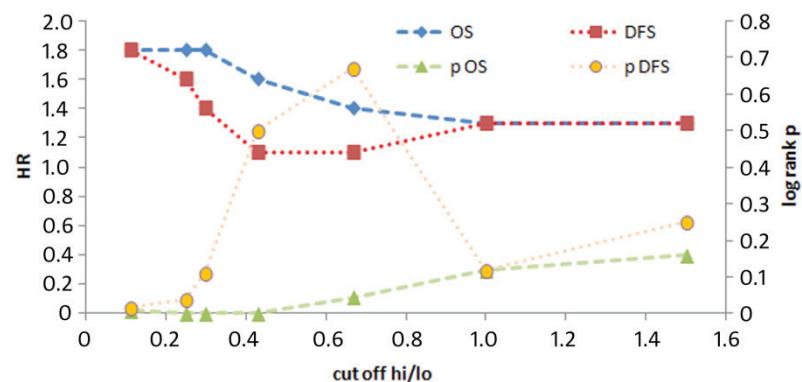
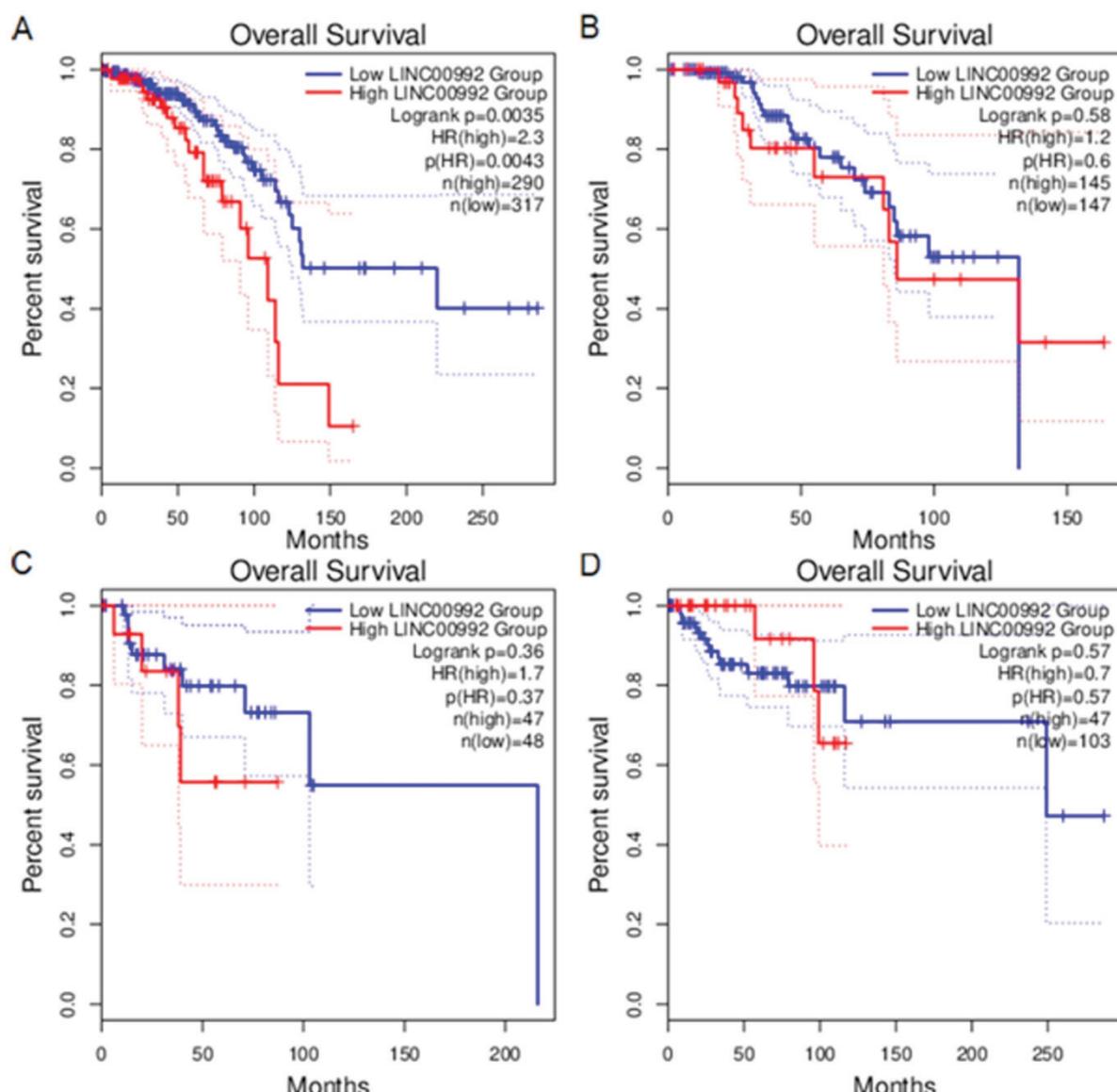


Supplementary. The tamoxifen-regulated, long non-coding RNA LINC00992 affects proliferation, migration, and expression of tamoxifen resistance-associated genes in MCF-7 breast cancer cells



cutoff	high	20	23	30	40	50	60
high	10	20	23	30	40	50	60
low	90	80	77	70	60	50	40
OS							
HR	1.8	1.8	1.8	1.6	1.4	1.3	1.3
log rank p	0.0096	0.00087	0.00081	0.0027	0.045	0.12	0.16
DFS							
HR	1.8	1.6	1.4	1.1	1.1	1.3	1.3
log rank p	0.018	0.04	0.11	0.5	0.67	0.12	0.25

