Supporting Information

Namdar et al. 10.1073/pnas.1013754107

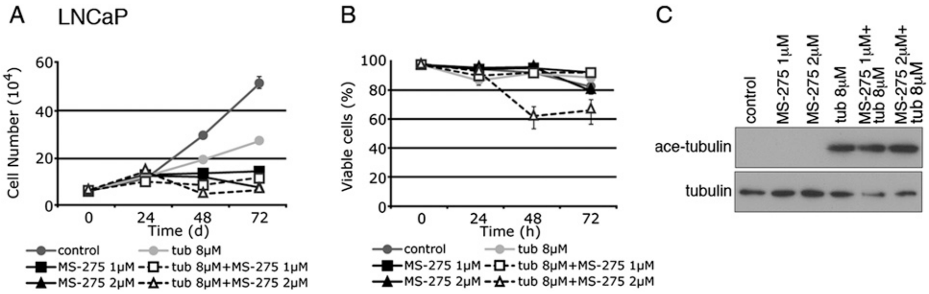

Fig. S1. Culture of LNCaP cells with MS-275 without and with tubacin. Cell growth (*A*) and viability (*B*) of LNCaP cells cultured with tubacin MS-275, and tubacin plus MS-275. (*C*) Western blot probing with antibodies against acetylated α-tubulin and α-tubulin in LNCaP cells cultured with tubacin, MS-275, and tubacin plus MS-275. MS-275 does not induce acetylation of α-tubulin, as does tubacin.

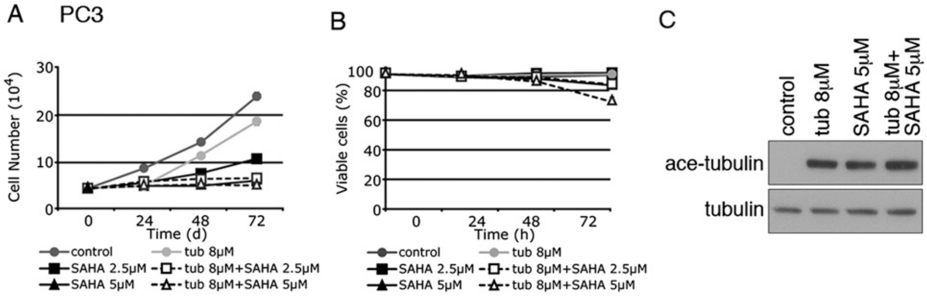

Fig. S2. Culture of PC3 cells with tubacin, SAHA, and tubacin plus SAHA. Cell growth (*A*) and viability (*B*) of PC3 cells cultured with tubacin, SAHA, and tubacin plus SAHA. (*C*) Western blot probing with antibodies against acetylated α-tubulin and α-tubulin in PC3 cells cultured with tubacin, SAHA, and tubacin plus SAHA.

Table S1. Genes up- or down-regulated by at least twofold following culture of LNCaP cells for 2 h, 8 h, and 24 h with tubacin, SAHA, and the combination of tubacin plus SAHA

Treatment	Total gene no.	Up-regulated genes	Down-regulated genes
SAHA			
2 h	37	21	16
8 h	628	326	302
24 h	1,951	962	989
Tubacin			
2 h	1	1	0
8 h	7	6	1
24 h	225	153	72
Tubacin + SAHA			
2 h	29	19	10
8 h	694	340	354
24 h	2,149	1,097	1,052

Table S2. *DDIT3* and *DDIT4* gene expression as a ratio of level of expression in culture with agent over culture with DMSO in LNCaP cells

Gene symbol	Tubacin			SAHA			Tubacin + SAHA		
	2 h	8 h	24 h	2 h	8 h	24 h	2 h	8 h	24 h
DDIT3	ND	2.22	7.04	2.18	ND	ND	2.1	2.5	22.36
DDIT4	2.01	5.54	6.8	ND	5.36	3.81	ND	6.4	7.09

ND, no detectable change of at least twofold.

