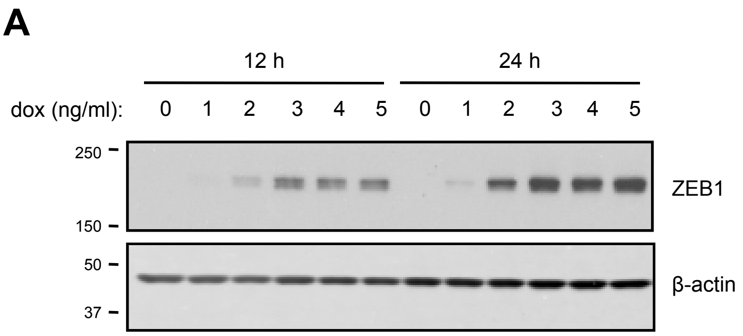
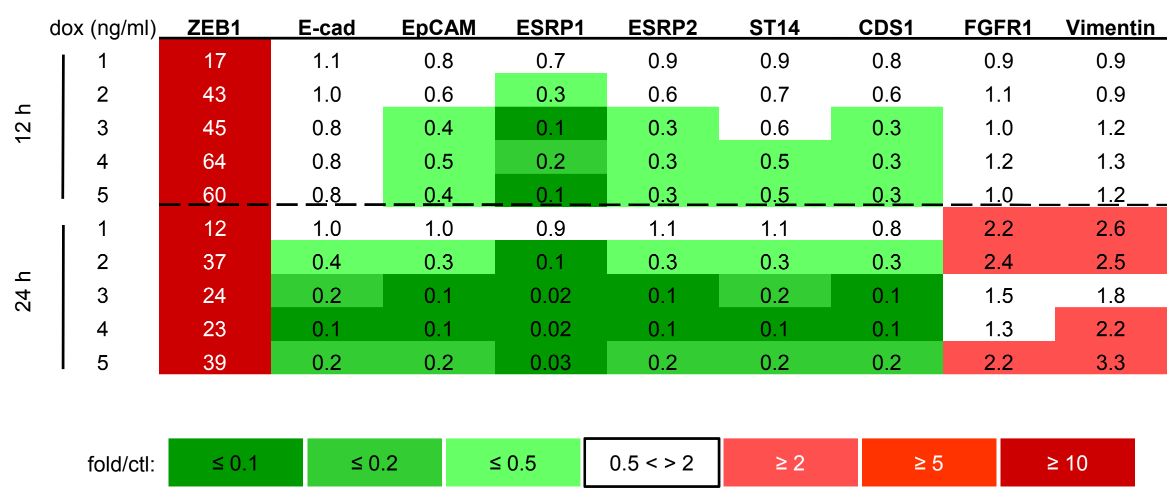
Figure S1