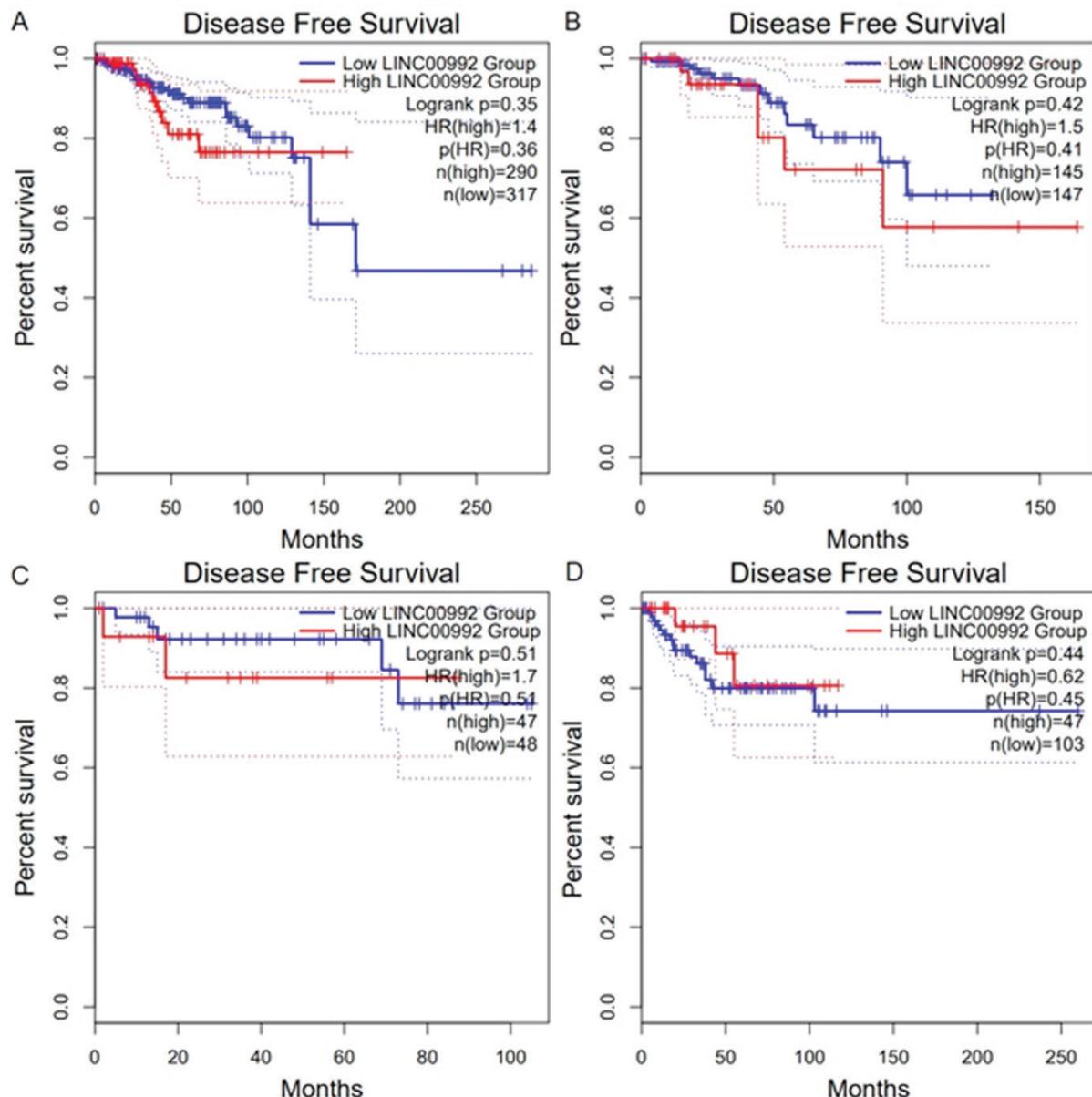
Suppl. Fig 1. Relationship of hazard ratio and statistical significance (log-rank p) to the cut-off values in Kaplan-Meier analysis for overall survival and disease-free survival using GEPIA2



Suppl. Fig. 2. Overall survival analysis comparing LINC00992 high and low expressing cases of the 4 intrinsic subtypes of breast cancer. Cut-off was set to 23% high and 77% low.

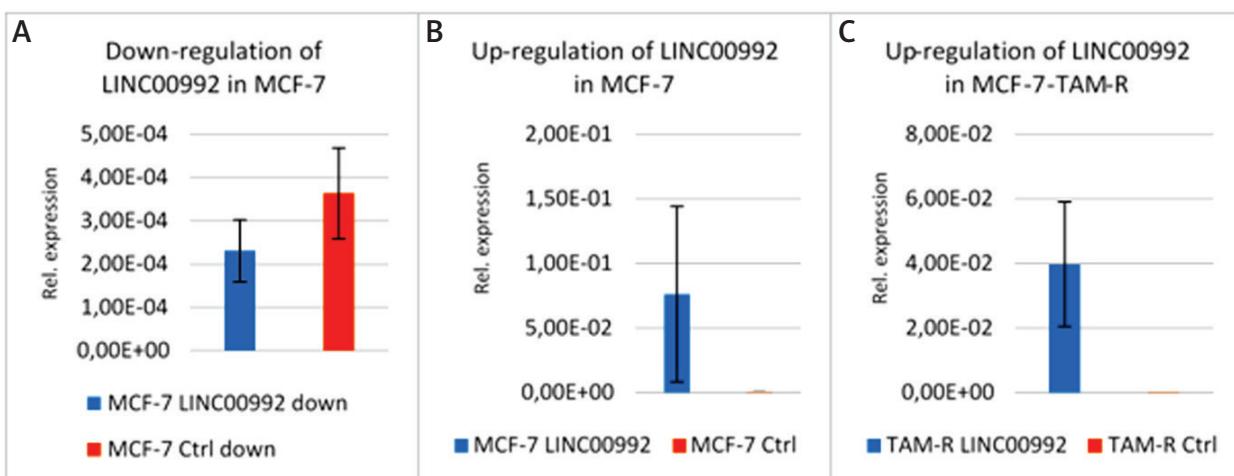
A – luminal A-subtype, B – luminal B-subtype, C – Her2-subtype, D – basal subtype