Table S3. Genes showing at least twofold down-regulation following culture of LNCaP cells with tubacin for 24 h

Gene symbol	Gene name	Fold change
MCM4	*H. sapiens* mini-chromosome maintenance complex component 4 (MCM4), transcript variant 1, mRNA	−3.13
CDCA7	*H. sapiens* cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA	−3.03
GINS2	*H. sapiens* GINS complex subunit 2 (Psf2 homologue) (GINS2), mRNA	−2.94
UHRF1	*H. sapiens* ubiquitin-like with PHD and ring finger domains 1 (UHRF1), transcript variant 1, mRNA	−2.92
LFNG	*H. sapiens* LFNG O-fucosylpeptide 3-β-N-acetylglucosaminyltransferase (LFNG), transcript variant 1, mRNA	−2.74
MYB	*H. sapiens* v-myb myeloblastosis viral oncogene homologue (avian) (MYB), transcript variant 2, mRNA	−2.68
LAMA1	*H. sapiens* laminin, α 1 (LAMA1), mRNA	−2.66
MCM10	*H. sapiens* minichromosome maintenance complex component 10 (MCM10), transcript variant 2, mRNA	−2.66
CDT1	*H. sapiens* chromatin licensing and DNA replication factor 1 (CDT1), mRNA	−2.63
TYMS	*H. sapiens* thymidylate synthetase (TYMS), mRNA	−2.61
NKX3-1	*H. sapiens* NK3 homeobox 1 (NKX3-1), mRNA	−2.56
NUDT1	*H. sapiens* nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1), transcript variant 2A, mRNA	−2.56
MCM6	*H. sapiens* minichromosome maintenance complex component 6 (MCM6), mRNA	−2.55
FKBP5	*H. sapiens* FK506 binding protein 5 (FKBP5), mRNA	−2.54
GEMIN4	*H. sapiens* gem (nuclear organelle) associated protein 4 (GEMIN4), mRNA	−2.49
MCM7	*H. sapiens* minichromosome maintenance complex component 7 (MCM7), transcript variant 2, mRNA	−2.48
STRA13	*H. sapiens* stimulated by retinoic acid 13 homologue (mouse) (STRA13), mRNA	−2.41
ASF1B	*H. sapiens* ASF1 anti-silencing function 1 homologue B (*S cerevisiae*) (ASF1B), mRNA	−2.41
LRRC45	*H. sapiens* leucine rich repeat containing 45 (LRRC45), mRNA	−2.4
TUBA3D	*H. sapiens* tubulin, α 3d (TUBA3D), mRNA	−2.39
SNRPA1	*H. sapiens* small nuclear ribonucleoprotein polypeptide A′ (SNRPA1), mRNA	−2.37
LOC399942	Predicted: *H. sapiens* similar to Tubulin α-2 chain (A-tubulin 2), transcript variant 5 (LOC399942), mRNA	−2.35
SLC25A19	*H. sapiens* solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 (SLC25A19), nuclear gene encoding mitochondrial protein, mRNA	−2.33
MCM5	*H. sapiens* minichromosome maintenance complex component 5 (MCM5), mRNA	−2.31
EXO1	*H. sapiens* exonuclease 1 (EXO1), transcript variant 1, mRNA	−2.3
UCHL5IP	*H. sapiens* UCHL5 interacting protein (UCHL5IP), transcript variant 1, mRNA	−2.3
PCNA	*H. sapiens* proliferating cell nuclear antigen (PCNA), transcript variant 2, mRNA	−2.26
CDK2	*H. sapiens* cyclin-dependent kinase 2 (CDK2), transcript variant 1, mRNA	−2.25
