Supplemental Table S1. Primer set sequences for qRT-PCR analysis.

Primer Set	Forward	Reverse
GDF15	GGGCAAGAACTCAGGACGG	TCTGGAGTCTTCGGAGTGCAA
IL-29	TATGTGGCCGATGGGAACCT	AGGGTGGGTTGACGTTCTCA
OAS-1	TGTCCAAGGTGGTAAAGGGTG	CCGGCGATTTAACTGATCCTG
MX1	GTTTCCGAAGTGGACATCGCA	CCATTCAGTAATAGAGGGTGGGA
IFTM1	TCGCCTACTCCGTGAAGTCT	ATGAGGATGCCCAGAATCAG
IL28A	CACCCTGCACCATATCCTCT	CACTGGCAACACAATTCAGG
IL28B	CTGCTGAAGGACTGCAAGTG	GAGGATATGGTGCAGGGTGT
Suz12	TGCAGTTCACTCTTCGTTGG	TGCTTCAGTTTGTTGCCTTG
GAPDH	GAGTCAACGGATTTGGTCGT	GACAAGCTTCCCGTTCTCAG

Supplemental Table S2. Univariate and multivariate Cox proportional hazard regression analyses of OS in the pancreatic cancer patient cohort (n=102).[a]

	Univariate		Multivariate	
	HR(95% CI)	p value	HR(95% CI)	p value
HOTAIR level (high vs low)	1.1619 to 4.2936	0.0165	1.1842 to 4.4320	0.0143
N stage	1.0534 to 3.2432	0.0331	1.0712 to 3.6031	0.0299
T stage	0.6232 to 1.8116	0.8245	0.4825 to 1.4304	0.5058

[a] Univariate and multivariate Cox proportional hazards regression analyses were carried out in the pancreatic cancer cohort (GSE21501) to evaluate the prognostic value of HOTAIR expression level in combination with other clinical variables including N stage and T stage. In the univariate analysis, HOTAIR level and N stage were significantly associated with Overall Survival (p=0.0165 and p=0.00331, respectively). Similarly, both HOTAIR level and N stage exhibited the significance (p=0.00143 and p=0.0299).

Supplemental Table S3. GSEA Analysis results (20 significant enrichment plots) using HOTAIR high (N=14) vs low (N=88) gene signatures obtained from pancreatic patient data (GSE21501).

GO TERM Biological Pathways	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
DNA_REPLICATION_INITIATION	15	0.78	2.08	0	0.04	0.04
REGULATION_OF_MITOSIS	40	0.60	1.89	0.02	0.12	0.22
CHROMOSOME_SEGREGATION	31	0.63	1.83	0	0.17	0.34
ORGANELLE_LOCALIZATION	23	0.55	1.81	0	0.15	0.35
M_PHASE_OF_MITOTIC_CELL_CYCLE	83	0.53	1.78	0.04	0.16	0.45
CELL_CYCLE_PROCESS	186	0.46	1.77	0.03	0.15	0.47
CYTOKINESIS	15	0.64	1.77	0.05	0.13	0.47
CELL_CYCLE_PHASE	166	0.45	1.77	0.05	0.11	0.47
ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	16	0.63	1.77	0	0.10	0.47
MITOSIS	81	0.53	1.75	0.04	0.10	0.52
MITOTIC_CELL_CYCLE	148	0.47	1.74	0.05	0.11	0.57
CELL_CYCLE_CHECKPOINT_GO_0000075	46	0.51	1.72	0.02	0.12	0.65
M_PHASE	110	0.51	1.71	0.06	0.12	0.67
DNA_PACKAGING	34	0.46	1.71	0	0.11	0.67
DNA_REPLICATION	100	0.42	1.71	0	0.11	0.68
CELL_DIVISION	17	0.60	1.70	0.06	0.10	0.69
SISTER_CHROMATID_SEGREGATION	17	0.65	1.69	0.04	0.11	0.71
DNA_DEPENDENT_DNA_REPLICATION	54	0.47	1.68	0	0.11	0.74
G1_PHASE	15	0.57	1.66	0	0.13	0.76
MITOCHONDRIAL_TRANSPORT	19	0.57	1.65	0.06	0.14	0.78

Supplemental Table S4. GSEA Analysis results using gene signature after HOTAIR KO in Panc1 cells (20 enriched biological pathways).

GO TERM Biological Pathways	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
ORGANELLE_LOCALIZATION	23	0.76	2.31	0	0	0
RNA_SPLICING_FACTOR_ACTIVITYTRANSESTERIFICATION_MECHANISM	16	0.81	2.21	0	0	0
MICROTUBULE_MOTOR_ACTIVITY	16	0.82	2.17	0	0	0
M_PHASE_OF_MITOTIC_CELL_CYCLE	83	0.58	2.15	0	0	0
CELL_DIVISION	17	0.82	2.13	0	0	0
SISTER_CHROMATID_SEGREGATION	17	0.76	2.11	0	0.004	0.02
REGULATION_OF_MITOSIS	40	0.64	2.11	0	0.003	0.02
CYTOKINESIS	15	0.80	2.09	0	0.003	0.02
SPINDLE	37	0.67	2.08	0	0.002	0.02
CHROMOSOME_SEGREGATION	31	0.68	2.08	0	0.002	0.02
CHROMOSOMEPERICENTRIC_REGION	31	0.69	2.05	0	0.003	0.03
MITOTIC_CELL_CYCLE	148	0.51	2.05	0	0.003	0.03
M_PHASE	112	0.51	2.02	0	0.003	0.03
MITOSIS	81	0.59	2.02	0	0.002	0.03
MITOTIC_SISTER_CHROMATID_SEGREGATION	16	0.78	2.00	0	0.002	0.03
ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	16	0.85	1.98	0	0.003	0.04
MOTOR_ACTIVITY	28	0.72	1.97	0	0.003	0.05
CELL_CYCLE_PROCESS	188	0.49	1.97	0	0.003	0.05
PROTEIN_DNA_COMPLEX_ASSEMBLY	48	0.61	1.97	0	0.003	0.05
RNA_SPLICING	82	0.54	1.92	0	0.009	0.16

