SUPPLEMENTAL FIGURES

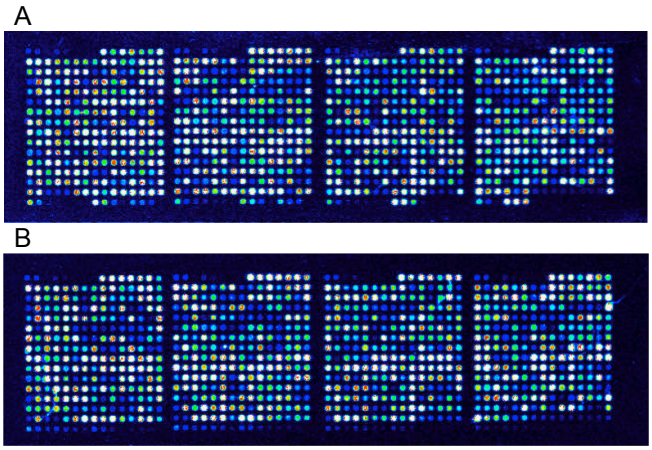

Figure S1. Anti-HIS (A) and anti-HA (B) probing of PF11+ chip

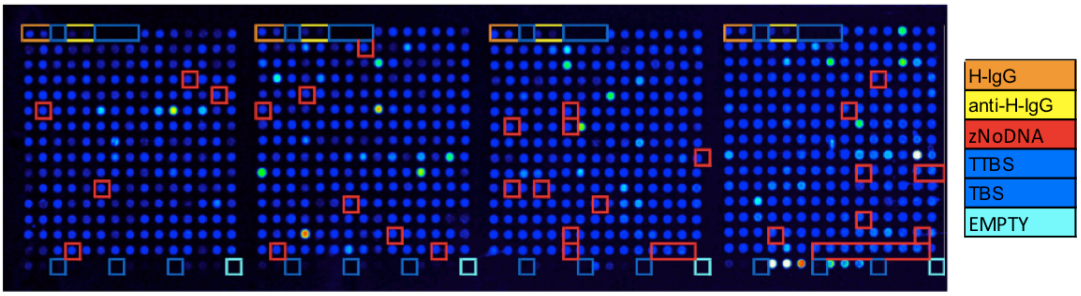

Figure S2. Control spot distribution in PF11+ chip

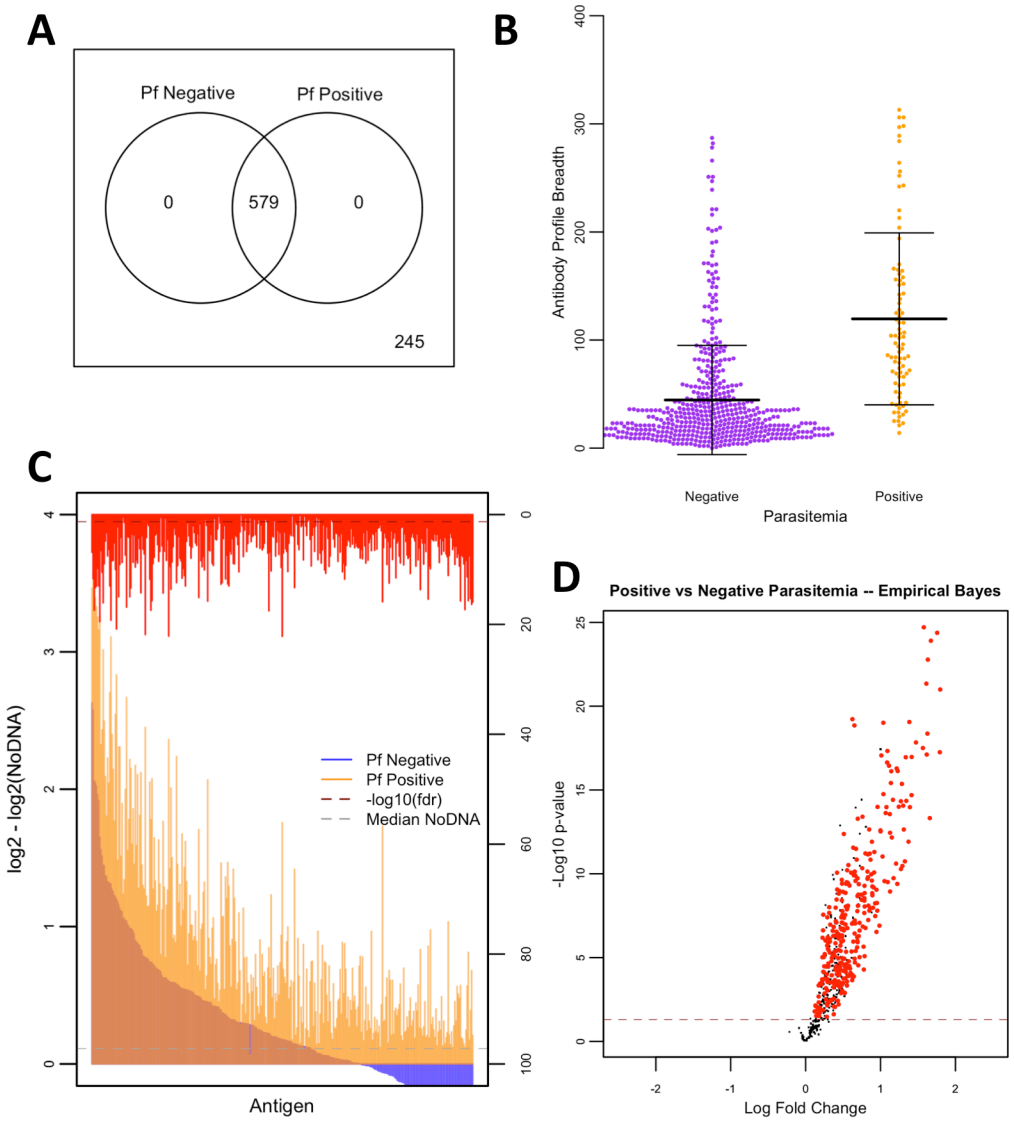

Figure S3. Antibody reactivity, breadth and magnitude profiles by parasitemia group
A) Antigen reactivity between parasitemia status is shown by Venn diagram with non-reactive antigens shown outside of the circles and shared antigens shown within the circles. B) Antibody breadth profiles are shown in boxplots with measurements as antibody breadth scores (P < 1E-15). C) A bar graph of antibody levels between parasitemia groups is represented by colored overlapping bars for each antigen, sorted by antibody level in the parasite negative group, and the red bars on the alternative y-axis represent inverse adjusted P-values with the dashed red line representing the