Table S1, related to Figure 1: Mass Spectrometry Analysis of FOXN3-containing Protein Complex

Band	**Identified proteins**	**Peptides**
217kDa	CHD4	ENEFSFEDNAIR
		KLERPPETPTVDPTVK
		APEPTPQQVAQQQ
		TEEPMETEPK
		NFEALNAR
		GAADVEKVEEK
152kDa	NSD2	ASTAASSALGFSK
		TPSCEVNR
		TSTTLSSEEK
148kDa	SAP180	VGAIVEVK
		KENIKPSLGSK
		NSDTAHIK
		NGDKDPDLKEPSNR
		SEVASIDR
		YCNTEECLK
		LLNNSDER
		MYEASIK
145kDa	SIN3A	EAGGNYTPALTEQEVYAQVAR
		DKSDSPAIQLR
		KAEQLMSDENCFK
		TMENVDSLDKLECR
		LDNTLGGTSEVIHR
		LDDQESPVYAAQQR
		YMNSDTTSPELR
		VLEAIQKK
		NPSIAVPIVLKR
		LDNTLGGTSEVIHRK
		SAEAYENFLR
		FKLNSYK
		IYADKAADIIDGLR
		VLEAIQK
		SEDYMYR
114kDa	SAP130	VVPQQITHTSPR
		GAAAAAVMSSSK
		AATDDDLHR
		LTNLQEGIIPK

		AMLQEIANQK
		HPQAGEIEAGGAGGGR
		KAMLQEIANQK
		LVMDQISEAR
		TLIPPQPPDVASPR
		GAAAAAVMSSSK
		QQLHTMAQK
		INELIQGNMQR
		ASPNPVAMETR
		EYIDEEGVR
		IQPDYPAER
54kDa	FOXN3	NGALLQVPPGVIQNGAR
		KVPSDTLPLKK
		SVSPVQDLDDDTPPSPAHSDMPYDAR
		STSPTSDSISSSSSSADDHYEFATK
		RNGALLQVPPGVIQNGAR
		KVPSDTLPLK
		GSLWCIDPEYR
		SCLNNITNR
		VPSDTLPLKK
		KVDKER
		QNLIQALKK
		HNLSLNK
		VPSDTLPLK
		NGITSCR
		SVSPVQDLDDDTPPSPAHSDMPYDAR
		SFGESVLR
		KPESSGISVSSGLSQCYGGSGFSK
55kDa	HDAC1	ISICSSDKR
		SIRPDNMSEYSK
		YYAVNYPLR
52kDa	HDAC2	SIRPDNMSEYSK
		ATAEEMTK
		YHSDEYIK
48kDa	RbAp48	TPSSDVLVFDYTK
		YMPQNPCIIATK
		INHEGEVNR
		HPSKPDPSGECNPDLR
		VINEEYK
		LMIWDTR
		TVALWDLR

48kDa	RbAp46	HPAKPDPSGECNPDLR
		YMPQNPHIIATK
		TPSSDVLVFDYTK
		EMFEDTVEER
		YMPQNPHIIATK
		EMFEDTVEER
		GEFGGFGSVTGK
		INHEGEVNR
		VINEEYK
		LMIWDTR
		TVALWDLR

Table S2, related to Figure 2

Known lncRNA name	NEAT1	MALAT1
Probe name	p2796	p30315
Fold of change (FC) (MCF-7) vs (MDA-MB-231)	4.627057885	-1.237074181
Log FC (MCF-7) vs (MDA-MB-231)	2.210095147	-0.306932014

Table S2. Microarray profiling of lncRNA expression in MCF-7 and MDA-MB-231 cells. Normalized fold of changes of NEAT1 or MALAT1 in MCF-7 cells over MDA-MB-231 cells are shown.