Supplemental Table S5. Most upregulated genes (50) after HOTAIR knockout in Panc1 cells.

Gene SYMBOL	DEFINITION	Fold Induction	p Value
MX1	Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA.	9.40	0.00044
OAS2	Homo sapiens 2'-5'-oligoadenylate synthetase 2, 69/71kDa (OAS2), transcript variant 1, mRNA.	7.24	0.00271
IFIT3	Homo sapiens interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), mRNA.	6.48	0.00114
OAS1	Homo sapiens 2',5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 3, mRNA.	5.62	0.00012
IFI6	Homo sapiens interferon, alpha-inducible protein 6 (IFI6), transcript variant 2, mRNA.	5.54	0.00135
VGF	Homo sapiens VGF nerve growth factor inducible (VGF), mRNA.	5.46	0.00023
IFIT1	Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 2, mRNA.	5.31	0.00334
OASL	Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, mRNA.	5.20	0.00001
OAS1	Homo sapiens 2',5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 3, mRNA.	5.08	0.00579
IL29	Homo sapiens interleukin 29 (interferon, lambda 1) (IL29), mRNA.	5.03	0.00000
IFIT3	Homo sapiens interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), mRNA.	4.96	0.00469
IFIT3	Homo sapiens interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), mRNA.	4.95	0.00410
IFIT2	Homo sapiens interferon-induced protein with tetratricopeptide repeats 2 (IFIT2), mRNA.	4.79	0.00103
IFI27	Homo sapiens interferon, alpha-inducible protein 27 (IFI27), transcript variant 2, mRNA.	4.75	0.00000
CCL5	Homo sapiens chemokine (C-C motif) ligand 5 (CCL5), mRNA.	4.47	0.00048
IFITM1	Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.	4.39	0.00023
ISG20	Homo sapiens interferon stimulated exonuclease gene 20kDa (ISG20), mRNA.	4.32	0.00963
OAS1	Homo sapiens 2',5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 2, mRNA.	4.30	0.00000
HERC5	Homo sapiens hect domain and RLD 5 (HERC5), mRNA.	4.03	0.00013
IRF7	Homo sapiens interferon regulatory factor 7 (IRF7), transcript variant b, mRNA.	4.02	0.00188
CCL5	Homo sapiens chemokine (C-C motif) ligand 5 (CCL5), mRNA.	4.01	0.00008
ISG15	Homo sapiens ISG15 ubiquitin-like modifier (ISG15), mRNA.	3.99	0.00491
HIST1H2BD	Homo sapiens histone cluster 1, H2bd (HIST1H2BD), transcript variant 2, mRNA.	3.96	0.00017
GDF15	Homo sapiens growth differentiation factor 15 (GDF15), mRNA.	3.92	0.00849
IL8	Homo sapiens interleukin 8 (IL8), mRNA.	3.79	0.00007
HIST1H2BD	Homo sapiens histone cluster 1, H2bd (HIST1H2BD), transcript variant 2, mRNA.	3.79	0.00315
PRIC285	Homo sapiens peroxisomal proliferator-activated receptor A interacting complex 285 (PRIC285), transcript variant 2, mRNA.	3.73	0.00003
SOD2	Homo sapiens superoxide dismutase 2, mitochondrial (SOD2), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA.	3.69	0.00383
UBE2L6	Homo sapiens ubiquitin-conjugating enzyme E2L 6 (UBE2L6), transcript variant 1, mRNA.	3.56	0.00104
CX3CL1	Homo sapiens chemokine (C-X3-C motif) ligand 1 (CX3CL1), mRNA.	3.50	0.01466
HMOX1	Homo sapiens heme oxygenase (decycling) 1 (HMOX1), mRNA.	3.44	0.00009
TTC9B	Homo sapiens tetratricopeptide repeat domain 9B (TTC9B), mRNA.	3.42	0.00003
IRF9	Homo sapiens interferon regulatory factor 9 (IRF9), mRNA.	3.42	0.00449
HIST2H2AA4	Homo sapiens histone cluster 2, H2aa4 (HIST2H2AA4), mRNA.	3.41	0.00640
HIST2H2AA3	Homo sapiens histone cluster 2, H2aa3 (HIST2H2AA3), mRNA.	3.38	0.00006
BST2	Homo sapiens bone marrow stromal cell antigen 2 (BST2), mRNA.	3.30	0.00757
LOC100129681	PREDICTED: Homo sapiens similar to NPC-A-7 (LOC100129681), mRNA.	3.26	0.00155
IL28A	Homo sapiens interleukin 28A (interferon, lambda 2) (IL28A), mRNA.	3.23	0.00265
PARP9	Homo sapiens poly (ADP-ribose) polymerase family, member 9 (PARP9), mRNA.	3.20	0.00901
SLC15A3	Homo sapiens solute carrier family 15, member 3 (SLC15A3), mRNA.	3.14	0.00003
IRF7	Homo sapiens interferon regulatory factor 7 (IRF7), transcript variant b, mRNA.	3.13	0.00075
PARP12	Homo sapiens poly (ADP-ribose) polymerase family, member 12 (PARP12), mRNA.	3.10	0.00001
XAF1	Homo sapiens XIAP associated factor 1 (XAF1), transcript variant 2, mRNA.	3.09	0.00143
IFIH1	Homo sapiens interferon induced with helicase C domain 1 (IFIH1), mRNA.	3.09	0.00070
HIST2H2AC	Homo sapiens histone cluster 2, H2ac (HIST2H2AC), mRNA.	3.08	0.00077
SAMD9	Homo sapiens sterile alpha motif domain containing 9 (SAMD9), mRNA.	3.06	0.00065
LINCR	Homo sapiens likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein (LINCR), mRNA.	3.04	0.00026
HIST2H2AA3	Homo sapiens histone cluster 2, H2aa3 (HIST2H2AA3), mRNA.	3.02	0.00985
SFN	Homo sapiens stratifin (SFN), mRNA.	2.99	0.00497
IL8	Homo sapiens interleukin 8 (IL8), mRNA.	2.95	0.00715