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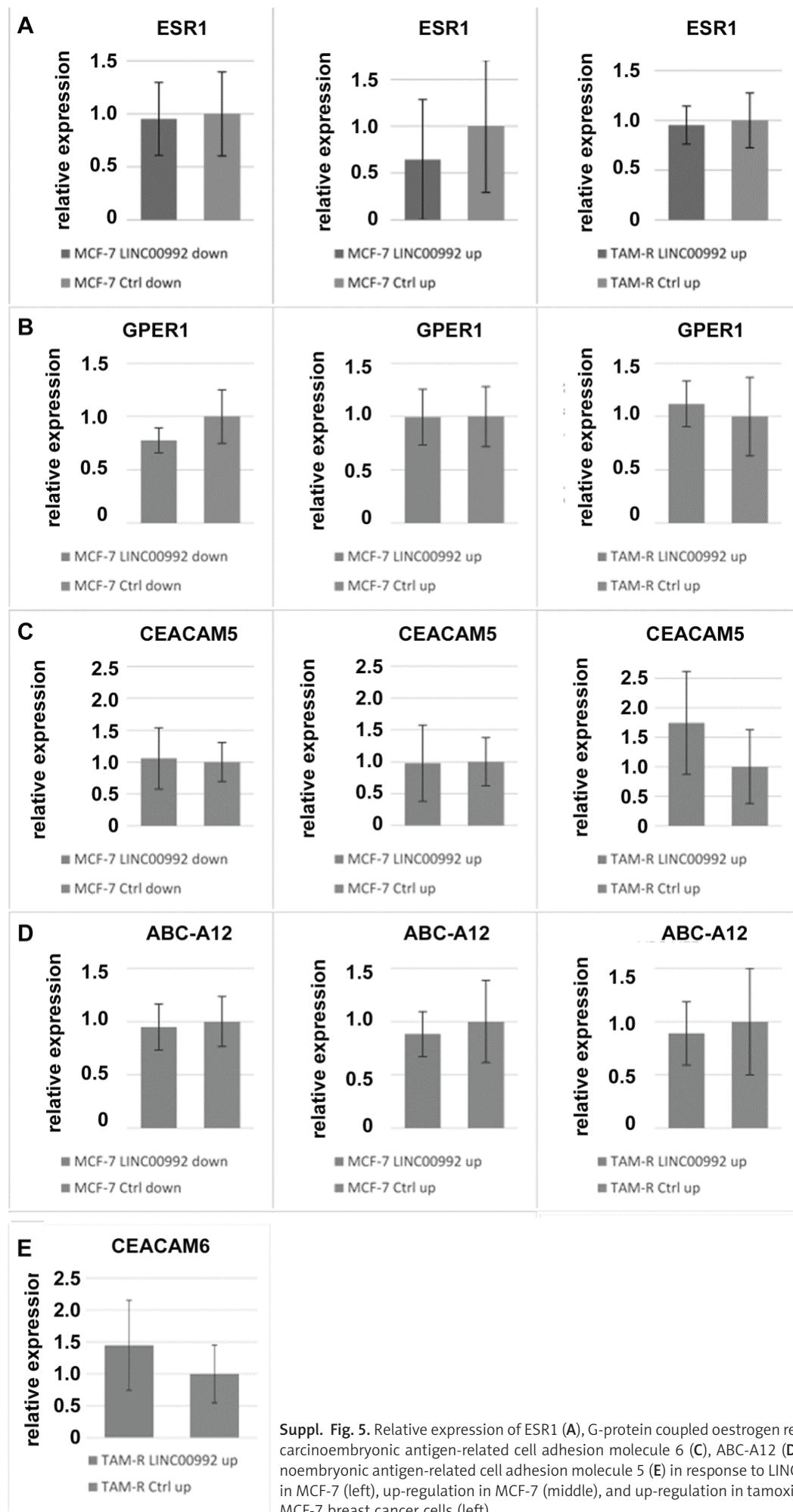
Suppl. Fig. 3. Disease-free survival analysis comparing LINC00992 high and low expressing cases of the 4 intrinsic subtypes of breast cancer. Cut-off was set to 23% high and 77% low

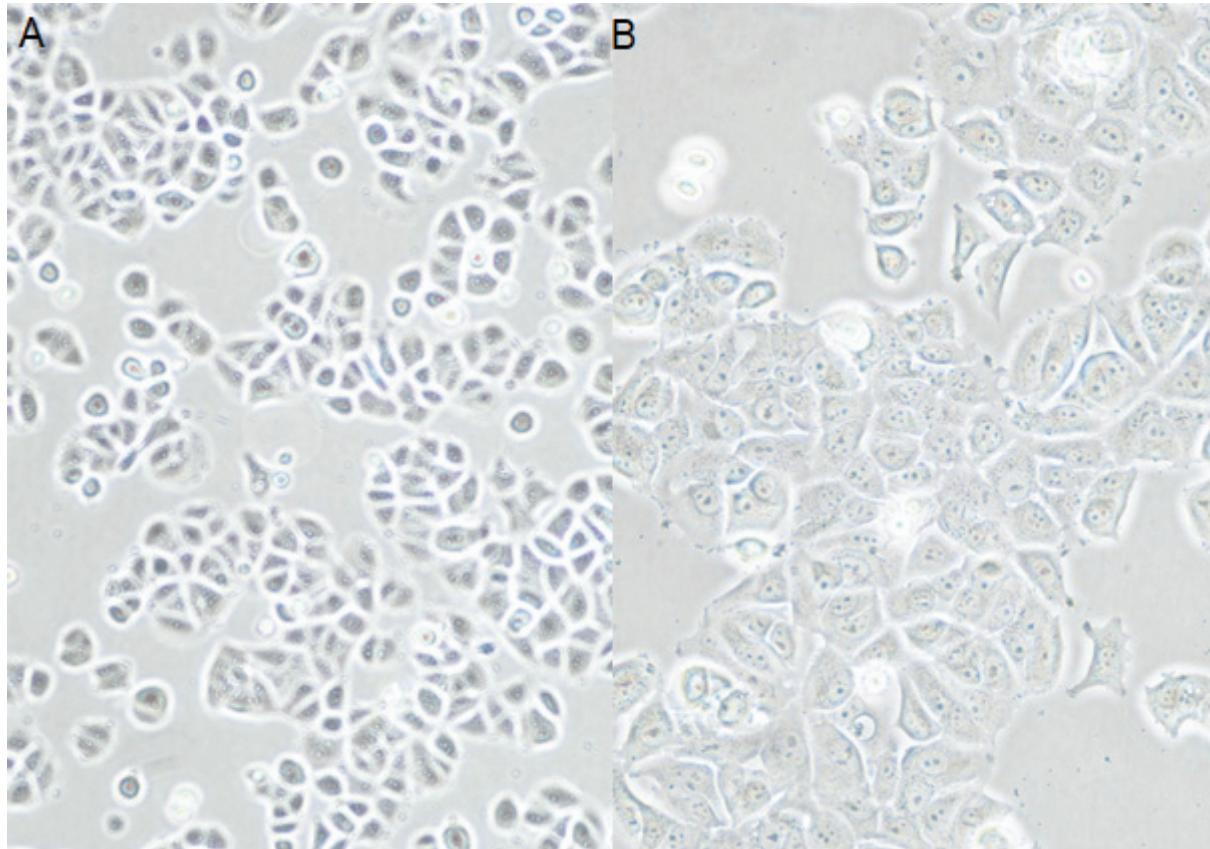
A – luminal A-subtype, B – luminal B-subtype, C – Her2-subtype, D – basal subtype



