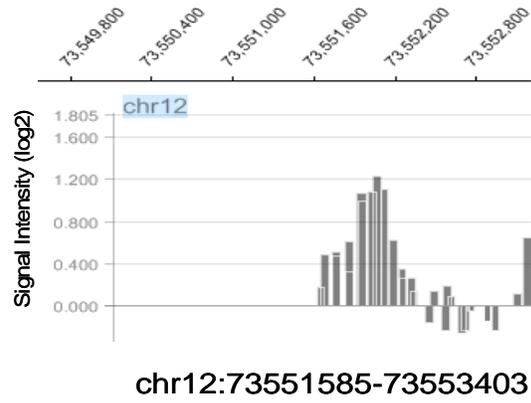
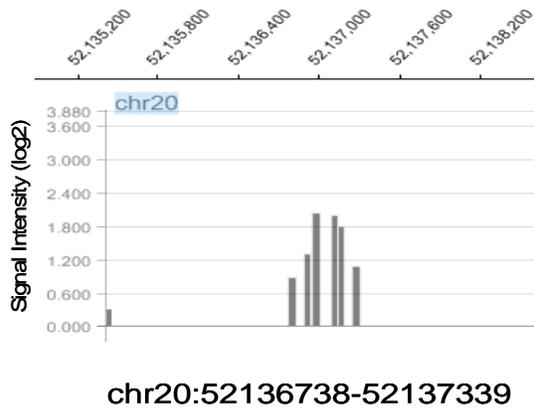
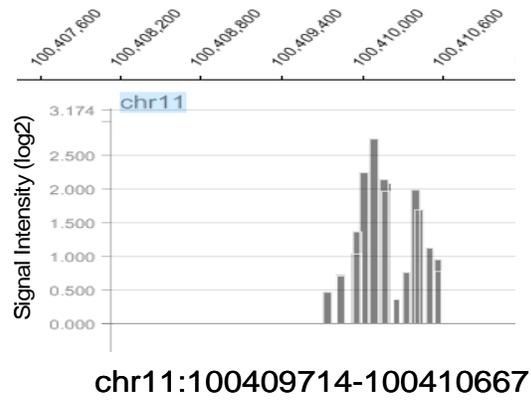
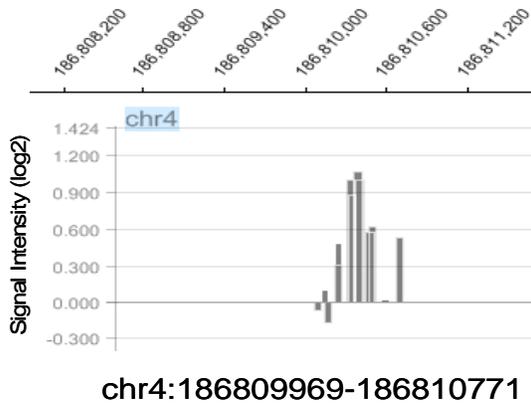


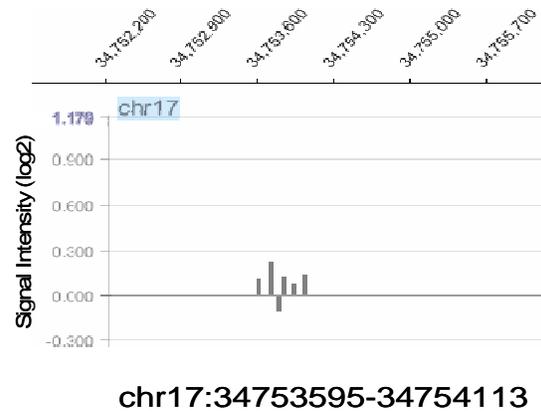
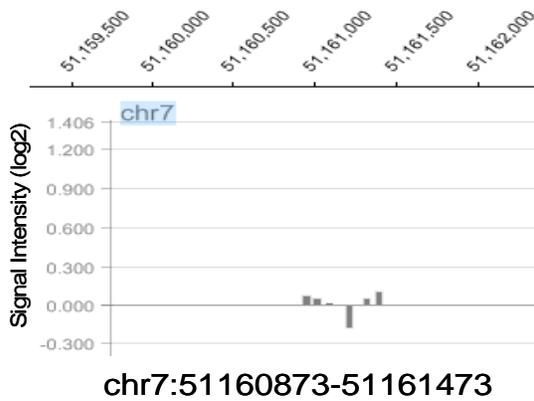
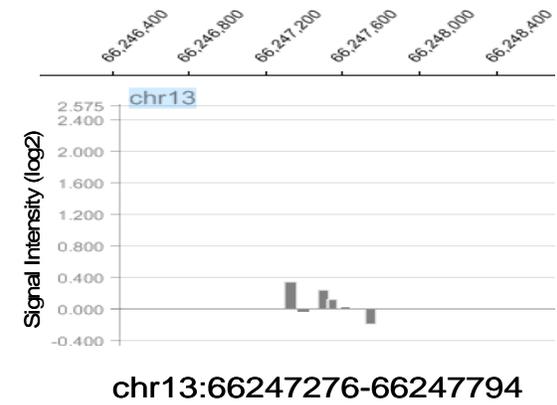
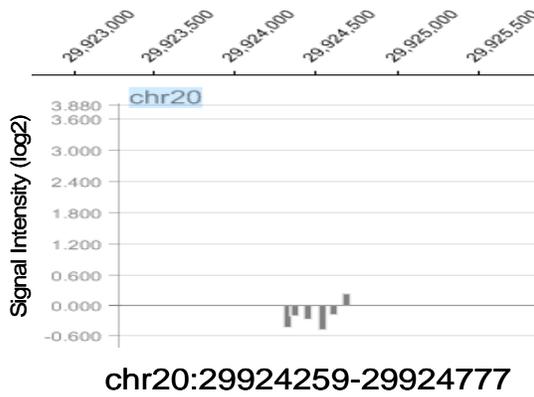
Supplemental Figure S1. ChIP-chip signal intensity peaks of several positive and negative ER binding regions. The regions were selected randomly from our ChIP-chip raw data. In the diagram, the Y-axis represents the log₂ signal intensity (ER ChIP over Input), and the X-axis represents the genomic locations. The regions being covered by our probes are indicated in each figure.

