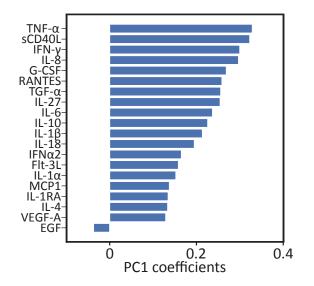
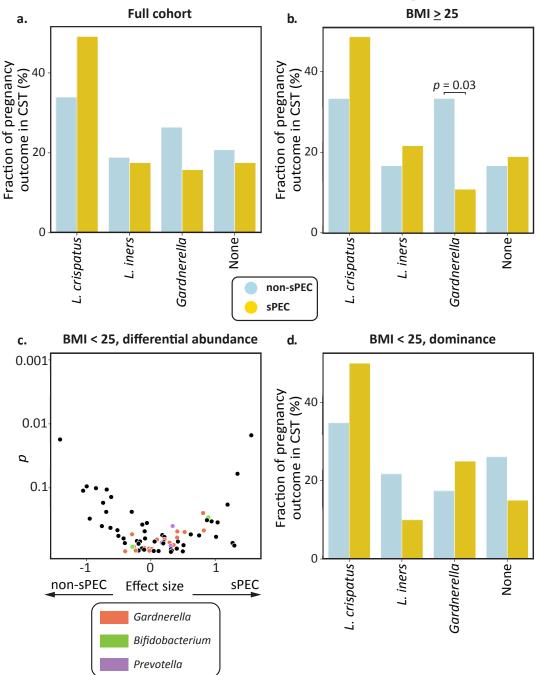
Supplementary Figures

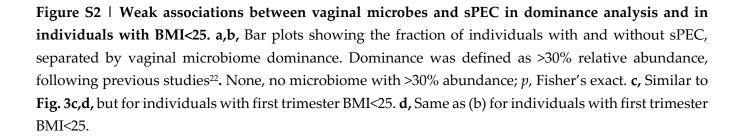


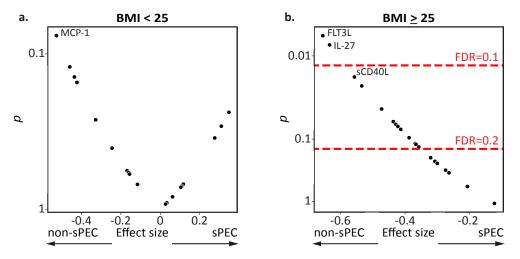
First principal component of host vaginal immune factors

Figure S1 | **The association of immune factor PC1 with sPEC is driven by multiple immune factors.** Barplot of the coefficients of the immune factors PC1.



Microbe dominance associations with sPEC are stronger for BMI \geq 25





Host immune factor associations with sPEC are stronger for BMI \geq 25

Figure S3 | Vaginal immune factors are more strongly associated with sPEC in individuals with BMI≥25. a,b, Same as Fig. 2d, stratified by BMI.

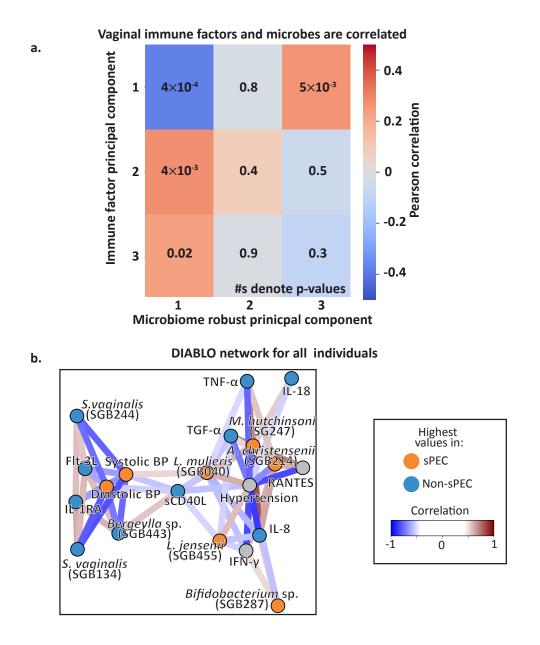


Figure S4 | **Associations between vaginal microbiome and immune factors in the context of sPEC. a.** Pearson correlations of the first three microbiome RPCs and the first three immune factors PCs. **b.** Similar to **Fig. 4d,e**, but for a DIABLO analysis which included all individuals regardless of BMI.

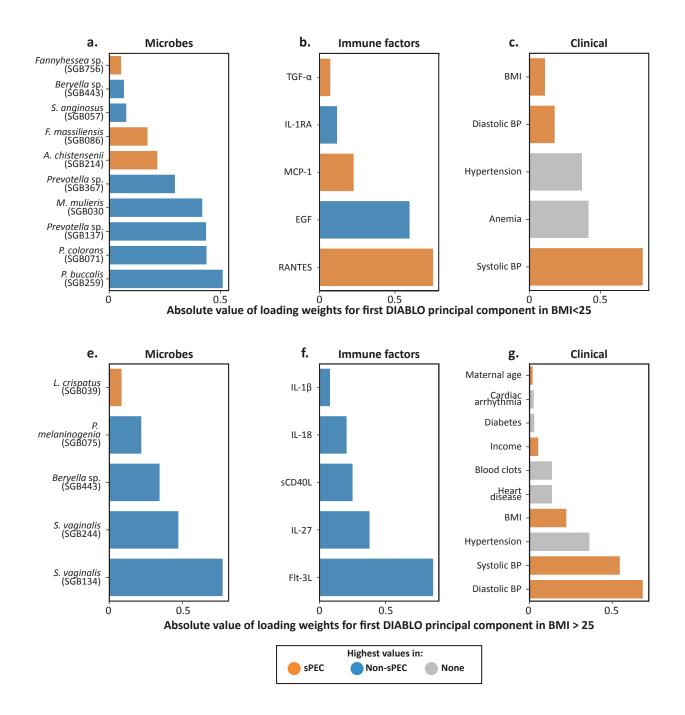


Figure S5 | **Associations of microbes, immune factors, and clinical covariates with sPEC in a sparse multivariate model. a-c,** Coefficients of fitted DIABLO model's associations with the first principal component of each data modality when trained on individuals with BMI<25, for microbes (a), immune factors (b), and clinical data (c). Colors of the bar denote the sPEC status that each variable is associated with. **d-f**, Same as a-c, but for a DIABLO model fitted using data from individuals with BMI≥25.

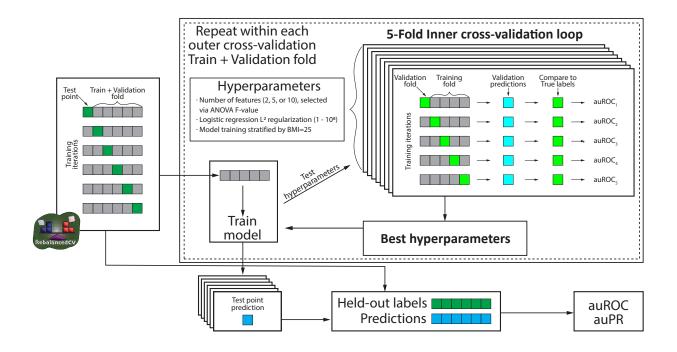


Figure S6 | **Description of our nested cross-validation pipeline.** The scheme used to evaluate predictive performance within the nuMoM2b dataset, using an inner 5-fold cross-validation structure to identify optimal hyperparameters, as described in **Methods**, with the 'Best hyperparameters' used to train a model which implements a prediction for its corresponding outer fold left-out point.