



Supplementary Figure S5. qPCR validation of endometrial disruption biomarkers. Comparison of gene expression fold change obtained with RNA-Sequencing (RNA-Seq) and quantitative PCR (qPCR) assays. Six differentially expressed genes (DEGS) were selected from (A) p1 vs. c1, (B) p2 vs. c1 and (C) c2 vs. c1 comparisons. In this context, p1 and p2 represent poor prognosis profiles 1 and 2, respectively, while c1 and c2 represent good prognosis profiles 1 and 2.