

**Supplementary Table S6.** Molecular and functional differences found among endometrial disruption profiles.

	p1 vs. c1		p1 vs. c2		p1 vs. p2		p2 vs. c1		p2 vs. c2		c2 vs. c1	
	3		0		0		47		0		1	
DEGs	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down
Functional groups	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down
Immune response (n = 26)	9	0	9	0	7	1	3	10	6	2	0	9
Nervous system and sensory perception (n = 6)	6	0	1	1	1	1	6	0	2	0	5	0
Signal transduction (n = 7)	3	2	2	2	0	0	2	0	0	0	1	0
Metabolism and energy production (n = 26)	3	2	3	3	0	2	1	12	3	6	0	0
Cellular movement and ciliary processes (n = 8)	2	6	0	0	0	0	0	3	0	2	0	1
Cellular adhesion and membranes (n = 11)	1	0	0	0	3	2	3	3	3	2	3	0
Gene expression and protein degradation (n = 13)	1	0	1	0	2	4	6	2	6	2	0	3
Proliferation and differentiation (n = 2)	1	1	1	0	0	0	0	0	0	0	0	0
Longevity and senescence (n = 2)	1	0	0	0	0	0	1	0	0	0	0	0
Angiogenesis and coagulation (n = 3)	0	0	0	0	0	2	2	0	1	0	0	0
<b>Total number of dysregulated functions</b>	27	11	17	6	13	12	24	30	21	14	9	13
	38		23		25		54		35		22	

The table shows the number of differentially expressed genes (DEGs) and the corresponding number of significantly up- or downregulated biological functions [False Discovery Rate (FDR) < 0.05], identified through a gene set enrichment analysis (GSEA), for each comparison. The number of biological functions in each functional group is indicated between brackets.