

## SUPPLEMENTARY MATERIAL

Table S1. Sequences of synthetic EREs, ER binding affinities and transcriptional activity in transfected cells

name	sequence	ER $\alpha$ binding (K <sub>d</sub> in nM).	ER $\beta$ binding (Kd in nM)	E <sub>2</sub> activation-ER $\alpha$ (10nM unless otherwise indicated)
ERec38	5'-CCAGGTCAGAGTGACCTGAGCTAAAATAACACATTCAG-3' (17bp ERE)	0.24 (39); 0.11 (108)	0.15 (24) 0.64 (108)	2-fold in MCF-7 cells (94); 4-fold in CHO-K1 cells transfected with ER $\alpha$ (24)
ERec13	5'-CTGGTCACTCTGACCGG-3'	1.08 (108)	1.72 (108)	1.85 in CHO-K1 cells transfected with ER $\alpha$ (108)
ERE15	5'-AGCTTCGAGGAGGTCACAGTGACCTGGAGCG-3'	0.15-0.25 (56) 0.15 (100 mM KCl) (198)		3.92-fold in CHO-K1 cells transfected with ER $\alpha$ (108)
ERec15	5'-TAGGTCAGAGTGACCTAG-3'	0.11 (108)	0.13 (108)	3.92-fold in CHO-K1 cells transfected with ER $\alpha$ (108)
ERec17	5'-CCAGGTCAGAGTGACCTGAG-3'	0.18 (108)	0.25 (108)	4.09-fold in CHO-K1 cells transfected with ER $\alpha$ (108)
ERec19	5'-CCAGGTCAGAGTGACCTGGAG-3'	0.25 (108)	0.41 (108)	4.66-fold in CHO-K1 cells transfected with ER $\alpha$ (108)
ERec17,4	5'-TCAGGTCAGAGTGACCTGAGCT-3'	0.11 (108)	0.45 (108)	3.12-in CHO-K1 cells transfected with ER $\alpha$ (108)
ERec17,6	5'-TCAGGTCAGAGTGACCTGAGCTAA-3'	0.25 (108)	0.34 (108)	3.99-fold in CHO-K1 cells transfected with ER $\alpha$ (108)
ERec17,11	5'-TCAGGTCAGAGTGACCTGAGCTAAAATAA-3'	0.10 (108)	0.19 (108)	4.89-fold in CHO-K1 cells transfected with ER $\alpha$ (108)
F-ERE	5'-AGCTTCGAGGAGGTCACAGTGACCTGGAGCGGATC-3'	8 at 200 mM KCl (109)		
F-ERE-mut A	5'-AGCTTCGAGGTGGTCACAGTGACCAAGGAGCGGATC-3'	200 at 200 mM KCl (109)		
F-ERE-mut B	5'-AGCTTCGAGGACGTCACAGTGACGTGGAGCGGATC-3'	336 at 200mM KCl (109)		
F-ERE-mut C	5'-AGCTTCGAGGAGGTCACAGTGAGCTGGAGCGGATC-3'	288 at 200mM KCl (109)		
F-ERE-mut D	5'-AGCTTCGAGGAGGACACAGTGTCTGGAGCGGATC-3'	272 at 200mM KCl (109)		
F-ERE-mut E	5'-AGCTTCGAGGAGGTCACAGTACCTGGAGCGGATC-3'	648 at 200mM KCl (109)		
F-ERE-mut E	5'-AGCTTCGAGGAGGTCACAGACCTGGAGCGGATC-3'	248 at 200mM KCl (109)		
EREmT	5'-AGCTTCGAGGAGGTCACAGTGATCTGGAGCG-3'	390 (100 mM KCl) (198)		
ERE''c''	5'-GGACACGATGTCC-3'	No binding (199)		
ERE mutant	5'-GGCCACAGTGAAC-3'			No activity (102)
EREmut1	5'-GGACACTGTGACC-3'			2.9-fold induction in MCF-7 cells (102)
EREmut4	5'-GGACACTGTGTCC-3'			4.3-fold induction in MCF-7 cells (102)
EREmut3	5'-GGACACTGTGTAC-3'			3.6-fold induction in MCF-7 cells (102)
PS2 mutant M1	5'-GGTCACGGTTGCC-3' (imperfect 13 bp ERE)			2-fold in HeLa cells transfected with HEO ER $\alpha$ (148);
PS2 mutant M1	5'-GGTCACGGTGGAG-3' (imperfect 13 bp ERE)			1.2-fold in HeLa cells transfected with HEO ER $\alpha$ vector (148);
VitERE mutant	5'-GGTCACGGTGGCC-3' (imperfect 13 bp ERE)			No induction (200)