Figure S1, related to Figure 4

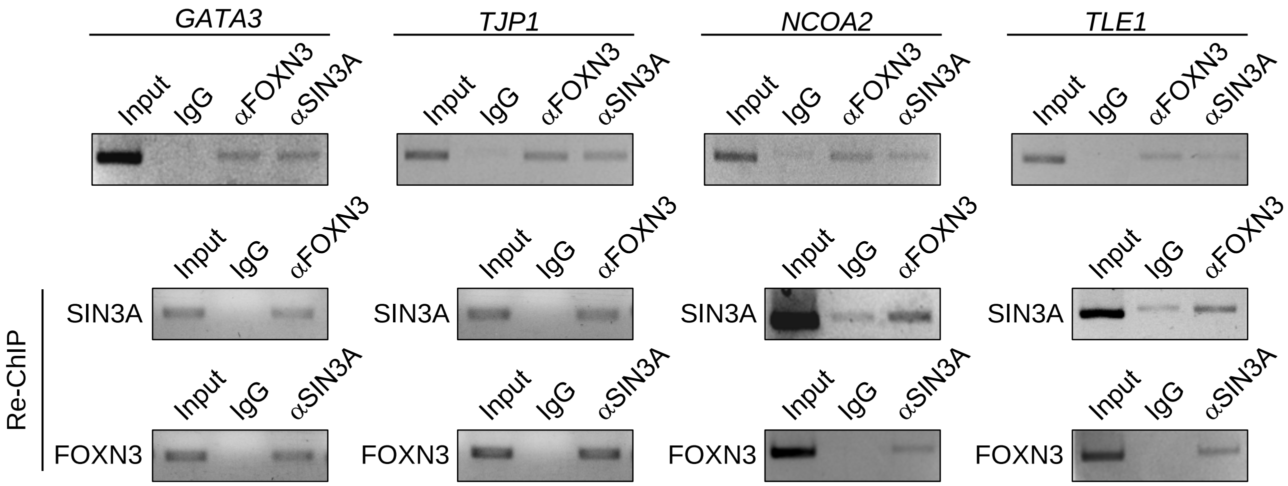

Figure S1. ChIP/Re-ChIP experiments on the promoter of the indicated genes with antibodies against the indicated proteins in MCF-7 cells.

Table S3, related to Figure 4

Pos	17	18	19	20	21	22	23	24	25	26	27	28	29
aa	E	K	P	I	D	R	E	K	T	S	P	L	L
T Score	1	1	1	1	1	1	1	1	0	1	1	1	0
Tag	+	+	+	+	+	+	+	+	+	+	+	+	+

Pos	139	140	141	142	143	144	145	146	147	148	149
aa	P	P	N	R	A	P	P	P	S	G	R
T Score	n/a	0	0	0	0	0	0	0	1	0	0
Tag	b	+	-	+	-	+	+	+	+	+	+

Table S3. Prediction of RBRs in SAP18 by RBRDetector. T Score denotes the prediction score generated by template-based prediction model. Tag denotes the target residue as buried (b), RNA-binding (+), or nonbinding (-).

Table S4. siRNA and shRNA sequences

siRNA sequences:

Control siRNA	UUCUCCGAACGUGUCACGU
FOXN3 siRNA	GGAGUCAGAGUAUUGGGAATT
NEAT1 siRNA-1	UGGUAAUGGUGGAGGAAGAUU
NEAT1 siRNA-2	GUGAGAAGUUGCUUAGAAAUU
NEAT1 siRNA-3	GGAGGAGUCAGGAGGAAUAUU
MALAT1 siRNA-1	GAGGUGUAAAGGGAUUUAUTT
MALAT1 siRNA-2	GGCAUUUGCAUCUUUAAAUTT
MALAT1 siRNA-3	CCCUCUAAAUAAGGAAUAATT

shRNA sequences:

shSCR	TTCTCCGAACGTGTCACGT
shFOXN3	GGAGUCAGAGUAUUGGGAATT
shSIN3A	CCCUCCAGUUAAGAAGAAATT
shNEAT1	GUGAGAAGUUGCUUAGAAAUU
shSAP18	GCGAGUUGCAGAUCUACACTT
shGATA3	GGCUCUACUACAAGCUUCATT

