

## **APPENDIX A**

### **RAW DATA FOR RNAi SCREEN**

This appendix lists the 74 genome maintenance genes identified in the RNAi screen (Table 1), and contains oligonucleotide-specific information from which the graphs in Chapter IV were generated. The quantitation of  $\gamma$ H2AX foci, the viability ratios and sensitivity indices from the HU viability assay, and the quantitation of mitotic cells from the HU recovery assay are listed in Tables 2, 4, and 5, respectively. This appendix also identifies the genome maintenance genes with tumor suppressor activity in Table 3.

**Table 1. Genes reproducibly demonstrating genome maintenance defects after RNAi silencing.** Genome maintenance defects were identified by activation of the DNA damage response (DDR), which results in the phosphorylation of the DDR substrates KAP1 and  $\gamma$ H2AX. The number of positive RNAi molecules/number tested is shown. APH=aphidicolin. The yellow highlighted boxes indicate where at least two of the siRNAs yielded adjusted *p* values of <0.05 and correspond to the thirty-seven highest confidence genome maintenance genes. The remaining genes had at least two siRNAs yielding unadjusted *p* values of <0.05 in either the untreated or aphidicolin treated samples. See Table 2 for raw data.

Entrez ID	Gene Name	Gene Symbol	P-KAP1 in HeLa		$\gamma$ H2AX in U2OS	
			shRNA without APH	shRNA with APH	siRNA without APH	siRNA with APH
29882	anaphase promoting complex subunit 2	ANAPC2	1/1	1/1	2/4	2/4
51433	anaphase promoting complex subunit 5	ANAPC5	1/3	2/3	2/4	2/4
648	BMI1 polycomb ring finger oncogene	BMI1	0/3	1/3	3/4	2/4
9577	brain and reproductive organ-expressed (TNFRSF1A modulator)	BRE	0/3	1/3	2/4	1/4
83990	BRCA1 interacting protein C-terminal helicase 1	BRIP1	1/3	1/3	1/4	3/4
55143	cell division cycle associated 8	CDCA8	1/3	1/3	3/4	1/4
9744	centaurin, beta 1	CENTB1	0/2	1/2	0/4	2/4
1111	CHK1 checkpoint homolog (S. pombe)	CHK1	1/2	2/2	3/4	3/4
11200	CHK2 checkpoint homolog (S. pombe)	CHK2	0/4	1/4	1/4	2/4
51550	cyclin-dependent kinase 2-interacting protein	CINP	2/5	3/5	3/4	2/4
23122	cytoplasmic linker associated protein 2	CLASP2	1/2	2/2	0/4	2/4
152330	contactin 4	CNTN4	0/3	1/3	2/4	1/4
22818	coatamer protein complex, subunit zeta 1 *KC gene*	COPZ1	1/3	1/3	0/4	3/4
1642	damage-specific DNA binding protein 1, 127kDa	DDB1	1/3	1/3	2/4	3/4
9077	DIRAS family, GTP-binding RAS-like 3	DIRAS3	1/3	1/3	2/4	2/4
1775	deoxyribonuclease I-like 2	DNASE1L2	1/3	2/3	2/5	2/5
2074	excision repair cross-complementing rodent repair deficiency, complementation group 6	ERCC6	1/2	1/2	0/4	2/4
161829	exonuclease 3'-5' domain-like 1	EXDL1	1/2	1/2	1/4	2/4
55120	Fanconi anemia, complementation group L	FANCL	0/3	2/3	2/5	1/5
6468	F-box and WD repeat domain containing 4	FBXW4	1/2	1/2	2/4	2/4
56776	formin 2	FMN2	1/3	1/3	2/4	0/4
26130	GTPase activating protein and VPS9 domains 1	GAPVD1	1/2	1/2	0/4	2/4
26354	guanine nucleotide binding protein-like 3 (nucleolar); nucleostemin	GNL3	1/2	2/2	2/4	2/4
51512	G-2 and S-phase expressed 1	GTSE1	0/3	1/3	2/4	1/4
9555	H2A histone family, member Y	H2AFY	0/3	2/3	1/4	3/4
57520	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	HECW2	0/3	1/3	2/4	2/4
8924	hect domain and RLD 2	HERC2	0/3	2/3	2/4	1/4
221613	histone cluster 1, H2aa	HIST1H2AA	0/1	1/1	2/4	2/4
3305	heat shock 70kDa protein 1-like	HSPA1L	1/2	1/2	2/4	2/4
3306	heat shock 70kDa protein 2	HSPA2	0/2	1/2	1/4	2/4
3576	interleukin 8	IL8	1/2	0/2	2/4	2/4
3659	interferon regulatory factor 1	IRF1	0/3	1/3	2/4	2/4
51438	melanoma antigen family C, 2	MAGEC2	0/3	1/3	0/4	2/4
23389	mediator complex subunit 13-like, thyroid hormone receptor associated protein 2	MED13L	0/3	2/3	2/4	2/4
284382	hypothetical protein MGC33407	MGC33407	1/1	1/1	2/4	2/4
9221	nucleolar and coiled-body phosphoprotein 1	NOLC1	1/3	1/3	1/4	2/4
4897	neuronal cell adhesion molecule	NRCAM	1/3	1/3	2/4	1/4
9381	otoferlin	OTOF	0/3	2/3	1/4	2/4