significance threshold. The grey dashed line represents median noDNA levels. D) The volcano plot shows inverse unadjusted P-values plotted against fold change. Red dots appearing to the right of zero fold change represent significant antigens after adjustment favoring the parasitemic children, while those appearing to the left represent significant antigens after adjustment favoring the parasite negative children. The red dashed line represent the threshold of statistical significance (P = 0.05).

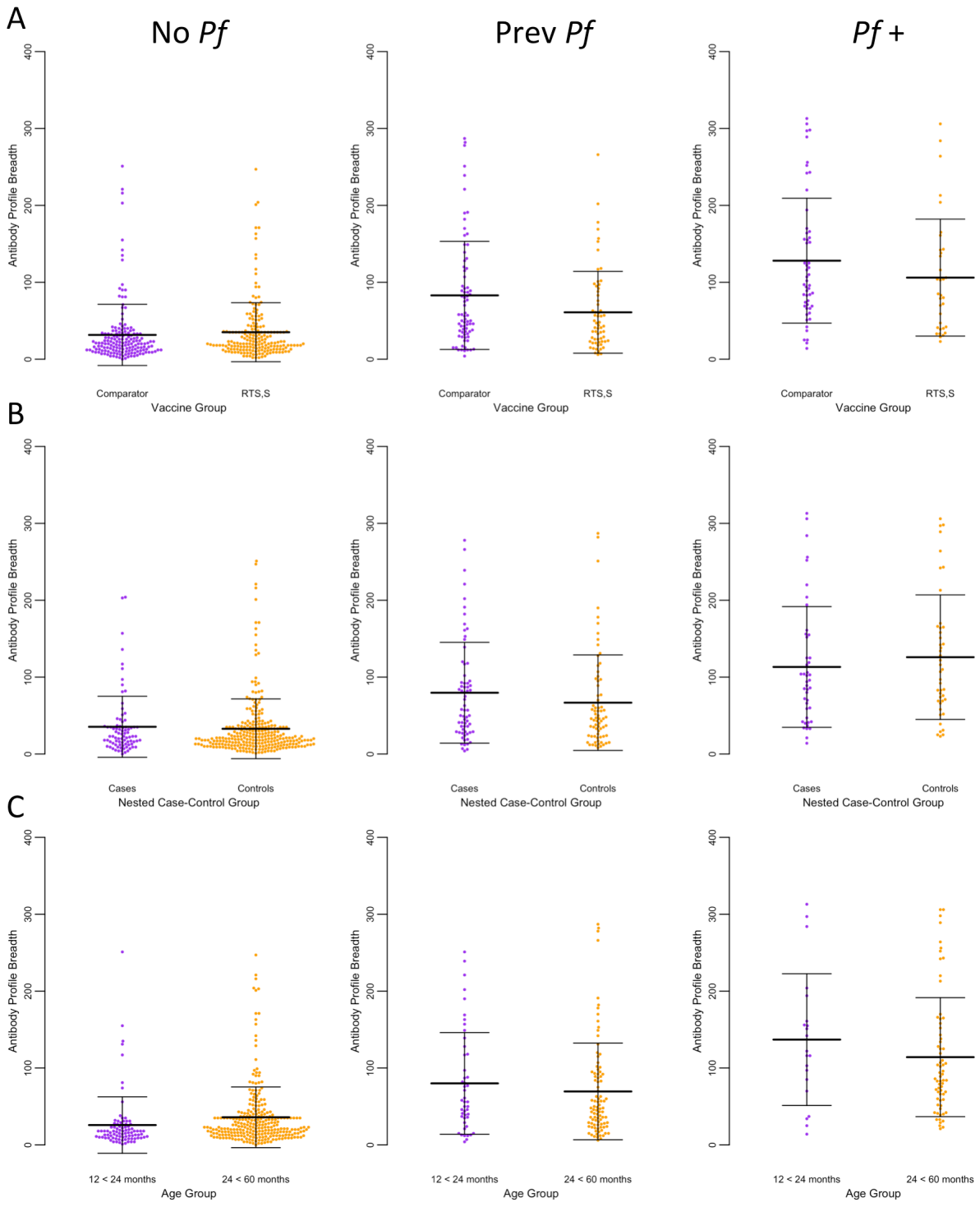

Figure S4. Antibody breadth by exposure group
Antibody breadth was stratified by the following exposure groups: children with no documented malaria exposures (No *Pf*), children with documented exposures to malaria during the 6 month surveillance period prior to sampling (Prev *Pf*) and children with exposure to malaria, or parasitemia at the time of sampling (*Pf* +). Dotplots plots show

