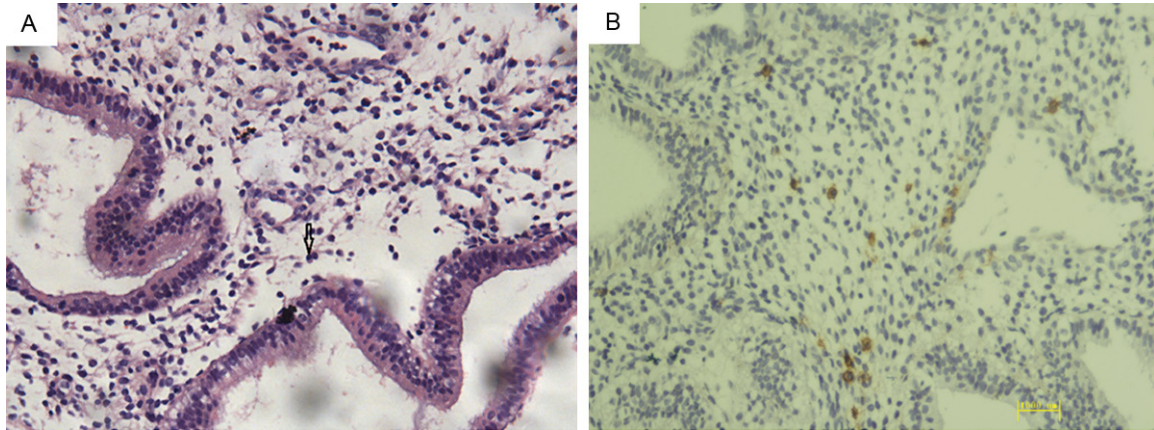


## Barcoded sequencing reveals diverse intrauterine microbiomes



**Figure S1.** Highlighted plasma cell based on immunohistochemical staining. A. A fragment of the endometrial curet-tage specimen stained by Hematoxylin and eosin (a,  $\times 200$ ) in which the specific cell (plasma cell, open arrow) can't be clearly recognized; B. The plasma cell syndecan-1 immunoreactivity is evident on the cell surface (syndecann-1,  $\times 200$ ) in a case of chronic endometritis.

**Table S1.** Number of quality sequences in 60 samples from vagina and intrauterine cavities of three groups

Group	Sampling site	Samples	Barcode sequences	Number of quality sequences
Group H	Vagina	7V	ACACATGTCTAC	8310
		8V	ACGCAACTGCTA	14162
		9V	AGCGTAGGTCGT	38817
		10V	ACATGTCACGTG	29729
		41V	ATACTATTGCGC	4810
		48V	ATCGCTCGAGGA	7577
		50V	ATTCTGTGAGCG	8260
		57V	AGTGGATGCTCT	8763
		60V	ATCGTACAACCTC	13147
		64V	ACGTTAGCACAC	6100
	Intrauterine cavities	7I	ACATGATCGTTC	6699
		8I	ACTGTCTGAAGCT	6600
		9I	ACACGAGCCACA	11649
		10I	ACGCGATACTGG	4912
		41I	ATGCACTGGCGA	6146
		48I	ATGCAGCTCAGT	5228
		50I	CACGGACTATAC	5203
		57I	ATAGCTCCATAC	11683
		60I	CAACACGCACGA	18762
		64I	ACTGTACGCGTA	9814
Group EP/CE	Vagina	22V	ACCGCAGAGTCA	12070
		23V	ACTCGATTCGAT	11828
		25V	AGATCTCTGCAT	10068
		36V	AGAGAGCAAGTG	11905
		39V	AGGCTACACGAC	7646
		49V	AATCAGTCTCGT	7950
		55V	AATCGTGACTCG	11148
		65V	CACGTCGATGGA	11069
		67V	ATAGGCGATCTC	7183
		68V	AGATACACGCGC	8438

