

**Table 2**

qRT-PCR outcomes and descriptive statistics for genes found to be significantly altered by BPA or EE2 exposure. Sample sizes for each group are in parentheses.

Gene Symbol	Comparison (n)	Relative Abundance	U	p-value
<i>Preselected genes of interest</i>				
<i>Esr2</i>	♂ 25 BPA (7) to ♂ Veh (6)	2.38	3	<0.01
	♀ 250 BPA (6) to ♀ Veh (7)	1.67	6	0.04
<i>Oxtr</i>	♂ Veh (7) to ♂ Veh (6)	0.70	8	0.08
	♂ 25 BPA (7) to ♂ Veh (6)	1.95	2	< 0.01
	♂ 250 BPA (7) to ♂ Veh (6)	1.37	6	0.04
	♀ 2.5 BPA (6) to ♀ Veh (7)	1.37	8	0.04
	♀ 25 BPA (6) to ♀ Veh (7)	1.90	4	<0.01
	♀ 250 BPA (6) to ♀ Veh (7)	1.97	5	0.02
	♀ 25000 BPA (6) to ♀ Veh (7)	1.58	4	<0.01
	♀ 0.5 EE2 (5) to ♀ Veh (7)	2.01	0	<0.01
<i>Avpr1a</i>	♂ 2.5 BPA (4) to ♂ Veh (6)	0.75	2	0.04
	♂ 25 BPA (7) to ♂ Veh (6)	2.27	0	<0.01
	♂ 250 BPA (7) to ♂ Veh (6)	1.56	4	<0.01
	♂ 0.5 EE2 (7) to ♂ Veh (6)	1.41	6	0.04
<i>Ar</i>	♂ 25 BPA (7) to ♂ Veh (6)	2.43	3	<0.01
	♀ 250 BPA (6) to ♀ Veh (7)	1.84	6	0.04
<i>Gadd45b</i>	♀ 0.5 EE2 to (5) ♀ Veh (7)	1.77	5	0.05
<i>Genes selected from RNAseq analysis</i>				
<b><i>Camk4</i></b>	♀ Veh (5) to ♂ Veh (5)	0.54	0	<0.01
	♂ 25 BPA (7) to ♂ Veh (5)	1.75	3	<0.01
	♀ 2.5 BPA (6) to ♀ Veh (5)	2.54	0	<0.01
	♀ 25 BPA (6) to ♀ Veh (5)	2.02	0	<0.01
	♀ 250 BPA (6) to ♀ Veh (5)	2.24	0	<0.01
	♀ 2500 BPA (6) to ♀ Veh (5)	1.68	5	0.08
	♀ 25000 BPA (6) to ♀ Veh (5)	2.48	0	<0.01
	♀ 00.5 EE2 (6) to ♀ Veh (5)	1.83	0	<0.01
	♀ 0.5 EE2 (5) to ♀ Veh (5)	2.52	0	<0.01
	<b><i>Grm5</i></b>	♂ 25 BPA (7) to ♂ Veh (6)	1.54	4
♀ 25 BPA (6) to ♀ Veh (4)		1.62	3	0.07
♀ 250 BPA (6) to ♀ Veh (4)		1.89	0	<0.01
♀ 2500 BPA (5) to ♀ Veh (4)		1.71	0	0.02
♀ 25000 BPA (6) to ♀ Veh (4)		2.01	2	0.04
♀ 0.05 EE2 (6) to ♀ Veh (4)		1.46	1	0.02
♀ 0.5 EE2 (3) to ♀ Veh (4)		2.14	0	0.06