antibody breadth score on the y-axis with means and standard deviation error bars and the following comparison groups on the x-axis: A) RTS,S and Comparator vaccinees; B) nested cases (subsequent cases of malaria) and controls (no subsequent cases of malaria); and C) age groups.

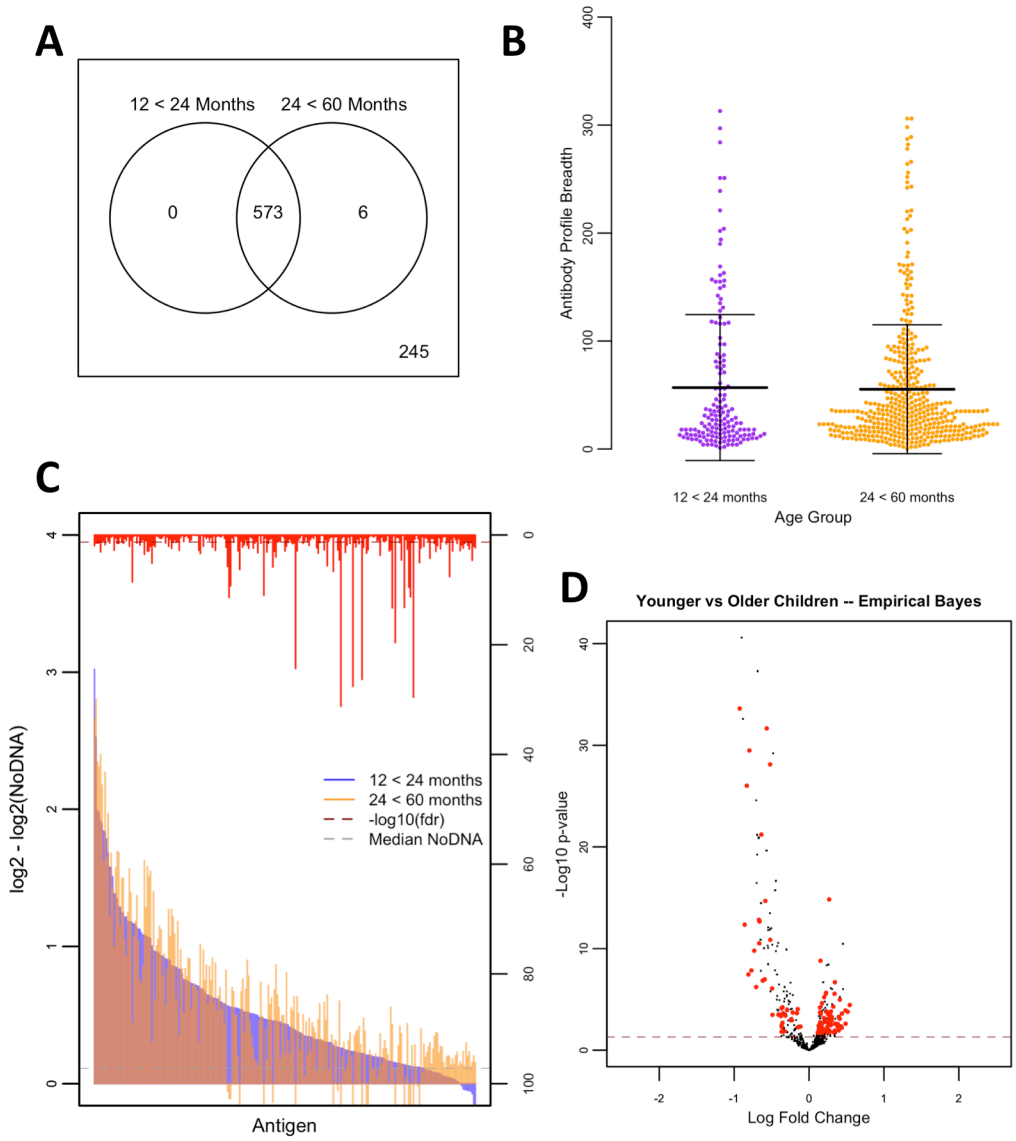

Figure S5. Antibody reactivity, breadth and magnitude profiles by age group
A) Antigen reactivity between age groups is shown by Venn diagram with non-reactive antigens shown outside of the circles and shared antigens shown within the circles. B) Antibody breadth profiles are shown in dotplots with measurements as antibody breadth scores (P = 0.02). Means are displayed with standard deviation error bars. C) A bar graph of antibody levels between age groups is represented by colored overlapping bars for each antigen, sorted by antibody level in the younger age group, and the red bars on the alternative y-axis represent inverse adjusted P-values with the dashed red line representing the significance threshold. The grey dashed line represents median noDNA levels. D) The volcano plot shows inverse unadjusted P-values plotted against fold change. Red dots appearing to the right of zero fold change represent significant antigens after adjustment favoring the older age group, while those appearing to the left represent significant antigens after adjustment favoring the younger age group. The red dashed line represent the threshold of statistical significance (P = 0.05).

