Supplementary Material

Fig. S1. Automatic Gating Strategy. (A) Lymphocytes were gated automatically, based upon a 2-dimensional curvature filter on forward scatter vs. side scatter parameters to exclude non-lymphoid cells (flowCore method *curv2Filter*, Hahne et al. 2009). (B) B lymphocytes were selected using an automatic range gate on CD19 (flowCore method *rangeGate*, Hahne et al. 2009). Shown are univariate histogram plots for each time point. The automatically selected threshold separating $CD19^+$ lymphocytes from $CD19^-$ lymphocytes is shown as a vertical line through all of the plots.

Fig. S2. Visualization of increased or decreased subsets in longitudinal studies. The lymphocyte gate was applied in all samples. $CD19^+$ lymphocytes were then analyzed by CF. Bivariate plots showing events in bins that are increased or decrease by 4-fold or greater relative to baseline. Each row of bivariate plots corresponds to a single time point in the study. The overall bivariate density is shown in the gray background of each panel. Superimposed on that are dots showing events in bins whose event density is increased (red) or decreased (blue) by 4-fold or greater relative to baseline.

Supplementary Material (cont.)

Fig. S3. Comparison of fingerprints using different baseline models. The left-hand panel shows fingerprints determined using the aggregate of the two baseline samples as the model (BL1+BL2), as discussed in the manuscript and shown in Figure 4A. The middle and right-hand panels show fingerprints determined using only Baseline 1 (BL1) or Baseline 2 (BL2) samples as the model, respectively. In the middle and right-hand panels, the sample used for the binning model shows a flat fingerprint, as expected. Prominent features of the post-transplant samples are recapitulated irrespective of which binning model was used.

Fig. S4. Fingerprints of a second transplant patient. Four baseline samples (BL1-BL4) were obtained over a one-year time period and were used to create the baseline binning model as described in section 3.2. The time points are listed as days following pancreatic islet transplantation.

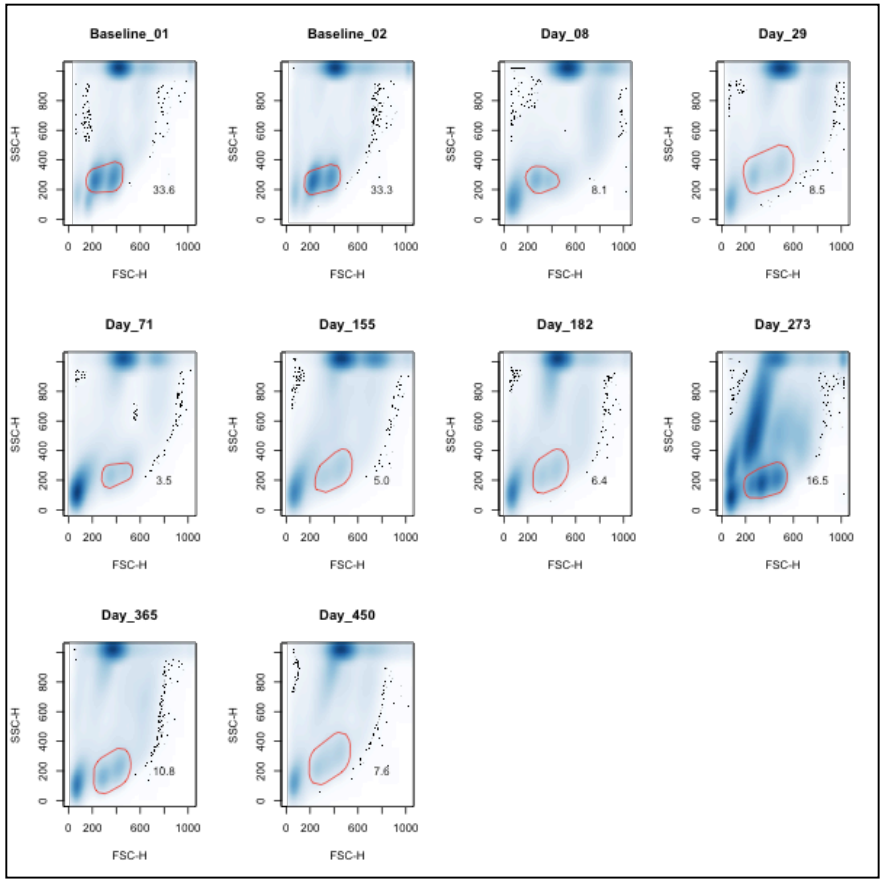
Supplementary Material (cont.)