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Group EP/CE	Intrauterine cavities	22I	ACGGTGAGTGTC	4978
		23I	AGACTGCGTACT	11874
		25I	AGCTATCCACGA	5059
		36I	AGCATATGAGAG	7220
		39I	AAGCTGCAGTCG	7222
		49I	ACGACGTCTTAG	8413
		55I	ACGAGTGCTATC	4881
		65I	CAGCACTAAGCG	8487
		67I	ATCTACTACACG	4238
		68I	AGCGCTGATGTG	11962
Group EP	Vagina	20V	ACCAGCGACTAG	9822
		21V	AGCTTGACAGCT	17823
		24V	AGCAGTCGCGAT	10470
		26V	AAGAGATGTCGA	20819
		27V	ACGTA CT CAGTG	3159
		40V	ACAGCTAGCTTG	5632
		44V	ACGTCTGTAGCA	4156
		46V	AGCCATACTGAC	12719
		52V	ACGTGAGAGAAT	3216
		61V	AGCGAGCTATCT	12102
	Intrauterine cavities	20I	ACGGATCGTCAG	4794
		21I	AACTGTGCGTAC	7113
		24I	AGGACGCACTGT	15654
		26I	ACAGCAGTGGTC	8018
		27I	ACTCGCACAGGA	4912
		40I	ACCTGTCTCTCT	3702
		44I	AGAGCAAGAGCA	7070
		46I	AGGTGTGATCGC	9370
	52I	ACTGACAGCCAT	9488	
	61I	AGTACTGCAGGC	8446	

**Table S2.** The mean relative abundance of the genus (>0.1%) in the samples of in the six groups

Genus	Group H (V)	Group H (I)	Group EP/CE (V)	Group EP/CE (I)	Group EP (V)	Group EP (I)
<i>Lactobacillus</i>	60.93%	6.23%	56.83%	33.44%	47.48%	38.86%
<i>Enterobacter</i>	3.27%	33.41%	1.08%	7.23%	4.47%	8.40%
<i>Pseudomonas</i>	2.44%	23.56%	0.92%	7.39%	1.78%	7.06%
<i>Gardnerella</i>	15.30%	3.55%	23.42%	6.95%	16.93%	5.54%
<i>Streptococcus</i>	1.32%	0.59%	3.08%	1.06%	14.55%	2.63%
<i>Prevotella</i>	6.28%	0.83%	2.64%	1.31%	0.86%	1.27%
<i>Bifidobacterium</i>	0.97%	0.58%	5.74%	1.46%	1.01%	4.82%
<i>Desulfosporosinus</i>	0.40%	4.33%	0.41%	5.45%	0.61%	4.28%
<i>Ralstonia</i>	0.12%	4.26%	0.09%	2.67%	0.13%	1.57%
<i>Veillonella</i>	0.34%	0.21%	0.19%	0.33%	3.83%	0.46%
<i>Atopobium</i>	1.81%	0.58%	0.46%	0.42%	0.57%	0.44%
<i>Thalassospira</i>	0.06%	0.79%	0.05%	1.69%	0.07%	1.23%
<i>Alteromonas</i>	0.07%	0.45%	0.06%	1.44%	0.06%	1.09%
<i>Megasphaera</i>	1.20%	0.52%	0.08%	0.13%	0.12%	0.13%
<i>Vibrio</i>	0.05%	0.74%	0.04%	1.16%	0.06%	0.73%
<i>Cupriavidus</i>	0.02%	0.92%	0.02%	0.61%	0.03%	0.44%

