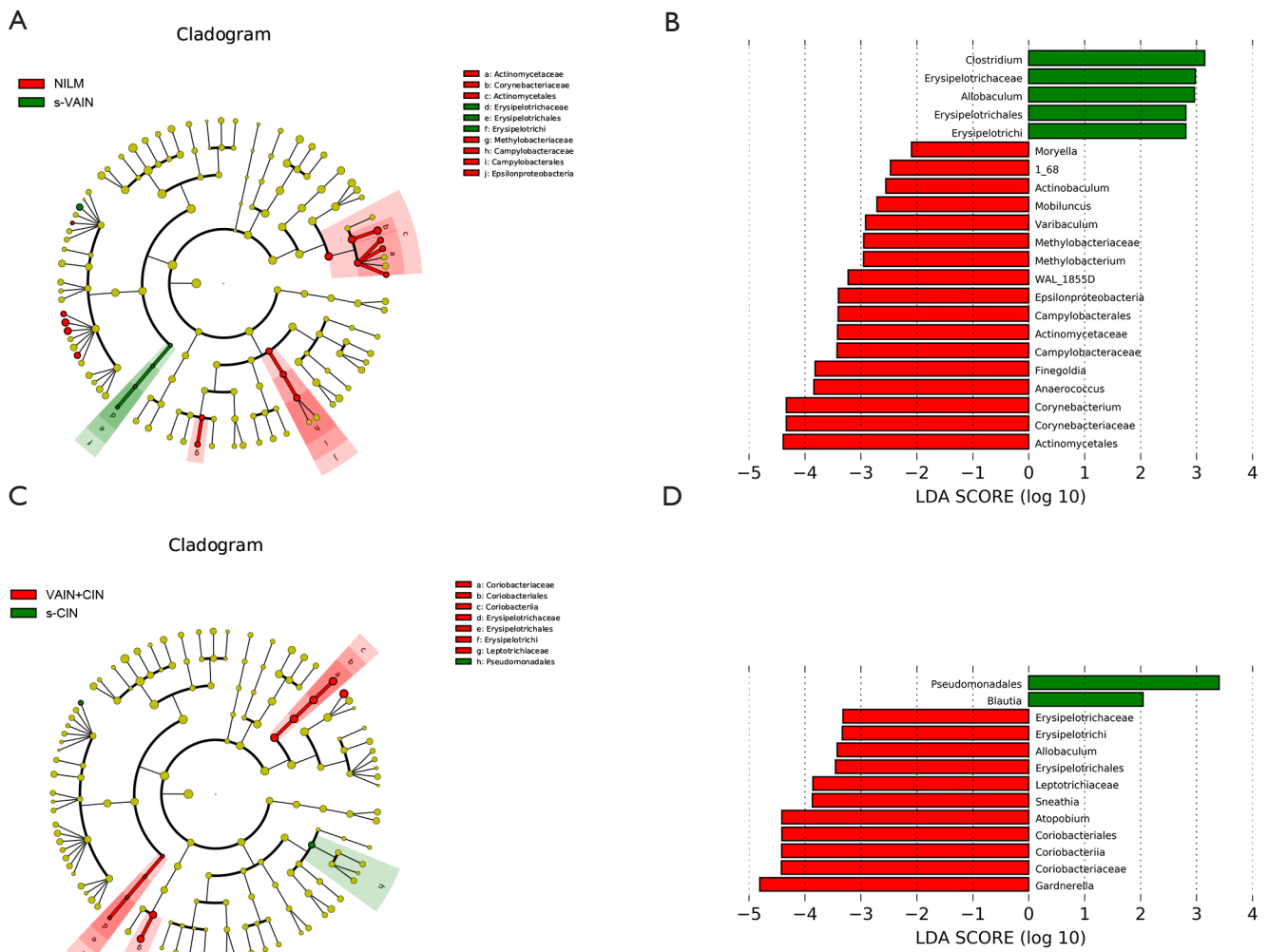
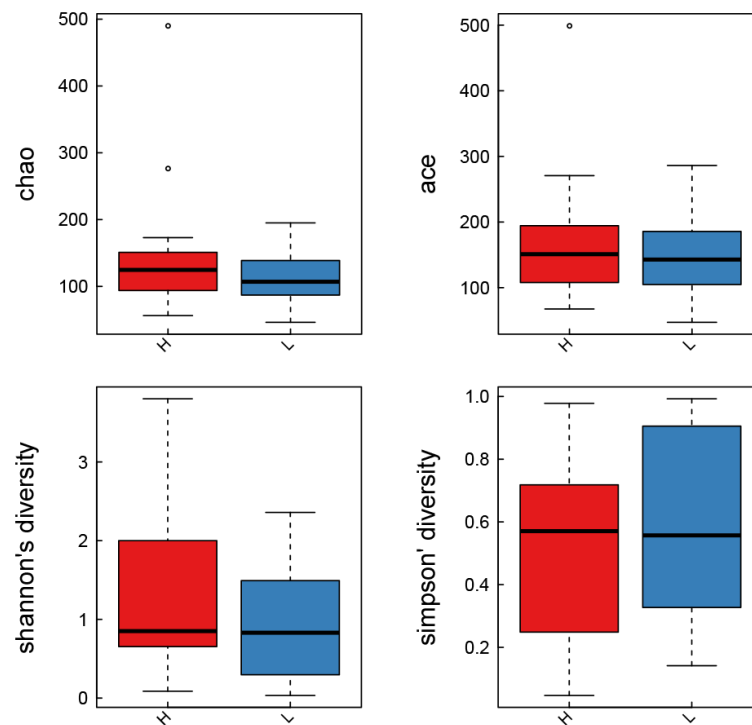


