



Nationwide profiling of vaginal microbiota in Chinese women reveals age-dependent shifts and predictive biomarkers for reproductive health

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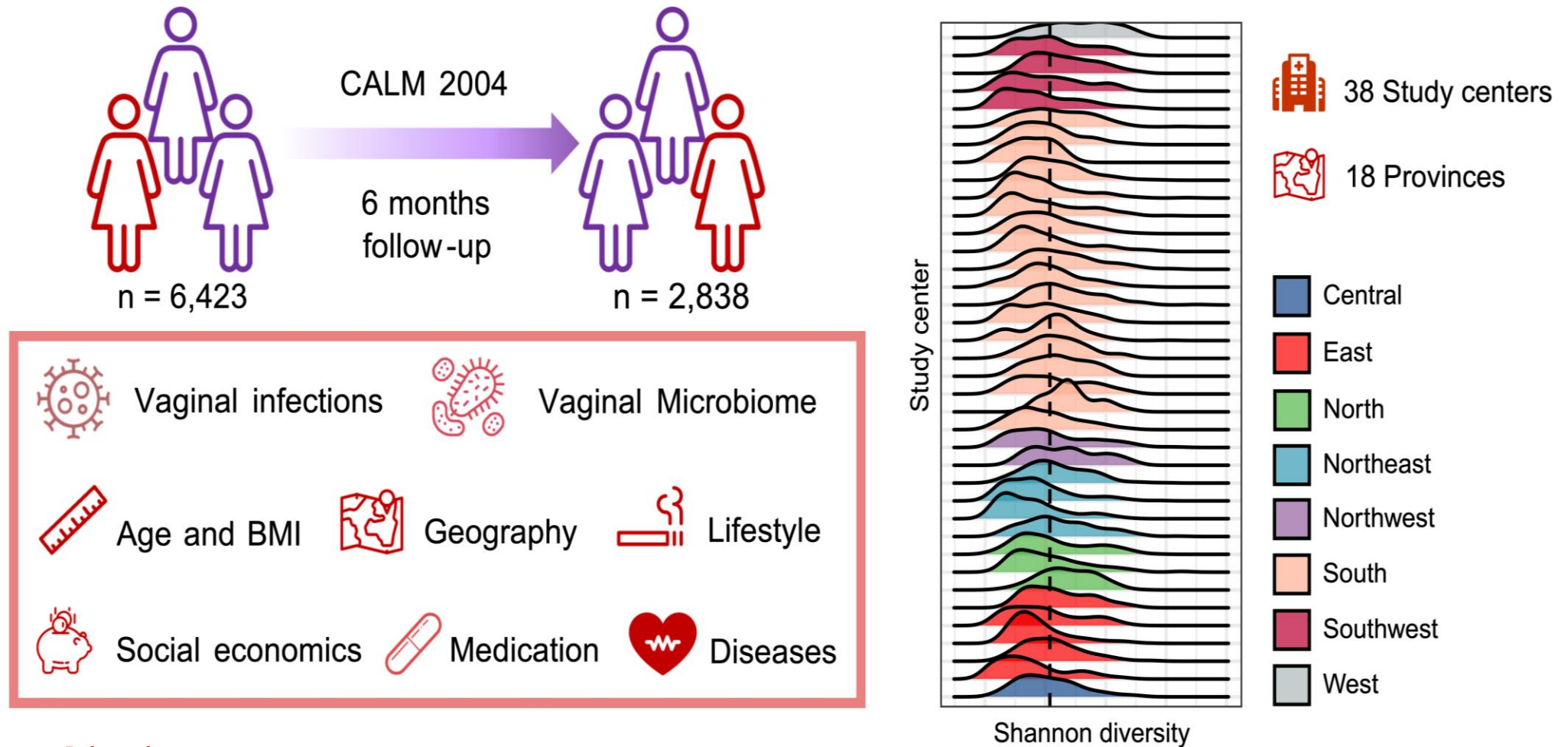
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Background



