Supplementary Table 1. A list of reported Human, Mouse and Rat ERα target genes[a]

Gene Symbol	UniGene ID	Start[b]	End[b]	ERE Sequence	Ref
Human Genes					
ABCG2	Hs.194720	-195	-171	acggcagggTGACCc	1
AGT	Hs.19383	102	116	aGGGCAtcgTGACCc	2
BCL2	Hs.79241	195	209	cGGTCGccaGGACCt	3,39*
BRCA1	Hs.194143	2022	2036	tGGTCAggcTGGTCt	4
C3 1	Hs.284394	-227	-215	aGGTGGcccTGACCc	5
C3 2	Hs.284394	32	46	cTGTCCctcTGACCc	5
CHAT	Hs.302002	508	522	aGGCTAcgaTGACGt	6
COMT 1	Hs.240013	-259	-245	cagggagtgTGACCc	7
COMT 2	Hs.240013	-478	-464	gagcatgggTGACCa	7
COX7A2	Hs.423404	452	466	gGGTCAaggTGACCc	8
CTSD	Hs.343475	-270	-256	gGGCCGggcTGACCc	9,40*
CYP1B1	Hs.154654	-63	-49	aGGTCGcgcTGCCCt	10
EBAG9	Hs.9222	6	20	gGGTCAgggTGACCt	8
EFEMP1	Hs.76224	-272	-258	aTGTCAacgTGTCCt	11
F12	Hs.1321	-30	-16	aGGGCAgctTGACCa	12
FOS	Hs.25647	90	101	cCGGCAgcgTGACCc	13,41*
HRAS	Hs.37003	1716	1730	agagtgcgcTGACCa	14
HOXA10	Hs.110637	-319	-307	gGGTCCcttAGAAGg	15
LCN2	Hs.204238	-823	-809	tGGTCTcagTGACCt	16
LTF	Hs.437457	-363	-349	aGGTCAaggCGATCt	17
NQO1	Hs.406515	-446	-432	gAGTCActgTGACTg	18
OVGP1	Hs.1154	-170	-156	gGGTCActgTGACTc	19
OXT	Hs.113216	-165	-151	cGGTGAcctTGACCc	20
PELP1 1	Hs.409251	-591	-577	acggcagggTGACCc	21
PELP1 2	Hs.409251	-1021	-1007	catccaccaTGACCt	21
PGR 1	Hs.2905	553	567	gGCAGGagcTGACCa	22

PGR 2	Hs.2905	1155	1169	aGGTCAccaGCTCTt	22
PTMA	Hs.459927	-765	-751	gGCTCTcagTGACCc	23
SERPINE1	Hs.414795	-427	-413	actccacagTGACCt	24
SERPINB9	Hs.104879	-197	-183	gGGGGAcccTGACCt	25
TERT	Hs.439911	-2687	-2673	tGGTCAggcTGATCt	26
TFAP2C 1	Hs.440411	120	134	tGGTCAccgTGACCc	27
TFAP2C 2	Hs.440411	68	82	cgtgtccagTGACCc	27
TFF1	Hs.350470	112	126	aGGTCAcggTGGCCa	28
TGFA 1	Hs.170009	-214	-200	gGGTCAgctGTGCCc	29
TGFA 2	Hs.170009	-190	-176	aGGTGAcggTAGCCg	29
VEGF	Hs.73793	-1560	-1546	tAATCAgacTGACTg	30,42,43*
Mouse Genes					
Agt	Mm.285467	-2379	-2365	aGGTCAcctTGACCc	31
Chat	Mm.256716	-2114	-2100	aGGCCAcgaTGACAt	32
Ltf	Mm.282359	-340	-326	aGGTCAaggTAACCc	17
Ovgp1	Mm.298812	-110	-96	cGGTCAttgTGACTc	33
Rat Genes					
Avp	Rn.9976	-4324	-4310	gGGCCAgccTGACCg	34
Ckb	Rn.1472	-558	-544	aGGTCAgaaCACCCt	35*
Prl 1	Rn.9759	-1568	-1554	tTGTCActaTGTCCt	36
Prl 2	Rn.9759	-1547	-1533	aGGTCAtaacgattt	36
Oxt 1	Rn.48915	-115	-101	gGAACAgttTGACCc	37
Oxt 2	Rn.48915	-160	-146	cGGTGAcctTGACCc	37
Vegf	Rn.1923	399	411	gGGGCAaagTGACTg	38

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[a]The experimentally verified ERE motifs are referred in the **Supplementary References** 1-43.

[b]The start and end positions are relative to TSS as reported.

The ERE Positional Weight Matrix (ERE_PWM)

Pos	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
A	18	8	5	4	1	29	7	7	7	0	1	39	1	1	6
C	8	3	3	9	33	4	21	15	14	0	0	1	43	39	18
G	13	31	34	9	8	10	11	15	19	4	44	3	0	1	6
T	7	4	4	24	4	3	7	9	6	42	1	3	2	5	16
Con	N	G	G	T	C	A	N	N	N	T	G	A	C	C	N

Sources: 48 experimentally verified ERE motifs from 40 ERα target genes of Human, Mouse, Rat. The PWM is consistent with PWM developed by O'Lone *et al.* (Ref 11 in main body).

The ERE Positional Weight Matrix (ERE_PWM_A) constructed without two genes (bcl-2 and c-fos).

Pos	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
A	18	8	5	4	1	29	7	7	6	0	1	37	1	1	6
C	7	3	3	8	31	4	20	14	13	0	0	1	41	37	17
G	12	29	32	9	8	8	10	14	19	3	42	3	0	1	6
T	7	4	4	23	4	3	7	9	6	41	1	3	2	5	15
Con	N	G	G	T	C	A	N	N	N	T	G	A	C	C	N

Sources: 46 experimentally verified ERE motifs from 38 ERα target genes of Human, Mouse, Rat. The PWM is consistent with PWM developed by O'Lone *et al.* (Ref 11 in main body).

***Note:** The genes such as bcl-2 (BCL2, 39) and c-fos (FOS, 40) have also been reported to be involved with an ERα/Sp1 pathway. The other genes such as cathepsin D (CTSD, 41), progesterone receptor (PR, 22), telomerase (TERT, 26), and Ckb (rat, 35) are thought that ERα and SP1 formed a complex in which both bind to ERE half-site and SP1

binding site. Stoner et al. (42) have found that E2 induced VEGF gene expression in ZR-75 cells through ERα/SP1 and ERα/SP3 interacting with a GC rich region in the promoter. However, studies from Taylor's group (30) and Perrot-Applanat's group (43) have identified an imperfect ERE consensus in the VEGF promoter when it was induced by E2 in MCF-7 cell. Two review papers lately published (Reference 11 in the main body of our manuscript, and Gruber et al. in *TRENDs in Endocrinology and Metabolism*, Vol. 15, 2004) have still quoted most of these genes as direct binding which may require an additional transcriptional factor such as Sp1. In either case, we have constructed the ERE_PWM_A after removing 2 ERE consensus from 2 genes (bcl-2 and c-fos) and found there is no effect to the PWM and therefore there is no effect to the CART model. That is because our PWM used a core region from positions 10 to 14 which represents a half site of ERE (TGACC) instead of a perfect ERE consensus (GGTCAnnnTGACC). We also analyzed the frequency of Sp1 binding sites which co-exists with ERE within the 455 bases promoter regions for three data sets (experimentally confirmed ERα targets, ChIP-on-chip data and OMGProm data set). The results and the **Table 3** were updated with new statistical data on a basis of new PWM and some explanation is in the section of Discussion.

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