

Supplementary Table 3. Genes up and down regulated by HQBA

Genes upregulated by HQBA

Column ID	Gene Title	Gene Symbol	p-value(MCF7 treatment vs. control)	Ratio(MCF7 treatment vs. control)	F(Treatment)
202912_at	adrenomedullin	ADM	3.81E-08	19.84	1,204.44
200632_s_at	N-myc downstream regulated 1	NDRG1	3.79E-08	15.23	1,206.51
214978_s_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting	PPFIA4	9.78E-08	13.11	878.46
228499_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	PFKFB4	3.05E-08	12.13	1,297.76
227337_at	ankyrin repeat domain 37	ANKRD37	1.49E-08	12.08	1,647.86
236180_at	---	---	1.05E-07	10.46	856.61
223553_s_at	docking protein 3	DOK3	1.31E-06	10.23	366.84
36711_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF	2.30E-08	9.61	1,426.57
202973_x_at	family with sequence similarity 13, member A1	FAM13A1	2.94E-10	8.28	6,116.26
219410_at	transmembrane protein 45A	TMEM45A	3.17E-05	7.91	123.40
226348_at	---	---	1.35E-08	7.86	1,705.92
235153_at	ring finger protein 183	RNF183	1.18E-06	7.66	380.47
209566_at	insulin induced gene 2	INSIG2	1.46E-07	7.35	767.60
227868_at	hypothetical LOC154761	LOC154761	1.13E-07	7.09	837.70
1558365_at	---	---	1.46E-06	7.03	353.54
202464_s_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	7.68E-09	6.70	2,058.66
226347_at	---	---	8.03E-08	6.51	938.48
227285_at	chromosome 1 open reading frame 51	C1orf51	4.29E-08	6.19	1,157.89
238551_at	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	FUT11	1.22E-08	6.06	1,764.54
202934_at	hexokinase 2	HK2	1.19E-07	6.02	823.16
228483_s_at	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	TAF9B	2.30E-06	6.01	303.17
226452_at	pyruvate dehydrogenase kinase, isozyme 1	PDK1	8.14E-08	5.93	934.13
221478_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	BNIP3L	3.54E-09	5.54	2,667.16
228770_at	G protein-coupled receptor 146	GPR146	1.07E-05	5.48	179.47
201968_s_at	phosphoglucomutase 1	PGM1	9.09E-08	5.46	900.22

221009_s_at	angiopoietin-like 4	ANGPTL4	5.13E-08	5.43	1,090.84
201313_at	enolase 2 (gamma, neuronal)	ENO2	1.89E-07	5.27	703.73
231786_at	homeobox A13	HOXA13	8.65E-05	5.07	86.82
239798_at	---	---	0.000194913	5.03	65.00
217047_s_at	family with sequence similarity 13, member A1	FAM13A1	2.86E-05	4.96	127.97
201848_s_at	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3	6.77E-09	4.94	2,146.81
210095_s_at	insulin-like growth factor binding protein 3 pleckstrin homology domain containing, family A (phosphoinositide binding specif	IGFBP3	8.63E-08	4.93	916.21
238013_at	---	PLEKHA2	3.44E-05	4.91	119.91
221497_x_at	egl nine homolog 1 (C. elegans)	EGLN1	1.15E-09	4.87	3,884.44
210512_s_at	vascular endothelial growth factor A	VEGFA	2.00E-07	4.83	691.14
227719_at	SMAD family member 9	SMAD9	2.69E-07	4.80	625.35
225750_at	---	---	3.62E-09	4.75	2,646.15
212558_at	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	SPRY1	1.23E-05	4.74	171.18
224314_s_at	egl nine homolog 1 (C. elegans)	EGLN1	3.81E-07	4.61	556.36
209446_s_at	chromosome 7 open reading frame 44	C7orf44	7.38E-06	4.58	203.89
235850_at	WD repeat domain 5B	WDR5B	1.03E-05	4.58	182.04
209189_at	v-fos FBJ murine osteosarcoma viral oncogene homolog	FOS	8.19E-08	4.57	932.27
212143_s_at	insulin-like growth factor binding protein 3	IGFBP3	2.03E-06	4.57	316.18
218507_at	hypoxia-inducible protein 2	HIG2	7.21E-09	4.44	2,102.35
201170_s_at	basic helix-loop-helix family, member e40	BHLHE40	1.46E-08	4.41	1,661.61
206686_at	pyruvate dehydrogenase kinase, isozyme 1	PDK1	4.47E-06	4.39	242.00
230630_at	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	AK3L1 /// AK3L2	5.38E-05	4.35	102.65
209122_at	adipose differentiation-related protein	ADFP	5.03E-08	4.25	1,097.44
1554452_a_at	hypoxia-inducible protein 2	HIG2	4.37E-10	4.24	5,361.32
201169_s_at	basic helix-loop-helix family, member e40	BHLHE40	1.94E-06	4.23	321.40
201849_at	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3	8.71E-08	4.17	913.43
226682_at	RAR-related orphan receptor A	RORA	2.65E-06	4.15	289.17
222847_s_at	egl nine homolog 3 (C. elegans)	EGLN3	2.78E-06	4.14	284.30
219232_s_at	egl nine homolog 3 (C. elegans)	EGLN3	9.13E-07	4.14	414.44
218498_s_at	ERO1-like (S. cerevisiae)	ERO1L	3.31E-07	4.12	583.32
223333_s_at	angiopoietin-like 4	ANGPTL4	7.03E-06	4.06	207.34