Supplemental Table S6. Most downregulated genes (50) after HOTAIR knockout in Panc1 cells.

SYMBOL	DEFINITION	Fold Change	T test p Value
RALA	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA.	0.23	0.00017
ARL6IP1	Homo sapiens ADP-ribosylation factor-like 6 interacting protein 1 (ARL6IP1), mRNA.	0.24	0.00028
GSTP1	Homo sapiens glutathione S-transferase pi (GSTP1), mRNA.	0.25	0.00402
UBQLN1	Homo sapiens ubiquilin 1 (UBQLN1), transcript variant 1, mRNA.	0.25	0.01206
C8orf59	Homo sapiens chromosome 8 open reading frame 59 (C8orf59), transcript variant 3, mRNA.	0.25	0.00195
CAV1	Homo sapiens caveolin 1, caveolae protein, 22kDa (CAV1), mRNA.	0.26	0.00447
SNORA12	Homo sapiens small nucleolar RNA, H/ACA box 12 (SNORA12), small nucleolar RNA.	0.27	0.00015
PTRF	Homo sapiens polymerase I and transcript release factor (PTRF), mRNA.	0.27	0.00000
RAC1	Homo sapiens ras-related C3 botulinum toxin substrate 1	0.28	0.00050
PRDX6	Homo sapiens peroxiredoxin 6 (PRDX6), mRNA.	0.29	0.00027
CAV1	Homo sapiens caveolin 1, caveolae protein, 22kDa (CAV1), mRNA.	0.29	0.00490
OSTC	Homo sapiens oligosaccharyltransferase complex subunit (OSTC), mRNA.	0.30	0.00005
	Homo sapiens cDNA: FLJ21333 fis, clone COL02535	0.30	0.00308
ALDH1A3	Homo sapiens aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), mRNA.	0.30	0.00067
PRKCA	Homo sapiens protein kinase C, alpha (PRKCA), mRNA.	0.31	0.00054
MELK	Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA.	0.32	0.00116
ALDH1A3	Homo sapiens aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), mRNA.	0.32	0.00263
KRT18P13	PREDICTED: Homo sapiens keratin 18 pseudogene 13 (KRT18P13), mRNA.	0.32	0.00009
CMTM6	Homo sapiens CKLF-like MARVEL transmembrane domain containing 6 (CMTM6), mRNA.	0.32	0.00858
FN3KRP	Homo sapiens fructosamine-3-kinase-related protein (FN3KRP), mRNA.	0.33	0.00008
LOC653226	PREDICTED: Homo sapiens similar to Signal recognition particle 9 kDa protein (SRP9)	0.34	0.00004
MELK	Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA.	0.35	0.00612
FLJ40504	Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA.	0.35	0.00590
MICB	Homo sapiens MHC class I polypeptide-related sequence B (MICB), mRNA.	0.35	0.00932
LOC646567	PREDICTED: Homo sapiens similar to HSPC307 (LOC646567), mRNA.	0.36	0.01902
PBX3	Homo sapiens pre-B-cell leukemia homeobox 3 (PBX3), mRNA.	0.36	0.00096
PPP2R1B	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform.	0.36	0.00602
TMEM167A	Homo sapiens transmembrane protein 167A (TMEM167A), mRNA.	0.36	0.00409
ARPC5	Homo sapiens actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA.	0.36	0.00003
ROD1	Homo sapiens ROD1 regulator of differentiation 1 (S. pombe) (ROD1), mRNA.	0.36	0.00001
OSTC	Homo sapiens oligosaccharyltransferase complex subunit (OSTC), mRNA.	0.37	0.00540
HNRPH3	Homo sapiens heterogeneous nuclear ribonucleoprotein H3 (2H9) (HNRPH3).	0.37	0.00001
OSTC	Homo sapiens oligosaccharyltransferase complex subunit (OSTC), mRNA.	0.38	0.00002
SRP9	Homo sapiens signal recognition particle 9kDa (SRP9), mRNA.	0.38	0.00240
MTHFD1L	Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (MTHFD1L), mRNA.	0.38	0.00002
FBXW11	Homo sapiens F-box and WD repeat domain containing 11 (FBXW11), transcript variant 1, mRNA.	0.38	0.00000
DHX33	Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 33 (DHX33), mRNA.	0.38	0.00020
CKAP4	Homo sapiens cytoskeleton-associated protein 4 (CKAP4), mRNA.	0.38	0.00102
NR2F6	Homo sapiens nuclear receptor subfamily 2, group F, member 6 (NR2F6), mRNA.	0.38	0.01179
PTPMT1	Homo sapiens protein tyrosine phosphatase, mitochondrial 1 (PTPMT1), nuclear gene encoding mitochondrial protein, mRNA.	0.39	0.00582
ITGA3	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant a, mRNA.	0.39	0.00111
TTPAL	Homo sapiens tocopherol (alpha) transfer protein-like (TTPAL), transcript variant 1, mRNA.	0.40	0.00125
MRPL19	Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), nuclear gene encoding mitochondrial protein, mRNA.	0.40	0.00547
LOC653226	PREDICTED: Homo sapiens similar to Signal recognition particle 9 kDa protein (SRP9) (LOC653226), mRNA.	0.40	0.00053
CNN2	Homo sapiens calponin 2 (CNN2), transcript variant 2, mRNA.	0.40	0.00175
CDCA8	Homo sapiens cell division cycle associated 8 (CDCA8), mRNA.	0.40	0.00394
PHF19	Homo sapiens PHD finger protein 19 (PHF19), transcript variant 2, mRNA.	0.40	0.00598
LOC399965	PREDICTED: Homo sapiens misc_RNA (LOC399965), miscRNA.	0.40	0.06446
ROD1	Homo sapiens ROD1 regulator of differentiation 1 (S. pombe) (ROD1), mRNA.	0.41	0.00796
LOC729317	PREDICTED: Homo sapiens similar to voltage-dependent anion channel 2 (LOC729317), mRNA.	0.41	0.01083