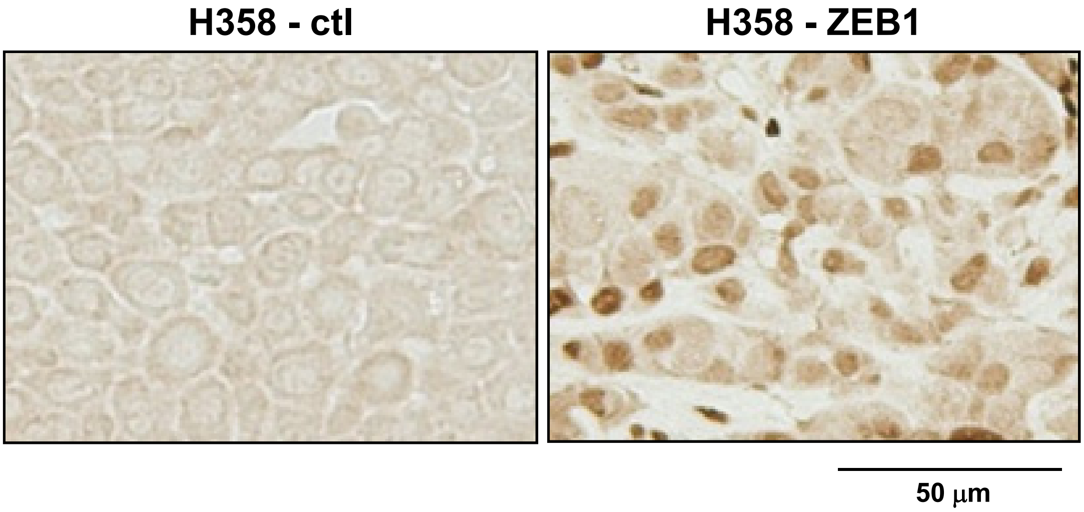



B

	dox (ng/ml)	ZEB1	E-cad	EpCAM	ESRP1	ESRP2	ST14	CDS1	FGFR1	Vimentin
12 h	1	17	1.1	0.8	0.7	0.9	0.9	0.8	0.9	0.9
	2	43	1.0	0.6	0.3	0.6	0.7	0.6	1.1	0.9
	3	45	0.8	0.4	0.1	0.3	0.6	0.3	1.0	1.2
	4	64	0.8	0.5	0.2	0.3	0.5	0.3	1.2	1.3
	5	60	0.8	0.4	0.1	0.3	0.5	0.3	1.0	1.2
24 h	1	12	1.0	1.0	0.9	1.1	1.1	0.8	2.2	2.6
	2	37	0.4	0.3	0.1	0.3	0.3	0.3	2.4	2.5
	3	24	0.2	0.1	0.02	0.1	0.2	0.1	1.5	1.8
	4	23	0.1	0.1	0.02	0.1	0.1	0.1	1.3	2.2
	5	39	0.2	0.2	0.03	0.2	0.2	0.2	2.2	3.3

fold/ctl: ≤ 0.1 | ≤ 0.2 | ≤ 0.5 | 0.5 < > 2 | ≥ 2 | ≥ 5 | ≥ 10

Figure S2



H358 - ctl

H358 - ZEB1

Table S1. DNA primer sequences for quantitative real-time RT-PCR

Gene	Forward Primer (5' to 3')	Reverse Primer (5' to 3')
EPCAM	CGCAGCTCAGGAAGAATGTG	TGAAGTACACTGGCATTGACGA
CDS1	TCCTCAGATAGAACCCCTGAGATTC	GTATCCACCAGTTTTTCCACCTTG
ESRP1	TCCTGCTGTTCTGGAAAGTCG	TCCGGTCTAACTAGCACTTCGTG
ST14	GGGACACACCCAGTATGGAGG	GAGGTTCTCGCAGGTGGTCTG
ESRP2	GGGTCTGGGAAGTCAAGACAATG	CTTCGAAAACAATTGACTGCTGG
CDH1 (E-cadherin)	CGGGAATGCAGTTGAGGATC	AGGATGGTGTAAGCGATGGC
VIM	TTTGAAGAAACTCCACGAAGAGGA	CCACATCGATTTGGACATGCT
FGFR1	TCAATGTTTCAGCTTGCCCA	ACCAAGTCCAAATGGCAAGG
SIRT1	AGCAGATTAGTAGGCGGCTTGA	TCAGCGCCATGGAAAATGTAA
ZEB1	AGCAGTGAAAGAGAAGGGAATGC	GGTCCTCTTCAGGTGCCTCAG
ZEB2	AGGCATATGGTGACGCACAA	CTTGAACTTGCGGTTACCTGC
SNAIL	CGCGCTCTTTCCTCGTCAG	TCCCAGATGAGCATTGGCAG
SLUG	AATATGTGAGCCTGGGCGC	CTCTGTTGCAGTGAGGGCAAG
CDH2 (N-cadherin)	TGTGGGAATCCGACGAATG	GTCATATGGTGGAGCTGTGGG

