

Table S5. Publicly Available Gene Expression Datasets from Breast, Colon and Lung Carcinomas with Follow-Up Clinical Data Used for This Study (Supplement for Figures 6 and 7)

Dataset	Outcome Event	n=?	Events	ER+ (n=?)	ER- (n=?)	% ER Neg	Other Info	GEO	Reference
Breast_1	Overall Survival	159	46	130	29	18%	x	GSE1456	(Pawitan et al., 2005)
Breast_2	5Y Met	295	78	226	69	23%	x	X	(van de Vijver et al., 2002)
Breast_3	Relapse	286	107	209	77	27%	x	GSE2034	(Wang et al., 2005)
Breast_4	5Y Status	102	42	68	34	33%	x	GSE3143	(Bild et al., 2006)
Breast_5	3Y Survival	108	15	75	30	28%	x	X	<a href="http://cancergenome.nih.gov/">http://cancergenome.nih.gov/</a>
Breast_6	5Y Met	200	28	156	44	22%	x	GSE11121	(Schmidt et al., 2008)
Breast_7	Overall Met	88	28	88	0	0%	x	GSE6532	(Loi et al., 2007)
Breast_8	5Y Met	77	6	77	0	0%	x	GSE9195	(Loi et al., 2008)
Breast_9	5Y Met	198	35	134	64	32%	x	GSE7390	(Desmedt et al., 2007)
Breast_10	3Y Met	81	12	45	36	44%	x	GSE2603	(Minn et al., 2005)
Lung_1	3Y Survival	50	27	NA	NA	NA	Lung Adeno-carcinoma	GSE3141	(Bild et al., 2006)
Lung_2	3Y Survival	37	9	NA	NA	NA	Lung Adeno-carcinoma	GSE19188	(Hou et al., 2010)
Colon_1	5Y Relapse	95	58	NA	NA	NA	x	GSE14333	(Jorissen et al., 2009)
Colon_2	5Y Survival	119	67	NA	NA	NA	x	GSE17538	(Smith et al., 2010)

Table S6. Multivariate Analysis of Breast Cancer-Specific Mortality by HSF1-Status (HSF1 High Positive or Low Positive versus HSF1-Negative, Supplement for Figure 6D).

Models	N		Hazard Ratio (95% CI)		
	Cases	Endpoints	None	Low	High
ER-positive, node negative cases:					
Model <sup>1</sup>	947	142	1.00	1.65 (1.02-2.66)	2.41 (1.45-3.99)
Model <sup>2</sup>	947	142	1.00	1.42 (0.88-2.31)	1.98 (1.17-3.33)

\*CI denotes confidence interval.

Model<sup>1</sup>: Adjust for age at diagnosis (years).

Model<sup>2</sup>: Adjust for age at diagnosis (years), date of diagnosis (months), disease stage (I, II, III), grade (I, II, III), radiation treatment (yes, no, missing), chemotherapy and hormonal treatment (no/no, yes/no, no/yes, yes/yes, missing).

**Table S7.** Oligonucleotides Used in this Study

<b>NAME</b>	<b>SEQUENCE</b>
AANAT/Ube2O-qPCR-F	GAGCCGTAGGTCCCTTCTTT
AANAT/Ube2O-qPCR-R	CTCAGGAACCTTCCAGACCA
CKS2-qPCR-F	ACCGACTACGTCATCACCAA
CKS2-qPCR-R	GTGGAAAGTTCCAGGACACG
Jarid2-qPCR-F	TTGGTTGCGCTTTTAGCTTT
Jarid2-qPCR-R	ACCCCAAGTCACAGAGATGG
Maf1/Sharpin-qPCR-F	TTTGCCACAAATGGACAC
Maf1/Sharpin-qPCR-R	CCCAAAGACCAGCTCTAACG
Pgk1-qPCR-F	TCTCGCACATTCTTCACGTC
Pgk1-qPCR-R	AGGAACCTTCCCAGACTTAGG
RBM23-qPCR-F	TTGGGGTTTCTCACCAGTTC
RBM23-qPCR-R	CTGCAGTGCTGCTTTTCTTG
HspA6-qPCR-F	GATCTGCCCGAACCTTCTC
HspA6-qPCR-R	AACTTTCGCGAACCTTTCC
HspA8-qPCR-F	CCACCCTGCCTCTTATACCC
HspA8-qPCR-R	GGCTTGTGATTGGGTCTTGT
HSPD1-qPCR-F	CGGCCGGCTTAGTCTAGTT
HSPD1-qPCR-R	ATTTGACCCTTGAGCCGTAG
BCL10-qPCR-F	TGAGTCATATGGGTGTGCTG
BCL10-qPCR-R	TCCCCTTAGCACAGAAGTGA
Ncor2-qPCR-F	GGGTGGAATTACAGCCTCAG
Ncor2-qPCR-R	TCCTGTAGCTCCCACACCTC
DHFR1-qPCR-F	ACCTGGTCGGCTGCACCT
DHFR1-qPCR-R	TTGCCCTGCCATGTCTCG
Intergenic-qPCR-F	ATGTCAGGCCCATGAACGAT
Intergenic-qPCR-R	GCATTCATGGAGTCCAGGCTTT