230710_at	---	---	1.60E-05	4.06	156.47
235857_at	potassium channel tetramerisation domain containing 11	KCTD11	4.27E-08	4.01	1,159.68
239619_at	---	---	1.73E-05	3.94	152.18
221479_s_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	BNIP3L	3.26E-09	3.94	2,740.24
236480_at	---	---	1.66E-05	3.93	154.32
223046_at	egl nine homolog 1 (C. elegans)	EGLN1	4.01E-09	3.92	2,556.89
219888_at	sperm associated antigen 4	SPAG4	2.51E-07	3.90	640.24
1568611_at	---	---	5.93E-07	3.87	479.33
202935_s_at	SRY (sex determining region Y)-box 9	SOX9	5.26E-05	3.84	103.42
235948_at	ribosomal modification protein rimK-like family member A	RIMKLA	3.60E-08	3.83	1,227.97
202887_s_at	DNA-damage-inducible transcript 4	DDIT4	1.36E-07	3.81	787.42
218149_s_at	zinc finger protein 395	ZNF395	1.30E-07	3.77	798.25
221123_x_at	zinc finger protein 395	ZNF395	6.17E-06	3.75	216.70
59625_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	3.01E-09	3.75	2,814.10
230612_at	WD repeat domain 73, mRNA (cDNA clone IMAGE:4547992)	WDR73	4.81E-06	3.72	236.00
227412_at	protein phosphatase 1, regulatory (inhibitor) subunit 3E	PPP1R3E	7.44E-07	3.67	444.05
44783_s_at	hairy/enhancer-of-split related with YRPW motif 1	HEY1	2.56E-09	3.64	2,970.41
212192_at	potassium channel tetramerisation domain containing 12	KCTD12	1.33E-05	3.63	166.74
206246_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	PFKFB4	8.21E-05	3.55	88.45
206307_s_at	forkhead box D1	FOXD1	9.55E-08	3.54	885.40
218274_s_at	ankyrin repeat and zinc finger domain containing 1	ANKZF1	3.60E-08	3.50	1,227.37
201667_at	gap junction protein, alpha 1, 43kDa	GJA1	8.30E-05	3.48	88.10
221567_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	4.27E-08	3.47	1,159.64
212689_s_at	jumonji domain containing 1A	JMJD1A	2.48E-10	3.45	6,478.76
223216_x_at	zinc finger protein 395	ZNF395	7.60E-06	3.44	201.82
232693_s_at	F-box protein 16 /// zinc finger protein 395	FBXO16 /// ZNF395	3.87E-05	3.41	115.17
225342_at	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	AK3L1 /// AK3L2	9.05E-09	3.41	1,948.89
211527_x_at	vascular endothelial growth factor A	VEGFA	3.85E-07	3.40	554.27
206685_at	HLA complex group 4	HCG4	2.39E-07	3.38	650.69
229001_at	protein phosphatase 1, regulatory (inhibitor) subunit 3E	PPP1R3E	6.86E-06	3.32	208.99
244385_at	Jumonji domain containing 2C (JMJD2C), mRNA	JMJD2C	4.37E-05	3.30	110.34

