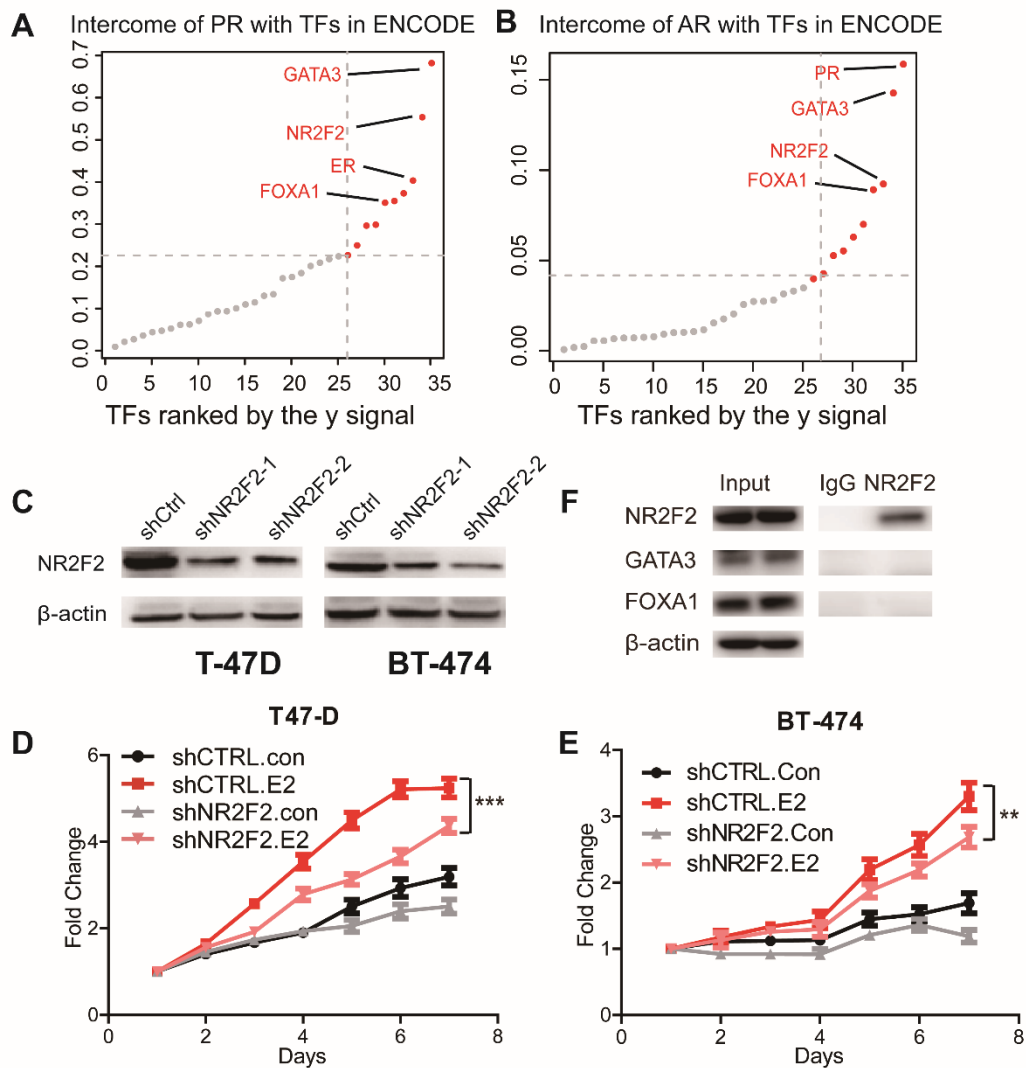


**Figure S1**

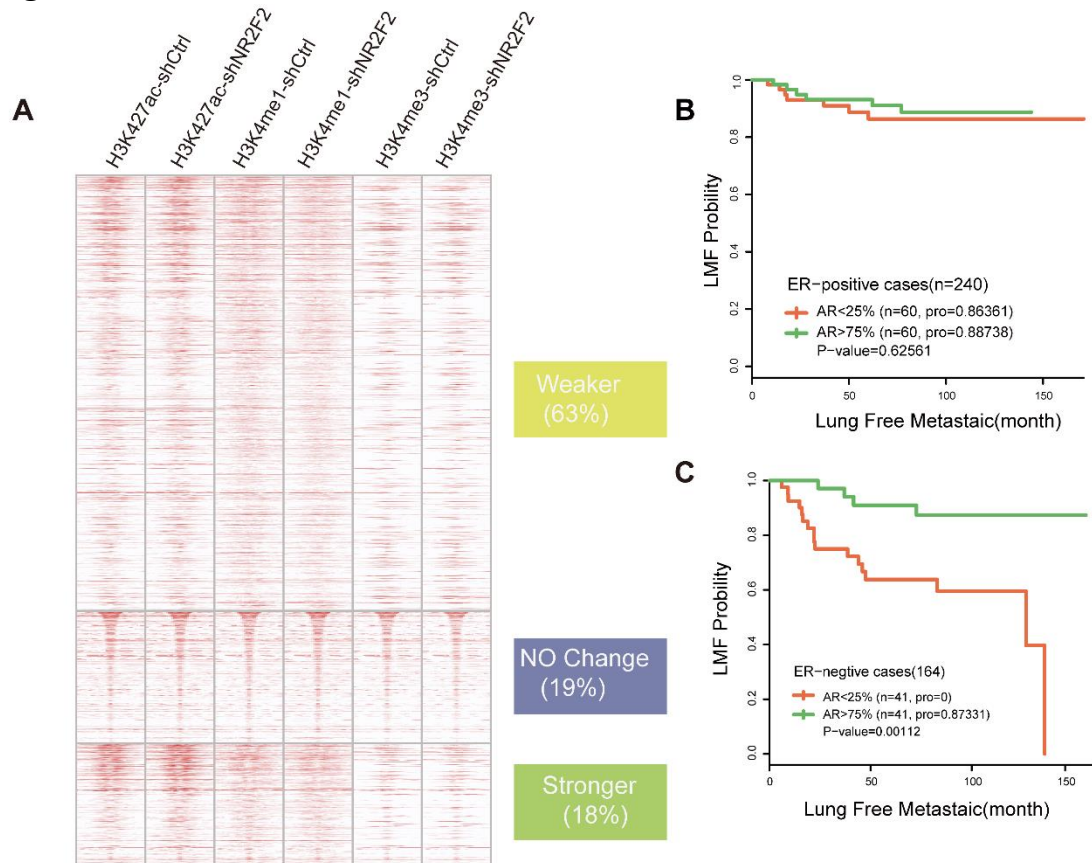


(A, B) Distribution of the overlap (value of y) of all transcription factors with the AR and PR.

(C) NR2F2 stable depletion via lentivirus-delivered shRNA reduces its protein levels in both BT-474 and T47-D cell lines.

(D, E) T-47D and BT-474 breast cancer cells depleted of NR2F2 fail to proliferate in response to oestrogen stimulation compared to cells subjected to the control treatment to a certain degree.

**Figure S2**



(A) Heatmap analyses of ChIP-seq signals of histone modification (H3K27ac, H3K4me3 and H3K4me1) in the control and shNR2F2 MCF-7 cells, ranked by ChIP-seq signals of ER. All ChIP-seq signals are displayed from -2.5 kb to +2.5 kb surrounding the center of each annotated ER peak.

(B, C) Kaplan-Meier product limit analysis of lung metastasis probability in ERa-positive and ERa-negative breast cancer patients, respectively. Patients were dichotomized by the median percent AR-positive nuclear area (>75% and <25%)