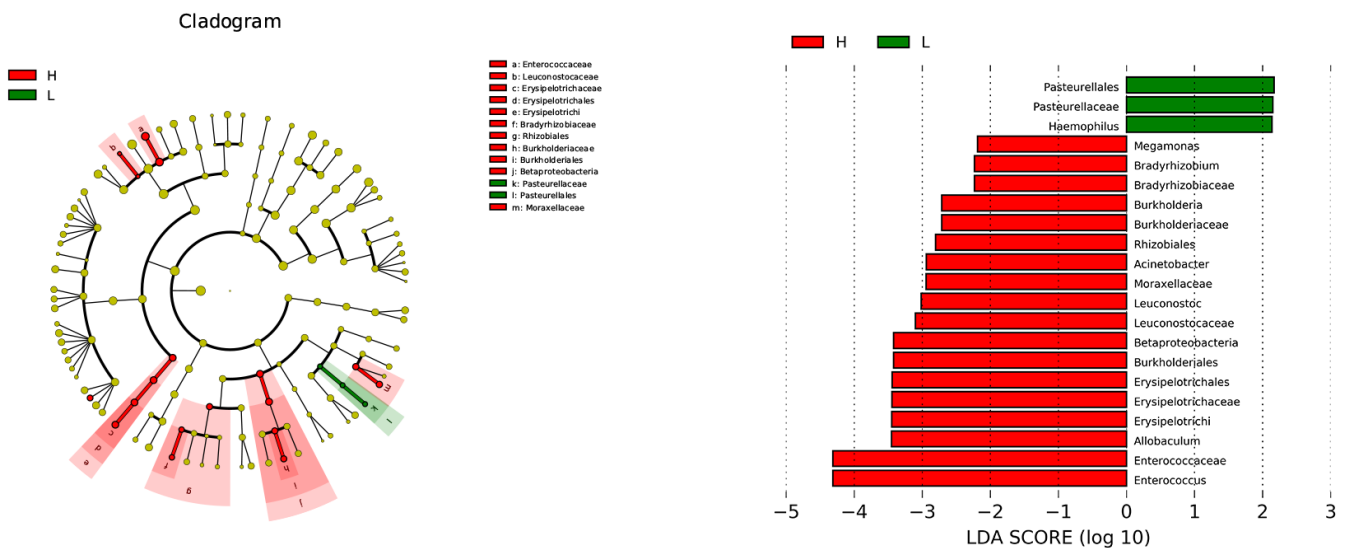
**Figure S1** The difference of vaginal microbiome between pre-menopausal and menopausal women by LEfSe analysis at the genus level. (A,B) Nm: menopausal women without VAIN, Np: pre-menopausal women without VAIN; Ym: menopausal women with VAIN; Yp: pre-menopausal women with VAIN. In group Nm, observing 68 significant different genera ( $P < 0.05$ ), In group Np, discovering as many as 9 genera enriched ( $P < 0.05$ ); (C,D) in group Ym, observing 47 significant different genera ( $P < 0.05$ ). In group Yp, discovering as many as 9 genera enriched ( $P < 0.05$ ); only taxa with absolute values of LDA scores  $> 2$  were presented.



