Supplementary files

Table S1.The primer sequences for qRT-PCR

Gene name	Forward (5'-3')	Reverse (5'-3')
β-actin	CTGCTATGTTGCTCTAGACTTCG	ATGCCACAGGATTCCATACC
Bax	CTGATGGCAACTTCAACTG	ATCTTCTTCCAGATGGTGAG
Bcl2	TGGATGACTGAGTACCTGAACC	ATCAAACAGAGGTCGCATGC
Caspase3	GCTGACTTCCTGTATGCTTA	GTTGCCACCTTCCTGTTAA
Gnrh	CATTCTACTGCTGACTGTGT	CCTGGCTTCCTCTTCAATC
Mapk1 (ERK)	CCAGCATTCAGAAGTCAGA	GGATACAGAGGCAAGAAGG
Hsd17b1	CTGTGTTGGATGTGAATGTG	CTTCGTGGAATGGCAGTC
Hsd17b2	CCTGCTTCCTTCTTCTGTAT	TATCTGCTCTGGCTTGGT
FSHR	TATGGCCCTCCTCGTACTCA	AAATTGGGGCCATGCAGAGA
Star	TCCTCGCTACGTTCAAGCTG	ACGTCGAACTTGACCCATCC
Esr1	TGCTCCTAACTTGCTCCT	GATGTGGTCCTTCTCTTCC
Esr2	CAACCTCCTGATGCTTCTT	TGCTCTTACTGTCCTCTGT
Cyp19a1	CTGAACATCGGAAGAATGC	TCACCTGGAATCGTCTCA

Table S2. Raw counts of estrous-stage distribution and cycle-pattern classification during the 10-day vaginal smear monitoring period

Table S2A. Group-level estrous-stage counts and percentages

Group	Mice for smear, n	Total observations	Proestrus, n (%)	Estrus, n (%)	Metestrus, n (%)	Diestrus, n (%)	Regular cycle,n (%)	Prolonged cycle, n (%)	Irregular cycle,n (%)	Disrupted cycle*,n (%)
Control	6	60	14 (23.33%)	18 (30.00%)	8 (13.33%)	20 (33.33%)	4 (66.67%)	1 (16.67%)	1 (16.67%)	2 (33.33%)
CTX model	6	60	22 (36.67%)	18 (30.00%)	2 (3.33%)	18 (30.00%)	0 (0.00%)	5 (83.33%)	1 (16.67%)	6 (100.00%)
CoQ10	6	60	22 (36.67%)	13 (21.67%)	9 (15.00%)	16 (26.67%)	1 (16.67%)	3 (50.00%)	2 (33.33%)	5 (83.33%)
SPH	6	60	15 (25.00%)	21 (35.00%)	11 (18.33%)	13 (21.67%)	2 (33.33%)	3 (50.00%)	1 (16.67%)	4 (66.67%)

*Disrupted cycle includes prolonged and irregular cycles during the 10-day monitoring period.

Table S2B. Individual mouse-level estrous-stage counts and cycle-pattern classification

Group	Proestrus	Estrus	Metestrus	Diestrus	Total observations	Cycle pattern
Control	2	4	2	2	10	Prolonged
Control	2	3	2	3	10	Regular
Control	2	2	1	5	10	Regular
Control	4	3	1	2	10	Irregular
Control	2	3	1	4	10	Regular
Control	2	3	1	4	10	Regular
CTX model	3	4	0	3	10	Prolonged
CTX model	4	3	0	3	10	Irregular
CTX model	4	3	1	2	10	Prolonged
CTX model	4	2	1	3	10	Prolonged
CTX model	3	4	0	3	10	Prolonged
CTX model	4	2	0	4	10	Prolonged
CoQ10	3	3	0	4	10	Prolonged
CoQ10	3	3	2	2	10	Regular
CoQ10	5	1	2	2	10	Prolonged
CoQ10	2	2	4	2	10	Irregular
CoQ10	5	1	1	3	10	Irregular
CoQ10	4	3	0	3	10	Prolonged
SPH	3	2	2	3	10	Prolonged
SPH	3	2	2	3	10	Regular
SPH	2	4	2	2	10	Irregular
SPH	2	4	1	3	10	Prolonged
SPH	2	5	2	1	10	Prolonged
SPH	3	4	2	1	10	Regular

Table S3. Raw follicle-count data from ovarian histological sections

Table S3A. Raw follicle counts in each counted replicate

Group	Mature follicles	Atretic follicles	Primordial follicles
Control	4	0	2
Control	0	0	10
Control	2	1	4
CTX model	3	5	6
CTX model	0	2	5
CTX model	0	1	6
CoQ10	0	0	2
CoQ10	0	5	10
CoQ10	2	2	4
SPH	2	0	4
SPH	0	6	5
SPH	0	1	10