Supplemental Table S7. List of 241 genes differentially regulated [HOTAIR KO (Panc-1) vs. Overexpression (MDA-MB-231)].

SYMBOL	DEFINITION	HOTAIR KO (Panc1) Fold Change	HOTAIR Overexpression (MDA-MB-231) Fold Change
ABCB6	Homo sapiens ATP-binding cassette	1.64	0.67
ABHD11	Homo sapiens abhydrolase domain containing 11 (ABHD11)	1.55	0.27
ABHD2	Homo sapiens abhydrolase domain containing 2 (ABHD2)	1.53	4.04
ACACA	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA)	0.61	3.03
ACCS	Homo sapiens 1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)	1.52	3.20
ACLY	Homo sapiens ATP citrate lyase (ACLY)	0.63	2.49
ACOT7	Homo sapiens acyl-CoA thioesterase 7 (ACOT7)	0.58	2.11
ADAR	Homo sapiens adenosine deaminase	1.74	2.20
ADARB1	Homo sapiens adenosine deaminase	0.58	2.46
ADD3	Homo sapiens adducin 3 (gamma) (ADD3)	0.65	2.98
AHNAK	Homo sapiens AHNAK nucleoprotein (AHNAK)	0.66	1.51
AKTIP	Homo sapiens AKT interacting protein (AKTIP)	0.56	3.83
ALDH1A3	Homo sapiens aldehyde dehydrogenase 1 family	0.32	2.16
ALG13	Homo sapiens asparagine-linked glycosylation 13 homolog (S. cerevisiae) (ALG13)	1.50	0.62
AMD1	Homo sapiens adenosylmethionine decarboxylase 1 (AMD1)	0.64	3.58
ANO6	Homo sapiens anoctamin 6 (ANO6)	0.63	0.64
APOL3	Homo sapiens apolipoprotein L	1.87	1.85
ARHGEF7	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 7 (ARHGEF7)	0.65	2.27
ARL14	Homo sapiens ADP-ribosylation factor-like 14 (ARL14)	1.61	2.15
ARMCX5	Homo sapiens armadillo repeat containing	0.54	2.24
ASPH	Homo sapiens aspartate beta-hydroxylase (ASPH)	1.96	1.84
ATF3	Homo sapiens activating transcription factor 3 (ATF3)	1.66	3.26
ATG4A	Homo sapiens ATG4 autophagy related 4 homolog A (S. cerevisiae) (ATG4A)	0.65	0.53
ATP2B4	Homo sapiens ATPase	0.62	2.18
B2M	Homo sapiens beta-2-microglobulin (B2M)	1.53	3.44
BAZ2B	Homo sapiens bromodomain adjacent to zinc finger domain	0.62	1.66
BCAS4	Homo sapiens breast carcinoma amplified sequence 4 (BCAS4)	0.65	1.80
BCL6	Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6)	1.52	2.25
BTBD3	Homo sapiens BTB (POZ) domain containing 3 (BTBD3)	0.66	2.17
C11orf49	Homo sapiens chromosome 11 open reading frame 49 (C11orf49)	0.64	2.10
C13orf29	PREDICTED: Homo sapiens misc_RNA (C13orf29)	1.57	1.84
C15orf57	Homo sapiens chromosome 15 open reading frame 57 (C15orf57)	1.62	2.49
C1orf86	Homo sapiens chromosome 1 open reading frame 86 (C1orf86)	1.54	2.63
C20orf160	Homo sapiens chromosome 20 open reading frame 160 (C20orf160)	0.48	2.64
C3orf21	Homo sapiens chromosome 3 open reading frame 21 (C3orf21)	0.42	0.66
C5orf41	Homo sapiens chromosome 5 open reading frame 41 (C5orf41)	1.62	1.93
CA8	Homo sapiens carbonic anhydrase VIII (CA8)	0.56	1.98
CALML4	Homo sapiens calmodulin-like 4 (CALML4)	0.62	1.72
CAPN12	Homo sapiens calpain 12 (CAPN12)	1.53	0.34
CASP1	Homo sapiens caspase 1	2.21	2.26
CASP4	Homo sapiens caspase 4	2.16	1.69
CATSPER2	Homo sapiens cation channel	1.74	2.23
CCL20	Homo sapiens chemokine (C-C motif) ligand 20 (CCL20)	2.24	2.30
CCNYL1	Homo sapiens cyclin Y-like 1 (CCNYL1)	1.62	2.16
CD44	Homo sapiens CD44 molecule (Indian blood group) (CD44)	0.59	2.12
CDK6	Homo sapiens cyclin-dependent kinase 6 (CDK6)	0.46	0.18
CDKN1A	Homo sapiens cyclin-dependent kinase inhibitor 1A (p21	2.59	2.06
CDKN2D	Homo sapiens cyclin-dependent kinase inhibitor 2D (p19	1.56	2.20
CERK	Homo sapiens ceramide kinase (CERK)	0.54	2.08
CHDH	Homo sapiens choline dehydrogenase (CHDH)	0.62	2.29

