

Table S1. Fluorescent quantitative PCR primers for marine medaka

Primer name	primer sequence	Genebank ID	Product size (bp)
<i>vtgr</i>	F:GACAACCCGGTCTACCTGAA; R:CTGGATTGAAGGAGGGATGA	XM_024262816.2	164
<i>vtg1</i>	F:TTGGCAGAGATGCAGCAGCGGT; R:GGAAATGCAGGACACCCCAGTAGCC	XM_024279512.2	83
<i>vtg2</i>	F:AAGCCCTCAACCACTGGCTCCCTAAT; R:TGGGCAGCGCCGTTCAAGATGTTGAT	XM_024279510.2	93
<i>star</i>	F:AGAAGGCTATCAGCATCCTCAGTG; R:AGGCAGTACCTTACTCAGGACCTT	XM_024276393.2	93
<i>lhr</i>	F:CCTGGTGGTGTGCTACTGCTAC; R:CGGCGGAGATGGCGAAGAAG	XM_024297983.2	162
<i>fshr</i>	F:GCGTGTGCGGCTGCTACC; R:CGAGATGGCGAAGAAGGAGATGG	XM_024285506.2	153
<i>erβ</i>	F:TGATCCAGGAGGCTGAGCTCCACGA; R:ACCGCTGACGGAGGCTGTTGTGAT	XM_024291918.2	121
<i>cyp19a</i>	F:ACCTCGCGTTTTTGGCAGCAAACA; R:TTTCCACAGCGCCACGTTGTTGT	XM_024296015.2	91
<i>cyp17a1</i>	F:CAGACTACAGCGACCACGTT; R:CTGGATAATGGATCAGGTAGGT	XM_024296725.1	220
<i>cyp11b</i>	F:GCATTGGCCTGTTCTCCTCATCT; R:CGGAGGGGTGGTTGTTAGCATT	XM_024267121.2	87
<i>cyp11a</i>	F:CGTTTGGGTTTACTGCTGGACTAC; R:GCGGTCAGCTTGGTTGAATATCC	XM_024282518.2	187
<i>era</i>	F:TCGCCGCTGTTGTGCTGTGATGTT; R:TCCTGGATCTGAGTGCGGGTCCGA	JF907629	84
<i>ara</i>	F:TTTGATGAACTGCGGACCTCCTAC; R:AACTGGTGCAATTTCTCACAACC	XM_024283708.2	144
<i>3βhsd</i>	F:TGGTCAACCCCGTCTATGTG; R:GGTGTCGTCAGTGGCGAAGT	XM_024260561.2	123
<i>17βhsd</i>	F:CGCTACCTCCACAAAGTTGTTGTC; R:AGTTCTGCCTCAACAGTTTCACCT	XM_024271605.2	138
<i>chgh</i>	F:ATGCCGACTATCCTGTGACC; R:AGCGTCCAAGAGTCAGAACC	XM_024282618.2	103
<i>chgl</i>	F:CAAAGTTCGTGTCTCGACCA; R:TCAGCATCAAGGGGATAAGC	XM_024281848.1	140
<i>fasn</i>	F:TCTCCTTACTGAACTGTGTAGCA; R:CCATTCCTGAGCAGACATACCA	XM_024261534.2	148
<i>dgat2</i>	F:CACTGTGCTGCTGATCTACATT; R:GAGGATCTCCTTCCACCTTGTT	XM_024266114.2	115
<i>apoba</i>	F:GGCTTCTTCTCTGAATCCATCTC;	XM_024266388.2	126