236513_at	---	---	0.000101326	3.29	82.10
227263_at	chromosome 8 open reading frame 58	C8orf58	1.51E-05	3.29	159.55
230864_at	serine/threonine-protein kinase NIM1	MGC42105	7.02E-06	3.27	207.36
1553220_at	family with sequence similarity 117, member B	FAM117B	0.000293302	3.23	56.06
204326_x_at	metallothionein 1X	MT1X	2.50E-07	3.23	640.70
224345_x_at	family with sequence similarity 162, member A	FAM162A	2.66E-10	3.21	6,324.77
203282_at	glucan (1,4-alpha-), branching enzyme 1	GBE1	7.99E-08	3.18	940.10
226431_at	family with sequence similarity 117, member B	FAM117B	3.93E-06	3.17	252.85
209535_s_at	---	---	3.16E-06	3.15	272.17
201250_s_at	solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	8.22E-08	3.15	931.37
202936_s_at	SR Y (sex determining region Y)-box 9	SOX9	2.34E-07	3.15	655.19
207543_s_at	prolyl 4-hydroxylase, alpha polypeptide I	P4HA1	3.78E-08	3.14	1,208.35
223193_x_at	family with sequence similarity 162, member A	FAM162A	1.10E-08	3.14	1,826.83
204348_s_at	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2 pleckstrin homology domain containing, family A (phosphoinositide binding specif	AK3L1 /// AK3L2	7.02E-08	3.12	981.92
225136_at	WD repeat and SOCS box-containing 1	PLEKHA2	1.96E-06	3.12	320.10
201294_s_at	vascular endothelial growth factor A	WSB1	8.26E-05	3.10	88.27
212171_x_at	vascular endothelial growth factor A	VEGFA	1.54E-06	3.10	347.33
205493_s_at	dihydropyrimidinase-like 4	DPYSL4	3.24E-07	3.08	587.37
204347_at	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	AK3L1 /// AK3L2	6.90E-08	3.08	987.61
202998_s_at	ectonucleoside triphosphate diphosphohydrolase 4 /// lysyl oxidase-like 2	ENTPD4 /// LOXL2	5.24E-05	3.07	103.58
220942_x_at	family with sequence similarity 162, member A	FAM162A	1.87E-08	3.05	1,529.32
223735_at	ADP-ribosylation factor-like 6	ARL6	5.12E-07	3.05	503.57
210513_s_at	vascular endothelial growth factor A	VEGFA	4.43E-06	3.04	242.59
240991_at	---	---	2.29E-07	3.03	659.91
243296_at	G0S9 mRNA, instability elements	NAMPT	0.000195631	3.00	64.91
211559_s_at	cyclin G2	CCNG2	8.47E-07	3.00	425.09
1552930_at	membrane metallo-endopeptidase-like 1	MMEL1	3.88E-06	2.98	253.84
208296_x_at	tumor necrosis factor, alpha-induced protein 8	TNFAIP8	6.92E-07	2.98	455.09
201295_s_at	WD repeat and SOCS box-containing 1	WSB1	0.000359255	2.94	52.05
202769_at	cyclin G2	CCNG2	4.44E-08	2.93	1,144.73
226542_at	---	---	2.44E-06	2.93	297.16

236462_at	---	---	0.000900924	2.90	36.95
230267_at	---	---	6.69E-06	2.90	210.88
223134_at	bobby sox homolog (Drosophila)	BBX	3.33E-05	2.87	121.36
225567_at	---	---	4.52E-07	2.86	525.14
217226_s_at	sideroflexin 3	SFXN3	5.44E-07	2.85	493.38
213015_at	bobby sox homolog (Drosophila)	BBX	9.71E-05	2.84	83.34
220974_x_at	sideroflexin 3	SFXN3	1.51E-06	2.82	349.98
201296_s_at	WD repeat and SOCS box-containing 1	WSB1	2.49E-06	2.80	295.28
236884_at	ribosomal modification protein rimK-like family member A	RIMKLA	7.34E-05	2.79	91.99
236266_at	Hypothetical protein LOC283666, mRNA (cDNA clone IMAGE:4750925)	RORA	0.00013974	2.77	73.23
224605_at	chromosome 4 open reading frame 3	C4orf3	5.35E-09	2.77	2,323.28
1564027_a_at	family with sequence similarity 115, member C	FAM115C	2.14E-06	2.77	310.54
213700_s_at	---	---	0.000239245	2.76	60.36
210426_x_at	RAR-related orphan receptor A pleckstrin homology domain containing, family A (phosphoinositide binding specif	RORA	8.89E-07	2.76	418.13
217677_at	ADP-ribosylation factor-like 6	PLEKHA2	0.000216053	2.75	62.63
235320_at	chromosome 4 open reading frame 3	ARL6	2.23E-05	2.74	139.39
224604_at	IKK interacting protein	C4orf3	2.50E-08	2.72	1,387.70
227295_at	stanniocalcin 1	IKIP	3.14E-06	2.72	272.69
204595_s_at	tumor necrosis factor, alpha-induced protein 8	STC1	1.13E-07	2.71	836.36
210260_s_at	metallothionein 1X	TNFAIP8	1.17E-06	2.71	381.04
208581_x_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncoge	MT1X	9.32E-08	2.70	892.94
201983_s_at	EF-hand calcium binding domain 3 /// similar to hypoxia-inducible protein 2	EGFR EFCAB3 ///	6.03E-05	2.69	98.59
1553392_at	very low density lipoprotein receptor	LOC100133744	0.00140056	2.69	31.19
209822_s_at	adenosine A2b receptor	VLDLR	8.82E-09	2.68	1,965.19
205891_at	hypothetical LOC387763	ADORA2B	1.97E-06	2.68	319.79
227099_s_at	zinc finger protein 160	LOC387763	8.17E-06	2.67	196.96
1567032_s_at	protein phosphatase 2, regulatory subunit B', beta isoform	ZNF160	4.12E-05	2.67	112.69
635_s_at	chromosome 18 open reading frame 19	PPP2R5B	0.000176049	2.67	67.42
235022_at	---	C18orf19	6.18E-07	2.67	472.86
227501_at	---	---	0.000101392	2.67	82.09