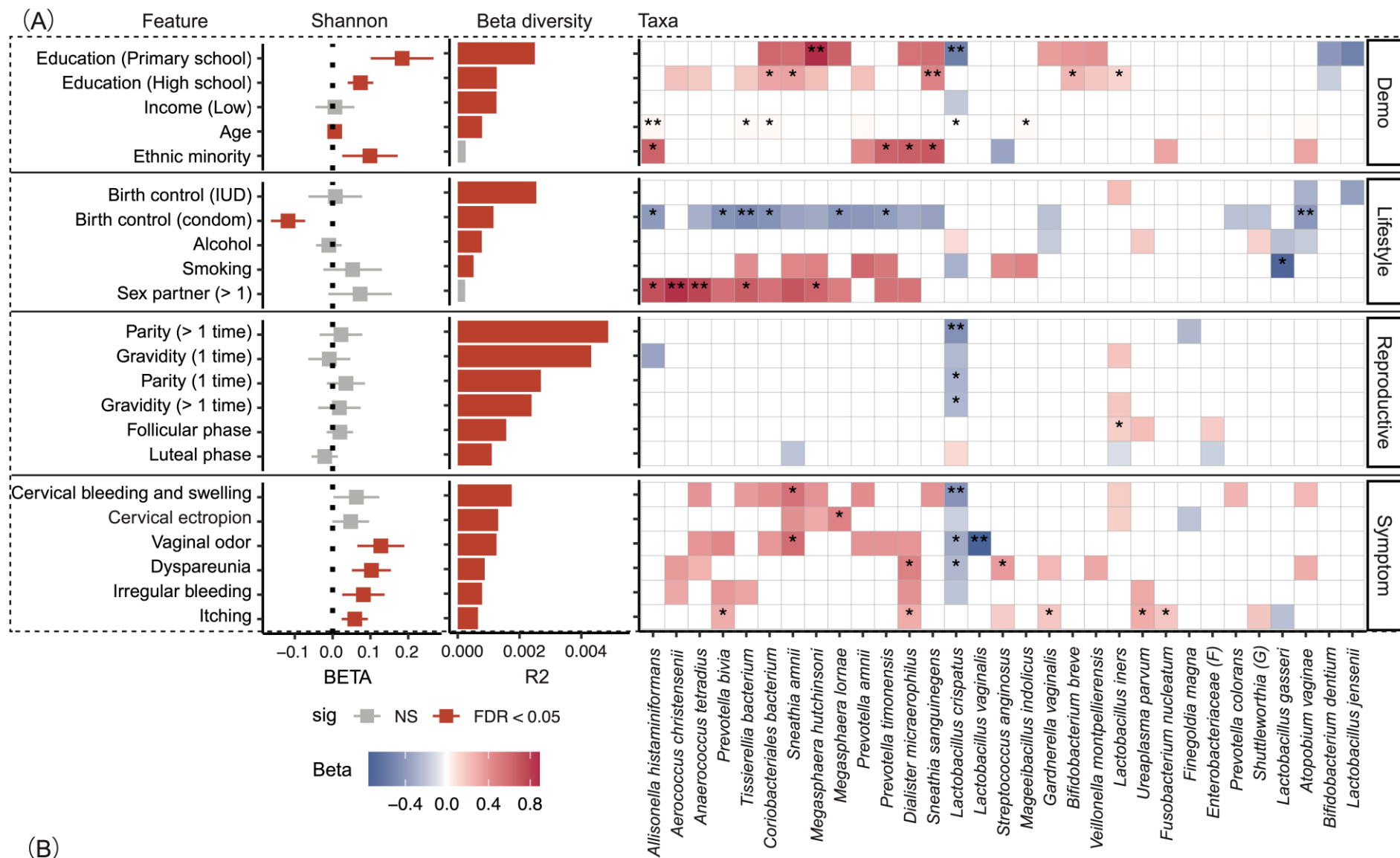
- **Our objectives:**

- Quantify the relative contributions of host factors to microbiota variation
- Explore how specific vaginal bacterial communities are shaped by host factors
- Provide a more comprehensive understanding of the role of vaginal microbiome in reproductive health among Chinese women



