Figure S1. Relative expression levels of E2F1 and E2F3 were significantly higher in T-47D and MDA-MB-231 compared with in MCF-10A. E2F1 expression was 1.59-fold higher in T-47D (P<0.001) and 1.81-fold higher in MDA-MB-231 cells (P<0.001) compared with in MCF-10A. E2F3 expression levels were 1.67 fold-higher in T-47D (P<0.001) and 1.5-fold higher in MDA-MB-231 cells (P<0.001) compared with MCF-10A cells. E2F1, E2F transcription factor 1; E2F3, E2F transcription factor 3.

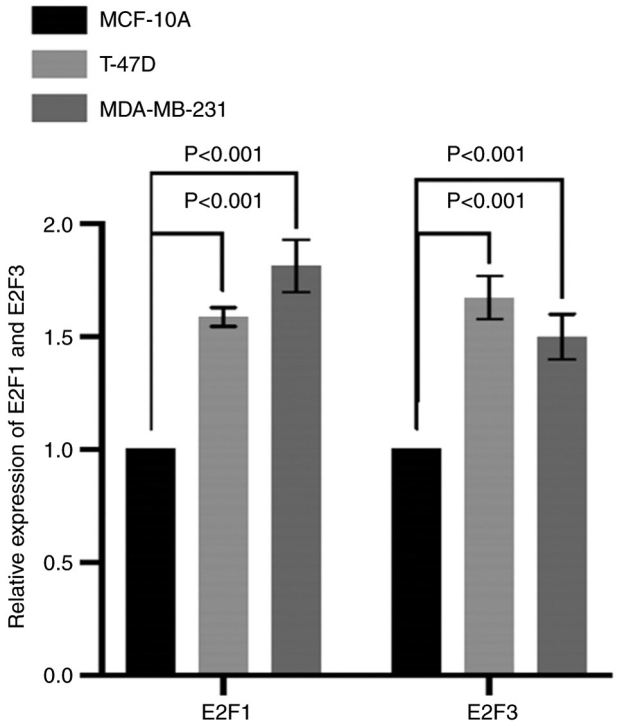

Figure S2. There is a positive correlation between E2F1 and E2F3 and miR-34a expression, and a negative correlation between E2F3 and miR-34a expression (data was obtained from datasets of TCGA breast cancer datasets) (https://portal.gdc.cancer.gov/). Correlation analyses of miRNA-seq and RNA-seq datasets of patients with breast cancer revealed a significantly positive correlation between E2F1 and E2F3 expression ($r=0.39$, $P=2.2\times10^{-16}$), a significantly negative correlation between E2F3 and miR-34a expression ($r=-0.17$, $P=2.19\times10^{-8}$) and a negative but not statistically significant correlation between E2F1 and miR-34a ($r=-0.001$, $P=0.96$). miR-34a, microRNA-34a; E2F1, E2F transcription factor 1; E2F3, E2F transcription factor 3; miRNA, microRNA.

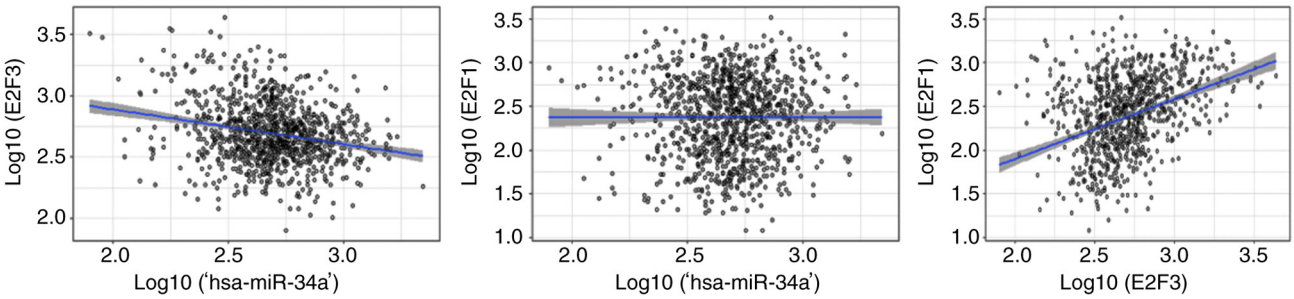

Table SI. Characteristics of populations and cancer types of the studies included in the meta-analysis.

Study	Country	Ethnicity	Cancer type	Sample size (cancer/normal) in *E2F1*	Sample size (cancer/normal) in *E2F3*	(Refs.)
The Cancer Genome Atlas, 2011	USA	American	Invasive Breast Carcinoma	76/61	76/61	(1)
Gluck *et al* 2012	USA	American	Invasive Breast Carcinoma	154/4	154/4	(2)
Curtis *et al* 2012 2	UK, Canada	British, Canadian	Invasive Breast Carcinoma	21/144		(3)
Curtis 2012 2	UK, Canada	British, Canadian	Breast Carcinoma	14/144		(3)

E2F1, E2F transcription factor 1; E2F3, E2F transcription factor 3.

Table SII. Oligo primer sequences of genes in the present study.

Gene	Primer	Base sequence
GAPDH	Forward	5'-GAAGGTGAAGGTCGGAGTC-3'
	Reverse	5'-GAAGATGGTGATGGGATTTC-3'
E2F3	Forward	5'-AAGAAATTAGATGAACTGATCCAAAGC-3'
	Reverse	5'-TAACATAAGCTAACCTTTGATTCTCTGAA-3'
E2F1	Forward	5'-CATCCAGGAAAAGGTGTGAAATC-3'
	Reverse	5'-AGGACGTTGGTGATGTCATAGATG-3'
miR-34a	Forward	5'-CGTCACCTCTTAGGCTTGGA-3'
	Reverse	5'-CATTGGTGTCGTTGTGCTCT-3'

miR, microRNA; E2F1, E2F transcription factor 1; E2F3, E2F transcription factor 3.

References

1. The Cancer Genome Atlas-Invasive Breast Carcinoma Gene Expression Data. Data link: http://tcga-data.nci.nih.gov/tcga/
2. Curtis C, Shah SP, Chin SF, Turashvili G, Rueda OM, Dunning MJ, Speed D, Lynch AG, Samarajiwa S, Yuan Y, *et al*: The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature 486: 346-352, 2012.
3. Glück S, Ross JS, Royce M, McKenna EF Jr, Perou CM, Avisar E and Wu L: TP53 genomics predict higher clinical and pathologic tumor response in operable early-stage breast cancer treated with docetaxel-capecitabine +/-trastuzumab. Breast Cancer Res Treat 132: 781-791, 2012.