Table S3B. Summary of follicle-count data

Group	Mature follicles	Atretic follicles	Primordial follicles
Control	2.00 ± 2.00	0.33 ± 0.58	5.33 ± 4.16
CTX model	1.00 ± 1.73	2.67 ± 2.08	5.67 ± 0.58
CoQ10	0.67 ± 1.15	2.33 ± 2.52	5.33 ± 4.16
SPH	0.67 ± 1.15	2.33 ± 3.21	6.33 ± 3.21

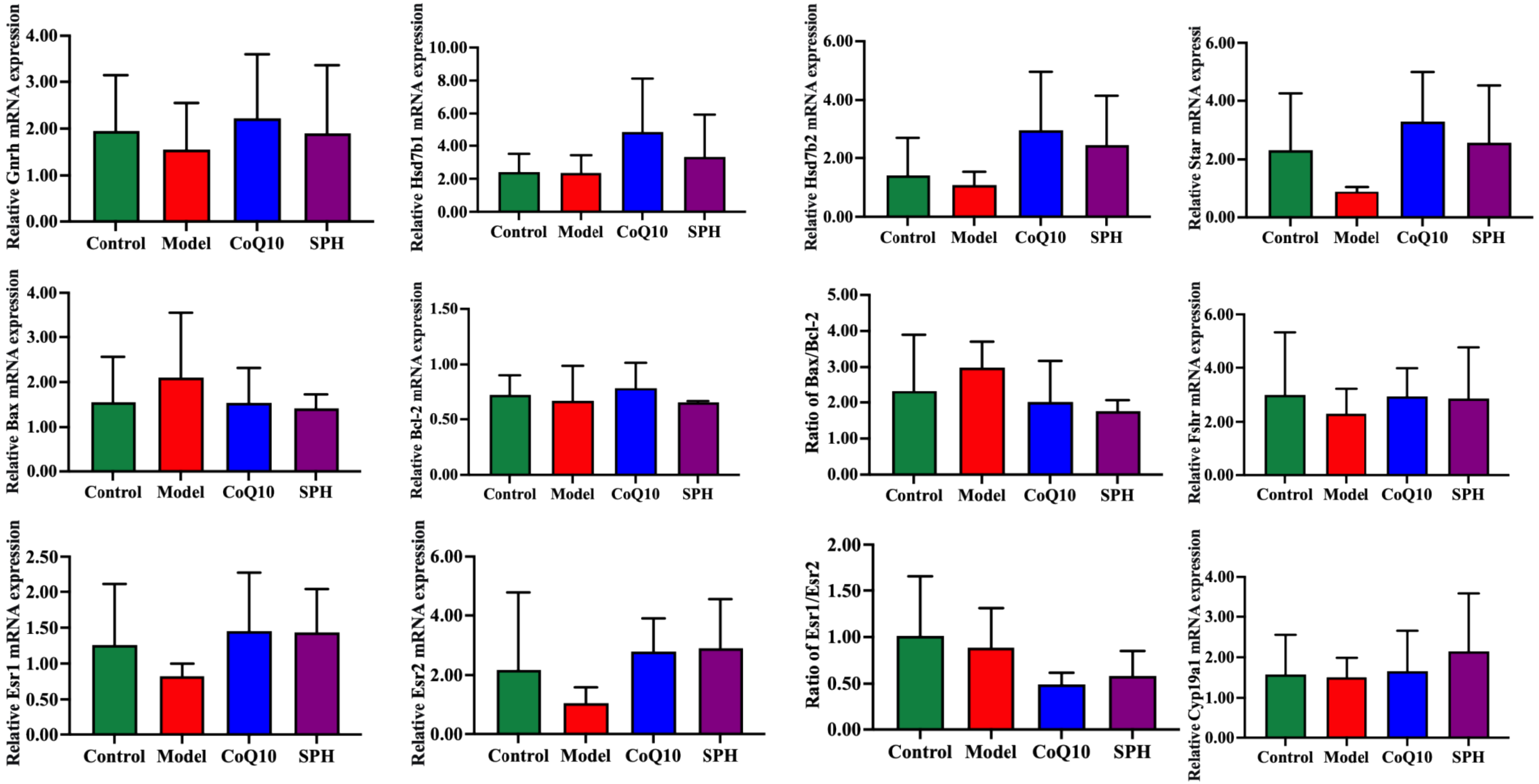

Figure S1 Effects of SPH on selected hypothalamic-related gene expression in CTX-induced POF mice. The mRNA levels of selected hypothalamic genes, excluding *Mapk1*, were measured by qRT-PCR. Each biological replicate consisted of pooled hypothalamic tissue from three mice; n = 3 pooled biological replicates per group. Data are presented as mean ± SD. Most examined hypothalamic genes did not show statistically significant differences among groups under the present experimental conditions.