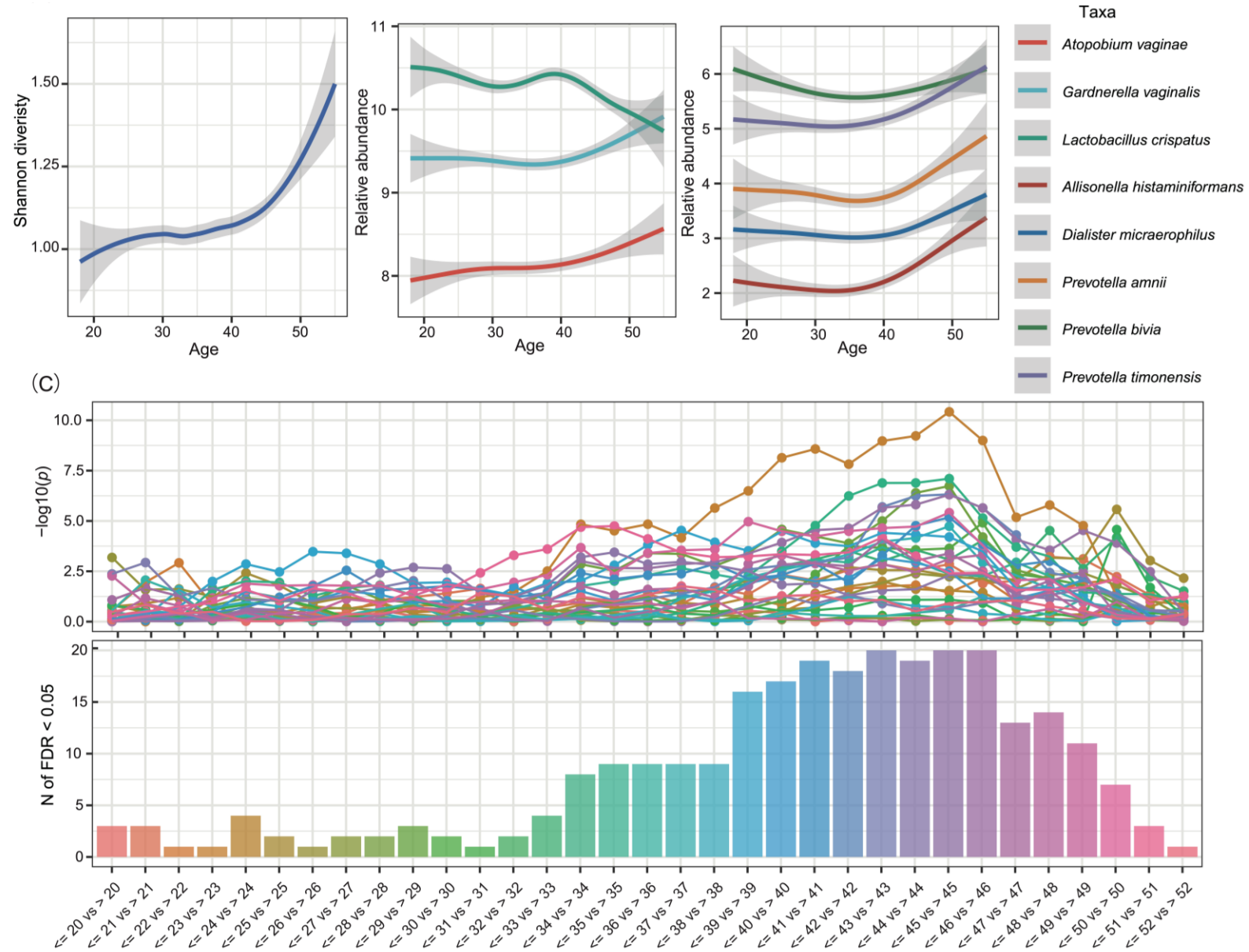
Associations of host factors with the vaginal microbiome

- Methods:** We assessed the associations between host features and vaginal microbiome characteristics, including beta diversity, Shannon diversity and the abundance of 31 core species.
- Overview:** Symptoms showed the strongest associations, followed by demographics, and lifestyles.
- Top features** with the greatest number of associations included condom use, age, number of sex partners, vaginal itching symptoms and middle education level.



