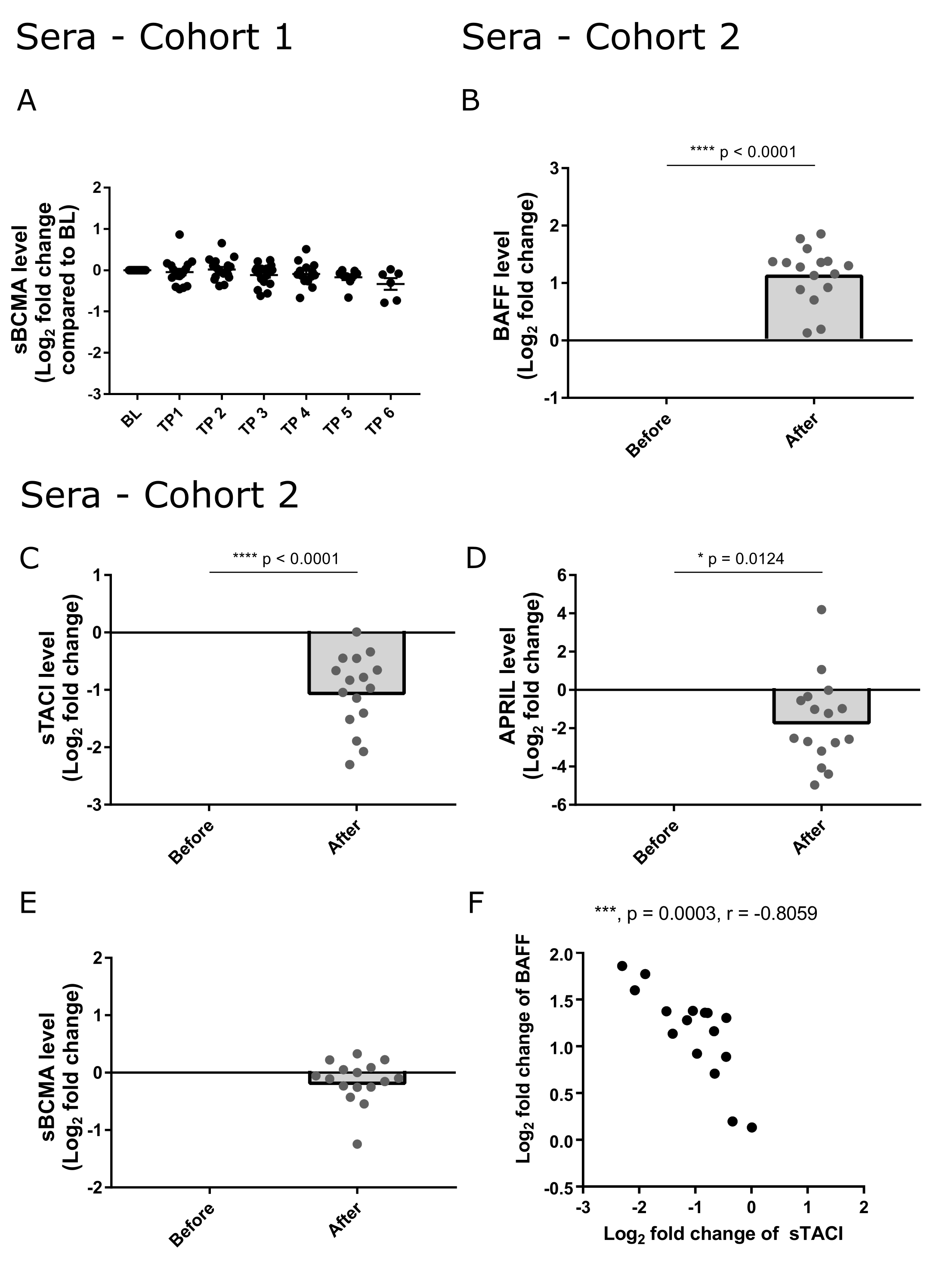
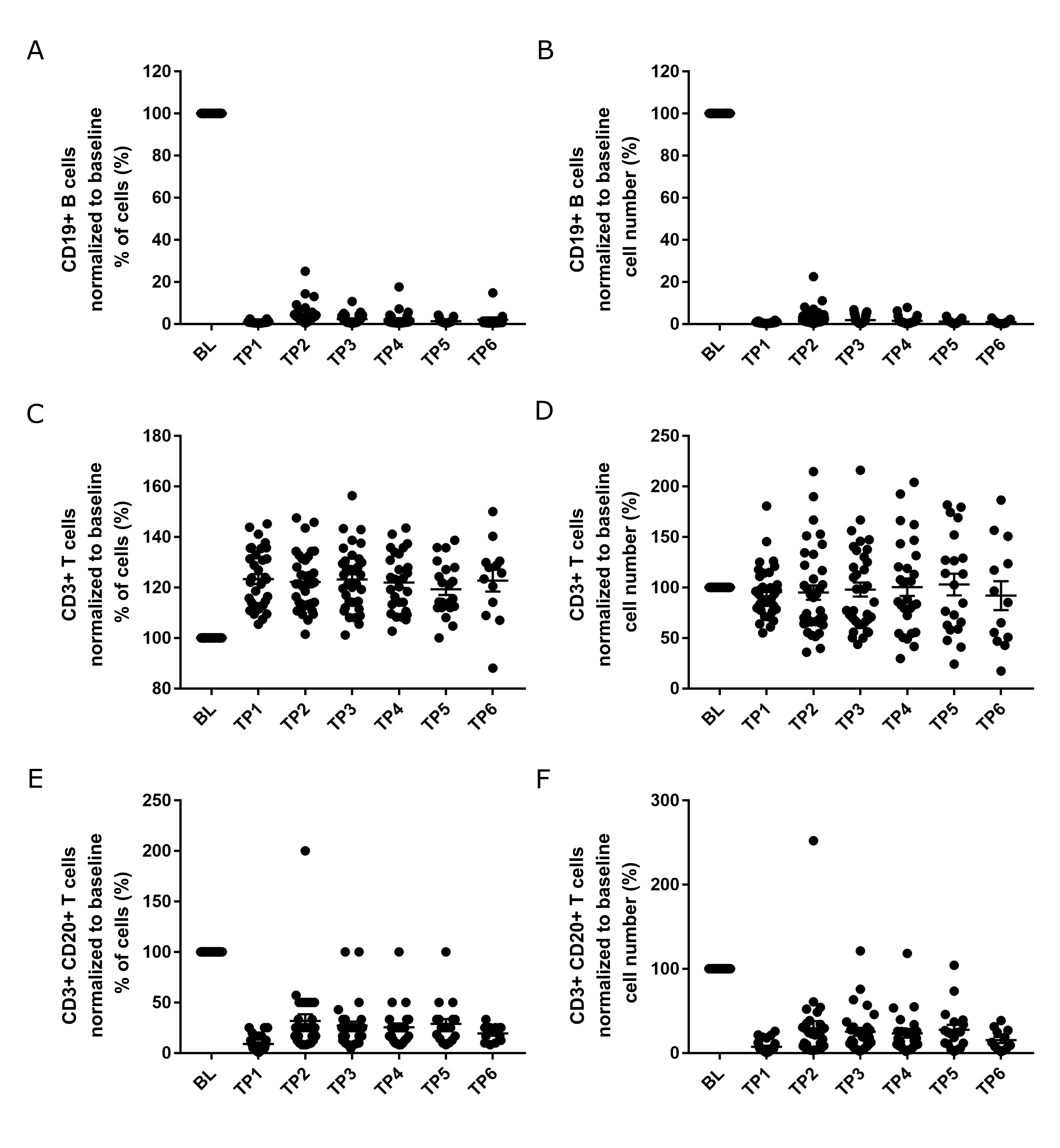
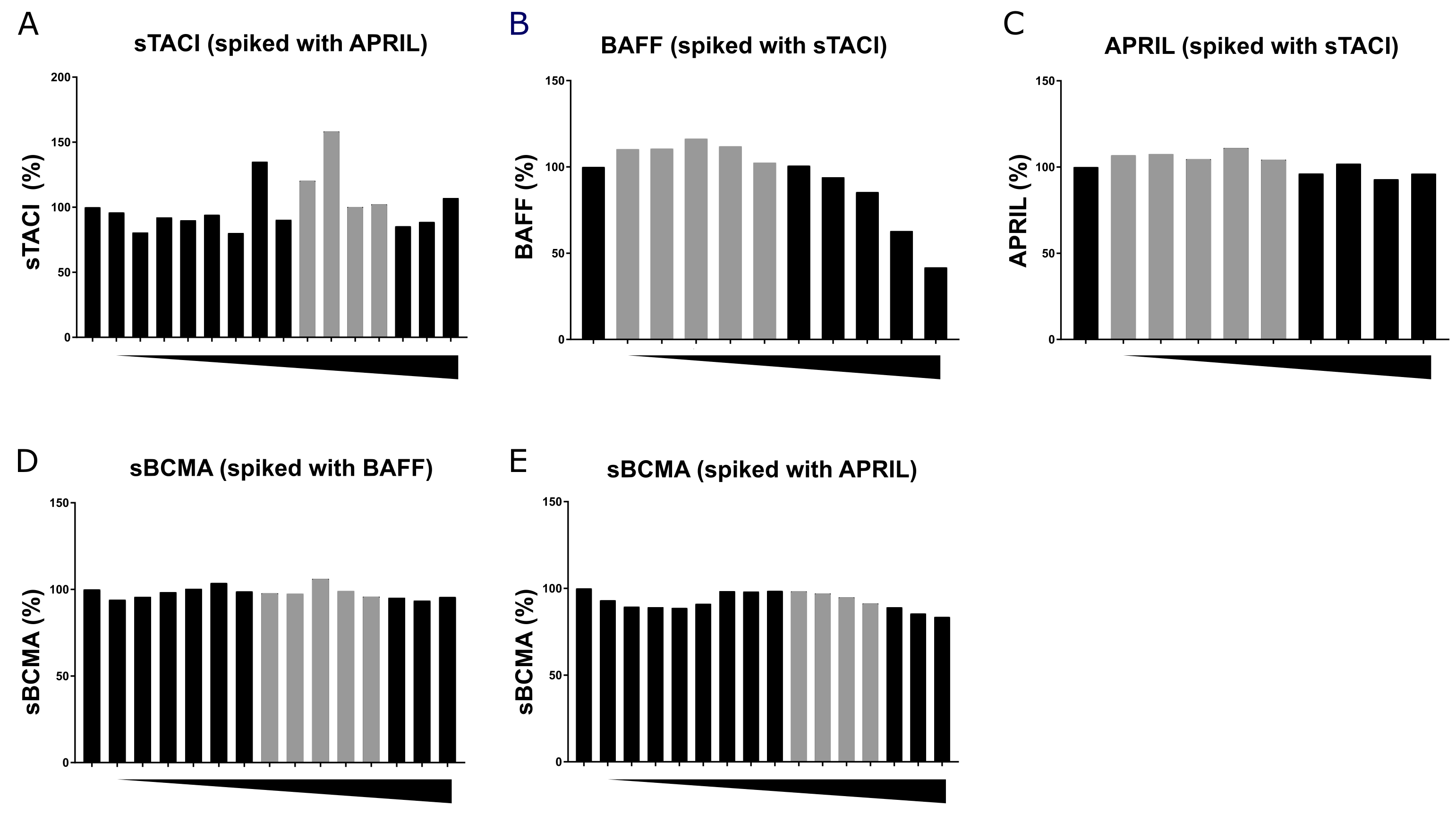
**eFigure 1: Effect of ocrelizumab treatment on lymphocyte subsets.** Lymphocyte subsets were analyzed from the patient cohort 1 longitudinally by FACS at baseline (BL; n=36), TP1 (mean 17 days; n=34), TP2 (mean 6 months; n=36), TP3 (mean 12.9 months; n=35), TP4 (mean 19.8 months; n=28), TP5 (mean 25.6 months; n=23) and TP6 (mean 31.2 months; n=13). We set the baseline values for each patient as 100 % and calculated the relative levels of the lymphocyte subsets (CD19+ B cells in Fig. 1A, CD3+ T cells in Fig 1B, CD3+CD20+ T cells in Fig. 1C). Raw values are provided in eTable 3. The data are shown as % of all lymphocytes (left) or as absolute cell count per µl (right). When the measured values were below 1 %, we used 0.5 % as a surrogate value. When there were no cells detectable, we used 0.1 % as surrogate. Data are given as arithmetic mean ± standard error of the mean (SEM).