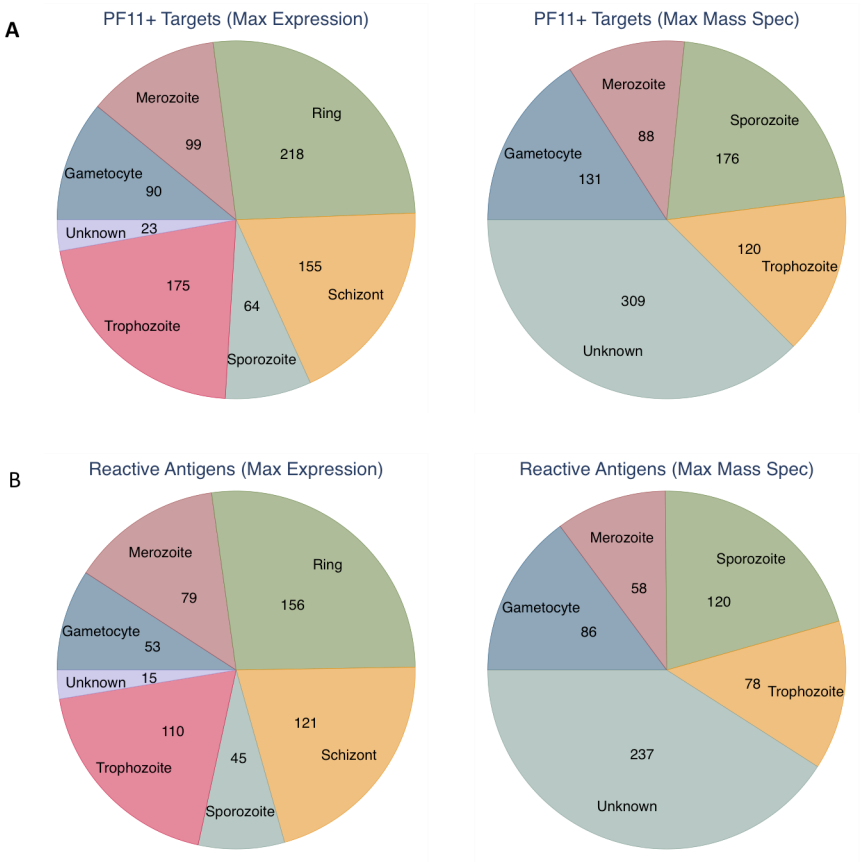

Figure S6. *P. falciparum* stage-specific distribution of target probes
The life cycle stages corresponding to the PF11+ chip target probes (A) are shown by maximum gene expression (left) and maximum mass spectrometry (right). Reactive targets above the 1% seropositivity threshold (B) are also shown.

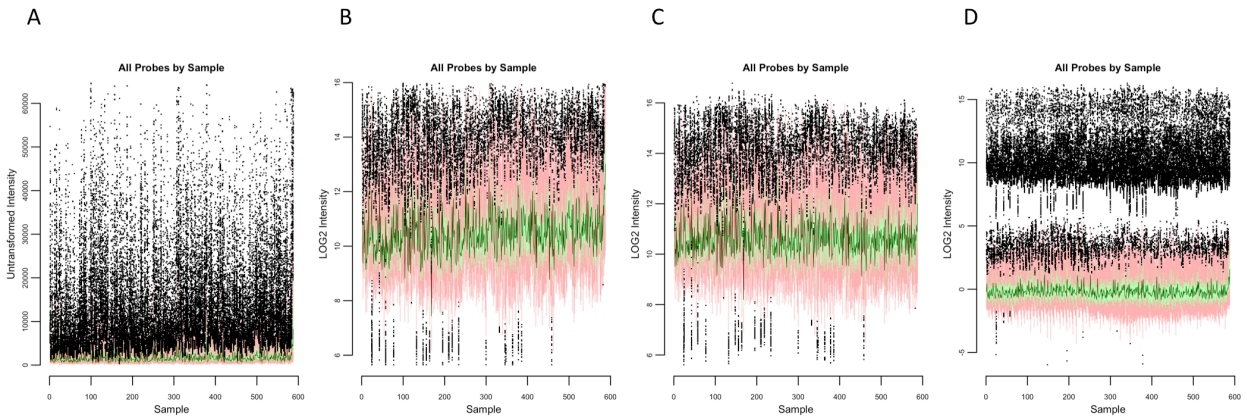

Figure S7.1. Distribution of signal intensities by sample for each step of the analysis pipeline

Signal intensities for all array probes are plotted as boxplots per sample (n=588) for A) raw data, B) Log_2-transformed data after local background adjustment, C) Linear Mixed Model-normalized data and D) data after noDNA subtraction. The upper mode of black signal intensities in (D) represents the Blank and Positive control probes, which are not affected by noDNA subtraction.

