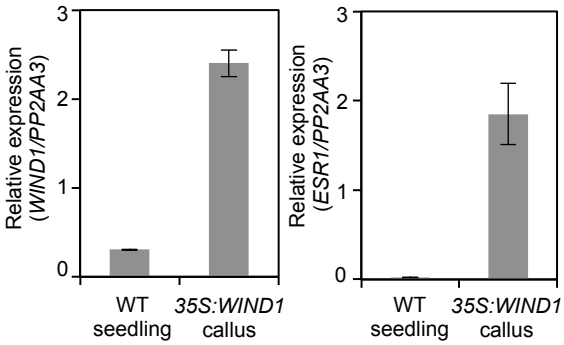
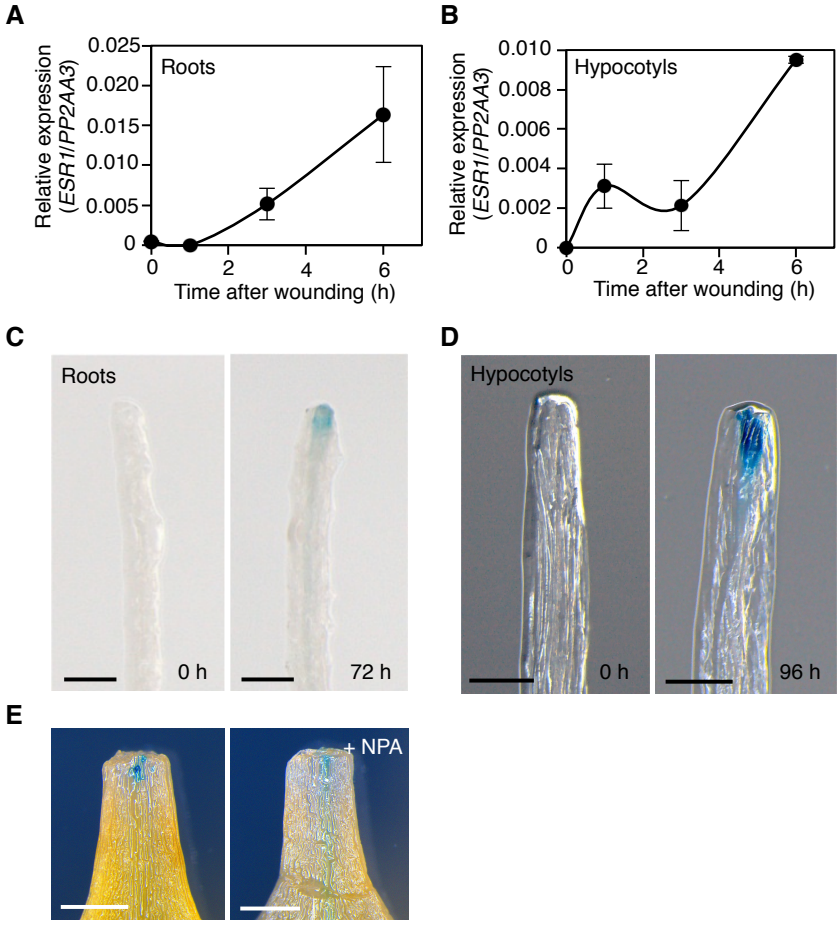


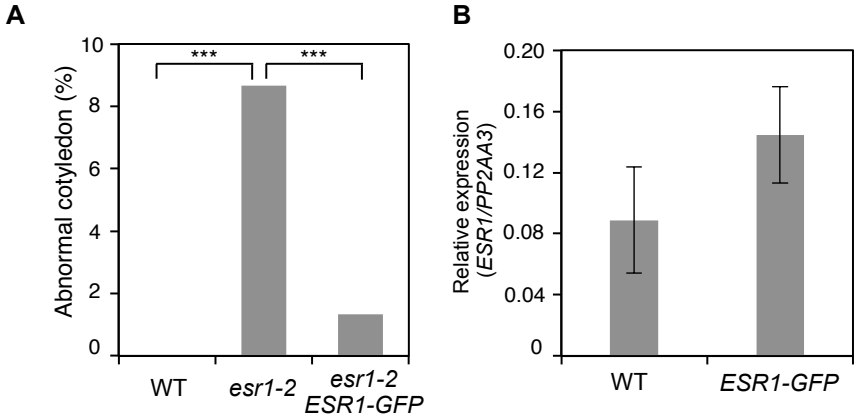
Supplemental Figure 1. *ESR1* is up-regulated in callus induced by WIND1 overexpression

RT-qPCR analysis of *WIND1* (left panel) and *ESR1* (right panel) expression in 14-day-old wild-type (WT) seedlings and *35S:WIND1* callus. Expression levels are normalised against those of the *PP2AA3* gene. Data are mean ± SE (n = 3, biological replicates).

