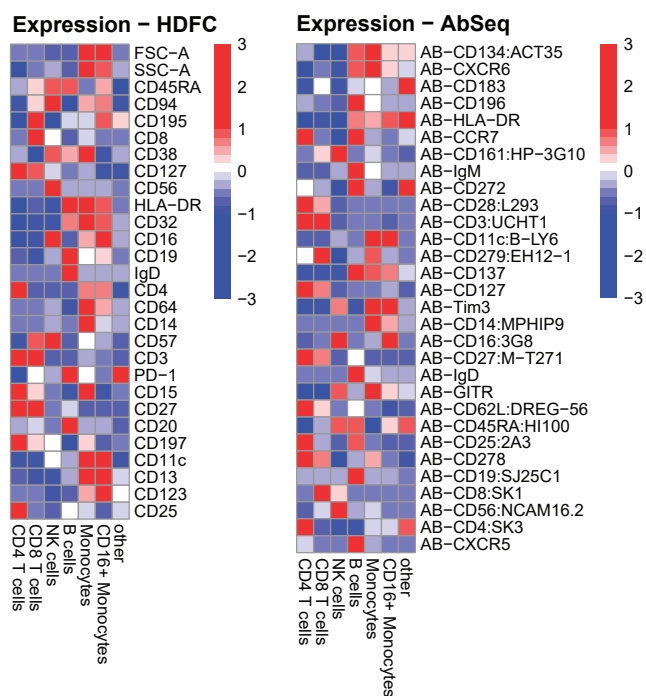


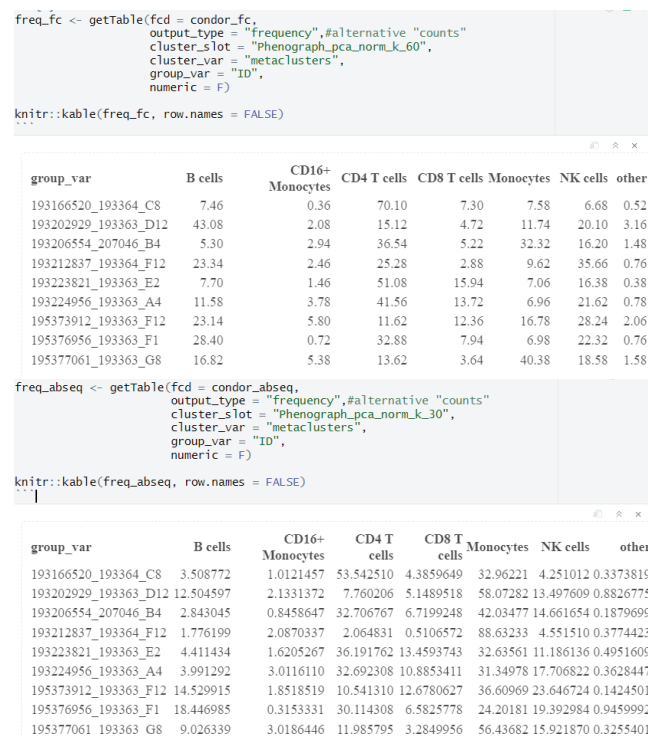
a



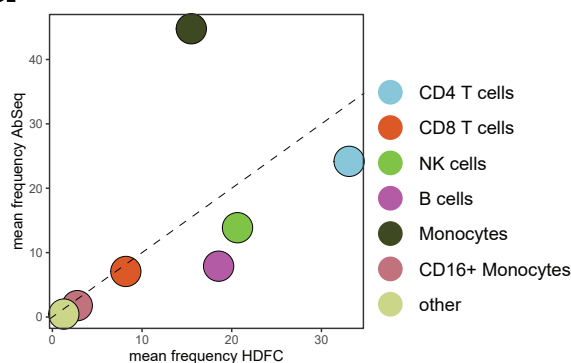
b



c



d



Supplementary Data 10: Exemplification of the cyCONDOR capabilities in the comparison between samples measured with multiple modalities. In this example the same samples were measured with both HDFC and AbSeq (CITE-seq). Thanks to the unified ecosystem provided by cyCONDOR is possible to easily compare the results of the two modalities. After data loading, batch correction, dimensionality reduction and clustering each dataset was annotated. **a:** UMAP dimensionality reduction of both dataset (HDFC left and AbSeq right) coloured by cell type. At this level is already possible to notice how the Monocytes cluster appears to be larger in AbSeq data compared to HDFC. **b:** Heatmap visualisation of marker expression: with a simple built-in cyCONDOR function is possible to plot marker expression of both modalities, here we can see a strong agreement between marker expression in the two modalities. **c:** From each condor object simple tabular summary results can be exported with cyCONDOR built-in function. Here with a single function (getTable) we export the cellular frequencies for each modality, those tables can be easily used to directly compare the result. **d:** Dotplot showing the correlation between the mean frequencies measured by HDFC and those recorded by AbSeq. Interestingly there is an increased frequency of monocytes and a decreased frequency of lymphocytes (B cells, NK cells CD4 T cells) in AbSeq data. This phenomenon can be explained by that in this dataset the cell calling of the cells is based on mRNA content. Due to the lower mRNA content of lymphocytes and the relatively bad quality of the sample (long-term storage) a loss of lymphocytes in favour of monocytes can be observed. This type of comparative analysis can be easily performed in cyCONDOR without the need of further tools.