	R:GTCCTCTGTACCTGTCTCTTC		
<i>apoc1</i>	F:GATGCGACCTACACTAAGATAAGA; R:ATGTTGAAGTGAACCAGTTTCCT	XM_024267688.2	137
<i>cyp7a1</i>	F:GTCTTCAAGAGTGCCTACAGTG; R:AAGGTGGATAAGGAGTCGTTCA	XM_024268797.1	132
<i>lpl</i>	F:ACTGAGTGGATGACGGATTACA; R:GTCTGAGCTTCTGCGTTGAATT	XM_024278730.2	144
<i>thf</i>	F:CTTCGTGGTTCTGGTTCT; R:GTTGTCCGCTAGTCTGAT	XM_024260306.2	171
<i>il-8</i>	F:TGCACTGCCGCTGCATCTTGACAG; R:TCTGGGTTCAAGCAAACCTCCTGGC	XM_024289379.2	149
<i>sod</i>	F:TGTACCAGTGCAGGGGCCTCACTTCA; R:TGCGGTCACATTTCCCAGGTCCCCA	XM_024266073.1	100
<i>gpx</i>	F:GTGTGCAGAAACGACGTGGCCTGGA; R:TCGCCTTCGATGTCGCTGGTGAGGA	XM_024270129.2	111
<i>cat</i>	F:GCCAACTACCTGCAGATCCCCGTCA; R:AGTTTGGAGCGCCGCCTTGGTTGT	XM_024265602.1	110
<i>cox-1</i>	F:AGTTCGACCCACGCTGCTGTTCA; R:AAGCTGTCGGGCATCAAAGGGTGC	XM_024299369.2	83
<i>cox-2</i>	F:CAGTGCTGACCGAGCATGGCATCA; R:TTACGACCACCAGCAACCCGTCCT	XM_024282897.2	129
<i>ppara</i>	F:AACAAAGATGGCCTCCTGGTGGCT; R:ATGGAGTTGAAGCGTGTGGCGAAC	XM_024293542.2	147
<i>pparβ</i>	F:TGCATTCCAGGGTTTGTGGACCTCT; R:CTTGTGACAAAGCCTTTACCGTTGGCT	XM_024293543.2	147
<i>rps4x</i>	F:TGCCACCAGGCTCTCCAACAT; R:TTGTCCCTCTCCTCTGCGATGG	XM_024287485.2	109
<i>actb2</i>	F:GCAGGTCATCACCATCGGCAAT; R:CCTCCAGACAGCACAGTGTTGG	XM_024272788.2	172

Table S2. The actual concentration of BPAF in water

Samples	Actual concentration at t ₀ (SD) (µg/L)	Actual concentration at t ₄₈ (SD) (µg/L)	Mean (SD) (µg/L)
Control	n.d	n.d	n.d
BPAF	199.15 (4.94)	177.51 (8.44)	188.33 (12.84)

The symbol SD stands for standard deviation. The recovery efficiency of BPAF was 84%, The detection limit of BPAF is 0.5µg/L.

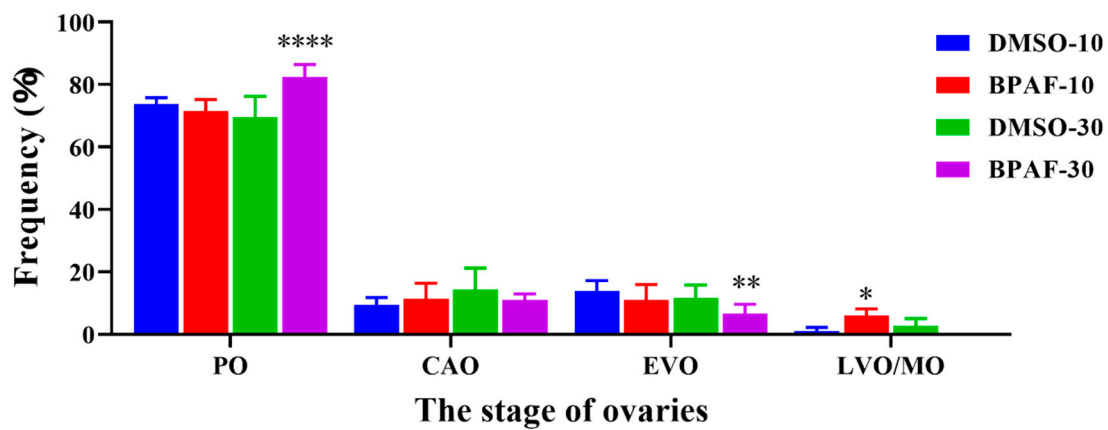


Figure S1 The alterations in relative percentages of each stage of ovaries.

Note: PO: perinucleolar oocytes; CAO: cortical alveolar oocytes; EVO: early vitellogenic oocytes; LVO/MO: late vitellogenic oocytes/mature oocytes; The results are represented as mean \pm S.D. (n = 8). Compared to the control (DMSO-10d), statistically significant differences are shown with asterisks (* $P \leq 0.05$, ** $P \leq 0.01$, and **** $P \leq 0.0001$).