Suppl. Fig. 4. Relative expression of LINC00992 determined by quantitative real-time polymerase chain reaction relative to RPL13 using the $2^{-\Delta ct}$ method. Error bars represent the first standard deviation. MCF-7 cells after transfection with the LINC00992 siRNA (down) and the control siRNA (Ctrl.) (A), overexpression of LINC00992 by transient plasmid transfection in MCF-7 cells (B), and overexpression of LINC00992 by transient plasmid transfection tamoxifen-adapted MCF-7 breast cancer cells (C)

Expression of LINC00992 was significantly altered ($p < 0.05$) in all 3 experimental groups compared to controls.

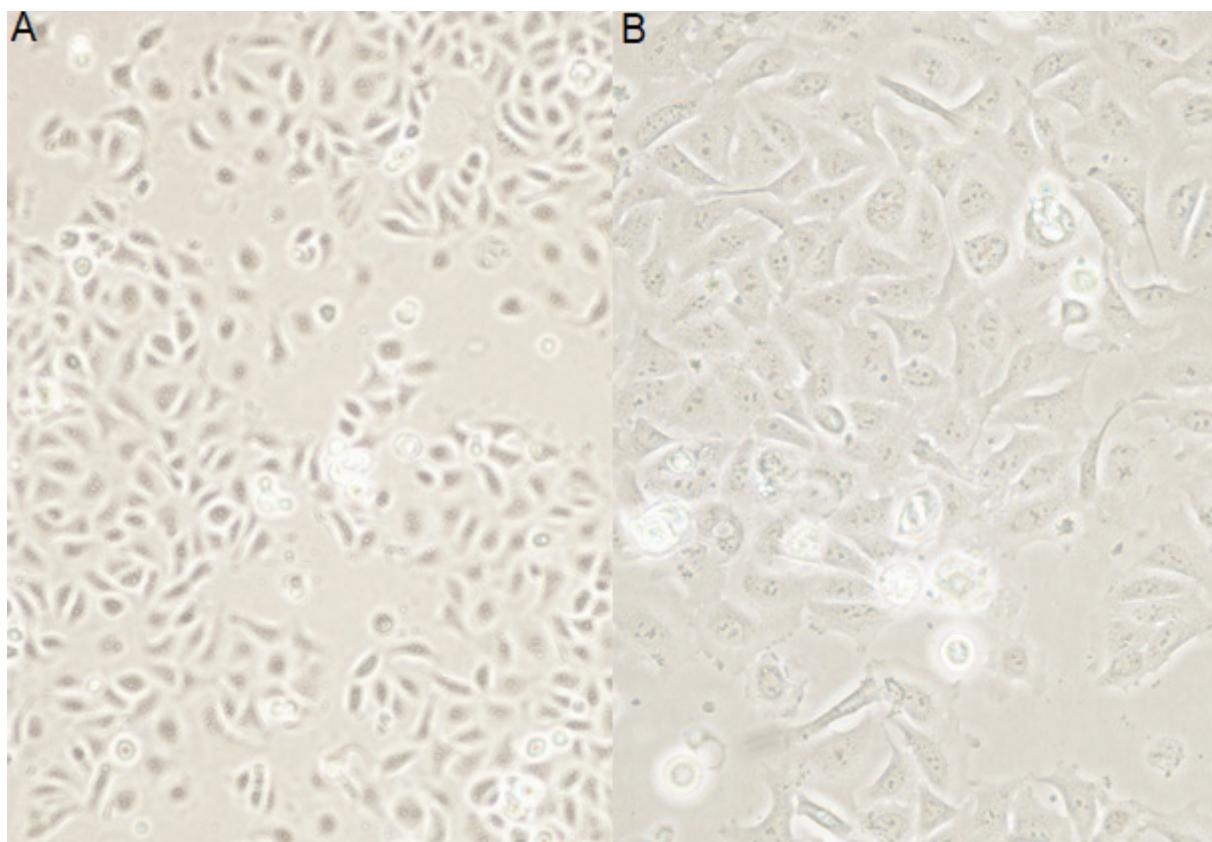




App. 14: A) Tenfold magnification of untreated MCF-7 cells in a culture flask. Grouped, cohesive, cylindrical and prismatic cells with formation of ductal or tubular duct structures in cross-section can be seen. B) Twenty-fold magnification of untreated MCF-7 cells in a culture flask. Ravenous growing, moderately pleiomorphic cells with clear adhesion of the cell membranes and shadowy formation of organoid, partly lobular structures can be seen.

Control cells are set to one (right column each).

Suppl. Fig 6. Morphology of MCF-7. Cells are untreated and photographed using phase contrast and 10 \times objective (A) and 20 \times for MCF-7 (B)



App 15: A) Tenfold magnification of untreated TAM-R cells in a culture flask. Clearly pleiomorphic, dissolutely growing cells without formation of cell assemblies or organoid structures, as well as clearly pleiomorphic cells can be seen. B) Twenty-fold magnification of untreated TAM-R cells in a culture flask. To be seen are poorly adherent, pleomorhic, polygonal to spindle-shaped cells with distinctly anisomorphic nuclei.