202770_s_at	cyclin G2	CCNG2	2.56E-06	2.67	292.42
238808_at	---	---	0.000942387	2.66	36.32
236241_at	mediator complex subunit 31	MED31	2.30E-05	2.65	137.83
202733_at	prolyl 4-hydroxylase, alpha polypeptide II	P4HA2	1.18E-07	2.65	825.54
227930_at	MRNA; cDNA DKFZp547H229 (from clone DKFZp547H229)	EIF2C4	7.45E-06	2.65	203.22
219622_at	RAB20, member RAS oncogene family	RAB20	9.66E-07	2.65	406.59
37433_at	protein inhibitor of activated STAT, 2	PIAS2	0.000147559	2.64	71.82
1568865_at	CDNA clone IMAGE:5264828	FNTB	0.00220135	2.61	26.10
210479_s_at	RAR-related orphan receptor A	RORA	2.88E-06	2.60	280.84
221530_s_at	basic helix-loop-helix family, member e41	BHLHE41	0.000150327	2.59	71.35
241348_at	zinc finger protein 654	ZNF654	9.81E-08	2.57	877.67
210561_s_at	WD repeat and SOCS box-containing 1	WSB1	1.33E-08	2.54	1,713.84
222851_at	zinc finger protein 654	ZNF654	3.62E-06	2.54	260.00
218898_at	family with sequence similarity 57, member A	FAM57A	5.65E-07	2.53	487.21
204284_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C	PPP1R3C	1.49E-05	2.53	160.16
244677_at	---	---	0.000661586	2.52	41.51
226863_at	family with sequence similarity 110, member C	FAM110C	2.90E-06	2.51	280.32
203986_at	starch binding domain 1	STBD1	2.49E-06	2.50	295.31
227409_at	protein phosphatase 1, regulatory (inhibitor) subunit 3E	PPP1R3E	2.60E-05	2.49	132.22
226464_at	chromosome 3 open reading frame 58	C3orf58	7.92E-09	2.48	2,037.00
1557803_at	---	---	2.42E-05	2.48	135.62
201673_s_at	glycogen synthase 1 (muscle)	GYS1	4.33E-05	2.47	110.69
202619_s_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	PLOD2	7.33E-06	2.47	204.39
224657_at	ERBB receptor feedback inhibitor 1	ERRFI1	1.56E-06	2.46	345.76
227044_at	---	---	1.72E-05	2.45	152.40
213629_x_at	metallothionein 1F	MT1F	3.80E-06	2.45	255.64
225307_at	zinc finger protein 511	ZNF511	2.56E-08	2.44	1,376.85
204596_s_at	stanniocalcin 1	STC1	3.82E-07	2.44	556.04
240549_at	---	---	0.00021612	2.44	62.62
203044_at	chondroitin sulfate synthase 1	CHSY1	5.44E-09	2.42	2,310.07
223467_at	RAS, dexamethasone-induced 1	RASD1	2.46E-08	2.41	1,394.71

228081_at	cyclin G2	CCNG2	1.91E-06	2.41	322.89
209598_at	paraneoplastic antigen MA2	PNMA2	0.000239059	2.40	60.38
231233_at	---	---	0.000100083	2.40	82.46
227210_at	---	---	4.14E-06	2.40	248.26
217841_s_at	protein phosphatase methylesterase 1	PPME1	1.91E-07	2.39	702.36
204900_x_at	Sin3A-associated protein, 30kDa	SAP30	5.07E-07	2.39	505.33
208935_s_at	lectin, galactoside-binding, soluble, 8	LGALS8	0.000160406	2.39	69.71
221203_s_at	YEATS domain containing 2	YEATS2	7.72E-08	2.38	950.84
217738_at	nicotinamide phosphoribosyltransferase	NAMPT	2.57E-06	2.38	291.93
221566_s_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	NOL3	6.56E-08	2.38	1,004.33
238096_at	hypothetical protein LOC284023	LOC284023	8.78E-07	2.38	419.95
205161_s_at	peroxisomal biogenesis factor 11 alpha	PEX11A	4.34E-07	2.38	532.50
218839_at	hairly/enhancer-of-split related with YRPW motif 1	HEY1	2.17E-05	2.38	140.64
217028_at	chemokine (C-X-C motif) receptor 4	CXCR4	0.00082952	2.37	38.12
220030_at	serine/threonine/tyrosine kinase 1	STYK1	0.000214773	2.37	62.76
208933_s_at	lectin, galactoside-binding, soluble, 8	LGALS8	3.37E-05	2.36	120.83
243857_at	Mrgx mRNA for MRGX	MORF4L2	0.00125841	2.36	32.51
228149_at	chromosome 7 open reading frame 60	C7orf60	2.92E-06	2.36	279.76
213016_at	bobby sox homolog (Drosophila)	BBX	3.09E-06	2.36	274.34
202672_s_at	activating transcription factor 3	ATF3	3.68E-06	2.36	258.55
243806_at	---	---	1.45E-05	2.36	161.80
229455_at	---	---	0.000427607	2.35	48.83
239043_at	zinc finger protein 404	ZNF404	0.000232642	2.34	60.98
227717_at	FLJ41603 protein	FLJ41603	2.78E-06	2.33	284.49
202022_at	aldolase C, fructose-bisphosphate	ALDOC	6.06E-08	2.33	1,031.53
201549_x_at	jumonji, AT rich interactive domain 1B	JARID1B	5.52E-07	2.32	491.24
226560_at	---	---	1.50E-06	2.32	350.37
226331_at	bobby sox homolog (Drosophila)	BBX	1.11E-05	2.31	177.39
202364_at	MAX interactor 1	MXI1	9.18E-07	2.31	413.62
205367_at	SH2B adaptor protein 2	SH2B2	5.71E-05	2.31	100.49
228262_at	MAP7 domain containing 2	MAP7D2	0.000484078	2.30	46.64

