

Supplementary Table 1: Study characteristics reporting microbiome changes in endometriosis patients.

References	Year	Study location	Mean age (years old)	Study period	Sample size	Diagnosis	Microbiome analysis
Akiyama et al., 2019	2019	Japan	Endometriosis: 33.9 ± 5.7 Control: 32.5 ± 6.0	N/A	Endometriosis: 30 Control: 39	Diagnosed via laparoscopic and pathology test (classified by rARSM score: Stage III and IV)	16S rRNA analysis (V5-V6 Regions) on Ion Torrent Platform
Ata et al., 2019 [1]	2019	Turkey	*Endometriosis: 28.5 (range: 26 - 31.3) Control: 27.5 (range: 25.8 - 30)	2016 - 2017	Endometriosis: 14 Control: 14	Classified based on the r-ASRM scores	16S rRNA analysis (V3 and V4 region)
Chen et al., 2020 [2]	2020	China	36.07 ± 5.57 (range: 18-45)	April 2018 - February 2019	68 patients: Cervical Canal: 67 Posterior Fornix: 65 Uterine Cavity (Endometrium): 2	Confirmed via laparoscopic and pathology test	16S rRNA analysis (V3-V4 region)
Hernandes et al., 2020 [3]	2020	Brazil	18 - 50	N/A	Endometriosis: 10 Control: 11	Confirmed with laparoscopic surgery and histopathology analysis	16S rRNA analysis (V3-V4 region)
Wei et al., 2020 [4]	2020	China	31.47 (range: 23 - 44)	N.A.	Endometriosis: 36 Control: 14	Confirmed with laparoscopic surgery and categorized based on r-ASRM	16S rRNA analysis (V4-V5 region)
Perrotta et al., 2020 [5]	2020	Brazil	Endometriosis: 34.9 ± 6.8 Control: 35.25 ± 6.9	N.A.	Endometriosis: 35 Control: 24	Confirmed by TVUS or MRI or previous surgery	16S rRNA analysis (V4 region)
Lee et al., 2021 [6]	2021	Korea	Endometriosis: 36.20 ± 1.30 Control: 39.40 ± 1.10	N/A	Endometriosis: 45 Control: 45	Confirmed by histological evaluation and classified according to r-ASRM	16S rRNA analysis (V3-V4 region)
Le et al., 2021 [7]	2021	United States	Endometriosis: 32.5 ± 1.1 Control: 32.6 ± 2.0	N/A	Endometriosis: 20 Control: 9	Confirmed by laparoscopy/laparotomy and classified according to r-ASRM	16S rRNA analysis (V4 region)

Svensson et al., 2021 [8]	2021	Sweden	Endometriosis: 37.8 (range: 32.8-43.3) Control: 37.0 (range: 32.0- 44.0)	September 2016 - N.A.	Endometriosis: 66 Control: 198	Confirmed by laparoscopy/laparotomy and classified according to ICD- 10 classification of endometriosis	16S rRNA analysis (V1-V3 region) on Illumina HiSeq platform
Wessels et al., 2021 [9]	2021	Canada	Endometriosis: 33.8 ± 5.8 Control: 35.1 ± 3.3	2011-2017	Endometriosis: 12 Control: 9	Confirmed by laparoscopy and pathology test, according to r-ASRM score	16S rRNA analysis (V3 region) on Illumina MiSeq platform
Huang et al., 2021 [10]	2021	China	Endometriosis: 38.3 ± 7.88 Control: 34.0 ± 10.8	June 2019 - October 2019	Endometriosis: 21 Control: 20	Confirmed by laparoscopy and pathology test	16S rRNA analysis (V4 region) on Ion Torrent platform
Shan et al., 2021 [11]	2021	China	Endometriosis/Control: 32 ± 2, 32 ± 3	March 2019 - September 2019	Endometriosis: 12 Control: 12	Confirmed by histology, according to r-ASRM score	16S rRNA analysis (V3-V4 region) on Illumina MiSeq platform
Chao et al., 2021 [12]	2021	China	Endometriosis: 39.89 ± 6.24 Control: 38.23 ± 7.80	July 2017 - December 2018	Endometriosis: 37 Control: 66	Confirmed by exploratory laparoscopy or surgical pathology	16S rRNA analysis (V4 region) on Illumina platform
Chang et al., 2022 [13]	2022	Taiwan	Endometriosis: 35.4 ± 6.7 Control: N.A.	N.A.	Endometriosis: 23 Control: 10	Based on r-ASRM score	16S rRNA analysis (V3, V4, V5 and V9 region) on Illumina platform
Oishi et al., 2022 [14]	2022	Japan	Endometriosis: 37.9 ± 6.4 Control: 35.2 ± 8.6	July 2019 - April 2020	Endometriosis: 18 Control: 18	Based on r-ASRM score	16S rRNA analysis (V1-V2 region) on Illumina MiSeq platform
Yuan et al., 2022 [15]	2022	China	Endometriosis: 35.28 ± 7.24 Control: 33.32 ± 8.04	January 2019 - December 2019	Endometriosis: 36 Control: 25	Confirmed via laparoscopy and pathology test (diagnosed as I-IV stages)	16S rRNA analysis (V4 region) on Illumina HiSeq platform
Lu et al., 2022 [16]	2022	China	Endometriosis: 36.75 ± 7.11 Control: 35 ± 6.61	30 September 2020 - 31st March 2021	Endometriosis: 16 Control: 18	Confirmed by imaging and pathology after surgery, according to r-ASRM score	16S rRNA analysis (V4 region) on Illumina HiSeq platform

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