**Figure S2** The difference of vaginal microbiome between VAIN and non-VAIN by LEfSe analysis at the genus level. (A,B) In group s-VAIN, observing 5 significant different genera ( $P < 0.05$ ), In group NILM, discovering as many as 17 genera enriched ( $P < 0.05$ ); (C,D) in group VAIN + CIN, observing 11 significant different genera ( $P < 0.05$ ). In group s-CIN, discovering as many as genera enriched ( $P < 0.05$ ); only taxa with absolute values of LDA scores  $> 2$  were presented.



**Figure S3** Bacteria species diversity and richness in VAIN1 compared with VAIN2/3. L: VAIN1; H: VAIN2/3; Shannon index,  $P=0.216$ ; Simpson index,  $P=0.320$ ; chao index,  $P=0.328$ ; ace index,  $P=0.779$ .



**Figure S4** The difference of vaginal microbiome between VAIN1 and VAIN2/3 by LefSe analysis at the genus level. L: VAIN1; H: VAIN2/3; In VAIN2/3, observing 18 significant different genera ( $P<0.05$ ). In VAIN1, discovering as many as 3 genera enriched ( $P<0.05$ ); only taxa with absolute values of LDA scores  $>2$  were presented.

1 **Table S1.** HPV types prevalence

	VAIN <sup>a</sup>	VAIN+CIN <sup>b</sup>	Number (%)
HPV16	9	6	15 (24.2)
HPV52	11	4	15 (24.2)
HPV53	9	1	10 (16.1)
HPV58	7	2	9 (14.5)
HPV66	7	2	9 (14.5)
HPV81	7	1	8 (12.9)
HPV56	6	2	8 (12.9)
HPV68	4	2	6 (9.7)
HPV33	4	2	6 (9.7)
HPV39	3	2	5 (8.1)
HPV59	3	1	4 (6.5)
HPV6	2	2	4 (6.5)
HPV35	3	0	3 (4.8)
HPV45	2	1	3 (4.8)
HPV31	2	0	2 (3.2)
HPV51	2	0	2 (3.2)
HPV18	2	0	2 (3.2)
HPV73	1	0	1 (1.6)

2 <sup>a</sup>VAIN, vaginal intraepithelial neoplasia

3 <sup>b</sup>CIN, cervical intraepithelial neoplasia

4

5 **Table S2.** Type-specific HPV viral load<sup>a</sup> (CIN versus VAIN+CIN)

<b>Log10-transformed HPV viral load</b>			
	CIN <sup>d</sup>	VAIN <sup>e</sup> +CIN	P
	Mean (SD)	Mean (SD)	
all	5.37±1.26	4.79±1.57	0.244
α9 <sup>b</sup> quantity	3.95±1.24	4.08±1.36	0.813
HPV16	4.90±0.25	4.00±1.37	0.415
HPV52	4.43±0.89	4.20±1.58	0.810
HPV58	2.54±0.76	4.36±2.15	0.375
α7 <sup>c</sup> quantity	5.99±0.82	4.66±2.64	0.393

6 <sup>a</sup>The mean and SD of the log10-transformed virus copy numbers per10,000 human cells  
7 were considered the type-specific HPV viral load. Values are presented as mean (SD,  
8 standard deviation) and compared using t test

9 <sup>b</sup>α9 species including HPV-16, -31, -33, -35, -52, -58

10 <sup>c</sup>α7 species including HPV-18, -39, -45, -59, -68

11 <sup>d</sup>CIN, cervical intraepithelial neoplasia

12 <sup>e</sup>VAIN, vaginal intraepithelial neoplasia

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