Table S5. Primers used in this study

qChIP primers:

GATA3	F	CCCCAGTCGCCCTTTACAAT
GATA3	R	ACAATAACCGCCCAGAGACG
TJP1	F	GCGTGTAGTACGTATTCGCCAT
TJP1	R	AGACGCTGCCTGTTGGTTTG
NCOA2	F	CGTCTTCATCTTGCGAGCAC
NCOA2	R	TCCTAGTTGCCGATCAAGCC
TLE1	F	CCTCGGCAAGTTCCACTTCT
TLE1	R	CCAGCTGCCGCTTGGTT
ESR1	F	AGACCTCTGCAGGTTACCGA
ESR1	R	TGCCATCCAGCCGATTTTCT
Control Region	F	AGCACTGTAACTCAATATACCCCA
Control Region	R	CCGGATGATGTGTCTCTGAATC

RT-PCR primers:

NEAT1	F	CCTAGCATGTTTGACAGGCG
NEAT1	R	TGCCACCTGGAAAATAAAGCG
MALAT1	F	GCTTGAGAAGATGAGGGTGTTT
MALAT1	R	ACCAACTTCCCCTTCTAGCTTC
GATA3	F	GTTGTGCTCGGAGGGTTTCT
GATA3	R	GCACGCTGGTAGCTCATACA
TJP1	F	AAGCTGTGGGTAACGCCATC
TJP1	R	GGGTTTTCCTTGGCTGACAC

GAPDH	F	CCCACTCCTCCACCTTTGAC
GAPDH	R	CATACCAGGAAATGAGCTTGACAA
CDH1	F	GAAATCACATCCTACACTGCCC
CDH1	R	GTAGCAACTGGAGAACCATTGTC
CTNNA1	F	ATGATCCCTGCTCTTCTGTG
CTNNA1	R	GATACCATCTTCCACAACTTTCAG
JUP1	F	GGACAAGAACCCAGACTACC
JUP1	R	GTGGCATCCATGTCATCTCC
FN1	F	GATAAATCAACAGTGGGAGCGG
FN1	R	GTCTCTTCAGCTTCAGGTTTACTC
VIM	F	ATTGAGATTGCCACCTACAG
VIM	R	ATCCAGATTAGTTTCCCTCAG
ESR1	F	GGGAATGATGAAAGGTGGGAT
ESR1	R	GGTTGGCAGCTCTCATGTCT
GREB1	F	GGCAGGACCAGCTTCTGA
GREB1	R	CTGTTCCCACCACCTTGG
TFF1	F	TTGTGGTTTTCCTGGTGTCA
TFF1	R	CCGAGCTCTGGGACTAATCA
KLF4	F	GGACACACGGGATGATGCTC
KLF4	R	TCATCTGAGCGGGCGAATTT
KLF7	F	ATTGTGTGGCACTTCCTCCT
KLF7	R	AAGCTGAGAAGTAGCCGGTG
KLF9	F	AGAAGAGGCACACTTGACGG

KLF9	R	GGGACCGAGTGTTGTTGACT
TAF3	F	CCCATGATTGGGTGTGACGA
TAF3	R	CATCTGGGGGTGGATGTGAC
RSF1	F	AGCAAGGTAAAACCCAAAGGC
RSF1	R	TTCGGCACGCTCTTTCTTCT
SOX4	F	CCCAGCAAGAAGGCGAGTTA
SOX4	R	CCTTCCAGTTCGTGTCCTCC
NOTCH2	F	TGAATCCCACAAAGCCTAGCA
NOTCH2	R	CTTGTCCCTGAGCAACCATCT
TLE1	F	CCTCGGCAAGTTCCACTTCT
TLE1	R	CCAGCTGCCGCTTGGTT
PTEN	F	GGCACAAGAGGCCCTAGATTT
PTEN	R	GGAATAGTTACTCCCTTTTTGTCTC