Reference:

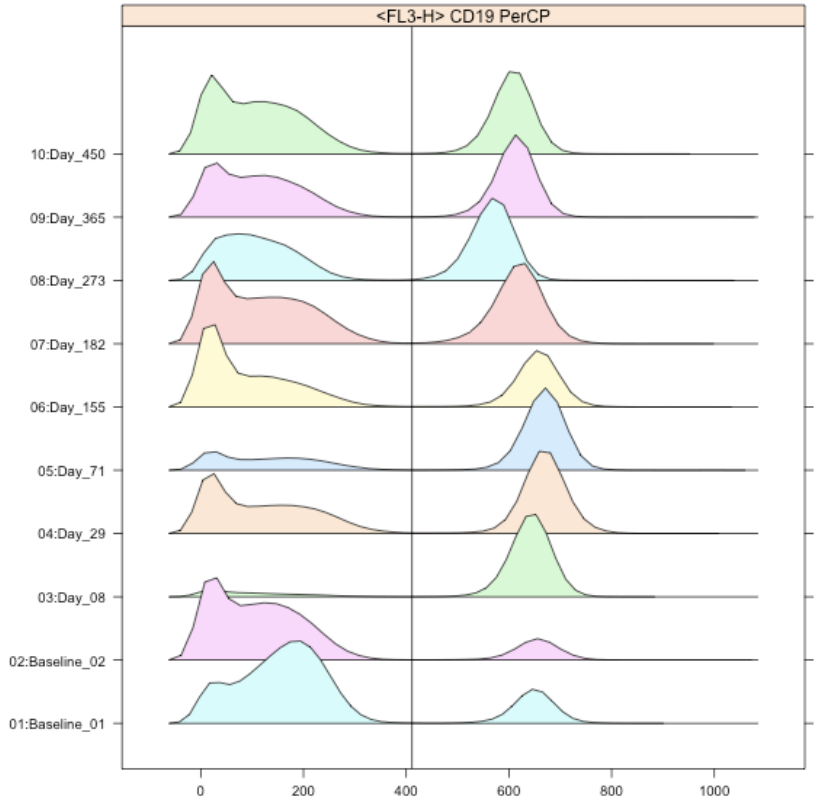
Hahne, F., LeMeur, N., Brinkman, R.R., Ellis, B., Haaland, P., Sarkar, D., Spidlen, J., Strain, E. and Gentleman, R., 2009. flowCore: a Bioconductor package for high throughput flow cytometry. BMC Bioinformatics 10, 106.

