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**Supplemental Table S1. Primers used for quantitative RT-PCR.**

| mRNA | Forward | Reverse | Genbank/EMBL Accession no. | Nucleotide no. |
|---|---|---|---|---|
| *PTGS2/ COX-2* | 5'-TGTGCAACACTTGAGTGG CT-3' | 5'-ACTTTCTGTACTGCGGGTGG-3' | AY151286 | 1381-1677 |
| *PTGES/ mPGES-1* | 5'-TCTTAGCCCCTTGGATTCCT-3' | 5'-ATTCTTAGCCCGGGATTCAG-3' | BC008280 | 695-898 |
| *GAPDH* | 5'-TGATGACATCAAGAAGGTGGTGAAG-3' | 5'-TCCTTGGAGGCCATGTAGGCCAT-3' | BC014085 | 1644-1883 |

**Supplemental Table S2. Demographic characteristics of the pregnancies used in the DNA methylome study using MeDIP.**

| Study group | (a) TL (n = 11) | (b) TNL-s (n = 10) | (c) TNL-I (n = 9) | (d) PTNL (n = 10) | (e) iPTL (n = 6) | (f) tPTL (n = 7) |
|---|---|---|---|---|---|---|
| Maternal age (yrs) | 34.7 ± 4.0 (28; 41) | 27.8 ± 4.3 (22; 35) | 32.8 ± 2.7 (27; 36) | 33.2 ± 6.0 (24; 40) | 32.8 ± 6.7 (23; 40) | 34.6 ± 11.1 (20; 55) |
| Parity | 0.7 ± 0.5 (0; 1) | 1.4 ± 0.7 (0; 2) | 0.7 ± 0.5 (0; 1) | 0.7 ± 0.8 (0; 2) | 1.0 ± 1.3 (0; 3) | 0.1 ± 0.4 (0; 1)[a] |
| Maternal BMI (kg/m$^2$) | 23.9 ± 3.0 (20; 29)[a] | 32.0 ± 4.4 (25; 41) | 25.0 ± 8.5 (19; 45) | 25.7 ± 6.5 (19; 35) | 23.8 ± 4.1 (19; 29) | 24.3 ± 6.3 (18; 35) |
| No. of women smoking during pregnancy | 0 | 0 | 0 | 0[c] | 0[d] | 0 |
| Race/Ethnicity | White (6)[e] | Hispanic White (8) | White (5)[f] | White (5)[c] | White (5)[d] | White (6)[f] |
| | Black (2) | Non-Hispanic White (1) | Black (1) | Black (2) | | |
| | Asian (1) | Asian (1) | | Pakistani (1) | | |
| Birth weight (g) | 3360 ± 373 (2670; 3990) | 3316 ± 268 (2987; 3731) | 3612 ± 357 (3070; 4280) | 1966 ± 544 (1225; 3110)[b] | 2403 ± 462 (2090; 3160)[b] | 2072 ± 486 (1523; 2855)[b] |
| No. of boys/girls | 7/4 | 6/4 | 6/3 | 4/6 | 2/4 | 9/5 |
| IUGR (< 2500 g) | 0 | 0 | 0 | 9 | 4 | 5 |
| Macrosomia (≥ 4000 g) | 0 | 0 | 1 | 0 | 0 | 0 |

Data are given as mean ± SD with range in parentheses, except where indicated differently. [a]*p<0.05 vs TNL-s group with one-way ANOVA followed by Bonferroni's post-hoc comparisons tests. [b]**p<0.01 vs. TL, TNL-s and TNL-I. [c,d,e,f]Data of 8, 5, 9 and 6 pregnancies.

