

Table S1. Demographic of endometrium for immunohistochemistry analysis

| Case ID | Diagnosis | Endometrium status | Age | Specimen type | Mean ± SD | P value* |
|----------------|-------------|----------------------|-----|---------------|------------|----------|
| For discovery | | | | | | |
| MAr-En-001 | Adenomyosis | proliferative | 40 | Frozen | 45.7 ± 3.5 | 0.91 |
| MAr-En-002 | Adenomyosis | weakly proliferative | 42 | Frozen | | |
| MAr-En-003 | Adenomyosis | proliferative | 48 | Frozen | 45.3 ± 3.5 | |
| MAr-En-004 | Adenomyosis | weakly proliferative | 54 | Frozen | | |
| MAr-En-005 | Adenomyosis | proliferative | 45 | Frozen | | |
| MAr-En-006 | Fibroids | proliferative | 48 | Frozen | | |
| MAr-En-007 | Fibroids | proliferative | 43 | Frozen | | |
| For validation | | | | | | |
| IHC-En-002 | Adenomyosis | early-secretory | 39 | FFPE | 46.7 ± 8.4 | 0.99 |
| IHC-En-003 | Adenomyosis | mid-secretory | 46 | FFPE | | |
| IHC-En-004 | Adenomyosis | mid-secretory | 48 | FFPE | 47 ± 4.2 | |
| IHC-En-005 | Adenomyosis | mid-secretory | 35 | FFPE | | |
| IHC-En-006 | Adenomyosis | mid-secretory | 50 | FFPE | | |
| IHC-En-007 | Adenomyosis | mid-secretory | 52 | FFPE | | |
| IHC-En-008 | Adenomyosis | mid-secretory | 45 | FFPE | | |
| IHC-En-009 | Adenomyosis | late-secretory | 49 | FFPE | | |
| IHC-En-010 | Adenomyosis | late-secretory | 43 | FFPE | | |
| IHC-En-011 | Adenomyosis | late-secretory | 34 | FFPE | | |
| IHC-En-012 | Adenomyosis | late-secretory | 43 | FFPE | | |
| IHC-En-013 | Adenomyosis | proliferative | 49 | FFPE | | |
| IHC-En-014 | Adenomyosis | proliferative | 53 | FFPE | | |
| IHC-En-015 | Adenomyosis | proliferative | 45 | FFPE | | |
| IHC-En-016 | Adenomyosis | proliferative | 41 | FFPE | | |
| IHC-En-017 | Adenomyosis | proliferative | 44 | FFPE | | |
| IHC-En-018 | Adenomyosis | proliferative | 44 | FFPE | | |
| IHC-En-019 | Adenomyosis | proliferative | 55 | FFPE | | |
| IHC-En-021 | Adenomyosis | proliferative | 34 | FFPE | | |
| IHC-En-022 | Adenomyosis | proliferative | 47 | FFPE | | |
| IHC-En-023 | Adenomyosis | proliferative | 43 | FFPE | | |
| IHC-En-024 | Adenomyosis | proliferative | 39 | FFPE | | |
| IHC-En-025 | Adenomyosis | proliferative | 54 | FFPE | | |
| IHC-En-026 | Adenomyosis | weakly proliferative | 39 | FFPE | | |
| IHC-En-027 | Adenomyosis | weakly proliferative | 57 | FFPE | | |
| IHC-En-028 | Adenomyosis | weakly proliferative | 40 | FFPE | | |
| IHC-En-029 | Adenomyosis | weakly proliferative | 53 | FFPE | | |
| IHC-En-030 | Fibroids | mid-secretory | 44 | FFPE | | |
| IHC-En-031 | Fibroids | mid-secretory | 44 | FFPE | | |
| IHC-En-032 | Fibroids | late-secretory | 48 | FFPE | | |
| IHC-En-033 | Fibroids | late-secretory | 44 | FFPE | | |
| IHC-En-034 | Fibroids | proliferative | 44 | FFPE | | |
| IHC-En-035 | Fibroids | proliferative | 45 | FFPE | | |
| IHC-En-036 | Fibroids | proliferative | 47 | FFPE | | |
| IHC-En-037 | Fibroids | proliferative | 52 | FFPE | | |
| IHC-En-038 | Fibroids | proliferative | 49 | FFPE | | |
| IHC-En-039 | Fibroids | proliferative | 42 | FFPE | | |
| IHC-En-040 | Fibroids | proliferative | 41 | FFPE | | |
| IHC-En-041 | Fibroids | weakly proliferative | 56 | FFPE | | |
| IHC-En-042 | Fibroids | weakly proliferative | 52 | FFPE | | |
| IHC-En-043 | Fibroids | weakly proliferative | 48 | FFPE | | |
| IHC-En-044 | Fibroids | weakly proliferative | 49 | FFPE | | |

*Two-tailed Welch-test. FFPE, formalin-fixed, paraffin-embedded.

Table S2. Functional enrichments of selected genes

| GO | Gene Name | P-value |
|---|---|---------|
| Low methylation and high gene expression in adenomyosis | | |
| 1. Multicellular organism development | <i>ZAR1, HOXC12, LMO2, ZNF541, PRM1, LIMD1, NKX2-4</i> | 3.9E-03 |
| 2. Regulation of transcription, DNA-templated | <i>HOXC12, BRF1, SOX1, HINT1, NKX6-2, SP5, LIMD1, NKX2-4, FZD7, ZNF23</i> | 1.0E-02 |
| 3. Potassium ion transport | <i>KCNMB3, KCNK9, KCNA6</i> | 2.4E-02 |
| 4. Spinal cord association neuron | <i>TAL1, GSX1</i> | 3.7E-02 |
| 5. Hypothalamus development differentiation | <i>RAX, GSX1</i> | 4.3E-02 |
| High methylation and low gene expression in adenomyosis | | |
| 1. Negative regulation of transcription from RNA polymerase II promoter | <i>BACH1, AEBP1, ZNF593, HIST1H1D, KLF11, FHL2, DUSP22, SMAD3, WHSC1, REST, WWTR1, GLI3, CHD8, SIN3A, ATN1, HEYL, GATAD2B, PTCH1, PRDM1</i> | 1.2E-04 |
| 2. Aorta development | <i>LTBP1, PRICKLE1, PRDM1, MYH10</i> | 5.7E-04 |
| 3. Osteoblast differentiation | <i>MRC2, FHL2, COL6A1, WWTR1, GPNMB, IGFBP3</i> | 2.8E-03 |
| 4. Negative regulation of canonical Wnt signaling pathway | <i>WNT5A, CHD8, PPP2R3A, PRICKLE1, BICC1, WWTR1, GLI3</i> | 4.1E-03 |
| 5. Negative regulation of transcription, DNA-templated | <i>WNT5A, CHD8, SIN3A, PRICKLE1, KLF11, HEYL, POU2F1, KCTD1, FHL2, LRRFIP1, REST, GLI3</i> | 6.7E-03 |
| 6. Negative regulation of fat cell differentiation | <i>WNT5A, SMAD3, ZADH2, WWTR1</i> | 6.7E-03 |
| 7. branching involved in ureteric bud morphogenesis | <i>PAX8, PTCH1, GLI3, HOXD11</i> | 6.7E-03 |
| 8. in utero embryonic development | <i>CHD8, SIN3A, SYF2, SMAD3, PTCH1, GLI3, MYH10</i> | 7.8E-03 |