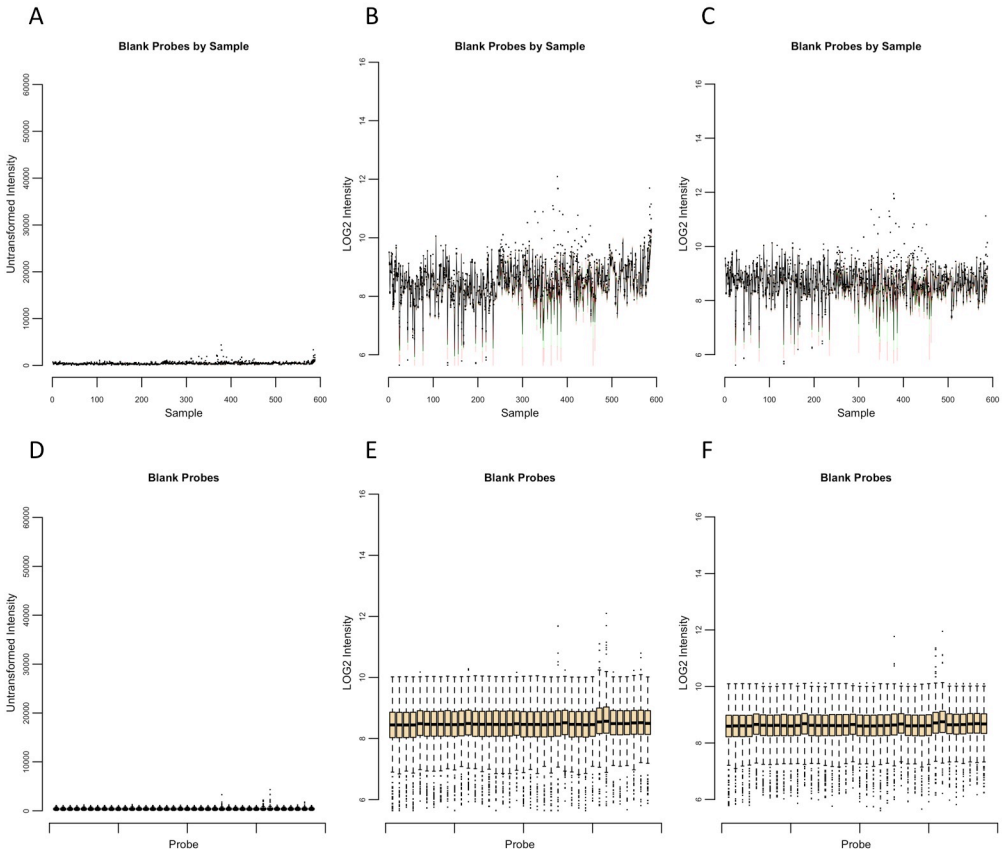

Figure S7.2. Distribution of Blank probe signal intensities

Plots (A) – (C) show signal intensities for Blank probes by sample as raw, Log_2-transformed/local background adjusted and LMM normalized data, respectively. Plots (D) – (F) represent Blank probes by probe position on the array for the same pipeline procedures. Post-noDNA subtraction is not included, since it is not applied to control probes.

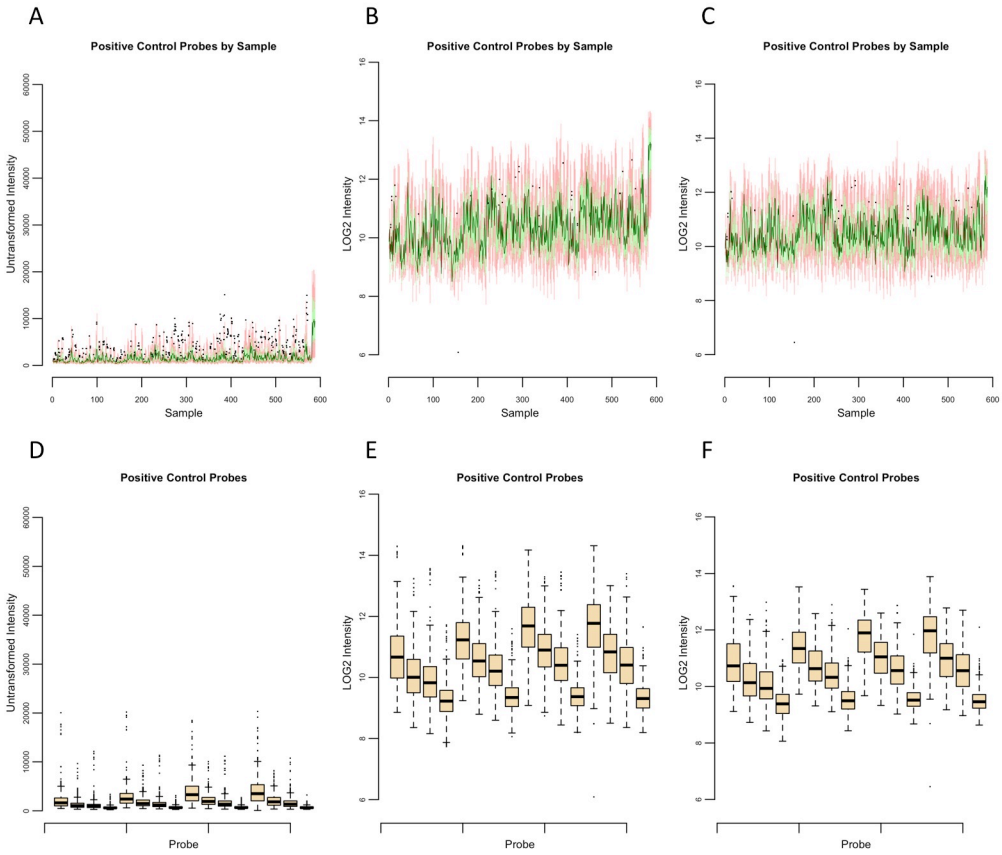

Figure S7.3. Distribution of Positive control probe signal intensities
Plots (A) – (C) show signal intensities for positive control probes by sample as raw, Log_2-transformed/local background adjusted and LMM normalized data, respectively. Plots (D) – (F) represent positive control probes by probe position on the array for the same pipeline procedures. Post-noDNA subtraction is not included, since it is not applied to control probes.