218096_at	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransf	AGPAT5	1.14E-07	2.30	833.70
238909_at	Calpactin I light chain, 5'UTR region	S100A10	7.14E-07	2.29	450.39
207980_s_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	CITED2	7.55E-06	2.29	202.32
201310_s_at	chromosome 5 open reading frame 13	C5orf13	6.30E-05	2.28	97.12
211919_s_at	chemokine (C-X-C motif) receptor 4	CXCR4	0.00049829	2.28	46.14
236249_at	IKK interacting protein	IKIP	3.22E-05	2.28	122.69
223172_s_at	mitochondrial protein 18 kDa	MTP18	2.14E-05	2.27	141.43
218276_s_at	salvador homolog 1 (Drosophila)	SAV1	5.45E-07	2.27	493.26
206448_at	zinc finger protein 365	ZNF365	2.74E-06	2.26	285.71
209201_x_at	chemokine (C-X-C motif) receptor 4	CXCR4	0.00033922	2.25	53.16
204859_s_at	apoptotic peptidase activating factor 1	APAF1	0.000180049	2.25	66.88
205199_at	carbonic anhydrase IX	CA9	7.82E-05	2.24	89.99
222646_s_at	ERO1-like (<i>S. cerevisiae</i>)	ERO1L	5.04E-07	2.24	506.29
211202_s_at	jumonji, AT rich interactive domain 1B	JARID1B	1.56E-07	2.24	750.78
230746_s_at	---	---	9.72E-07	2.24	405.76
234725_s_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cyt	SEMA4B	1.91E-06	2.23	322.87
243683_at	Mrgx mRNA for MRGX	MORF4L2	0.00165492	2.23	29.22
228280_at	zinc finger CCCH-type, antiviral 1-like	ZC3HAV1L	0.000117049	2.23	78.01
226275_at	MAX dimerization protein 1	MXD1	3.53E-06	2.22	262.20
238700_at	---	---	1.55E-06	2.22	346.60
226621_at	---	---	2.74E-08	2.21	1,345.29
231431_s_at	---	---	6.72E-06	2.21	210.48
218697_at	NCK interacting protein with SH3 domain	NCKIPSD	0.000229188	2.20	61.31
229390_at	family with sequence similarity 26, member F	FAM26F	0.000257608	2.20	58.77
228846_at	MAX dimerization protein 1	MXD1	1.50E-06	2.20	350.32
224496_s_at	transmembrane protein 107	TMEM107	8.80E-05	2.19	86.31
217165_x_at	metallothionein 1F	MT1F	1.18E-06	2.19	380.34
226199_at	uracil phosphoribosyltransferase (FUR1) homolog (<i>S. cerevisiae</i>)	UPRT	4.00E-05	2.19	113.83
242017_at	---	---	0.000781195	2.18	39.00
202620_s_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	PLOD2	7.31E-07	2.18	446.65
209318_x_at	pleiomorphic adenoma gene-like 1	PLAGL1	6.24E-05	2.18	97.40

240063_at	glucuronidase, beta pseudogene	LOC441046	5.79E-05	2.17	100.04
225962_at	zinc and ring finger 1	ZNRF1	8.11E-05	2.17	88.82
214624_at	uroplakin 1A	UPK1A	0.000620848	2.17	42.51
201918_at	solute carrier family 25, member 36	SLC25A36	0.000699382	2.17	40.66
206461_x_at	metallothionein 1H	MT1H	7.33E-06	2.16	204.35
219239_s_at	zinc finger protein 654	ZNF654	1.67E-05	2.16	153.92
232008_s_at	bobby sox homolog (Drosophila)	BBX	6.34E-07	2.16	468.80
210132_at	ephrin-A3	EFNA3	6.65E-06	2.16	211.31
242149_at	chromosome 18 open reading frame 19	C18orf19	6.77E-05	2.16	94.65
243463_s_at	Ras-like without CAAX 1	RIT1	0.000213915	2.15	62.85
217739_s_at	nicotinamide phosphoribosyltransferase	NAMPT	8.67E-07	2.15	421.75
223135_s_at	bobby sox homolog (Drosophila)	BBX	2.71E-06	2.15	286.71
209357_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	CITED2	1.25E-06	2.15	372.72
232968_at	fibronectin type III and ankyrin repeat domains 1	FANK1	4.20E-06	2.13	247.10
223045_at	egl nine homolog 1 (C. elegans)	EGLN1	0.000715056	2.12	40.32
235202_x_at	IKK interacting protein	IKIP	0.000370049	2.12	51.49
228696_at	solute carrier family 45, member 3	SLC45A3	0.00110892	2.12	34.13
228304_at	---	---	0.000231727	2.11	61.06
243179_at	CDNA FLJ33993 fis, clone DFNES2007757	LOC100130360	5.14E-05	2.11	104.24
227084_at	dystrobrevin, alpha	DTNA	1.07E-05	2.10	179.32
215446_s_at	lysyl oxidase	LOX	9.64E-05	2.10	83.55
227068_at	phosphoglycerate kinase 1	PGK1	4.09E-08	2.10	1,176.86
235571_at	---	---	3.51E-05	2.10	119.12
1555007_s_at	WD repeat domain 66	WDR66	0.00199916	2.10	27.12
240258_at	enolase 1, (alpha)	ENO1	4.78E-05	2.10	106.95
227247_at	Homo sapiens, clone IMAGE:4617677, mRNA	PLEKHA8	0.000102831	2.09	81.68
200737_at	phosphoglycerate kinase 1	PGK1	2.83E-07	2.09	615.22
49077_at	protein phosphatase methylesterase 1	PPME1	2.42E-06	2.08	297.85
213664_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter	SLC1A1	0.000239411	2.08	60.35
228307_at	elastin microfibril interfacer 3	EMILIN3	7.21E-05	2.08	92.58
201548_s_at	jumonji, AT rich interactive domain 1B	JARID1B	3.97E-06	2.08	251.88