ADH1A	*H. sapiens* alcohol dehydrogenase 1A (class I), α polypeptide (ADH1A), mRNA	−2.23
CDCA5	*H. sapiens* cell division cycle associated 5 (CDCA5), mRNA	−2.23
CDC25A	*H. sapiens* cell division cycle 25 homologue A (*S pombe*) (CDC25A), transcript variant 1, mRNA	−2.21
ATAD2	*H. sapiens* ATPase family, AAA domain containing 2 (ATAD2), mRNA	−2.21
MCM4	*H. sapiens* minichromosome maintenance complex component 4 (MCM4), transcript variant 2, mRNA	−2.21
LYAR	*H. sapiens* Ly1 antibody reactive homologue (mouse) (LYAR), mRNA	−2.19
LOC647000	Predicted: *H. sapiens* similar to tubulin, β 5 (LOC647000), mRNA	−2.16
RAD54L	*H. sapiens* RAD54-like (*S cerevisiae*) (RAD54L), mRNA	−2.14
MCM7	*H. sapiens* minichromosome maintenance complex component 7 (MCM7), transcript variant 1, mRNA	−2.14
NPTX2	*H. sapiens* neuronal pentraxin II (NPTX2), mRNA	−2.11
RDH13	*H. sapiens* retinol dehydrogenase 13 (all-trans/9-cis) (RDH13), mRNA	−2.11
CCNA2	*H. sapiens* cyclin A2 (CCNA2), mRNA	−2.11
C20orf72	*H. sapiens* chromosome 20 ORF 72 (C20orf72), mRNA	−2.11
XRCC3	*H. sapiens* x-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), transcript variant 3, mRNA	−2.11
UNG	*H. sapiens* uracil-DNA glycosylase (UNG), transcript variant 1, mRNA	−2.1
BIRC5	*H. sapiens* baculoviral IAP repeat-containing 5 (BIRC5), transcript variant 1, mRNA	−2.1
FAM83D	*H. sapiens* family with sequence similarity 83, member D (FAM83D), mRNA	−2.1
CDC45L	*H. sapiens* CDC45 cell division cycle 45-like (*S. cerevisiae*) (CDC45L), mRNA	−2.09
PAQR4	*H. sapiens* progestin and adipoQ receptor family member IV (PAQR4), mRNA	−2.09
FEN1	*H. sapiens* flap structure-specific endonuclease 1 (FEN1), mRNA	−2.09
BCL2L12	*H. sapiens* BCL2-like 12 (proline rich) (BCL2L12), transcript variant 3, mRNA.	−2.09
MCM2	*H. sapiens* minichromosome maintenance complex component 2 (MCM2), mRNA	−2.08
XTP3TPA	*H. sapiens* XTP3-transactivated protein A (XTP3TPA), mRNA	−2.07
SLC29A1	*H. sapiens* solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA	−2.06
ARHGDIA	*H. sapiens* Rho GDP dissociation inhibitor (GDI) α (ARHGDIA), mRNA	−2.06
RRM2	*H. sapiens* ribonucleotide reductase M2 polypeptide (RRM2), mRNA	−2.06
LOC652595	Predicted: *H. sapiens* similar to U2 small nuclear ribonucleoprotein A (U2 snRNP-A) (LOC652595), mRNA	−2.06
MCM10	*H. sapiens* minichromosome maintenance complex component 10 (MCM10), transcript variant 2, mRNA	−2.05
YWHAH	*H. sapiens* tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (YWHAH), mRNA	−2.04
CCNF	*H. sapiens* cyclin F (CCNF), mRNA.	−2.04
ADH1C	*H. sapiens* alcohol dehydrogenase 1C (class I), γ-polypeptide (ADH1C), mRNA	−2.04