SYMBOL	DEFINITION	HOTAIR KO (Panc1) Fold Change	HOTAIR Overexpression (MDA-MB-231) Fold Change
CLEC16A	Homo sapiens C-type lectin domain family 16	0.62	0.32
CNN2	Homo sapiens calponin 2 (CNN2)	0.61	2.65
COL11A1	Homo sapiens collagen	0.60	2.36
COL5A2	Homo sapiens collagen	0.62	2.20
COMMD10	Homo sapiens COMM domain containing 10 (COMMD10)	0.61	2.94
CORO6	Homo sapiens coronin 6 (CORO6)	1.85	1.77
CPD	Homo sapiens carboxypeptidase D (CPD)	0.60	0.65
CREB1	Homo sapiens cAMP responsive element binding protein 1 (CREB1)	1.59	0.65
CTBP2	Homo sapiens C-terminal binding protein 2 (CTBP2)	0.66	38.05
CTDSP1	Homo sapiens CTD (carboxy-terminal domain	0.66	2.60
CTDSP2	Homo sapiens CTD (carboxy-terminal domain	0.44	1.68
CX3CL1	Homo sapiens chemokine (C-X3-C motif) ligand 1 (CX3CL1)	3.50	0.39
CXCL1	Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity	1.73	0.62
DAGLB	Homo sapiens diacylglycerol lipase	1.51	0.41
DGKD	Homo sapiens diacylglycerol kinase	1.77	2.28
DHRS3	Homo sapiens dehydrogenase/reductase (SDR family) member 3 (DHRS3)	0.62	1.58
DHX58	Homo sapiens DEXH (Asp-Glu-X-His) box polypeptide 58 (DHX58)	1.72	1.94
DIAPH3	Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3)	0.62	3.46
DICER1	Homo sapiens Dicer1	0.59	2.54
DKFZp686O24166	Homo sapiens hypothetical protein DKFZp686O24166 (DKFZp686O24166)	1.51	2.29
DTL	Homo sapiens denticleless homolog (Drosophila) (DTL)	0.54	0.67
DTX3	Homo sapiens deltex homolog 3 (Drosophila) (DTX3)	1.61	1.74
DUSP19	Homo sapiens dual specificity phosphatase 19 (DUSP19)	1.64	3.00
E2F5	Homo sapiens E2F transcription factor 5	0.55	1.86
EAF1	Homo sapiens ELL associated factor 1 (EAF1)	0.66	2.05
EFEMP1	Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1)	0.57	2.25
EGR1	Homo sapiens early growth response 1 (EGR1)	1.51	1.55
EIF4B	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B)	0.54	2.15
ELL	Homo sapiens elongation factor RNA polymerase II (ELL)	1.56	2.45
ELP4	Homo sapiens elongation protein 4 homolog (S. cerevisiae) (ELP4)	0.63	1.77
EPSTI1	Homo sapiens epithelial stromal interaction 1 (breast) (EPSTI1)	1.99	3.60
ERCC1	Homo sapiens excision repair cross-complementing rodent repair deficiency	1.64	2.11
ETS2	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2)	0.50	1.85
EVL	Homo sapiens Enah/Vasp-like (EVL)	0.52	0.30
F2RL2	Homo sapiens coagulation factor II (thrombin) receptor-like 2 (F2RL2)	1.85	2.39
FAF1	Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1)	0.58	2.06
FAM102A	Homo sapiens family with sequence similarity 102	1.52	0.62
FAM119A	Homo sapiens family with sequence similarity 119	1.69	2.19
FAM120A	Homo sapiens family with sequence similarity 120A (FAM120A)	0.65	1.74
FAM13B	Homo sapiens family with sequence similarity 13	0.67	2.21
FAM46C	Homo sapiens family with sequence similarity 46	0.64	1.56
FAM72D	Homo sapiens family with sequence similarity 72	0.61	1.60
FBLN1	Homo sapiens fibulin 1 (FBLN1)	0.66	8.85
FBXO17	Homo sapiens F-box protein 17 (FBXO17)	0.66	0.64
FBXO32	Homo sapiens F-box protein 32 (FBXO32)	1.57	1.81
FBXW11	Homo sapiens F-box and WD repeat domain containing 11 (FBXW11)	0.53	1.77
FLJ46906	PREDICTED: Homo sapiens hypothetical gene supported by AK128874	1.79	1.84
FXYD5	Homo sapiens FXYD domain containing ion transport regulator 5 (FXYD5)	1.52	1.62
GBP4	Homo sapiens guanylate binding protein 4 (GBP4)	2.25	1.81
GNB5	Homo sapiens guanine nucleotide binding protein (G protein)	1.54	2.66
GOSR1	Homo sapiens golgi SNAP receptor complex member 1 (GOSR1)	0.52	1.63
GPX7	Homo sapiens glutathione peroxidase 7 (GPX7)	0.49	1.73
GTSE1	Homo sapiens G-2 and S-phase expressed 1 (GTSE1)	0.59	1.92
HAS3	Homo sapiens hyaluronan synthase 3 (HAS3)	1.84	1.85