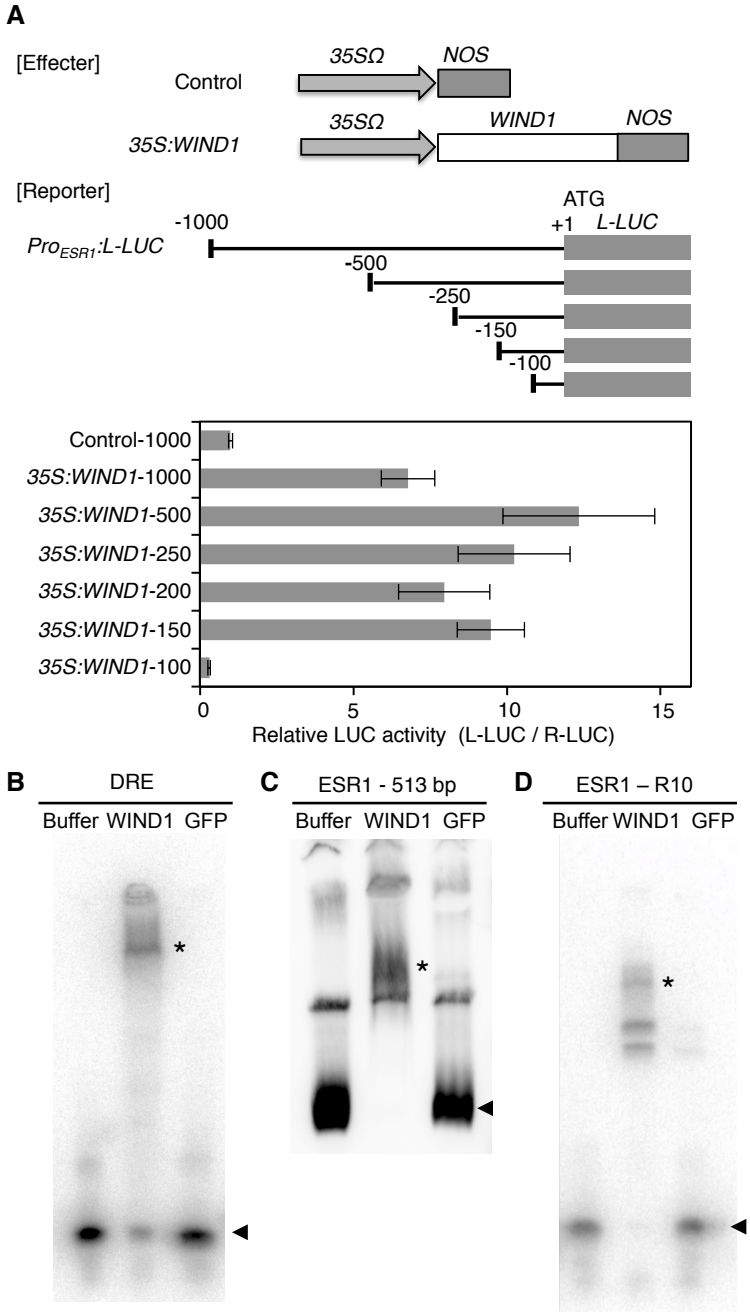


Supplemental Figure 2. Wounding activates the *ESR1* expression in roots and hypocotyls.