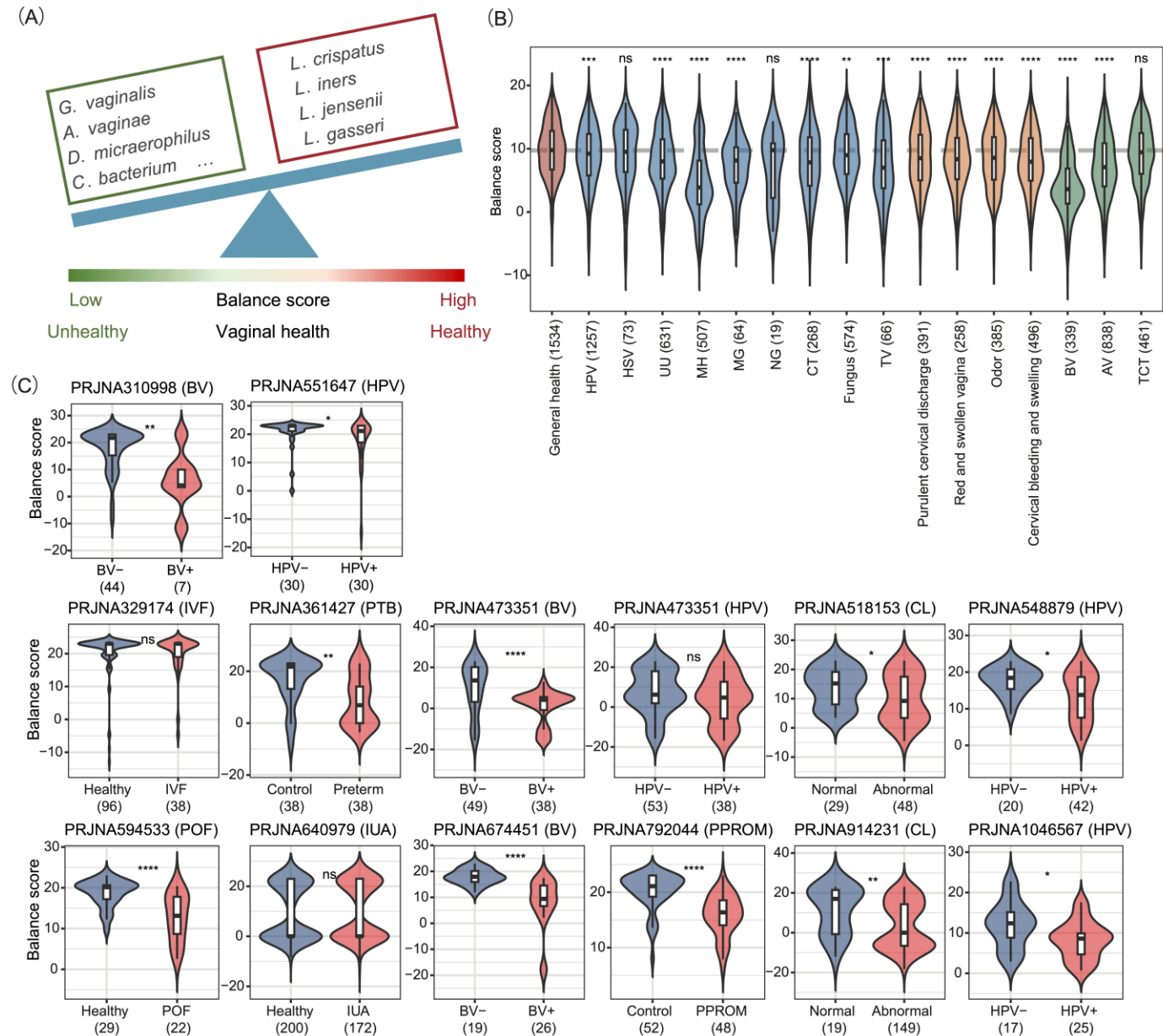
Significant shift in the vaginal microbiota occurs around 40 years old

Significant shift: Our study reveals a marked shift in the vaginal microbiome beginning around age 40, prior to the typical onset of menopause, characterized by a decline in *Lactobacillus. crispatus* and enrichment of dysbiosis-associated taxa.