232002_at	---	---	0.00141083	2.08	31.10
221523_s_at	Ras-related GTP binding D	RRAGD	0.00176517	2.07	28.49
208936_x_at	lectin, galactoside-binding, soluble, 8	LGALS8	7.11E-08	2.07	977.60
230523_at	---	---	3.03E-05	2.07	125.43
228914_at	---	---	0.000211079	2.07	63.16
207992_s_at	adenosine monophosphate deaminase (isoform E)	AMPD3	0.000644973	2.07	41.91
212492_s_at	jumonji domain containing 2B	JMJD2B	0.000184814	2.06	66.25
207785_s_at	recombination signal binding protein for immunoglobulin kappa J region	RBPJ	8.53E-07	2.06	424.12
222662_at	protein phosphatase 1, regulatory (inhibitor) subunit 3B	PPP1R3B	0.000121761	2.05	76.92
205160_at	MRNA full length insert cDNA clone EUROIMAGE 202740	PEX11A	6.24E-06	2.05	215.90
223441_at	solute carrier family 17 (anion/sugar transporter), member 5	SLC17A5	0.000516001	2.05	45.55
212850_s_at	low density lipoprotein receptor-related protein 4	LRP4	0.00119818	2.05	33.13
212444_at	---	---	1.25E-05	2.05	170.15
222383_s_at	arachidonate lipoxygenase 3	ALOXE3	0.000132369	2.05	74.66
225239_at	---	---	0.00134043	2.05	31.72
204521_at	chromosome 12 open reading frame 24	C12orf24	5.55E-06	2.04	224.70
206070_s_at	EPH receptor A3	EPHA3	1.22E-05	2.04	171.48
212188_at	potassium channel tetramerisation domain containing 12	KCTD12	0.000344968	2.04	52.83
212368_at	zinc finger protein 292	ZNF292	5.23E-05	2.04	103.62
236223_s_at	Small G protein RIBB	RIT1	3.52E-05	2.04	118.99
228033_at	E2F transcription factor 7	E2F7	4.60E-07	2.03	522.12
228919_at	---	---	0.000187154	2.03	65.95
201917_s_at	solute carrier family 25, member 36	SLC25A36	0.000143128	2.02	72.61
212185_x_at	metallothionein 2A	MT2A	4.04E-06	2.02	250.32
239315_at	family with sequence similarity 115, member C	FAM115C	2.96E-05	2.02	126.39
1555167_s_at	nicotinamide phosphoribosyltransferase	NAMPT	8.46E-06	2.02	194.57
226114_at	zinc finger protein 436	ZNF436	5.06E-05	2.01	104.83
228188_at	FOS-like antigen 2	FOSL2	2.18E-06	2.01	308.95
212366_at	zinc finger protein 292	ZNF292	0.000393001	2.01	50.37
204172_at	coproporphyrinogen oxidase	CPOX	0.000160283	2.00	69.73
209034_at	proline-rich nuclear receptor coactivator 1	PNRC1	1.60E-05	2.00	156.30