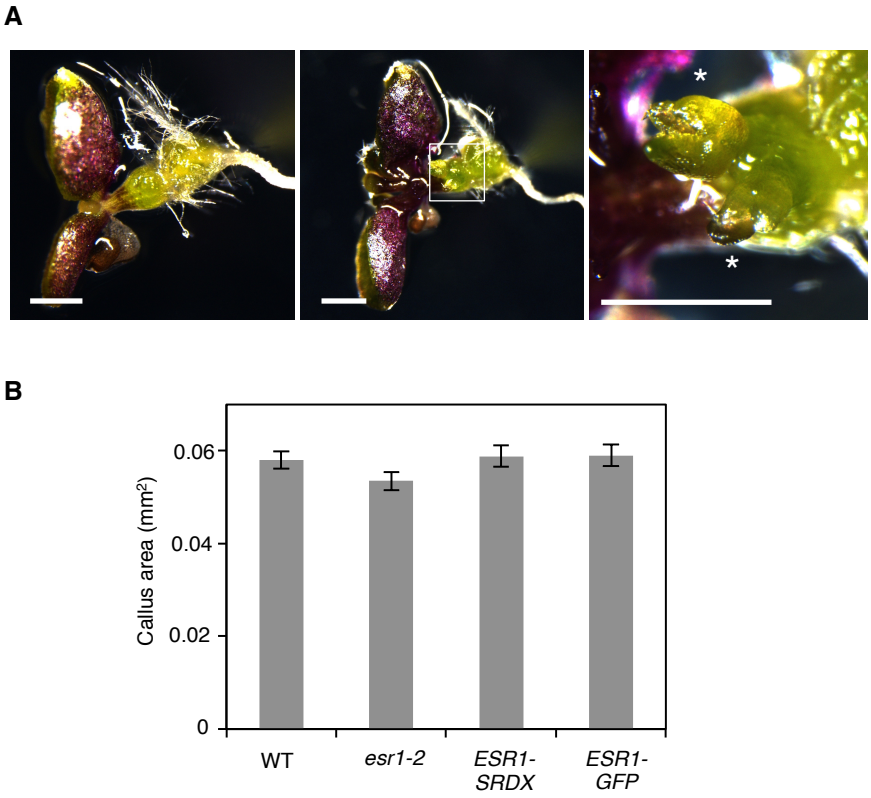
(**A**, **B**) RT-qPCR analysis of *ESR1* expression in root (**A**) and hypocotyl (**B**) explants after wounding. 14-day-old, light-grown roots and 7-day-old, dark-grown hypocotyls were cut and their explants were cultured on phytohormone-free MS medium. The *ESR1* expression is increased within the few hours after wounding. Mean expression levels are normalized against those of *PP2AA3*. Data are mean ± SE (n = 3, biological replicates). (**C**, **D**) Induction of the *ESR1* promoter activity in cut roots (**C**) and hypocotyls (**D**) of Pro_{ESR1}*:GUS* plants as visualized by GUS staining. Representative images of root explants at 0 and 72 h and hypocotyl explants at 0 and 96 h after wounding are shown. (**E**) Inhibition of polar auxin transport by 1 μM N-1-naphthylphthalamic acid (NPA) does not prevent the *ESR1* activation at wound sites. Representative images of petiole explants at 48 h after wounding are shown. Scale bars = 250 μm in (**C**) and (**D**), and 500 μm in (**E**).



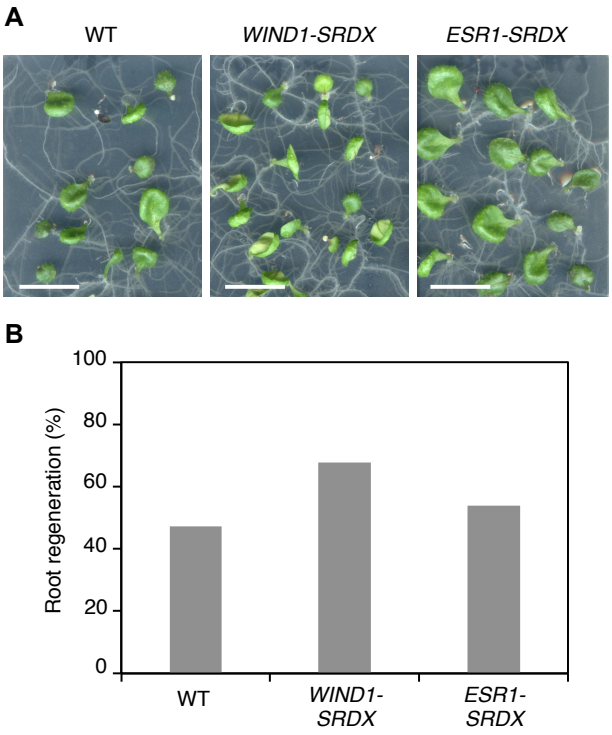
Supplemental Figure 3. Characterization of *Pro$_{ESR1}$:ESR1-GFP* plants.
(**A**) ESR1-GFP proteins, expressed by the *ESR1* promoter, complement the cotyledon phenotype in *esr1-2* mutants transformed with the *Pro$_{ESR1}$:ESR1-GFP* (*ESR1-GFP*) vector. The frequency of abnormal, i.e., single, triple or fused, cotyledons was scored in WT, *esr1-2* and *esr1-2 ESR1-GFP* plants (n ≥ 950 per genotype). Statistical significance was determined by a proportion test (***p < 0.001). (**B**) RT-qPCR analysis of *ESR1* expression in *ESR1-GFP* plants. Total RNA was extracted from wound sites of leaf explants at 3 h after wounding. Mean expression levels are normalized against those of *PP2AA3*. Data are mean ± SE (n = 3, biological replicates).