A microbiome balance score indicating vaginal health

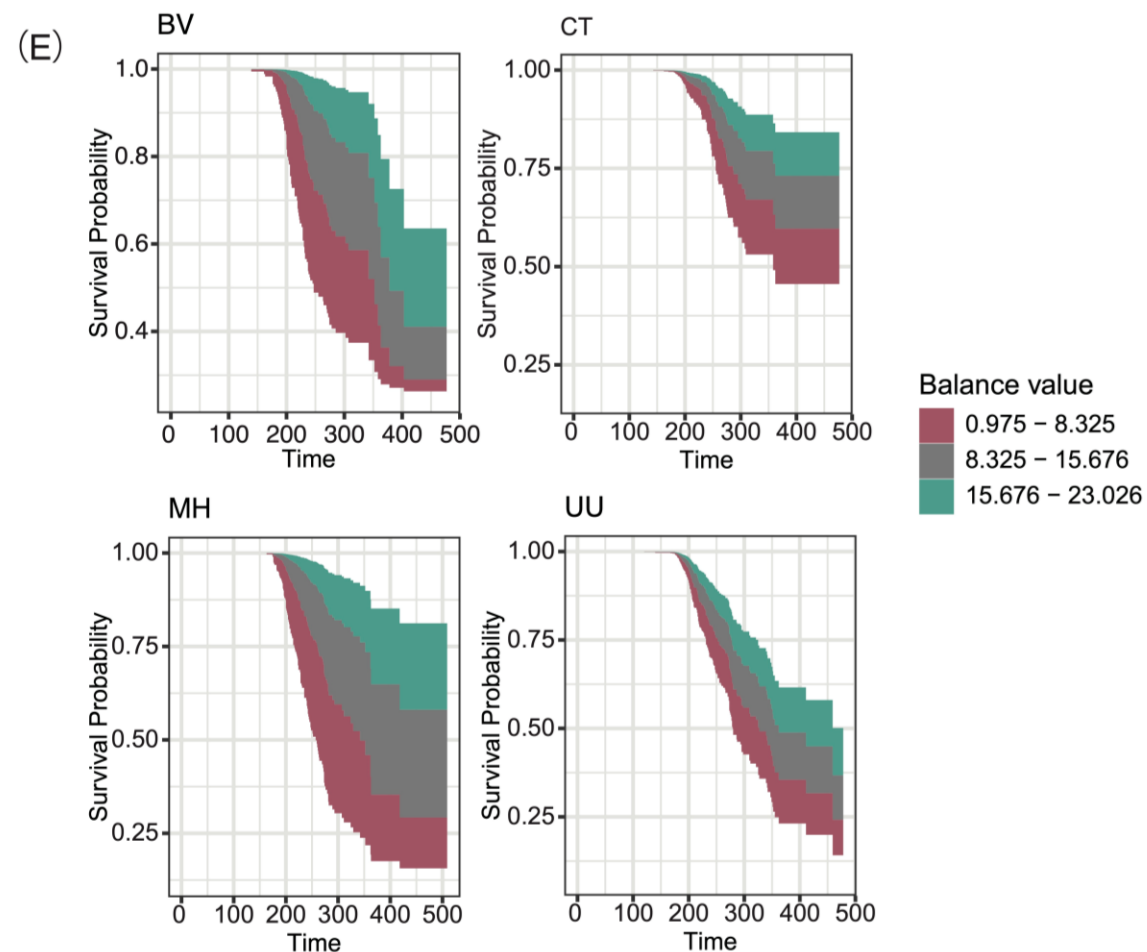
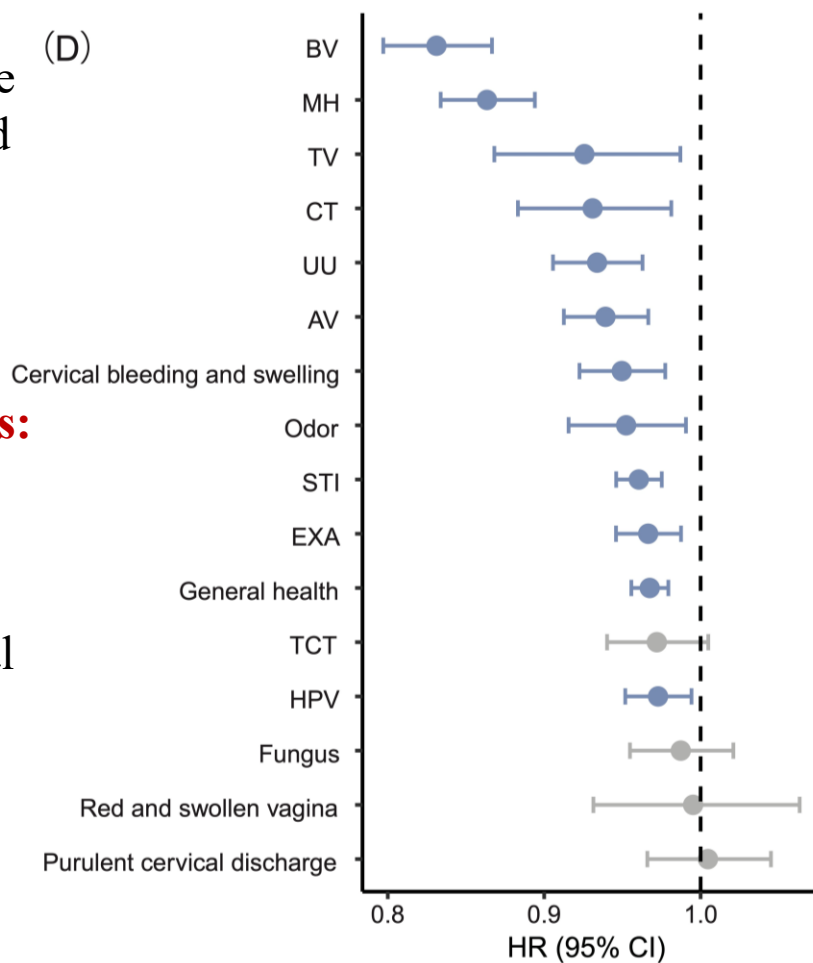