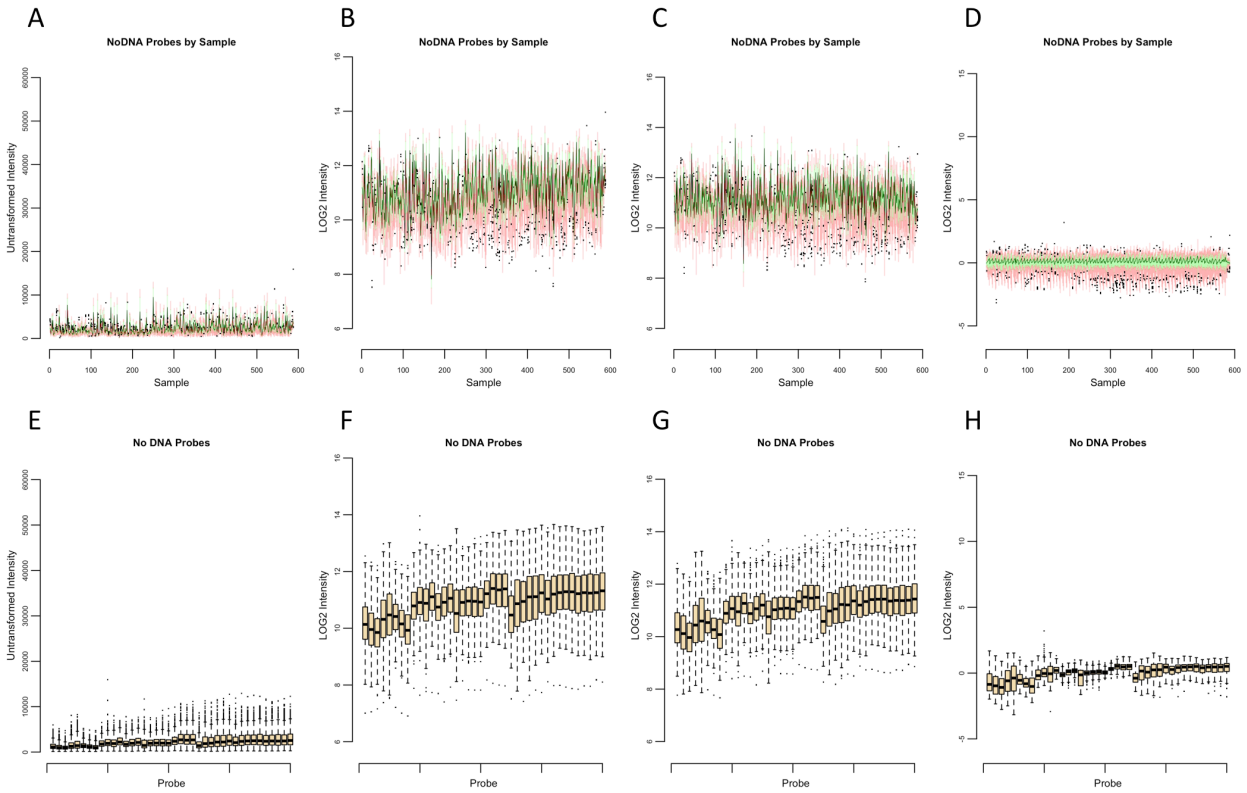

Figure S7.4. Distribution of noDNA background probe signal intensities
Plots (A) – (D) show signal intensities for noDNA background probes by sample as raw, Log_2-transformed/local background adjusted, LMM normalized and noDNA subtracted data, respectively. Plots (E) – (H) represent noDNA background probes by probe position on the array for the same pipeline procedures.