Table S3. Cont.

Gene symbol	Gene name	Fold change
IRX3	*H. sapiens* Iroquois homeobox 3 (IRX3), mRNA	−2.04
E2F2	*H. sapiens* E2F transcription factor 2 (E2F2), mRNA	−2.03
FN3KRP	*H. sapiens* fructosamine-3-kinase-related protein (FN3KRP), mRNA	−2.03
SLC29A1	*H. sapiens* solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA	−2.03
CCNE2	*H. sapiens* cyclin E2 (CCNE2), transcript variant 2, mRNA	−2.03
SUV39H1	*H. sapiens* suppressor of variegation 3–9 homologue 1 (*Drosophila*) (SUV39H1), mRNA	−2.02
DNMT1	*H. sapiens* DNA (cytosine-5-)-methyltransferase 1 (DNMT1), mRNA	−2.01
C11orf82	*H. sapiens* chromosome 11 ORF 82 (C11orf82), mRNA	−2.01
SLBP	*H. sapiens* stem-loop binding protein (SLBP), mRNA	−2.01
NOL5A	*H. sapiens* nucleolar protein 5A (56 kDa with KKE/D repeat) (NOL5A), mRNA	−2.01
NP	*H. sapiens* nucleoside phosphorylase (NP), mRNA	−2.01
GAL	Homo sapiens galanin prepropeptide (GAL), mRNA	−2.01
LOC642031	Predicted: *H. sapiens* hypothetical protein LOC642031 (LOC642031), mRNA	−2

Table S4. DNA damage and repair genes showing at least twofold down-regulation following culture of LNCaP cells with SAHA for 24 h

Gene symbol	Gene name	Fold change
BIRC5	*H. sapiens* baculoviral IAP repeat-containing 5 (BIRC5), transcript variant 1, mRNA	−5.18
BRCA1	*H. sapiens* breast cancer 1, early onset (BRCA1), transcript variant BRCA1-delta14-17, mRNA	−2.15
CCND1	*H. sapiens* cyclin D1 (CCND1), mRNA	−10.06
CDC25A	*H. sapiens* cell division cycle 25 homologue A (*S. pombe*) (CDC25A), transcript variant 1, mRNA.	−4.5
CDC25C	*H. sapiens* cell division cycle 25 homologue C (*S. pombe*) (CDC25C), transcript variant 1, mRNA	−2.18
CHEK1	*H. sapiens* CHK1 checkpoint homologue (*S. pombe*) (CHEK1), mRNA	−4.51
CHEK2	*H. sapiens* CHK2 checkpoint homologue (*S. pombe*) (CHEK2), transcript variant 1, mRNA	−2
E2F2	*H. sapiens* E2F transcription factor 2 (E2F2), mRNA	−3.05
FANCG	*H. sapiens* Fanconi anemia, complementation group G (FANCG), mRNA	−2.43
FOXM1	*H. sapiens* forkhead box M1 (FOXM1), transcript variant 2, mRNA	−4.11
H2AFX	*H. sapiens* H2A histone family, member X (H2AFX), mRNA.	−3.24
HIPK2	*H. sapiens* homeodomain interacting protein kinase 2 (HIPK2), mRNA	−2.5
MYB	*H. sapiens* v-myb myeloblastosis viral oncogene homologue (avian) (MYB), transcript variant 2, mRNA	−2.61
MYC	*H. sapiens* v-myc myelocytomatosis viral oncogene homologue (avian) (MYC), mRNA	−4.26
NME1	*H. sapiens* nonmetastatic cells 1, protein (NM23A) expressed in (NME1), transcript variant 1, mRNA	−3.12
NUPR1	*H. sapiens* nuclear protein 1 (NUPR1), transcript variant 1, mRNA	−3.65
PBK	*H. sapiens* PDZ binding kinase (PBK), mRNA	−2.29
PHLDA3	*H. sapiens* Homo sapiens pleckstrin homology-like domain, family A, member 3 (PHLDA3), mRNA	−2.12
PLK1	*H. sapiens* polo-like kinase 1 (Drosophila) (PLK1), mRNA	−2.13
RAD54L	*H. sapiens* RAD54-like (*S. cerevisiae*) (RAD54L), mRNA	−2.89
SFRS2	*H. sapiens* splicing factor, arginine/serine-rich 2 (SFRS2), mRNA	−2.15
TOP2A	*H. sapiens* topoisomerase (DNA) II-α170 kDa (TOP2A), mRNA	−5.13
TOPBP1	*H. sapiens* topoisomerase (DNA) II binding protein 1 (TOPBP1), mRNA	−2.1
TP53	*H. sapiens* tumor protein p53 (TP53), mRNA	−2.24
XRCC3	*H. sapiens* x-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), transcript variant 3, mRNA	−2.65