

Supplemental Information

Table S3. Functional enrichment of E2 affected genes in ECC-1

p-value	genes in category	genes affected by E2 in ECC-1	Overlap	Term	Category
2.01E-09	90	849	25	REAC:192823	Viral mRNA Translation
2.01E-09	90	849	25	REAC:192841	Viral Protein Synthesis
2.01E-09	90	849	25	REAC:192704	Synthesis of PB1-F2
8.24E-09	111	849	27	REAC:157279	3' -UTR-mediated translational regulation
8.24E-09	111	849	27	REAC:156827	L13a-mediated translational silencing of Ceruloplasmin expression
2.65E-02	50	849	11	REAC:156826	Dissociation of L13a from the 60s ribosomal subunit
1.90E-07	126	849	27	REAC:72766	Translation
5.84E-09	94	849	25	REAC:156842	Eukaryotic Translation Elongation
2.64E-09	91	849	25	REAC:156902	Peptide chain elongation
1.53E-09	89	849	25	REAC:156912	Peptide transfer from P-site tRNA to the A-site tRNA
2.01E-09	90	849	25	REAC:156907	Aminoacyl-tRNA binds to the ribosome at the A-site
2.64E-09	91	849	25	REAC:156915	Translocation of ribosome by 3 bases in the 3' direction
2.01E-09	90	849	25	REAC:156923	Hydrolysis of eEF1A:GTP
4.70E-08	119	849	27	REAC:72613	Eukaryotic Translation Initiation
4.70E-08	119	849	27	REAC:72737	Cap-dependent Translation Initiation
7.18E-10	101	849	27	REAC:72689	Formation of a pool of free 40S subunits
2.01E-09	90	849	25	REAC:72673	Release of 40S and 60S subunits from the 80S ribosome
2.44E-06	51	849	16	REAC:72676	eIF3 and eIF1A bind to the 40S subunit
6.17E-06	54	849	16	REAC:72695	Formation of the ternary complex, and

					subsequently, the 43S complex
6.17E-06	54	849	16	REAC:72691	Formation of the 43S pre-initiation complex
5.37E-05	62	849	16	REAC:72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S
4.18E-05	61	849	16	REAC:72649	Translation initiation complex formation
4.18E-05	61	849	16	REAC:156808	Formation of translation initiation complexes yielding circularized Ceruloplasmin mRNA in a 'closed-loop' conformation
3.25E-05	60	849	16	REAC:157849	Formation of translation initiation complexes containing mRNA that does not circularize
4.18E-05	61	849	16	REAC:72702	Ribosomal scanning and start codon recognition
3.25E-05	60	849	16	REAC:72621	Ribosomal scanning
4.18E-05	61	849	16	REAC:72697	Start codon recognition
1.03E-08	112	849	27	REAC:72706	GTP hydrolysis and joining of the 60S ribosomal subunit
4.18E-05	61	849	16	REAC:72619	eIF2:GTP is hydrolyzed, eIFs are released
2.01E-09	90	849	25	REAC:72672	The 60S subunit joins the translation initiation complex
2.01E-09	90	849	25	REAC:72671	eIF5B:GTP is hydrolyzed and released
2.64E-09	91	849	25	REAC:72764	Eukaryotic Translation Termination
2.64E-09	91	849	25	REAC:141671	Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex
2.64E-09	91	849	25	REAC:141691	GTP bound eRF3:eRF1 complex

2.64E-09	91	849	25	REAC:141673	binds the peptidyl tRNA:mRNA:80S Ribosome complex GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptid e:80S Ribosome complex
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Table S4. Association between ESR1 binding and gene expression
ECC-1

Gene categories	Total genes	Genes associated with E2 only ESR1 sites	Genes associated with E2+GEN ESR1 sites	Genes associated with E2+GEN+BPA ESR1 sites
E2 only up	352	90	33	20
E2+GEN up	156	15	61	23
E2+GEN+BPA up	54	4	6	34
E2 only down	401	74	17	6
E2+GEN down	47	7	13	1
E2+GEN+BPA down	2	0	0	1
T-47D				
Gene categories	Total genes	Genes associated with E2 only ESR1 sites	Genes associated with E2+GEN ESR1 sites	Genes associated with E2+GEN+BPA ESR1 sites
E2 only up	337	86	31	26
E2+GEN up	105	7	35	38
E2+GEN+BPA up	1	0	0	0
E2 only down	158	31	15	6
E2+GEN down	14	2	2	2
E2+GEN+BPA down	0	0	0	0

Table S5. QPCR primer sequences

Primer	Sequence
TGFA Forward	AGGTCCGAAAACACTGTGAGT
TGFA Reverse	AGCAAGCGGTTCTTCCCTTC
ZNF608 Forward	CCTTGTATGGGATTCCCGAGA
ZNF608 Reverse	CGCTGCTCACACTTTGACC
DOK7 Forward	TCCTGTTCGACTGCATCGTC
DOK7 Reverse	GGGGACTTGGGTCTGGTAG
SLC22A5 Forward	GAAGGCCCCACTCACAATCTC
SLC22A5 Reverse	GGTCACGAACAGCACATTCTT
CTCF Forward	ACCTGTTCTGTGACTGTACC
CTCF Reverse	ATGGGTTCACTTTCCGCAAGG

