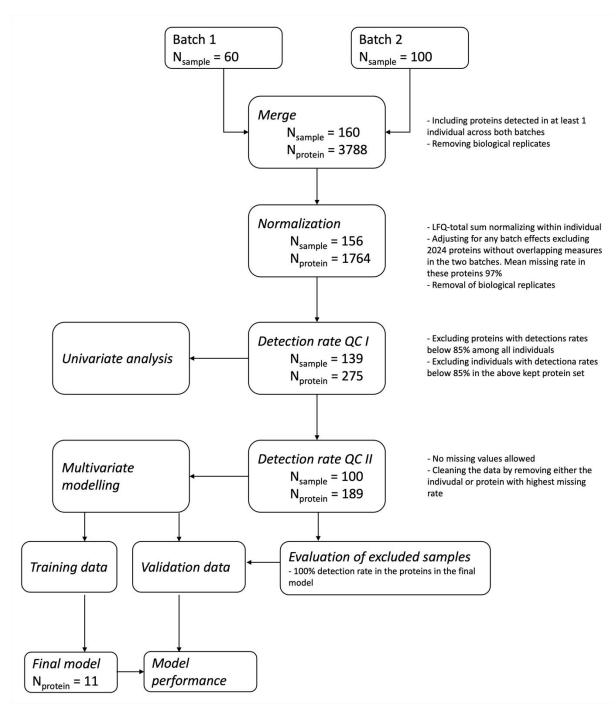
Supplemental information

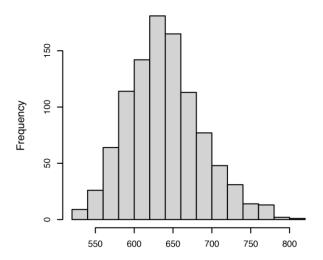
Toward ovarian cancer screening
with protein biomarkers using
dried, self-sampled cervico-vaginal fluid

Julia Hedlund Lindberg, Anna Widgren, Emma Ivansson, Inger Gustavsson, Karin Stålberg, Ulf Gyllensten, Karin Sundfeldt, Jonas Bergquist, and Stefan Enroth

Supplementary Material

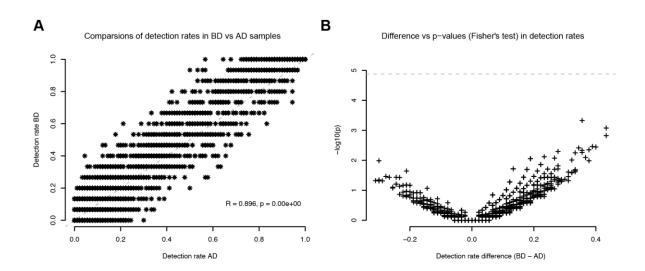


Supplementary Figure 1: Flowchart of sample use, related to STAR Methods. From top to bottom, samples from the two batches were first merged and then normalized before two sets of quality control (QC) filters were applied before univariate or multivariate analyses. The chart also shows (bottom left) the split of the data into a training and replication proportion before the model generation.



Nr. proteins detected in at least 4 or 5 randomly selected Controls

Supplementary Figure 2: Detection rates in controls, related to STAR Methods. Frequencies (y-axis) of number of commonly detected proteins (x-axis) in 4 out of 5 randomly selected controls from 1000 runs. Total number of controls to choose from was 40.



Supplementary Figure 3: Protein detection rates in samples collected before or at diagnose, related to Figure 1 and STAR Methods. (A) Comparisons of individual detection rates in samples collected before diagnose (y-axis) and at time of diagnose (x-axis). (B) Volcano plot illustrating difference in detection rate estimates (x-axis) and significance levels (y-axis, two-sided Fisher's test) for difference in the observed detection rates. The horizontal dashed grey line indicate multiple hypothesis testing adjusted (Bonferroni) significance level.