Supplemental Figure 4. WIND1 directly binds the *ESR1* promoter *in vitro*.
(**A**) WIND1-induced transient activation of *ESR1* expression in Arabidopsis culture cells. Co-bombardment of an effecter construct, *35S:WIND1*, and a reporter construct, *Pro$_{ESR1}$:L-LUC*, causes reproducible induction of 1,000-bp *ESR1* promoter as judged by the relative lucifererase activity. Promoter deletion analyses showed that the 150-bp promoter sequence is sufficient for the *ESR1* activation by WIND1. Data are mean ± SE (n = 3, technical replicates). 35SΩ, cauliflower mosaic virus 35S promoter with the tobacco mosaic virus omega translation amplification sequence; NOS, *Agrobacterium* nopaline synthase transcriptional terminator; L-LUC, firefly luciferase; R-LUC, *Renilla* luciferase. (**B**) An EMSA shows that MBP-WIND1-His6 (WIND1) proteins bind the Dehydration Responsive Element (DRE) sequence, shifting the position of the DRE probe. (**C**) MBP-WIND1-His6 (WIND1) proteins bind the 513-bp promoter sequence of *ESR1*. (**D**) MBP-WIND1-His6 (WIND1) proteins bind the R10 sequence, located between -153 and -104 bp from the *ESR1* translational start site, *in vitro*. Arrowhead and asterisk show free and shifted DNA probes, respectively. Note that the incubation of these probes with buffer alone or MBP-GFP-His6 (GFP) proteins does not cause the same band shift, indicating that the band shift is caused by WIND1's binding to the probes. The DRE probe in (**B**) and ESR1 R10 probe in (**D**) were detected radioactively, and the 513-bp ESR1 probe in (**C**) was detected chemiluminescently.



Supplemental Figure 5. ESR1 overexpression induces callus with competency for shoot regeneration.
(A) Callus that develop in unwounded *XVE-ESR1* plants regenerate shoots on SIM. (Left panel) Callus developing from unwounded *XVE-ESR1* plants cultured in the presence of 10 µM 17b-estradiol. (Middle panel) Regenerating shoots from same *XVE-ESR1* plants after transfer to SIM. (Right panel) Magnified view of regenerating shoots. Asterisks mark regenerating shoots. (**B**) ESR1 is not required for *in vitro* callus formation. Root explants of WT, *esr1-2*, *ESR1-SRDX* and *ESR1-GFP* seedlings were cultured on CIM for 4 days and the projected area of callus was quantified. Data are mean ± SE (n = 9 per genotype). Scale bars = 500 µm in (**A**).



Supplemental Figure 6. WIND1 and ESR1 are not required for root regeneration from leaf explants.

(**A**) Root regeneration at wound sites of WT, *WIND1-SRDX* and *ESR1-SRDX* leaf explants. Leaf explants were cultured on phytohormone-free MS medium and root regeneration phenotypes were recorded 20 days after wounding. (**B**) Quantitative analysis of root regeneration phenotypes at 10 days after wounding Data are shown as frequency (%) of explants regenerating roots (n ≥ 20 per genotype). Scale bars = 10 mm in (**A**).