SYMBOL	DEFINITION	HOTAIR KO (Panc1) Fold Change	HOTAIR Overexpression (MDA-MB-231) Fold Change
HIST1H2AC	Homo sapiens histone cluster 1	2.80	1.82
HIST1H2BD	Homo sapiens histone cluster 1	3.79	0.66
HIST1H4C	Homo sapiens histone cluster 1	0.60	1.87
HLA-B	Homo sapiens major histocompatibility complex	2.51	0.52
HOXC4	Homo sapiens homeobox C4 (HOXC4)	0.59	2.36
HSBP1	Homo sapiens heat shock factor binding protein 1 (HSBP1)	0.58	1.76
IDH1	Homo sapiens isocitrate dehydrogenase 1 (NADP+)	0.63	0.60
IFI44L	Homo sapiens interferon-induced protein 44-like (IFI44L)	1.53	1.50
IFI6	Homo sapiens interferon	2.38	1.66
IL17RB	Homo sapiens interleukin 17 receptor B (IL17RB)	0.50	0.31
IL27RA	Homo sapiens interleukin 27 receptor	1.53	0.67
IL28A	Homo sapiens interleukin 28A (interferon	3.23	0.28
IL28B	Homo sapiens interleukin 28B (interferon	1.92	2.69
IL8	Homo sapiens interleukin 8 (IL8)	2.95	1.61
INSIG1	Homo sapiens insulin induced gene 1 (INSIG1)	0.66	0.54
ITGA3	Homo sapiens integrin	0.39	1.83
KCNMA1	Homo sapiens potassium large conductance calcium-activated channel	0.46	3.64
KIF23	Homo sapiens kinesin family member 23 (KIF23)	0.59	1.52
KIF3B	Homo sapiens kinesin family member 3B (KIF3B)	0.45	0.66
KLC1	Homo sapiens kinesin light chain 1 (KLC1)	1.57	2.82
KLF2	Homo sapiens Kruppel-like factor 2 (lung) (KLF2)	1.66	0.67
KRT18	Homo sapiens keratin 18 (KRT18)	0.61	1.57
LAMC2	Homo sapiens laminin	1.65	1.67
LGALS8	Homo sapiens lectin	1.55	2.20
LHPP	Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP)	0.57	4.08
LONP2	Homo sapiens lon peptidase 2	0.63	1.80
LRP8	Homo sapiens low density lipoprotein receptor-related protein 8	0.49	2.21
LYST	Homo sapiens lysosomal trafficking regulator (LYST)	1.61	0.66
MAP1S	Homo sapiens microtubule-associated protein 1S (MAP1S)	1.53	2.08
MAPK8IP2	Homo sapiens mitogen-activated protein kinase 8 interacting protein 2 (MAPK8IP2)	1.62	2.66
MCFD2	Homo sapiens multiple coagulation factor deficiency 2 (MCFD2)	0.48	3.54
MLLT6	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog	1.59	3.54
MNT	Homo sapiens MAX binding protein (MNT)	1.66	0.63
MRPL13	Homo sapiens mitochondrial ribosomal protein L13 (MRPL13)	0.50	2.17
MRPS6	Homo sapiens mitochondrial ribosomal protein S6 (MRPS6)	0.46	1.64
MSI2	Homo sapiens musashi homolog 2 (Drosophila) (MSI2)	2.04	4.89
MTO1	Homo sapiens mitochondrial translation optimization 1 homolog (S. cerevisiae) (MTO1)	0.64	1.85
MXRA5	Homo sapiens matrix-remodelling associated 5 (MXRA5)	0.64	2.12
MYBL1	Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1)	0.63	1.65
MYO3B	Homo sapiens myosin IIIB (MYO3B)	1.53	0.10
NAMPT	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT)	1.52	2.57
NCAPD2	Homo sapiens non-SMC condensin I complex	0.61	3.16
NEBL	Homo sapiens nebulette (NEBL)	0.66	23.20
NETO2	Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 2 (NETO2)	0.47	2.12
NFKB2	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) (NFKB2)	1.64	1.59
NLK	Homo sapiens nemo-like kinase (NLK)	0.62	1.53
NME4	Homo sapiens non-metastatic cells 4	0.41	3.83
NRG1	Homo sapiens neuregulin 1 (NRG1)	2.59	5.26
NRIP3	Homo sapiens nuclear receptor interacting protein 3 (NRIP3)	1.52	2.61
NT5C3	Homo sapiens 5'-nucleotidase	1.53	3.54
NT5DC1	Homo sapiens 5'-nucleotidase domain containing 1 (NT5DC1)	0.42	0.66
NUMB	Homo sapiens numb homolog (Drosophila) (NUMB)	0.49	1.71