Table S4. DNA primer sequences for quantitative real-time RT-PCR

	Spearman R value [1]							
Affym. ID	**ZEB1**	**ZEB2**	**SNAIL**	**SLUG**	**TWIST1**	**Symbol**	**Study**	**Genes proposed as markers in NSCLC**
202489_s_at	***-0.76***	***-0.54***	-0.26	0.28	-0.10	FXYD3	(6)	FXYD domain containing ion transport regulator 3
204855_at	***-0.71***	-0.50	-0.25	0.48	0.01	SERPINB5	(2)	serpin peptidase inhibitor, clade B (ovalbumin), member 5
203453_at	***-0.71***	***-0.63***	-0.35	0.05	-0.11	SCNN1A	(5)	sodium channel, nonvoltage-gated 1 alpha
226213_at	***-0.60***	-0.39	0.04	-0.12	-0.30	ERBB3	(8, 4)	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
205455_at	***-0.60***	-0.44	-0.12	0.11	-0.04	MST1R	(6)	macrophage stimulating 1 receptor (c-met-related tyrosine kinase) RON
204891_s_at	***-0.56***	-0.35	-0.02	0.28	-0.05	LCK	(8, 4)	lymphocyte-specific protein tyrosine kinase
201250_s_at	***-0.56***	-0.37	-0.17	0.21	-0.10	SLC2A1	(6)	solute carrier family 2 (facilitated glucose transporter), member 1
207388_s_at	-0.42	-0.23	-0.06	0.29	-0.03	PTGES	(5)	prostaglandin E synthase
204351_at	-0.42	-0.41	-0.11	-0.07	-0.51	S100P	(6)	S100 calcium binding protein P
201150_s_at	-0.39	-0.25	0.07	0.35	0.16	TIMP3	(3)	TIMP metallopeptidase inhibitor 3
200872_at	-0.38	-0.14	-0.19	0.28	0.07	S100A10	(3)	S100 calcium binding protein A10
218498_s_at	-0.33	-0.18	0.25	-0.15	-0.32	ERO1L	(5)	ERO1-like (S. cerevisiae)
234883_x_at	-0.30	-0.21	-0.24	0.18	0.19	TRBV7-3	(6)	T cell receptor beta variable 7-3
230378_at	-0.22	-0.01	0.25	0.31	-0.24	SCGB3A1	(2)	secretoglobin, family 3A, member 1
208893_s_at	-0.21	-0.29	0.21	-0.03	-0.27	DUSP6	(4)	dual specificity phosphatase 6
202414_at	-0.18	0.02	***-0.68***	0.24	0.51	ERCC5	(1)	excision repair cross-complementing rodent repair deficiency, complementation group 5
204135_at	-0.15	0.04	0.14	0.41	0.07	FILIP1L	(3)	filamin A interacting protein 1-like
207011_s_at	-0.15	-0.01	-0.17	-0.03	0.37	PTK7	(5)	PTK7 protein tyrosine kinase 7
200989_at	-0.12	-0.15	0.07	0.11	-0.19	HIF1A	(7, 3)	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
38707_r_at	-0.11	-0.20	***0.57***	-0.21	-0.47	E2F4	(2)	E2F transcription factor 4, p107/p130-binding
212724_at	-0.09	-0.16	0.02	0.24	0.05	RND3	(8)	Rho family GTPase 3
201655_s_at	-0.08	0.13	-0.14	0.11	0.35	HSPG2	(2)	heparan sulfate proteoglycan 2
206337_at	-0.07	-0.10	0.39	-0.06	-0.42	CCR7	(7)	chemokine (C-C motif) receptor 7
204778_x_at	-0.05	0.17	-0.22	0.21	0.18	HOXB7	(2)	homeobox B7
204026_s_at	-0.02	-0.07	-0.28	0.02	0.36	ZWINT	(5)	ZW10 interactor
203414_at	-0.02	-0.05	0.21	-0.03	-0.27	MMD	(4)	monocyte to macrophage differentiation-associated
220454_s_at	0.01	-0.05	0.33	-0.35	-0.41	SEMA6A	(3)	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
212249_at	0.02	0.02	-0.14	-0.40	-0.38	PIK3R1	(3)	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)
2028_s_at	0.07	0.02	0.44	0.04	-0.02	E2F1	(2)	E2F transcription factor 1
212884_x_at	0.08	0.15	0.30	0.07	0.15	APOE	(6)	apolipoprotein E
201168_x_at	0.08	0.18	0.29	0.15	-0.09	ARHGDIA	(3)	Rho GDP dissociation inhibitor (GDI) alpha
225439_at	0.08	0.06	-0.20	0.33	0.50	NUDCD1	(2)	NudC domain containing 1
212801_at	0.12	0.05	-0.21	-0.11	0.25	CIT	(5, 3)	citron (rho-interacting, serine/threonine kinase 21)
201890_at	0.12	0.16	0.13	0.13	-0.03	RRM2	(2)	ribonucleotide reductase M2 polypeptide
219671_at	0.14	-0.01	0.44	-0.23	-0.23	HPCAL4	(3)	hippocalcin like 4
202459_s_at	0.14	0.02	0.29	-0.32	-0.21	LPIN2	(6)	lipin 2
201071_x_at	0.15	0.13	-0.45	-0.21	0.09	SF3B1	(2)	splicing factor 3b, subunit 1, 155kDa
221455_s_at	0.21	0.16	-0.01	0.38	0.29	WNT3	(8)	wingless-type MMTV integration site family, member 3
201069_at	0.21	0.33	0.16	0.42	0.43	MMP2	(3)	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
211851_x_at	0.23	0.17	0.14	-0.08	0.05	BRCA1	(1)	breast cancer 1, early onset
238977_at	0.23	0.18	0.28	-0.07	-0.21	MCM6	(2)	minichromosome maintenance complex component 6
204729_s_at	0.24	0.06	0.30	0.02	-0.32	STX1A	(7)	syntaxin 1A (brain)
203089_s_at	0.28	0.15	0.19	-0.24	-0.18	HTRA2	(3)	HtrA serine peptidase 2
209969_s_at	0.44	0.42	0.02	-0.07	0.07	STAT1	(4)	signal transducer and activator of transcription 1, 91kDa
228131_at	0.48	0.49	-0.19	-0.12	0.41	ERCC1	(1)	excision repair cross-complementing rodent repair deficiency, complementation group 1

1 Significant R values are bolded and italicized. Genes of interest are highlighted in blue.