Suppl. Fig 7. Morphology of tamoxifen-adapted MCF-7 breast cancer cells. Cells are untreated and photographed using phase contrast and 10 \times objective (A) and 20 \times for MCF-7 (B)

Suppl. Table 1. Down- and up-regulation of LINC00992 in MCF-7 and up-regulation in tamoxifen-adapted MCF-7 breast cancer cells

LINC00992	MCF-7 LINC00-992 siRNA	MCF-7 LINC00-992 Ctrl siRNA	MCF-7 LINC00-992 up	MCF-7 Ctrl (up)	TAM-R LINC00-992 up	TAM-R Ctrl (up)
Average	2.31E-04	3.64E-04	7.61E-02	1.54E-04	3.98E-02	6.44E-06
Standard deviation	7.17E-05	1.05E-04	6.78E-02	8.34E-05	1.93E-02	3.20E-06
Samples	7	7	8	8	9	9
p ($T \geq t$) (2-sided)		*0.018		*0.016		*0.0002

Ctrl – control group

* $p < 0.05$ **Suppl. Table 2.** Results of gene expression analysis using NanoString nCounter® for down-regulation of LINC00992 in MCF-7 (relative gene expression to RPL13) with statistical testing

LINC00992 down	Average	s.d.	Ctrl		Log ₂ Fc		p ($T \geq t$) (2-sided)
			Average	s.d.	Average	s.d.	
LINC00992	5.82	3.37	5.01	1.11	0.03	1.10	0.723
ABC-A12	293.68	75.59	345.57	58.33	-0.25	0.15	0.057
ADAMTS9	38.67	3.50	37.11	7.61	0.08	0.26	0.738
AMIGO2	3145.14	1098.57	3484.05	1150.35	-0.15	0.03	*0.014
AR	91.85	12.78	87.00	12.60	0.08	0.19	0.566
ARHGAP26	93.93	18.77	91.31	15.42	0.03	0.07	0.422
BAMBI	3155.44	1182.23	2746.24	1061.84	0.21	0.17	0.149
BDKRB2	58.69	4.30	66.36	20.13	-0.14	0.32	0.501
BMP5	646.07	340.85	699.79	330.20	-0.16	0.14	0.103
BPIFB1	90.64	64.54	113.86	85.50	-0.35	0.21	0.237
C1orf226	260.23	84.59	268.68	104.39	-0.02	0.22	0.710
CA2	6287.32	1516.66	6127.02	1358.14	0.03	0.10	0.586
CEACAM6	274.56	205.45	235.72	143.89	-0.05	0.59	0.389
DEFB1	13.14	5.26	11.63	4.02	0.14	0.16	0.217
DHRS3	564.05	367.52	482.55	353.74	0.26	0.25	0.140
EPAS1	799.84	524.86	583.60	370.93	0.42	0.12	0.139
FAXDC2	169.76	109.70	206.13	99.29	-0.36	0.29	0.218
FOLH1	13.17	5.05	10.90	5.07	0.31	0.53	0.522
GPER1	199.87	151.21	189.14	141.73	0.07	0.01	0.189
GPR68	336.63	203.57	384.79	178.19	-0.26	0.20	0.142
GPX2	94.42	46.47	79.06	35.37	0.22	0.14	0.154
GREB1	1038.97	692.21	1152.56	670.80	-0.19	0.17	0.184
KLK11	602.92	418.30	688.49	334.96	-0.30	0.34	0.301
KRT4	17.63	13.10	21.70	15.62	-0.44	0.45	0.381
LINC00632	7.89	2.55	7.14	2.06	0.14	0.68	0.763
LINC00683	60.32	5.29	54.19	8.08	0.16	0.10	0.072
LINC01213	69.53	18.69	59.97	7.92	0.19	0.20	0.265
LOC101929547	120.98	49.90	133.75	39.64	-0.18	0.16	0.212
PIP	16.61	8.55	17.75	5.52	-0.18	0.55	0.815
PTGER4	61.51	9.77	60.52	6.93	0.02	0.08	0.643
RAMP3	877.69	267.02	1062.80	256.18	-0.29	0.33	0.315
RGS22	19.16	7.12	22.73	11.47	-0.20	0.26	0.344
SEMA5A	134.30	77.62	120.54	65.65	0.12	0.15	0.340
SIM1	66.15	39.83	85.19	26.14	-0.48	0.59	0.307
SOX3	496.64	141.43	570.90	108.04	-0.23	0.18	0.098
SPINK4	52.06	20.69	54.32	15.59	-0.09	0.25	0.670

LINC00992 down	Average	s.d.	Ctrl		Log ₂ Fc		<i>p</i> ($T \geq t$) (2-sided)
			Average	s.d.	Average	s.d.	
TARP	27.77	14.25	25.63	13.27	0.11	0.13	0.216
TFF3	1513.86	774.85	1740.42	932.56	-0.20	0.14	0.189
UBD	17.84	11.23	13.45	13.31	0.60	0.96	0.407
VAV3	1244.45	269.09	1390.30	253.20	-0.17	0.09	0.078
XR_133213	23.49	4.01	14.44	6.07	0.80	0.72	0.127
ZNF462	27.10	14.85	28.39	17.53	-0.05	0.22	0.650
ACTB	176504.02	63580.86	164397.88	46247.71	0.07	0.17	0.390
CLTC	15536.62	4978.70	14900.99	4396.86	0.05	0.05	0.202
GUSB	1312.16	19.57	1279.49	49.28	0.04	0.06	0.406
HPRT1	4039.63	592.60	3749.45	514.14	0.11	0.08	0.140
PGK1	13937.78	6943.68	13319.77	7485.90	0.10	0.12	0.277
RPL13	8013.89	0.00	8013.89	0.00	0.00	0.00	0.423

CEACAM – carcinoembryonic antigen-related cell adhesion molecule, Ctrl – control group, GPER1 – G-protein coupled oestrogen receptor 1, SIM1 – single-minded homologue 1, UBD – ubiquitin D, ZNF462 – zinc finger protein 462
Orange background – LINC00992, blue – housekeeping genes

Suppl. Table 3. Results of gene expression analysis using NanoString nCounter® for up-regulation of LINC00992 (relative gene expression to RPL13) in MCF-7 with statistical testing