Supplementary Fig. S1

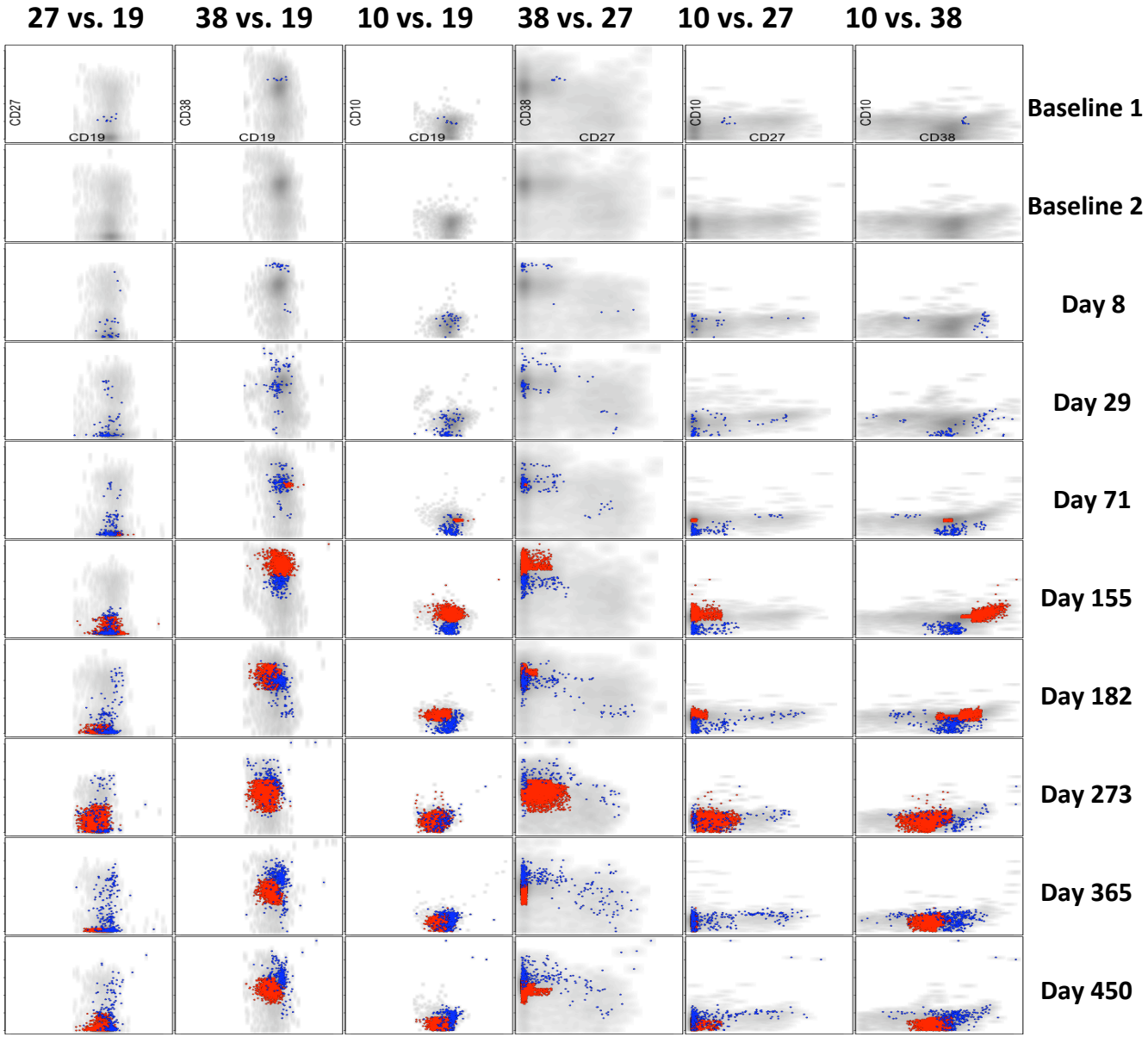
A



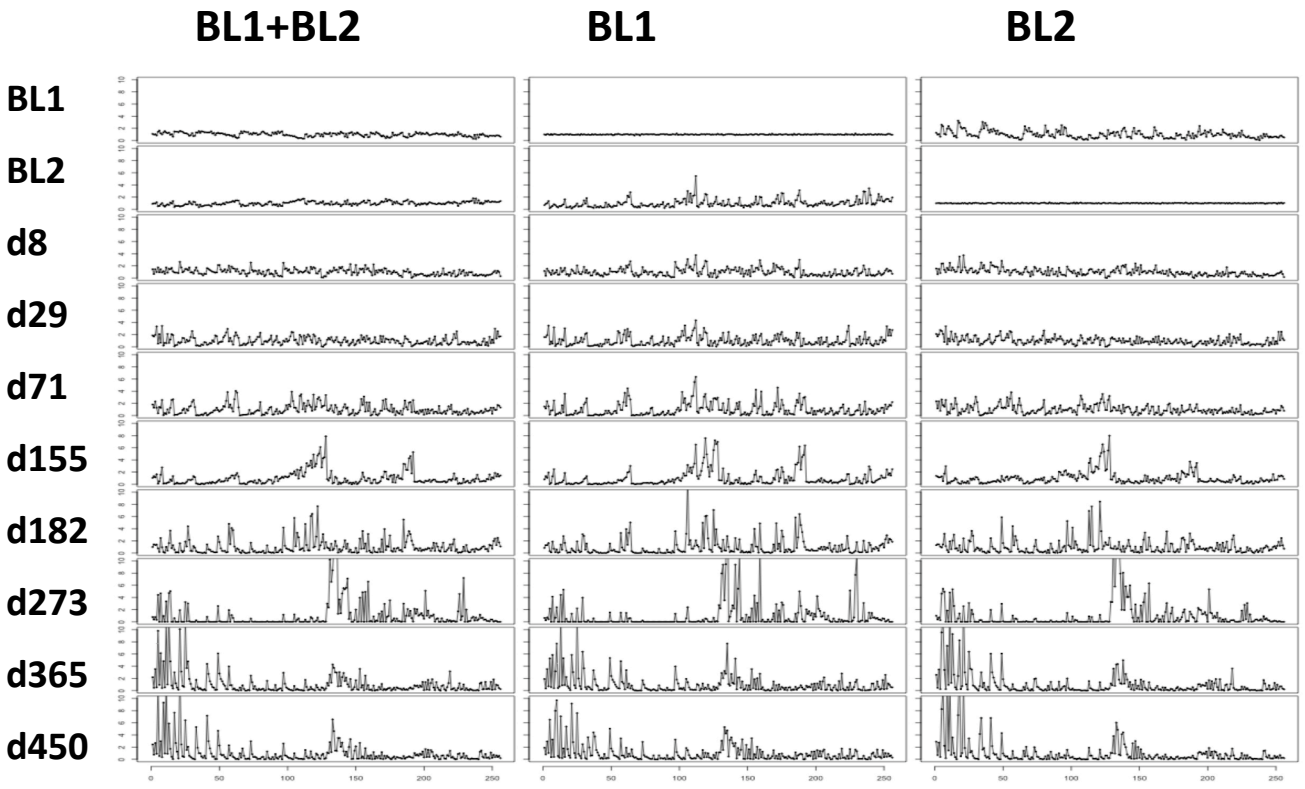
B



Supplementary Fig. S2



Supplementary Fig. S3



Supplementary Fig. S4