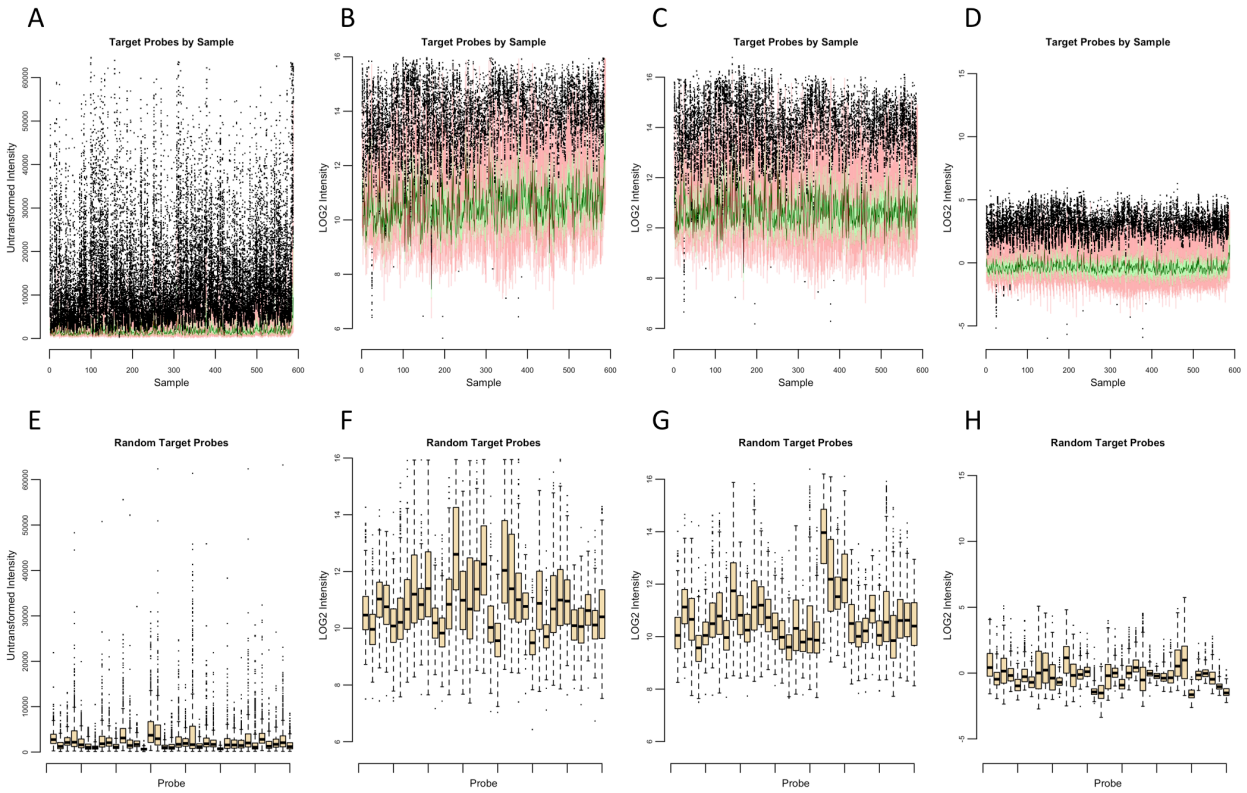

Figure S7.5. Distribution of *P. falciparum* target probe signal intensities
Plots (A) – (D) show signal intensities for *P. falciparum* target probes by sample as raw, Log_2-transformed/local background adjusted, LMM normalized and noDNA subtracted data, respectively. Plots (E) – (H) represent random target probes by probe position on the array for the same pipeline procedures, but is of limited usefulness, as the same probes are not shown across plots.