Table S1. Continued

C3M1	5'-CAGGTGGCCCTTACTCTGGGAGAGT-3'			4-fold induction with ER $\alpha$ in HepG2 cells treated with 100 nM E <sub>2</sub> (163)
ERE mutant	5'-GATCACAGTGATC-3'	185 (138)		
C3m2	5'-GGACACCCCTGGCC-3'			6-fold in HepG2 transfected with ER $\alpha$ (201)
mmERE	5'-TCAGATTTCAGAAATCTGA-3'	No binding (202)		
mutERE	5'-CCGTCACAGTGACCT-3'	No binding (203)		Transcriptional activation in yeast is 20% of that for 15bp ERE palindrome (203)
2bp spacer	5'-GGTCAAGTGATC-3'	No binding (49)		
overERE	5'-AGCTGCTCAGGTGACCTGACCTGACCTCTACT-3'	Two ER $\alpha$ dimers bind (128)		4-fold higher transcriptional activity than a consensus ERE in HepG2 cells with 100 nM E <sub>2</sub> (128)
mt-fos-ERE	5'-TCGACCTTTATCCATTTACCACAGCCCAGGCCATG-3'	ER $\alpha$ binds (145)	No binding (145)	
EREZ20	5'-CCAGGTCAGAGTGGCCTGAGCTAAAAAATACACATTCAG-3'			
EREZ22	5'-CCAGGTCAGAGTAGCCTGAGCTAAAAAATACACATTCAG-3'	1.39 (39)		
EREZ23	5'-CCAGGTCAGAGTGTCTGAGCTAAAAAATACACATTCAG-3'	1.58 (39)		
EREZ25	5'-CCAGGTCAGAGAAATGACCTGAGCTAAAAAATACACATTCAG-3'	No binding (39)		
EREZ26	5'-CCAGGTCAGGTGACCTGAGCTAAAAAATACACATTCAG-3'	1.51 (39)		
EREZ27	5'-CCGGTCAGAGTGACCGAGCTAAAAAATACACATTCAG-3'	0.36 (39)		
EREm(-)	5'-CTGGTCACTCTGACC-3'	0.81 (44)		
EREhs(-)	5'-CTGGTCACTCTGCCGGTCAGAGTGACCAGCTGGTCACTC-3'	1.65 (44)		
GCERec	5'-CCAGGTCAGAGTGACCTGAGCTGACAGGACTGACCAG-3'	0.28 (44)		
ERExx(+)	5'-CCAGGTCAGAGTGACCGACGTTAAAAAATAACAATTCAG-3'	1.56 (44)		
EREc(-)	5'-CCAGGTCAGAGTGACCTGAG-3'	2.02 (45)		
EREp13	5'-CCC GCGAGATATGGT CAGAGTGACCGAGATTCCTA-3'	6.9 (21)		
EREp13d1	5'-CCC GCGAGATATGGG CAGAGTGACCGAGATTCCTA-3'	No binding (21)		
EREp13g(-6)c	5'-CCC GCGAGATATCGT CAGAGTGACCGAGATTCCTA-3'	No binding (21)		
EREp13(-5)c	5'-CCC GCGAGATATGCT CAGAGTGACCGAGATTCCTA-3'	No binding (21)		
EREp13(-3)g	5'-CCC GCGAGATATGGT GAGAGTGACCGAGATTCCTA-3'	No binding (21)		
EREp13(-2)t	5'-CCC GCGAGATATGGT CTGAGTGACCGAGATTCCTA-3'	No binding (21)		
EREp13d1+A	5'-CCC GCGAGATATAGGG CAGAGTGACCGAGATTCCTA-3'	Binding, but Kd ND (21)		
EREp13d1+A	5'-CCC GCGAGATATGGG CAGAGTGACCGAGATTCCTA-3'	Binding, but Kd ND (21)		
EREp15	5'-CCC GCGAGATATAGGT CAGAGTGACCTGAGATTCCTA-3'	0.54 (21)		
EREp15d2	5'-CCC GCGAGATATAGGG CTGAGTGACCTGAGATTCCTA-3'	20 (21)		
EREp17	5'-CCC GCGAGATACAGGT CAGAGTGACCTGAGATTCCTA-3'	0.25 (21)		
EREc17d2	5'-CCC GCGAGATACAGGG CTGAGTGACCTGAGATTCCTA-3'	20 (21)		
CAR oxytocin	5'-GGTGACCTTGAAC-3'			4-fold in P19 EC transfected with ER $\alpha$ cells and treated with 100 nM E <sub>2</sub> (204)
GTR oxytocin	5'-GGTGGCCTTGACC-3'			6-fold in P19 EC transfected with ER $\alpha$ cells and treated with 100 nM E <sub>2</sub> (204)

The underlined nucleotides constitute the consensus ERE half-site IR sequence and nucleotides in bold type are altered from the consensus.