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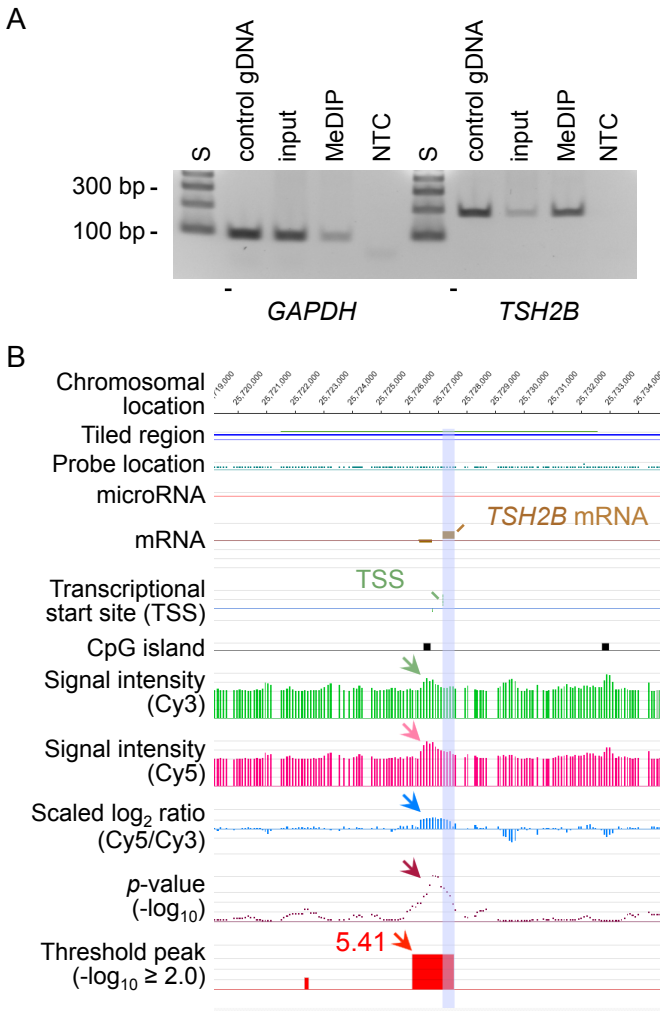
**Supplemental Table S3. Control gene methylation detected in the human myometrium.**

| Positive controls | Locus | Cytosine methylation | CpG island | Peak score[#] |
|---|---|---|---|---|
| *TSH2B (HIST1H2BA)*[§] | 6p22.2 | Detected | 5' | 4.63 ± 0.46 (4.22; 5.41) |
| *H1T (HIST1H1T)*[§] | 6p21.3 | Detected | 5' | 3.39 ± 0.30 (3.12; 3.89) |
| *PRM1* (protamine 1) | 16p13.2 | Detected | 3' | 3.23 ± 0.37 (2.83; 3.75) |
| Negative controls | | | | |
| *GAPDH* | 12p13.31 | Not detected | 5' | N/A |
| *HIST1H1E* | 6p21.3 | Not detected | 5' | N/A |
| *HIST1H2AC* | 6p22.1 | Not detected | 5' | N/A |

[#]Data are given as mean ± SD with range in parentheses. N/A, not applicable. [§]Testis-specific histone variants that are expressed exclusively in testis. The CpG sites of these histone variant genes are methylated in somatic cells but not in testis.




**Supplemental Figure S1.** (A) Selective enrichment of methylated DNA fragments in the MeDIP preparation. The whole genome-amplified products from immunoprecipitated and non-immunoprecipitated (input) DNA fragments were subjected to PCR amplification with primer pairs specific to the *GAPDH* and *TSH2B* genomic regions. The region amplified with the *TSH2B* primer pair corresponds to genomic locus that is unmethylated in testis and highly methylated in all somatic cells tested and was used as a control gene representing inactive methylated regions. *GAPDH* primer pair is designed from the constitutively active promoter region and used as an unmethylated negative control gene. Preferential amplification was detected for the unmethylated *GAPDH* promoter region in the input DNA and for the methylated *TSH2B* promoter region in the MeDIP DNA preparations. The expected products for the *GAPDH* and *TSH2B* primer pairs from genomic DNA template are 88 bp and 170 bp, respectively. A 100 bp ladder was used as a DNA size marker (lane S). No amplification was detected in the no template controls (NTC). Untreated genomic DNA samples were used as a positive control template in the PCR amplification assays. (B) Cytosine methylation at the positive control gene *TSH2B* was readily detected in the human myometrium methylome using MeDIP-chip analysis. Statistically significant p-values were determined by 750 bp sliding window analysis.