**Epigenetic and Transcriptional Alterations in Human Adipose Tissue of Polycystic Ovary Syndrome**

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**Study participants.** Women with PCOS and controls were recruited by advertising in local newspapers and in frequently visited places in the community. All women were ≥18 and ≤ 38 years of age. The eligibility criteria for women with PCOS were at least two of the following three signs; polycystic ovarian morphology (PCO), clinical signs of hyperandrogenism and oligo/amenorrhea. The criteria for ultrasound-verified PCO were ≥12 follicles 2–9 mm and/or ovarian volume ≥10 ml in one or both ovaries. A self-reported Ferriman-Gallwey (FG) score ≥8 was defined as hirsutism and acne was defined by a positive response to the question Do you have acne? Oligomenorrhea was defined as an intermenstrual interval >45 days and <8 menstrual bleedings in the past year. Amenorrhea was defined as <3 menstruations per year.

Exclusion criteria for controls were evidence of PCO morphology, excessive acne or hirsutism, or menstrual irregularities (cycles >35 days). Exclusion criteria for all women were any signs of other endocrine disorders such as hyperprolactinemia (s-prolactin <27μg/l), nonclassic congenital adrenal hyperplasia (17β hydroprogesterone <3nmol/l), and androgen-secreting tumors or autoimmune disorder, cancer, type I or type II diabetes or cardiovascular disease. Moreover, women had not received any pharmacological treatment within 12 weeks before inclusion, had not been pregnant, and had not been breastfeeding for 6 months before inclusion.

**Supplementary Table Legends**

**Table S1:** Genes differently expressed in adipose tissue from women with PCOS (n=64) and controls (n=30) ($Q < 0.05$) sorted in alphabetic order (cohort 1).

**Table S2.** Significant gene sets contributing to Z-score for expression pathways that are up-regulated in adipose tissue from women with PCOS versus controls (cohort 1).

**Table S3.** Significant gene sets contributing to Z-score for expression pathways that are down-regulated in adipose tissue from women with PCOS versus controls (cohort 1).

**Table S4.** Selected genes of relevance for PCOS found to be differentially expressed in cohort 1 were biological validated in cohort 2.

**Table S5:** Differential methylation in adipose tissue from women with PCOS and controls $P < 0.05$. (XLS)

**Table S6:** Differential methylation of CpG-sites in adipose tissue from women with PCOS and controls applying a $Q < 0.15$. (XLS)

**Table S7:** Significant gene sets with differential methylated genes in adipose tissue from women with PCOS versus controls. IPA analyses with $P < 0.05$. (XLS)

**Table S8.** Significant gene sets contributing to Z-score for differential methylated methylation pathways that are up-regulated in adipose tissue from women with PCOS versus controls (cohort 1).

**Table S9.** Significant gene sets contributing to Z-score for differential methylated methylation pathways that are down-regulated in adipose tissue from women with PCOS versus controls (cohort 1).

**Table S10:** Differential methylation in adipose tissue from women with PCOS and controls based on the cross reactive probes $P < 0.05$. (XLS)

**Table S11:** Differential DNA methylation in adipose tissue ($Q < 0.15$ and the range of difference in β-value is 0.3 - 3%) concurrent with an inverse change in mRNA expression ($P < 0.05$) of the nearest gene between PCOS women and controls (cohort 1).

**Table S12:** Differential methylation of DNA methyltransferases (*DNMTs*), a family of enzymes catalyzing the transfer of a methyl group to DNA, in adipose tissue from women with PCOS and controls.

**Table S13.** Spearman correlations with correction for multiple testing ($Q < 0.05$) between methylation and expression for significantly differentially expressed genes and CPG sites within the cis distance 500 kb upstream and 100 kb downstream of the gene.