Name	Sequence
PRIMERS FOR GENOTYPING	
ESR1f	ATGGAAAAAGCCTTGAGAAACTTC
Spm8	GTTTTGGCCGACACTCCTTAC
ESR1r	CTATCCCCACGATCTTCGGCAAGT
ESR1 Cf	CGGTGGTTTATCGTTGGGATCA
GFP Nr	TTGAAGTCGATGCCCTTCAG
SRDXr	AGCGAAACCCAAACGGAGTTCTAG
PRIMERS FOR CLONING	
ESR1 XVE XhoIf	ACGTTAATTAAATGGAAAAAGCCTTGAGAAACTT
ESR1 XVE SpeIr	AACCACTAGTCTATCCCCACGATCTTCGGCAAGTA
ESR1 Genome SpeIf	AGGACTAGTTTAACAGTATAAAAACAGTTATCATTT
ESR1 Genome SmaIr	AATCCCGGGTCCCCACGATCTTCGGCAAGTACAGCCT
ESR1pro1000 WT SacIIf	TCCCCGCGGCGCAGCCATTACAACGCTAT
ESR1pro500 WT SacIIf	TCCCCGCGGTGTGAAATGACTGTTGGTCGAT
ESR1pro250 WT SacIIf	TCCCCGCGGGTTTTAAGTGCAACTCAAAAGTTTC
ESR1pro200 WTSacIIf	TCCCCGCGGCTACTATACTGTATGTGCAA
ESR1pro150 WT SacIIf	TCCCCGCGGCAAACTTCACAAAATTTAAT
ESR1p150 m1 SacIIf	TCCCCGCGGCAAACTTCACCTTGCTTAATTAAGCAAGTATACCATTTATGTACCTATAAATAG
ESR1p150 m2 SacIIf	TCCCCGCGGCAAACTTCACCTTGCTTAATTAAATTTTTATACCATTTATGTA
ESR1p150 m3 SacIIf	TCCCCGCGGCAAACTTCACAAAATTTAATTAAGCAAGTATACCATTTATGTACCTATAAATAG
ESR1p150m4 SacIIf	TCCCCGCGGCAAACTTCACGTTGACAGTAAGTGAACCTATACCATTTATGTACCTATAAATAG
ESR1p150m5 SacIIf	TCCCCGCGGAAAAATTAAAAAAATTTAATTAAATTTTTATACCATTTATGTACCTATAAATAG
ESR1pro100 WTSacIIf	TCCCCGCGGATAGATAGAAGAAGCTCCAT
ESR1pro SpeIr	GGACTAGTTTTTGGTTTCTAGGGTTTTG
PRIMERS FOR RT-qPCR	
ESR1 Rf	ACAGCTGTCATTATGCCTGAACCA
ESR1 Rr	GGTAGAGGAATCTAACGGTAGAGA
at1G12980Rf1	CGGTGGTTTATCGTTGGGATCA
at1G12980Rr1	CAGCCTAACTGAGTTCCGTACA
WIND1 Rf	GATCTCACATCGGAGGCGATT
WIND1 Rf	CCACCGATCGAAACCGAATTC
PP2AA3 Rf	GACCAAGTGAACCAGGTTATTGG
PP2AA3 Rr	TACTCTCCAGTGCCTGTCTTCA
ARR5 Rf	CATCTTGCCTCGTATCGATAG
ARR5 Rr	GCTTCAAGCTCTCTCTTGTGCA
ESR2 Rf	GCTGACTTCCATGTCGAAGGA
ESR2 Rr	TCTGCTGCATCTTAGCTGAATC
CUC1 Rf	CAGCAGCAGCAGCGTTCTTT
CUC1 Rr	AATGACGGAGGAGGAGGAAGAA
WUS Rf	GCAAAGCCTCTGTTTGGTCTAGAA
WUS Rr	AGCGTACGTCGATGTTCCAGATA
STM Rf	CCTTACCCTTCGGAGCAACAA
STM Rr	TCCAATGCCGTTTCCTCTGGTTTA
PLT3 Rf	GACTCGACCGGGTCTAACAA
PLT3 Rr	CAGCCGGATTTGGTGCCATAA
PLT5 Rf	GTCGATGGCAGGCACGAATT
PLT5 Rr	TGCAGCTTCCTCTTGAGTGCTAAA
PLT7 Rf	GGTGTCACAAGGCATCATCAACAA
PLT7 Rr	GTTGCAAAGGTTCCGAGGTAAAGA
PLT1 Rf	AGCACTGAGGAAGAAGCAGCAGA
PLT1 Rr	CCGGTTGATCTCGAAGTTGGTCAC
PLT2 Rf	GGCCGAGTTGCTGGAAACAAAGAT
PLT2 Rr	TGCTTCTTCCTCCGTGCTGAATG
RAP2.6L Rf	ACGCTCAGTTGCTTACGAGTAACA
RAP2.6L Rr	TGCGTCTGTTGGGAGGAAGAA
PRIMERS FOR CHIP-qPCR	
ESR1p P1f	CACCATTTACTCTGTCTTTCA
ESR1p P1r	ATGGGAGAGTTGGAGTCGTT
ESR1p P2f	CTCAAATGATGGTAGTAATTAAAC
ESR1p P2r	GTCTATTAGAACAATATAAGAATT
ESR1p P3f	GGCAGTTTTAGAAATAATGGAATT
ESR1p P3r	CATTTAAATTTACTTGCTATCTTG
ESR1p P4f	ACAGCTGTCATTATGCCTGAACCA
ESR1p P4r	GGTAGAGGAATCTAACGGTAGAGA
ESR1p P5f	CGGTGGTTTATCGTTGGGATCA
ESR1p P5r	CAGCCTAACTGAGTTCCGTACA