LINC00992 up	Average	s.d.	Ctrl		Log ₂ Fc		<i>p</i> ($T \geq t$) (2-sided)
			Average	s.d.	Average	s.d.	
LINC00992	4776.51	1984.62	4.82	3.61	10.10	1.66	0.053
ABC-A12	506.62	153.87	475.86	170.88	0.12	0.15	0.238
ADAMTS9	51.11	7.79	46.81	12.93	0.15	0.21	0.364
AMIGO2	4634.55	3061.14	4531.56	2985.96	-0.01	0.16	0.741
AR	144.73	12.35	129.04	5.40	0.16	0.12	0.149
ARHGAP26	212.68	72.90	232.56	102.21	-0.09	0.24	0.438
BAMBI	6474.20	2158.32	5812.28	1321.95	0.12	0.18	0.304
BDKRB2	202.69	14.53	199.44	41.35	0.04	0.19	0.855
BMP5	899.03	342.55	912.34	373.55	-0.01	0.05	0.581
BPIFB1	217.66	76.54	194.02	67.10	0.16	0.09	0.155
C1orf226	364.21	108.16	368.43	100.70	-0.03	0.20	0.893
CA2	7521.95	2254.10	7556.45	1498.11	-0.04	0.28	0.966
CEACAM6	462.20	395.25	396.40	314.45	0.14	0.27	0.317
DEFB1	12.90	10.04	11.93	0.78	-0.17	1.20	0.890
DHRS3	439.32	255.79	457.51	211.12	-0.16	0.43	0.724
EPAS1	786.36	634.19	633.93	331.44	0.13	0.43	0.503
FAXDC2	134.34	58.59	135.45	42.45	-0.08	0.39	0.951
FOLH1	21.21	1.80	16.70	10.41	0.56	1.08	0.549
GPER1	301.23	183.09	273.94	169.27	0.15	0.04	0.087
GPR68	241.22	109.40	257.32	58.00	-0.20	0.47	0.655
GPX2	126.64	37.24	115.55	27.42	0.12	0.08	0.202
GREB1	670.79	586.88	627.01	560.46	-0.07	0.38	0.390
KLK11	649.05	261.46	772.42	72.10	-0.35	0.72	0.517
KRT4	26.70	15.72	18.30	1.14	0.37	0.81	0.432
LINC00632	16.42	4.37	12.26	2.40	0.40	0.45	0.230
LINC00683	50.43	21.36	53.15	13.66	-0.15	0.36	0.675
LINC01213	68.80	19.31	57.19	10.76	0.25	0.17	0.191
LOC101929547	163.69	84.73	182.11	69.77	-0.24	0.37	0.290

LINC00992 up	Average	s.d.	Ctrl		$\log_2 Fc$		$p (T \geq t)$ (2-sided)
			Average	s.d.	Average	s.d.	
PIP	18.62	2.83	18.77	5.75	0.03	0.38	0.958
PTGER4	171.11	36.93	158.98	26.80	0.10	0.13	0.339
RAMP3	573.56	398.73	630.34	253.61	-0.42	0.91	0.651
RGS22	24.08	4.66	17.41	5.48	0.51	0.44	0.159
SEMA5A	104.95	52.35	88.66	36.12	0.21	0.29	0.318
SIM1	42.44	21.18	50.76	19.86	-0.35	0.52	0.353
SOX3	533.26	263.65	548.72	230.17	-0.08	0.16	0.676
SPINK4	49.78	9.44	66.22	19.77	-0.39	0.53	0.351
TARP	83.62	52.61	57.46	36.34	0.50	0.27	0.138
TFF3	2400.58	1463.37	2418.07	1317.54	-0.09	0.21	0.859
UBD	72.02	45.86	155.81	63.79	-1.19	0.76	0.127
VAV3	1207.84	285.06	1195.92	310.19	0.02	0.06	0.748
XR_133213	21.94	4.52	23.50	4.16	-0.10	0.34	0.669
ZNF462	43.21	6.36	58.52	28.13	-0.29	0.67	0.353
ACTB	228537.07	31032.86	217941.68	5434.70	0.06	0.16	0.548
CLTC	21673.34	1366.71	19750.48	794.40	0.13	0.15	0.258
GUSB	1680.11	273.95	1625.74	253.92	0.05	0.12	0.582
HPRT1	4338.31	355.54	4147.21	275.34	0.06	0.09	0.358
PGK1	9781.71	187.28	9543.43	518.37	0.04	0.10	0.612
RPL13	8013.89	0.00	8013.89	0.00	0.00	0.00	0.667

CEACAM – carcinoembryonic antigen-related cell adhesion molecule, Ctrl – control group, GPER1 – G-protein coupled oestrogen receptor 1, SIM1 – single-minded homologue 1, UBD – ubiquitin D, ZNF462 – zinc finger protein 462
Orange background – LINC00992, blue – housekeeping genes

Suppl. Table 4. Results of PAM50 gene expression analysis using NanoString nCounter® for down-regulation of LINC00992 in MCF-7 (relative gene expression to RPL13) with statistical testing

LINC00992 down	Average	s.d.	Ctrl		$\log_2 Fc$		$p (T \geq t)$ (2-sided)
			Average	s.d.	Average	s.d.	
ACTR3B	1300.00	40.50	1370.00	66.00	-0.07	0.04	0.24
ANLN	3590.00	161.00	3630.00	134.00	-0.01	0.01	0.80
BAG1	4910.00	698.00	4730.00	775.00	0.06	0.03	0.78
BCL2	6.20	8.97	6.71	9.82	-0.06	0.04	0.95
BIRC5	5920.00	304.00	6070.00	247.00	-0.04	0.04	0.55
BLVRA	3140.00	386.00	3040.00	260.00	0.04	0.03	0.73
CCNB1	22200.00	2220.00	22700.00	195.00	-0.04	0.09	0.73
CCNE1	1200.00	191.00	1160.00	73.00	0.04	0.11	0.76
CDC20	2910.00	163.00	2930.00	267.00	-0.01	0.05	0.93
CDC6	1830.00	121.00	1890.00	143.00	-0.05	0.01	0.60
CDCA1	243.00	17.70	271.00	39.90	-0.15	0.07	0.35
CDH3	778.00	217.00	759.00	159.00	0.01	0.11	0.91
CENPF	1060.00	103.00	1050.00	102.00	0.01	0.09	0.95
CEP55	2100.00	252.00	2230.00	74.90	-0.09	0.12	0.46
CXXC5	8350.00	1300.00	9030.00	1000.00	-0.12	0.07	0.52
EGFR	72.70	8.63	67.70	10.80	0.11	0.23	0.57
ERBB2	691.00	86.40	686.00	32.40	0.00	0.10	0.93
ESR1	4500.00	1160.00	4610.00	1050.00	-0.04	0.05	0.91
EXO1	1430.00	113.00	1480.00	126.00	-0.04	0.01	0.67
FGFR4	422.00	77.00	455.00	72.70	-0.11	0.05	0.63