Supplemental Figure S2. Frequency of number of ERE motifs found in ER binding regions. Cells containing ER α and/or ER β , as indicated, were treated with E2, and the frequency of EREs within ER binding regions was determined.

Regions binding ER:



Regions not binding ER:



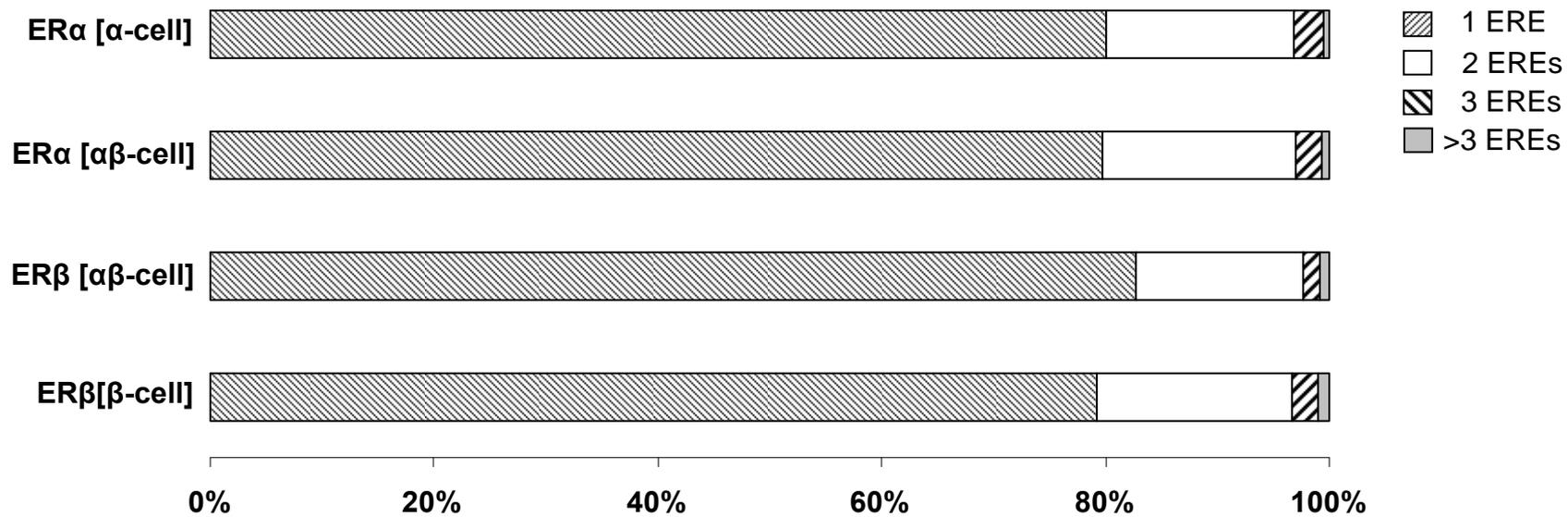


Figure S2

Supplemental Table S1. Validation of ChIP-chip binding sites. ER α and ER β chromatin binding (by conventional ChIP assays) was measured by quantitative PCR after 45 min of E₂ treatment of MCF-7 cells differentially expressing ER α and/or ER β . The binding sites were considered validated if their qPCR enrichment (ER ChIP over Input) was greater than 2 fold, with values at different sites ranging up to 400 fold.

	ER α [α -cell]	ER α [$\alpha\beta$ -cell]	ER β [$\alpha\beta$ -cell]	ER β [β -cell]
Number of random binding sites tested	12 sites	12 sites	9 sites	9 sites
Number of validated binding sites	11 sites	11 sites	8 sites	9 sites
False-positive error rate	8.3%	8.3%	11.1%	0%

Supplemental Table S2. Distribution of ER binding sites mapped onto the five categories of sites on the NimbleGen arrays.

	Binding sites	Ligand	Cat 1	Cat 2	Cat 3	Cat 4	Cat 5
1	ER α [α cells]	E2	42%	13%	30%	14%	1%
2	ER α [α cells]	PPT	40%	14%	36%	10%	~0%
3	ER α [$\alpha\beta$ cells]	E2	39%	13%	36%	11%	1%
4	ER β [$\alpha\beta$ cells]	E2	32%	15%	42%	15%	1%
5	ER α [$\alpha\beta$ cells]	PPT	39%	13%	35%	12%	1%
6	ER β [$\alpha\beta$ cells]	ERB-041	17%	27%	47%	9%	~0%
7	ER β [β cells]	E2	23%	21%	44%	11%	1%
8	ER β [β cells]	ERB-041	9%	40%	32%	18%	1%

Cat 1: ChIP-chip ER binding regions (taken from Carroll et al. 2006)*

Cat 2: ChIP-PET ER binding regions (taken from Lin et al. 2007)*

Cat 3: Overlapping ER binding regions from both ChIP-chip and ChIP-PET

Cat 4: Computational predicted ERE regions (taken from Vega et al. 2006)

Cat 5: Control regions

*Binding regions from Cat 3 have been removed from Cat 1 and Cat 2 to avoid double-counting