**eFigure 2: Effect of ocrelizumab treatment on components of the BAFF/APRIL system in serum of patients.**

Serum levels of sBCMA (A) were evaluated from patient cohort 1 by ELISA from 17 patients receiving ocrelizumab at baseline (BL) (n=17), TP1 (mean 18 days; n=17), TP2 (mean 6.7 months; n=17), TP3 (mean 12.9 months; n=17), TP4 (mean 19.1 months; n=14), TP5 (mean 25.2 months; n=10) and TP6 (mean 31.3 months; n=7). Serum levels of BAFF (B), sTACI (C), APRIL (D), sBCMA (E) were evaluated in the patient cohort 2 (n=16) at baseline and after ocrelizumab treatment (12 to 19 months). Raw values are provided in eTable 3. Data are presented as log2 fold change compared to baseline. We performed a one-sample t test to compare baseline and follow up samples. p-values are shown if they were < 0.05. Data are given as arithmetic mean ± standard error of the mean (SEM). Negative correlation between BAFF and sTACI levels are shown by the Pearson correlation analyses of log2 fold change of BAFF to log2 fold change of sTACI in serum of patient cohort 2 (F).



**eFigure 3: Spiking experiments: interference of complex formation on protein detection.**

**(A)** The detection of sTACI (500 pg/ml) was evaluated with the addition of APRIL from 30 ng/ml to 0 ng/ml. **(B)** BAFF (300 pg/ml) detection was evaluated with the addition of sTACI from 6000 pg/ml down to 0 pg/ml. **(C)** APRIL (1500pg/ml) detection was evaluated with addition of sTACI from 6000 pg/ml to 0 pg/ml**.** **(D)** The detection of sBCMA (20 ng/ml) was evaluated with addition of BAFF from 15ng/ml to 0 ng/ml-and **(E)** APRIL from 30 ng/ml to 0 ng/ml**.** The triangles below the x-axes represent titration of interaction partners added to the samples. The data is presented in % of detection compared to the sample detection without interaction partners. The bars in grey represent physiological levels of the spiked APRIL (A), sTACI (B,C), BAFF (D) and APRIL (E).