LINC00992 down	Average	s.d.	Ctrl		Log ₂ Fc		<i>p</i> ($T \geq t$) (2-sided)
			Average	s.d.	Average	s.d.	
FOXA1	10800.00	384.00	11100.00	1420.00	-0.03	0.13	0.75
FOXC1	444.00	9.37	434.00	18.70	0.03	0.04	0.48
GPR160	3410.00	293.00	3660.00	431.00	-0.10	0.05	0.45
GRB7	248.00	41.40	270.00	24.60	-0.13	0.06	0.48
KIF2C	1490.00	150.00	1540.00	260.00	-0.03	0.15	0.83
KNTC2	2700.00	361.00	2930.00	357.00	-0.12	0.01	0.48
KRT14	57.70	4.59	60.10	11.10	-0.04	0.21	0.76
KRT17	1.06	0.06	1.11	0.13	-0.07	0.05	0.56
KRT5	1.06	0.06	1.11	0.13	-0.07	0.05	0.56
MAPT	579.00	79.70	643.00	88.00	-0.15	0.16	0.40
MDM2	11600.00	535.00	12000.00	421.00	-0.06	0.06	0.31
MELK	2190.00	99.50	2310.00	157.00	-0.08	0.02	0.34
MIA	1.06	0.06	1.11	0.13	-0.07	0.05	0.56
MKI67	3770.00	262.00	3830.00	291.00	-0.02	0.05	0.78
MLPH	2390.00	246.00	2630.00	373.00	-0.13	0.03	0.42
MMP11	20.60	20.60	25.70	17.20	-1.11	0.37	0.76
MYBL2	2490.00	335.00	2620.00	107.00	-0.08	0.10	0.57
MYC	7210.00	520.00	6780.00	86.50	0.09	0.06	0.29
NAT1	202.00	16.90	224.00	8.13	-0.15	0.04	0.14
ORC6L	2020.00	154.00	1990.00	294.00	0.03	0.08	0.91
PGR	179.00	170.00	254.00	138.00	-0.85	0.42	0.59
PHGDH	1410.00	269.00	1470.00	138.00	-0.07	0.09	0.77
PTTG1	7520.00	356.00	7930.00	283.00	-0.08	0.05	0.20
RRM2	24200.00	1360.00	24000.00	1900.00	0.02	0.04	0.88
SFRP1	1.06	0.06	1.11	0.13	-0.07	0.05	0.56
SLC39A6	78700.00	25000.00	80600.00	27400.00	-0.02	0.04	0.93
TMEM45B	511.00	283.00	409.00	120.00	0.23	0.28	0.61
TYMS	5320.00	980.00	5710.00	991.00	-0.10	0.01	0.65
UBE2C	8120.00	614.00	8380.00	783.00	-0.05	0.05	0.67
UBE2T	1180.00	169.00	1130.00	74.20	0.05	0.15	0.68
ACTB	792000.00	132000.00	783000.00	87600.00	0.01	0.04	0.93
GUSB	1430.00	217.00	1460.00	148.00	-0.04	0.05	0.85
MRPL19	4610.00	382.00	4720.00	113.00	-0.04	0.08	0.67
PSMC4	5890.00	405.00	5670.00	197.00	0.05	0.03	0.46
PUM1	1990.00	199.00	1960.00	62.80	0.02	0.06	0.84
RPLPO	110000.00	16900.00	114000.00	27300.00	-0.03	0.07	0.87
SF3A1	2130.00	98.90	2170.00	132.00	-0.03	0.01	0.66
TFRC	7940.00	326.00	7610.00	385.00	0.06	0.08	0.32

Ctrl – control group

Suppl. Table 5. Results of PAM50 gene expression analysis using NanoString nCounter® for up-regulation of LINC00992 (relative gene expression to RPL13) with statistical testing

LINC00992 up	Average	s.d.	Ctrl		Log ₂ Fc		<i>p</i> ($T \geq t$) (2-sided)
			Average	s.d.	Average	s.d.	
ACTR3B	1400.00	72.50	1420.00	76.30	-0.02	0.06	0.73
ANLN	4490.00	460.00	4670.00	239.00	-0.06	0.04	0.58
BAG1	4740.00	911.00	4630.00	761.00	0.03	0.05	0.89
BCL2	7.91	11.80	5.09	7.08	0.33	0.26	0.74
BIRC5	6320.00	93.60	6650.00	510.00	-0.07	0.07	0.38
BLVRA	3350.00	696.00	3580.00	750.00	-0.10	0.01	0.71
CCNB1	19700.00	2180.00	20300.00	540.00	-0.05	0.08	0.71
CCNE1	1390.00	370.00	1380.00	279.00	-0.01	0.06	0.98
CDC20	2430.00	477.00	2680.00	524.00	-0.14	0.04	0.58
CDC6	1770.00	277.00	1980.00	218.00	-0.17	0.03	0.36
CDCA1	273.00	39.10	296.00	40.20	-0.12	0.01	0.52
CDH3	993.00	239.00	915.00	164.00	0.11	0.05	0.67
CENPF	1150.00	196.00	1290.00	184.00	-0.17	0.08	0.41
CEP55	2250.00	365.00	2310.00	170.00	-0.05	0.07	0.81
CXXC5	10600.00	3600.00	10700.00	3120.00	-0.03	0.05	0.97
EGFR	23.40	21.20	22.70	11.70	-1.00	0.87	0.96
ERBB2	702.00	120.00	673.00	50.60	0.05	0.09	0.73
ESR1	5300.00	1010.00	5430.00	836.00	-0.04	0.04	0.87
EXO1	1520.00	68.30	1640.00	76.70	-0.11	0.01	0.12
FGFR4	469.00	13.50	491.00	45.20	-0.06	0.07	0.49
FOXA1	9800.00	1160.00	10500.00	2690.00	-0.08	0.10	0.71
FOXC1	343.00	17.30	338.00	5.79	0.02	0.05	0.70
GPR160	5150.00	2500.00	5040.00	2400.00	0.02	0.04	0.96
GRB7	281.00	121.00	300.00	69.50	-0.15	0.18	0.83
KIF2C	1310.00	187.00	1410.00	189.00	-0.11	0.08	0.55
KNTC2	2840.00	520.00	3230.00	542.00	-0.19	0.03	0.41
KRT14	42.20	28.80	45.10	30.70	0.02	0.28	0.91
KRT17	1.11	0.11	1.13	0.23	-0.01	0.16	0.92
KRT5	1.11	0.11	1.13	0.23	-0.01	0.16	0.92
MAPT	644.00	275.00	655.00	252.00	-0.04	0.03	0.96
MDM2	9020.00	724.00	8790.00	916.00	0.04	0.02	0.75
MELK	2190.00	240.00	2250.00	110.00	-0.04	0.05	0.71
MIA	1.11	0.11	1.13	0.23	-0.01	0.16	0.92
MKI67	4140.00	397.00	4460.00	555.00	-0.11	0.02	0.46
MLPH	2320.00	827.00	2540.00	1060.00	-0.11	0.07	0.79
MMP11	20.90	5.06	32.30	2.92	-0.65	0.08	*0.04
MYBL2	2680.00	328.00	2770.00	231.00	-0.05	0.09	0.75
MYC	6420.00	1540.00	6080.00	1500.00	0.08	0.02	0.80
NAT1	226.00	29.10	220.00	38.40	0.04	0.13	0.85
ORC6L	2000.00	435.00	1960.00	356.00	0.02	0.04	0.90
PGR	382.00	288.00	435.00	287.00	-0.21	0.16	0.83
PHGDH	1840.00	376.00	2040.00	238.00	-0.17	0.09	0.47
PTTG1	7460.00	862.00	7780.00	1220.00	-0.06	0.03	0.73
RRM2	23600.00	3610.00	23100.00	3460.00	0.03	0.03	0.87
SFRP1	1.11	0.11	1.13	0.23	-0.01	0.16	0.92
SLC39A6	71600.00	10900.00	79300.00	10600.00	-0.15	0.02	0.43