SYMBOL	DEFINITION	HOTAIR KO (Panc1) Fold Change	HOTAIR Overexpression (MDA-MB-231) Fold Change
OAS1	Homo sapiens 2'	4.30	1.78
OAS2	Homo sapiens 2'-5'-oligoadenylate synthetase 2	1.62	2.11
OPN3	Homo sapiens opsin 3 (OPN3)	0.61	1.94
PAIP2	Homo sapiens poly(A) binding protein interacting protein 2 (PAIP2)	0.59	2.80
PARP14	Homo sapiens poly (ADP-ribose) polymerase family	2.79	1.69
PBX3	Homo sapiens pre-B-cell leukemia homeobox 3 (PBX3)	0.36	0.61
PCDH7	Homo sapiens protocadherin 7 (PCDH7)	1.87	1.89
PEMT	Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT)	0.60	2.52
PFN2	Homo sapiens profilin 2 (PFN2)	0.59	0.62
PLAGL2	Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2)	0.64	1.60
PLEKHM1	PREDICTED: Homo sapiens pleckstrin homology domain containing	2.05	3.16
PLSCR1	Homo sapiens phospholipid scramblase 1 (PLSCR1)	1.99	0.65
PNMA3	Homo sapiens paraneoplastic antigen MA3 (PNMA3)	1.70	4.93
POFUT1	Homo sapiens protein O-fucosyltransferase 1 (POFUT1)	0.62	1.84
POLDIP3	Homo sapiens polymerase (DNA-directed)	0.66	6.71
PPP2R2B	Homo sapiens protein phosphatase 2 (formerly 2A)	0.62	2.97
PTBP2	Homo sapiens polypyrimidine tract binding protein 2 (PTBP2)	1.63	0.63
PTPLAD1	Homo sapiens protein tyrosine phosphatase-like A domain containing 1 (PTPLAD1)	0.66	1.99
RAB3IL1	Homo sapiens RAB3A interacting protein (rabin3)-like 1 (RAB3IL1)	1.65	2.86
RAB5B	Homo sapiens RAB5B	0.58	0.62
RAP1GAP	Homo sapiens RAP1 GTPase activating protein (RAP1GAP)	2.72	4.68
RASA1	Homo sapiens RAS p21 protein activator (GTPase activating protein) 1 (RASA1)	0.58	2.24
RHEB	Homo sapiens Ras homolog enriched in brain (RHEB)	0.62	0.66
RHOU	Homo sapiens ras homolog gene family	0.62	0.66
RIPPLY2	Homo sapiens ripply2 homolog (zebrafish) (RIPPLY2)	1.77	3.28
RNASEN	Homo sapiens ribonuclease III	0.60	0.66
RNF145	Homo sapiens ring finger protein 145 (RNF145)	0.55	0.65
RPS6KB1	Homo sapiens ribosomal protein S6 kinase	0.67	1.77
RTN3	Homo sapiens reticulon 3 (RTN3)	0.60	1.61
SF3B4	Homo sapiens splicing factor 3b	0.42	1.56
SLC12A2	Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters)	0.58	3.78
SLC22A18	Homo sapiens solute carrier family 22 (organic cation transporter)	2.01	1.57
SLC30A5	Homo sapiens solute carrier family 30 (zinc transporter)	0.64	1.67
SLC36A1	Homo sapiens solute carrier family 36 (proton/amino acid symporter)	1.52	0.65
SLC44A2	Homo sapiens solute carrier family 44	1.86	1.97
SLC7A11	Homo sapiens solute carrier family 7	1.64	1.72
SLFN11	Homo sapiens schlafen family member 11 (SLFN11)	0.61	3.34
SMAD5	Homo sapiens SMAD family member 5 (SMAD5)	0.63	0.66
SMARCD1	Homo sapiens SWI/SNF related	0.56	1.63
SOX4	Homo sapiens SRY (sex determining region Y)-box 4 (SOX4)	0.63	2.54
SP1	Homo sapiens Sp1 transcription factor (SP1)	0.57	2.15
SP100	Homo sapiens SP100 nuclear antigen (SP100)	1.82	0.64
SP110	Homo sapiens SP110 nuclear body protein (SP110)	1.84	0.58
SPAG9	Homo sapiens sperm associated antigen 9 (SPAG9)	1.53	3.43
SPAST	Homo sapiens spastin (SPAST)	0.66	3.24
SPHK1	Homo sapiens sphingosine kinase 1 (SPHK1)	1.89	1.98
SRPK2	Homo sapiens SFRS protein kinase 2 (SRPK2)	1.61	0.53
SSTR2	Homo sapiens somatostatin receptor 2 (SSTR2)	1.53	1.65
ST5	Homo sapiens suppression of tumorigenicity 5 (ST5)	1.61	2.48
STX11	Homo sapiens syntaxin 11 (STX11)	1.80	0.63
SYP	Homo sapiens synaptophysin (SYP)	1.54	2.46
SYT11	Homo sapiens synaptotagmin XI (SYT11)	1.65	2.20
TAF12	Homo sapiens TAF12 RNA polymerase II	0.63	1.81
TCIRG1	Homo sapiens T-cell	1.52	2.15