Genes down-regulated by HQBA

Column ID	Gene Title	Gene Symbol	p-value (Treatment)	Ratio(MCF7 treatment vs. control)	F(Treatment)
222902_s_at	defects in morphology 1 homolog (S. cerevisiae)	DEM1	2.30E-05	0.67	137.88
211580_s_at	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	PIK3R3	4.26E-04	0.66	48.91
213116_at	NIMA (never in mitosis gene a)-related kinase 3	NEK3	2.08E-03	0.66	26.73
213005_s_at	KN motif and ankyrin repeat domains 1	KANK1	1.30E-03	0.66	32.12
227750_at	kalirin, RhoGEF kinase	KALRN	3.81E-05	0.66	115.74
204826_at	cyclin F	CCNF	9.01E-04	0.66	36.95
220038_at	chromosome 8 open reading frame 44 /// serum/glucocorticoid regulated kinase fam	C8orf44 /// SGK3	1.45E-03	0.66	30.73
209567_at	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	RRS1	6.33E-05	0.66	96.95
225473_at	chromosome 20 open reading frame 117	C20orf117	4.29E-04	0.66	48.75
220215_at	zinc finger protein 669	ZNF669	2.62E-04	0.66	58.37
215359_x_at	zinc finger protein 44	ZNF44	1.96E-03	0.66	27.32
219765_at	zinc finger protein 329	ZNF329	1.64E-03	0.66	29.33
222883_at	chromosome 1 open reading frame 163	C1orf163	2.11E-04	0.66	63.14
204162_at	NDC80 homolog, kinetochore complex component (S. cerevisiae)	NDC80	5.20E-04	0.65	45.43
235289_at	eukaryotic translation initiation factor 5A2	EIF5A2	4.61E-04	0.65	47.50
205928_at	zinc finger protein 443	ZNF443	1.02E-04	0.65	81.80
236313_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	6.62E-04	0.65	41.51
213352_at	transmembrane and coiled-coil domain family 1	TMCC1	2.34E-04	0.65	60.84
221268_s_at	sphingosine-1-phosphate phosphatase 1	SGPP1	2.72E-04	0.65	57.59
212660_at	PHD finger protein 15	PHF15	1.17E-05	0.65	174.16
202150_s_at	neural precursor cell expressed, developmentally down-regulated 9	NEDD9	5.79E-05	0.65	100.02
200790_at	ornithine decarboxylase 1	ODC1	3.21E-04	0.65	54.24
242463_x_at	zinc finger protein 600	ZNF600	4.39E-04	0.65	48.35
222958_s_at	DEP domain containing 1	DEPDC1	1.62E-03	0.65	29.47
202437_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	3.95E-04	0.64	50.27
204914_s_at	SRY (sex determining region Y)-box 11	SOX11	2.15E-04	0.64	62.76

220295_x_at	DEP domain containing 1	DEPDC1	1.10E-03	0.64	34.21
206261_at	zinc finger protein 239	ZNF239	8.78E-06	0.64	192.16
220721_at	zinc finger protein 614	ZNF614	4.54E-04	0.64	47.74
213916_at	zinc finger protein 20	ZNF20	1.72E-04	0.64	68.00
221213_s_at	zinc finger protein 280D	ZNF280D	6.24E-04	0.64	42.44
227445_at	zinc finger protein 689	ZNF689	6.28E-05	0.64	97.22
211721_s_at	zinc finger protein 551	ZNF551	8.85E-05	0.64	86.13
242828_at	fidgetin	FIGN	1.92E-03	0.64	27.58
225748_at	LTV1 homolog (<i>S. cerevisiae</i>)	LTV1	5.33E-06	0.64	227.85
213351_s_at	transmembrane and coiled-coil domain family 1	TMCC1	1.36E-03	0.64	31.57
224365_s_at	tigger transposable element derived 7	TIGD7	7.35E-04	0.64	39.91
210447_at	glutamate dehydrogenase 2	GLUD2	5.69E-04	0.63	43.91
225917_at	---	---	1.81E-03	0.63	28.20
217202_s_at	glutamate-ammonia ligase (glutamine synthetase)	GLUL	2.08E-05	0.63	142.88
227294_at	zinc finger protein 689	ZNF689	2.65E-06	0.63	288.94
202436_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	3.09E-04	0.63	55.00
203373_at	suppressor of cytokine signaling 2	SOCS2	2.20E-05	0.63	140.17
204092_s_at	aurora kinase A	AURKA	5.12E-04	0.63	45.66
203372_s_at	suppressor of cytokine signaling 2	SOCS2	1.13E-03	0.63	33.89
230960_at	immunoglobulin superfamily, DCC subclass, member 3	IGDCC3	1.27E-03	0.63	32.35
206182_at	zinc finger protein 134	ZNF134	1.49E-04	0.62	71.55
226021_at	retinol dehydrogenase 10 (all-trans)	RDH10	3.95E-04	0.61	50.28
231741_at	sphingosine-1-phosphate receptor 3	S1PR3	4.16E-04	0.61	49.31
204709_s_at	kinesin family member 23	KIF23	1.52E-03	0.61	30.22
222670_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	MAFB	1.51E-04	0.61	71.20
219010_at	chromosome 1 open reading frame 106	C1orf106	3.86E-05	0.61	115.25
230421_at	similar to hypothetical protein 9630041N07	DKFZp686E2433	9.70E-05	0.61	83.38
235061_at	protein phosphatase 1K (PP2C domain containing) hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix	PPM1K	3.24E-04	0.61	54.04
200989_at	transcription	HIF1A	3.19E-07	0.61	590.60
232645_at	hypothetical LOC153684	LOC153684	8.94E-05	0.60	85.81

