Gene set enrichment analysis (GSEA) showing pathways expressed in pregnant compared to non-pregnant patients.

(A) Sorted gene enrichment analysis using PIANO. Genes were ranked from the more expressed in pregnant women to the more repressed and each Gene Ontology (GO) functional class was scored according to this ranking (i.e. GO classes presenting a big proportion of highly expressed or repressed genes obtaining higher scores). Depending on the metric used to compute the enrichment score, a given GO class could rank high with a metric while it could rank low with another one. We thus computed the median rank obtained by each GO class according to each scoring metrics that we considered (here mean, median, sum, fisher, stouffer). Classes ranking high (i.e. that enrich the top up-regulated or the top repressed genes) whatever metrics we consider are considered as more reliable. Each box of the boxplots represent the ranks obtained by a given gene ontology class according to the considered metrics. GO classes are ranked according the median rank.

(B) Significantly differentially expressed genes enrichment analysis using DAVID. Differentially expressed genes in pregnant women versus non-pregnant women were compared to all gene ontology classes. The enrichment significance was then computed using the hypergeometric probability that estimates the probability that a given enrichment is obtained by chance considering the number of differentially expressed genes and the GO class size.

Although both approaches are based on a very different principle, the results delivered by the second approach confirms those obtained by the first one.