Supplementary Table 1. Data Used in analysis.

ChIP-Seq	MCF7	MDA-MB-231	
ChIP-Seq	FOXA1.E2	HDAC2 RAD21	H3K4me1
	FOXA1.Con	MYC ESRRA	H3K27ac
	GATA3.E2	TCF12 CTCF	
	GATA3.Con	SIN3A MTA1	
	ER.E2	TCF12 SRF	
	ER.Con	MAX MAZ	
	H3K4me1.E2	JUND EGR1	
	H3K4me1.Con	FOXM1 PML	
	H3K4me2.E2	E2F1 REST	
	H3K4me2.Con	FOSL2 GABPA	
	H3K27ac.E2	TEAD4 RFX5	
	H3K27ac.Con	MNT MAFK	
	CEBPB	TCF7L2 GTF2F1	
	NR2F2	ELF1 HSF1	
	PR	ZNF217 TAF1	
	CEBPb		
	AR		
	NR2F2-Con	H3K4me3-shCtrl	
	NR2F2-E2	H3K4me3-shNR2F2	
	ER-shCtrl-E2	H3K4me1-shCtrl	
ER-shNR2F2-E2	H3K4me1-shNR2F2		
RNA-Seq	shNR2F2-con		
	shCtrl-con		
	shNR2F2-E2.12h		
	shCtrl-E2.12h		
ATAC-Seq	ATAC-Seq-shCtrl		ATAC-seq
	ATAC-Seq-shNR2F2		
GRO-Seq	GRO-Seq.E2		
	GRO-Seq.Con		
DNase-Seq	DNase-Seq.E2		
	DNase-Seq.Con		

Note: data used in black font is downloaded from public dataset and in blue is newly generated by our lab.