206695_x_at	zinc finger protein 43	ZNF43	1.01E-06	0.60	400.40
235728_at	zinc finger protein 3 homolog (mouse)	ZFP3	2.18E-04	0.60	62.46
227045_at	zinc finger protein 614	ZNF614	1.06E-03	0.60	34.69
204519_s_at	plasma membrane proteolipid (plasmolipin)	PLLP	1.10E-03	0.60	34.29
204937_s_at	zinc finger protein 274	ZNF274	4.81E-06	0.60	235.99
208079_s_at	aurora kinase A	AURKA	5.83E-05	0.60	99.78
220936_s_at	H2A histone family, member J	H2AFJ	2.18E-03	0.59	26.20
218490_s_at	zinc finger protein 302	ZNF302	1.30E-03	0.59	32.10
227687_at	hydroletharus syndrome 1	HYLS1	1.66E-05	0.59	154.53
225687_at	family with sequence similarity 83, member D	FAM83D	1.71E-03	0.59	28.88
203817_at	guanylate cyclase 1, soluble, beta 3	GUCY1B3	6.49E-04	0.59	41.81
207304_at	zinc finger protein 45	ZNF45	7.44E-05	0.59	91.58
215001_s_at	glutamate-ammonia ligase (glutamine synthetase)	GLUL	5.42E-06	0.59	226.59
232278_s_at	DEP domain containing 1	DEPDC1	1.37E-03	0.59	31.42
202435_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	8.31E-05	0.58	88.08
202149_at	neural precursor cell expressed, developmentally down-regulated 9	NEDD9	3.86E-05	0.58	115.26
218574_s_at	LIM and cysteine-rich domains 1	LMCD1	4.67E-06	0.58	238.34
218559_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	MAFB	2.00E-04	0.58	64.44
204913_s_at	SRY (sex determining region Y)-box 11	SOX11	2.33E-03	0.57	25.52
202870_s_at	cell division cycle 20 homolog (S. cerevisiae)	CDC20	7.41E-04	0.57	39.78
214751_at	zinc finger protein 468	ZNF468	6.55E-05	0.57	95.78
200648_s_at	glutamate-ammonia ligase (glutamine synthetase)	GLUL	1.25E-06	0.57	372.71
240633_at	docking protein 7	DOK7	9.25E-06	0.57	188.72
218987_at	activating transcription factor 7 interacting protein	ATF7IP	3.54E-05	0.56	118.74
213721_at	SRY (sex determining region Y)-box 2	SOX2	9.71E-05	0.55	83.34
219615_s_at	potassium channel, subfamily K, member 5	KCNK5	1.83E-04	0.55	66.55
238149_at	zinc finger protein 818 pseudogene	ZNF818P	2.44E-03	0.55	25.06
243174_at	---	---	3.50E-05	0.55	119.24
238148_s_at	zinc finger protein 818 pseudogene	ZNF818P	8.37E-04	0.54	37.99
227670_at	zinc finger protein 75a	ZNF75A	4.42E-05	0.53	109.94
218694_at	armadillo repeat containing, X-linked 1	ARMCX1	7.64E-06	0.53	201.49

228038_at	SRY (sex determining region Y)-box 2	SOX2	2.35E-07	0.52	655.00
228176_at	sphingosine-1-phosphate receptor 3	S1PR3	5.32E-06	0.52	228.06
204962_s_at	centromere protein A	CENPA	1.07E-03	0.51	34.60
209631_s_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	GPR37	7.42E-05	0.51	91.67
202434_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	1.03E-03	0.51	35.13
211778_s_at	ovo-like 2 (Drosophila)	OVOL2	1.35E-04	0.51	74.21
201739_at	serum/glucocorticoid regulated kinase 1	SGK1	9.55E-06	0.50	186.69
205749_at	cytochrome P450, family 1, subfamily A, polypeptide 1	CYP1A1	1.29E-04	0.50	75.43
206900_x_at	zinc finger protein 253	ZNF253	1.10E-07	0.49	844.11
229518_at	family with sequence similarity 46, member B	FAM46B	1.45E-04	0.49	72.21
206683_at	zinc finger protein 165	ZNF165	1.76E-05	0.49	151.18
225834_at	family with sequence similarity 72, member A /// family with sequence similarity	FAM72A ///			
209987_s_at	achaete-scute complex homolog 1 (Drosophila)	FAM72B /// GCUD2	7.05E-05	0.47	93.34
242919_at	zinc finger protein 253	ASCL1	2.16E-03	0.46	26.30
213780_at	trichohyalin	ZNF253	9.64E-07	0.41	406.96
		TCHH	1.48E-04	0.37	71.78
		HIST1H4A ///			
		HIST1H4B ///			
		HIST1H4C ///			
		HIST1H4D ///			
		HIST1H4E ///			
		HIST1H4F ///			
		HIST1H4H ///			
		HIST1H4I ///			
		HIST1H4J ///			
		HIST1H4K ///			
		HIST1H4L ///			
		HIST2H4A ///			
		HIST2H4B ///			
205967_at	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c ///	HIST4H4	1.31E-06	0.23	367.10