



Supplementary Figure S2 Correlation between RNA-Seq and microarray. Correlation of average gene expression in endometrium between RNA-Seq and microarray in different menstrual cycle stages (a = menstrual/M, b = proliferative/P, c = early secretory/ES, d = mid secretory/MS, and e = late secretory/LS). The correlations were performed by taking the average expression of 161 samples for 10,054 genes shared between both platforms. Each dot represents the average expression of each gene across the samples.