## Barcoded sequencing reveals diverse intrauterine microbiomes

<i>Actinomyces</i>	0.04%	0.03%	0.05%	0.06%	0.87%	0.06%
<i>Acinetobacter</i>	0.01%	0.10%	0.02%	0.77%	0.03%	0.14%
<i>Sphingomonas</i>	0.03%	0.77%	0.04%	0.66%	0.04%	0.39%
<i>Ureaplasma</i>	0.05%	0.03%	0.16%	0.07%	0.72%	0.14%
<i>Marinobacter</i>	0.03%	0.24%	0.02%	0.56%	0.04%	0.40%
<i>Sneathia</i>	0.55%	0.13%	0.03%	0.04%	0.01%	0.03%
<i>Klebsiella</i>	0.09%	0.53%	0.04%	0.17%	0.10%	0.18%
<i>Pelomonas</i>	0.02%	0.51%	0.02%	0.46%	0.02%	0.21%
<i>Muricauda</i>	0.01%	0.19%	0.01%	0.47%	0.01%	0.23%
<i>Corynebacterium</i>	0.06%	0.06%	0.45%	0.23%	0.22%	0.32%
<i>Stenotrophomonas</i>	0.00%	0.02%	0.01%	0.44%	0.01%	0.02%
<i>Erythrobacter</i>	0.01%	0.22%	0.02%	0.39%	0.01%	0.33%
<i>Dialister</i>	0.38%	0.14%	0.06%	0.09%	0.14%	0.09%
<i>Escherichia</i>	0.03%	0.18%	0.03%	0.27%	0.06%	0.37%
<i>Bacillus</i>	0.02%	0.17%	0.02%	0.36%	0.02%	0.20%
<i>Staphylococcus</i>	0.03%	0.03%	0.03%	0.21%	0.32%	0.08%
<i>Mobiluncus</i>	0.32%	0.16%	0.10%	0.07%	0.06%	0.06%
<i>Singulisphaera</i>	0.01%	0.16%	0.01%	0.25%	0.01%	0.31%
<i>Halomonas</i>	0.01%	0.11%	0.01%	0.30%	0.01%	0.21%
<i>Methylobacterium</i>	0.02%	0.19%	0.01%	0.29%	0.01%	0.13%
<i>Loktanella</i>	0.01%	0.09%	0.01%	0.25%	0.01%	0.19%
<i>Gramella</i>	0.01%	0.07%	0.00%	0.21%	0.01%	0.15%
<i>Fusobacterium</i>	0.00%	0.02%	0.04%	0.04%	0.02%	0.20%
<i>Anaerococcus</i>	0.03%	0.04%	0.20%	0.18%	0.15%	0.13%
<i>Thermus</i>	0.00%	0.04%	0.00%	0.19%	0.00%	0.05%
<i>Porphyromonas</i>	0.03%	0.02%	0.08%	0.19%	0.01%	0.07%
<i>Azorhizophilus</i>	0.18%	0.04%	0.14%	0.14%	0.14%	0.10%
<i>Aquabacterium</i>	0.01%	0.10%	0.01%	0.17%	0.02%	0.07%
<i>Enhydrobacter</i>	0.00%	0.06%	0.00%	0.16%	0.00%	0.05%
<i>Opitutus</i>	0.01%	0.07%	0.01%	0.16%	0.01%	0.09%
<i>Tolumonas</i>	0.03%	0.15%	0.02%	0.07%	0.04%	0.06%
<i>Blastopirellula</i>	0.01%	0.06%	0.01%	0.15%	0.01%	0.12%
<i>Campylobacter</i>	0.02%	0.01%	0.08%	0.14%	0.02%	0.02%
<i>Gemmata</i>	0.01%	0.11%	0.01%	0.14%	0.01%	0.13%
<i>Ktedonobacter</i>	0.01%	0.07%	0.00%	0.12%	0.01%	0.14%
<i>Thiothrix</i>	0.08%	0.14%	0.05%	0.12%	0.08%	0.09%
<i>Planctomyces</i>	0.02%	0.03%	0.02%	0.13%	0.03%	0.13%
<i>Bacteroides</i>	0.00%	0.01%	0.02%	0.03%	0.00%	0.13%
<i>Pseudoalteromonas</i>	0.00%	0.05%	0.00%	0.13%	0.00%	0.09%
<i>Howardella</i>	0.02%	0.00%	0.02%	0.01%	0.13%	0.01%
<i>Simkania</i>	0.00%	0.10%	0.00%	0.12%	0.00%	0.05%
<i>Anaeroglobus</i>	0.01%	0.02%	0.02%	0.04%	0.03%	0.12%
<i>Thermogymnomonas</i>	0.00%	0.06%	0.00%	0.12%	0.00%	0.05%
<i>Methylophaga</i>	0.00%	0.05%	0.01%	0.11%	0.00%	0.07%
<i>Dechloromonas</i>	0.01%	0.08%	0.01%	0.11%	0.01%	0.06%
<i>Finegoldia</i>	0.06%	0.06%	0.07%	0.07%	0.11%	0.08%
<i>Peptoniphilus</i>	0.08%	0.04%	0.10%	0.11%	0.07%	0.08%
<i>Deinococcus</i>	0.00%	0.05%	0.00%	0.11%	0.00%	0.06%
<i>Kangiella</i>	0.01%	0.02%	0.01%	0.11%	0.00%	0.08%

Notes: The relative abundance of genus were calculated as the average value of samples in the same group.

## Barcoded sequencing reveals diverse intrauterine microbiomes

**Table S3.** Microbial biodiversity of the six sample groups revealed by Miseq sequencing

Group	OTUs	Chao1	Shannon	Simpson
Group H (V)	176	514	2.78	0.61
Group EP/CE (V)	178	526	2.66	0.60
Group EP (V)	186	549	2.78	0.60
Group H (I)	331	789	4.07	0.77
Group EP/CE (I)	501	1112	5.66	0.93
Group EP (I)	454	1036	5.19	0.88

Notes: OTUs were defined at 97% sequence identity level. For each sample, 3000 sequences were randomly selected to calculate the number of the OTUs, chao1, Shannon index and simpson index, the average values of the same group were then calculated to represent the value of the corresponding group.