LINC00992 up	Average	s.d.	Ctrl		$\log_2 F_c$		$p (T \geq t)$ (2-sided)
			Average	s.d.	Average	s.d.	
TMEM45B	395.00	189.00	289.00	59.80	0.34	0.35	0.44
TYMS	5740.00	316.00	6090.00	213.00	-0.09	0.02	0.20
UBE2C	8400.00	254.00	8710.00	837.00	-0.05	0.06	0.60
UBE2T	1240.00	158.00	1240.00	176.00	0.00	0.05	0.99
ACTB	731000.00	194000.00	711000.00	133000.00	0.02	0.09	0.89
GUSB	1400.00	329.00	1450.00	222.00	-0.06	0.06	0.84
MRPL19	4570.00	637.00	4630.00	253.00	-0.03	0.09	0.89
PSMC4	4700.00	1120.00	4600.00	1030.00	0.03	0.02	0.92
PUM1	1790.00	225.00	1800.00	171.00	-0.01	0.08	0.99
RPLPO	161000.00	30700.00	156000.00	27200.00	0.04	0.02	0.84
SF3A1	2020.00	143.00	2000.00	100.00	0.01	0.02	0.90
TFRC	8590.00	366.00	8480.00	383.00	0.02	0.04	0.73

Ctrl – control group

Suppl. Table 6. Primers used for quantitative real-time polymerase chain reaction

Gene	Primer	Sequence	Producer
ABC-A12	Forward	5'-TGC-TGG-AGA-GTG-TTT-TGG-GC-3'	Integrated DNA technologies, B-3001 Leuven, Belgium
	Reverse	5'-TTC-CCT-ATC-AAG-GCC-AGT-GC-3'	
CEACAM5	Forward	5'-GGA-CCA-CAG-TCA-CGA-CGA-3'	biomers.net GmbH, Ulm, Germany
	Reverse	5'-ACC-CCT-GGA-CGG-TAA-TAG-GT-3'	
CEACAM6	Forward	5'-TCA-GCG-TCA-AAA-GAA-ACG-ATG-C-3'	Integrated DNA technologies, B-3001 Leuven, Belgium
	Reverse	5'-TCA-GAT-TTT-CCC-CTG-GAC-GG-3'	
ESR1	Forward	5'-TGG-GAA-AAG-GCT-CAA-ATG-CC-3'	Integrated DNA technologies, B-3001 Leuven, Belgium
	Reverse	5'-GCA-AAG-CTG-CGA-CAA-AAC-CG-3'	
GPER1	Forward	5'-TGG-TGC-TGG-TCT-TCT-TCG-TC-3'	Integrated DNA technologies, B-3001 Leuven, Belgium
	Reverse	5'-GCT-TGT-CCC-TGA-AGG-TCT-CC-3'	
LINC00992	Forward	5'-GGT-GGA-AGA-CAG-GTC-CAT-GA-3'	biomers.net GmbH, Ulm, Germany
	Reverse	5'-AGG-TGC-AAG-ATG-AGA-TAT-GTT-G-3'	
RPL13	Forward	5'-CCT-GGA-GGA-GAA-GAG-GAA-AGA-GA-3'	biomers.net GmbH, Ulm, Germany
	Reverse	5'-TTG-AGG-ACC-TCT-GTG-TAT-TTG-TCA-A-3'	
UBD/FAT10	Forward	5'-CAT-AGA-TGG-CTC-CCA-ATG-C-3'	Integrated DNA technologies, B-3001 Leuven, Belgium
	Reverse	5'-CCT-GAC-TCC-ACA-AGA-AAC-AAG-G-3'	
ZNF462	Forward	5'-TTC-TCC-TCC-GGC-TAC-ATC-CA-3'	Integrated DNA technologies, B-3001 Leuven, Belgium
	Reverse	5'-TTA-ACC-CGT-CCA-ACC-AGC-TC-3'	

CEACAM – carcinoembryonic antigen-related cell adhesion molecule, GPER1 – G-protein coupled oestrogen receptor 1, UBD – ubiquitin D, ZNF462 – zinc finger 462. The primers for FOLH1 and single-minded homologue 1 were ordered as RealTime Ready Custom Single Assay (product number: 05532957001) from Roche Molecular Systems (Basel, Switzerland). Therefore, sequences cannot be provided.