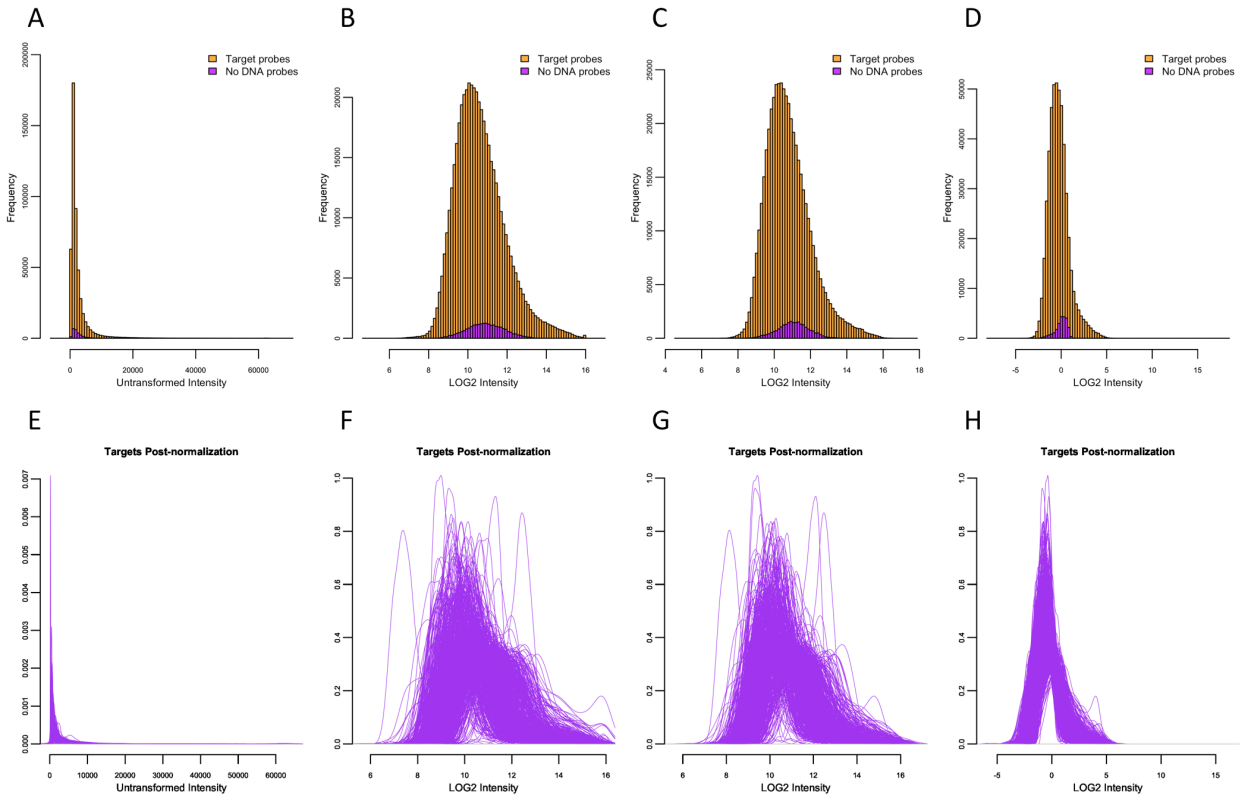

Figure S7.6. Distribution of noDNA and target signal intensities for the dataset
Plots (A) – (D) show histograms of signal intensities for target (orange bars) and noDNA background (purple bars) probes as raw, Log_2-transformed/local background adjusted, LMM normalized and noDNA subtracted data, respectively. Plots (E) – (H) show density plots of signal intensity for all probes for the same pipeline procedures, where each purple line represents a sample.

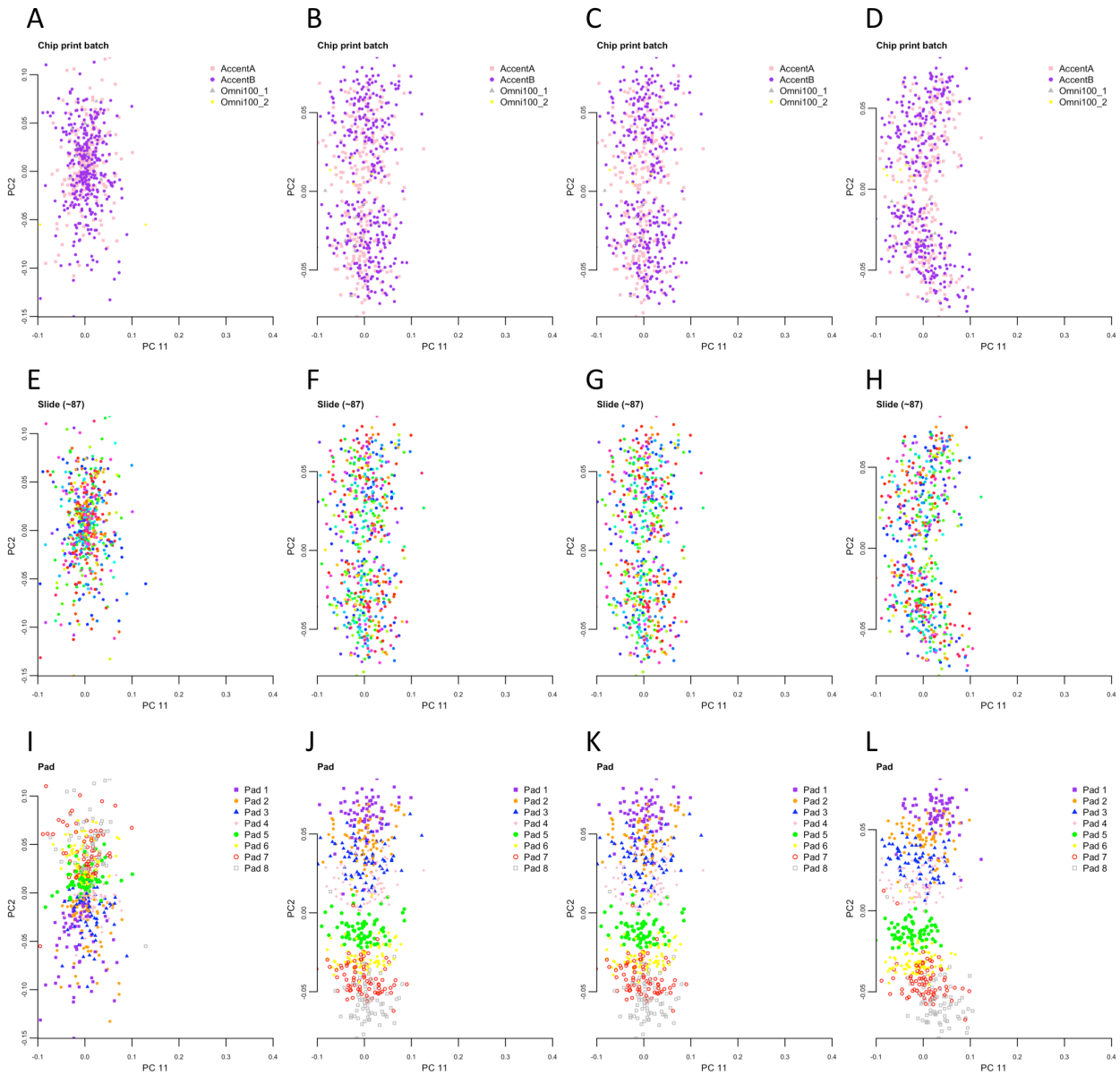

Figure S8. Principal Component Analysis of nuisance factors for each step of the analysis pipeline

Plots (A) – (D) show PCA plots of batch effects for raw, Log_2-transformed/local background adjusted, LMM normalized and noDNA subtracted data, respectively. Plots (E) – (H) show Slide effects, and plots (I) – (L) show Pad effects for the same pipeline procedures, respectively.