Supplemental Table 1. A list of PCR primers used in this study.

Probe name	Name of the oligonucleotide	Sequence
DRE	DRE element probe s	TTGATACTACCGACATGAGTTGATACTACCGACATGAGTT
	DRE element probe antisense a	AACTCATGTCGGTAGTATCAACTCATGTCGGTAGTATCAA
ESR1-513bp	ESR1 -513s	CATGTGTGAAATGACTGTTGGTCG
	[Bio-ON]ESR1+3as	[Bio-ON]CATTTTTGGTTTCTAGGGTTTTGGTTTG
R1	ESR1 -513to-464s	CATGTGTGAAATGACTGTTGGTCGATTTTTAACTTTAATAAATAAAAAAG
	ESR1 -513to-464as	CTTTTTTATTTATTAAAGTTAAAAATCGACCAACAGTCATTTCACACATG
R2	ESR1 -473to-424s	AATAAAAAAGCAATAAGAACGTGGTTTTATTTCGCCACTCCCACTTGCAT
	ESR1 -473to-424as	ATGCAAGTGGGAGTGGCGAAATAAAACCACGTTCTTATTGCTTTTTTATT
R3	ESR1 -433to-384s	CCACTTGCATCGTCATCATCAAAGAAAAACACTAATGTCTAGACCAAAGA
	ESR1 -433to-384as	TCTTTGGTCTAGACATTAGTGTTTTTCTTTGATGATGACGATGCAAGTGG
R4	ESR1 -393to-344s	AGACCAAAGATTTAAAACATCTACCCCATATATATATGATGAACAAGATA
	ESR1 -393to-344as	TATCTTGTTCATCATATATATATGGGGTAGATGTTTTAAATCTTTGGTCT
R5	ESR1 -353to-304s	GAACAAGATAGCAAGTAAATTTAAATGTAAAATTAAATTTTAGTTTGCTA
	ESR1 -353to-304as	TAGCAAACTAAAATTTAATTTTACATTTAAATTTACTTGCTATCTTGTTC
R6	ESR1 -313to-264s	TAGTTTGCTAAGATTAATATACAAAAGAAGTATTATCAATTTATCAGTTA
	ESR1 -313to-264as	TAACTGATAAATTGATAATACTTCTTTTGTATATTAATCTTAGCAAACTA
R7	ESR1 -273to-224s	TTATCAGTTATTAATCAAATCAAGTTTTAAGTGCAACTCAAAAGTTTCCA
	ESR1 -273to-224as	TGGAAACTTTTGAGTTGCACTTAAAACTTGATTTGATTAATAACTGATAA
R8	ESR1 -233to-18 s	AAAGTTTCCATGCTTATATAGTTATTTGTATACTACTATACTGTATGTGC
	ESR1 -233to-184as	GCACATACAGTATAGTAGTATACAAATAACTATATAAGCATGGAAACTTT
R9	ESR1 -193to-144s	CTGTATGTGCAAGAAAAGCATTTATACTCTTCGCCATATATTTCAAACTT
	ESR1 -193to-144as	AAGTTTGAAATATATGGCGAAGAGTATAAATGCTTTTCTTGCACATACAG
R10	ESR1 -153to-104s	TTTCAAACTTCACAAAATTTAATTAAATTTTTATACCATTTATGTACCTA
	ESR1 -153to-104as	TAGGTACATAAATGGTATAAAAATTTAATTAAATTTTGTGAAGTTTGAAA
R11	ESR1 -113to-64s	TATGTACCTATAAATAGATAGAAGAAGCTCCATCTCTTTCAAACTATCAA
	ESR1 -113to-64as	TTGATAGTTTGAAAGAGATGGAGCTTCTTCTATCTATTTATAGGTACATA

Supplemental Table 2. A list of oligonucleotides used in EMSA.