SYMBOL	DEFINITION	HOTAIR KO (Panc1) Fold Change	HOTAIR Overexpression (MDA-MB-231) Fold Change
TDRD7	Homo sapiens tudor domain containing 7 (TDRD7)	1.89	8.95
TICAM1	Homo sapiens toll-like receptor adaptor molecule 1 (TICAM1)	1.63	1.64
TMC6	Homo sapiens transmembrane channel-like 6 (TMC6)	1.57	2.60
TMEM140	Homo sapiens transmembrane protein 140 (TMEM140)	1.98	0.51
TMEM151A	Homo sapiens transmembrane protein 151A (TMEM151A)	1.54	3.05
TMEM159	Homo sapiens transmembrane protein 159 (TMEM159)	1.55	1.92
TNFRSF1B	Homo sapiens tumor necrosis factor receptor superfamily	1.99	2.33
TOMM34	Homo sapiens translocase of outer mitochondrial membrane 34 (TOMM34)	1.57	0.65
TTC9B	Homo sapiens tetratricopeptide repeat domain 9B (TTC9B)	3.42	1.74
TUBA4A	Homo sapiens tubulin	1.62	2.39
TYMP	Homo sapiens thymidine phosphorylase (TYMP)	1.53	11.95
UAP1	Homo sapiens UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1)	0.61	1.58
UBA2	Homo sapiens ubiquitin-like modifier activating enzyme 2 (UBA2)	0.61	1.52
UBE2L6	Homo sapiens ubiquitin-conjugating enzyme E2L 6 (UBE2L6)	2.46	2.18
UBFD1	Homo sapiens ubiquitin family domain containing 1 (UBFD1)	1.59	1.56
UBIAD1	Homo sapiens UbiA prenyltransferase domain containing 1 (UBIAD1)	1.62	1.91
UBQLN1	Homo sapiens ubiquilin 1 (UBQLN1)	0.25	1.51
USP12	Homo sapiens ubiquitin specific peptidase 12 (USP12)	0.62	2.13
VPS26A	Homo sapiens vacuolar protein sorting 26 homolog A (S. pombe) (VPS26A)	0.66	1.91
VWA1	Homo sapiens von Willebrand factor A domain containing 1 (VWA1)	0.65	3.04
WDR26	Homo sapiens WD repeat domain 26 (WDR26)	0.62	2.55
XAF1	Homo sapiens XIAP associated factor 1 (XAF1)	1.77	2.65
ZAK	Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK)	1.55	2.44
ZBTB4	Homo sapiens zinc finger and BTB domain containing 4 (ZBTB4)	0.59	0.63
ZC3HAV1	Homo sapiens zinc finger CCCH-type	2.45	1.72
ZCCHC7	Homo sapiens zinc finger	0.46	0.67
ZFYVE26	Homo sapiens zinc finger	1.54	0.64
ZNF318	Homo sapiens zinc finger protein 318 (ZNF318)	0.56	3.98
ZNF483	Homo sapiens zinc finger protein 483 (ZNF483)	1.52	1.58
ZNFX1	Homo sapiens zinc finger	2.06	2.21
ZSWIM4	Homo sapiens zinc finger	1.84	1.52

Supplemental Table S8. Common genes regulated by PRC2/HOTAIR in MDA-MB-231 and after knockdown of HOTAIR in Panc-1 cells.

Gene Symbol	Description	HOTAIR Overexpression (MDA-MB-231) Fold Change	HOTAIR KO (Panc-1) Fold Change
API5	apoptosis inhibitor 5	0.85	0.44
BRD7	Bromodomain containing 7	1.26	0.50
GSTP1	Glutathione S-transferase pi 1	0.69	0.24
KIAA1751	KIAA1751	0.82	1.00
MICB	MHC class I polypeptide-related sequence B	0.83	0.35
OCIAD2	OCIA domain containing 2	1.00	1.43
OXSR1	oxidative-stress responsive 1	1.10	0.60
RSAD2	Radical S-adenosyl methionine domain containing 2	1.34	2.25
SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	0.89	0.65