- **Methods:** Using a log ratio of healthy-enriched to healthy-depleted taxa, we developed a vaginal microbiome balance score (BS) .
- **Features:** BS was significantly lower in unhealthy individuals, including those with sexually transmitted infections, symptoms, or vaginal diseases.
- **Validation:** The BS can be replicated in publicly available vaginal microbiome datasets on women's reproductive health.



A microbiome balance score indicating vaginal health

- Methods:** We examined whether the baseline BS predicted the progression of vaginal health outcomes using longitudinal data.
- Prediction potentials:** A higher BS was significantly associated with a lower risk of bacterial vaginosis (BV), *Mycoplasma hominis* (MH), *Trichomonas vaginalis* (TV), and *Chlamydia trachomatis* (CT) at 6-month follow-up.





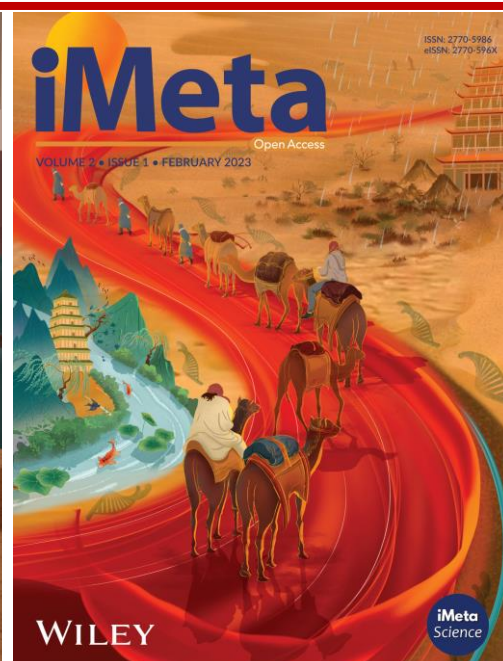
Summary

- ❑ We characterized the vaginal microbiota of 6,423 Chinese women of reproductive age across 18 provinces and assessed associations with 33 host factors.
- ❑ We observed a striking compositional transition around age 40, marked by declining *Lactobacillus crispatus* and enrichment of dysbiosis-associated taxa including *Gardnerella vaginalis*, independent of lifestyle or sociodemographic influences.
- ❑ Sexual behavior, contraceptive use, and educational attainment emerged as key determinants of community structure.
- ❑ We derived a microbiome balance score, validated it in external cohorts, and demonstrated its predictive power for incident bacterial vaginosis and sexually transmitted infections.

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