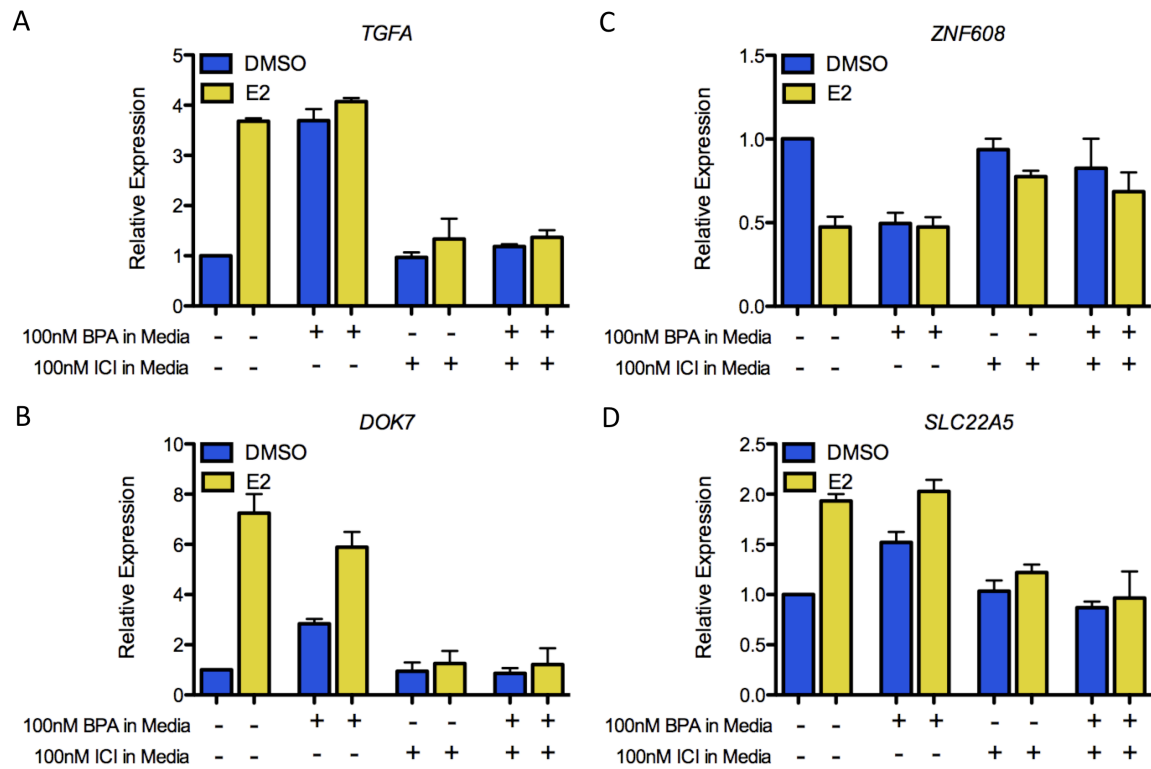


Figure S1. Expression changes in response to long-term BPA exposure are dependent on ESR1. Relative expression measurements are shown for TGFA (A), DOK7 (B), ZNF608 (C) and SLC22A5 (D) for cells treated with combinations of BPA and ICI 182,780 for five days. Cells were then treated with either DMSO (blue) or E2 (yellow) for four hours. Expression was then measured by qPCR and error bars represent s.e.m.

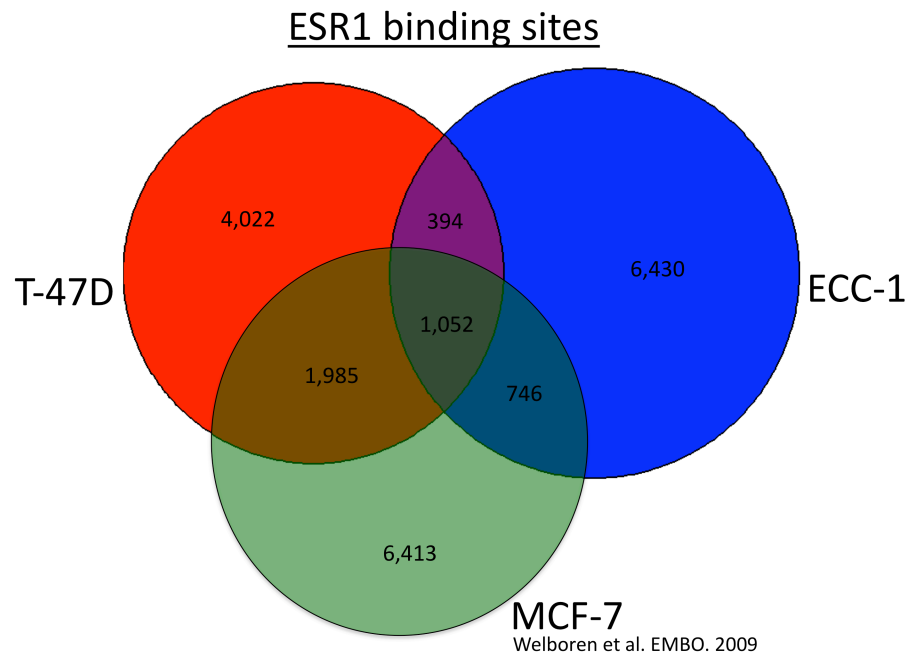


Figure S2. Overlap between ESR1 binding sites in MCF-7, ECC-1 and T-47D. The overlap between ESR1 binding sites in T-47D, MCF-7 and ECC-1 is shown as a venn diagram. ESR1 binding sites in MCF-7 are more similar to T-47D than ECC-1.