**Table 1 (continued). Genes reproducibly demonstrating genome maintenance defects after RNAi silencing.**  
Genome maintenance defects were identified by activation of the DNA damage response (DDR), which results in the phosphorylation of the DDR substrates KAP1 and  $\gamma$ H2AX. The number of positive RNAi molecules/number tested is shown. APH=aphidicolin. The yellow highlighted boxes indicate where at least two of the siRNAs yielded adjusted *p* values of <0.05 and correspond to the thirty-seven highest confidence genome maintenance genes. The remaining genes had at least two siRNAs yielding unadjusted *p* values of <0.05 in either the untreated or aphidicolin treated samples. See Table 2 for raw data.

Entrez ID	Gene Name	Gene Symbol	P-KAP1 in HeLa		$\gamma$ H2AX in U2OS	
			shRNA without APH	shRNA with APH	siRNA without APH	siRNA with APH
80301	pleckstrin homology domain containing, family Q member 1	PLEKHO2	1/3	1/3	2/4	2/4
5422	polymerase (DNA directed), alpha 1	POLA	1/3	1/3	4/4	4/4
5423	polymerase (DNA directed), beta	POLB	2/3	2/3	2/4	2/4
5424	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	POLD1	2/3	3/3	1/4	3/4
5426	polymerase (DNA directed), epsilon	POLE	1/1	1/1	3/4	4/4
5427	polymerase (DNA directed), epsilon 2 (p59 subunit)	POLE2	0/3	3/3	1/4	3/4
54776	protein phosphatase 1, regulatory (inhibitor) subunit 12C	PPP1R12C	0/2	1/2	1/4	2/4
5518	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	PPP2R1A	1/2	1/2	1/4	2/4
5557	primase, polypeptide 1, 49kDa	PRIM1	0/3	1/3	3/4	2/4
5714	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	PSMD8	0/3	2/3	3/4	2/4
5929	retinoblastoma binding protein 5	RBBP5	1/3	1/3	2/4	2/4
5937	RNA binding motif, single stranded interacting protein 1	RBMS1	1/3	1/3	2/4	1/4
23186	REST corepressor 1	RCOR1	1/3	1/3	0/4	2/4
5985	replication factor C (activator 1) 5, 36.5kDa	RFC5	0/4	1/4	0/4	2/4
117584	ring finger and FYVE-like domain containing 1	RFFL	1/4	1/4	0/4	2/4
6240	Ribonucleotide reductase M1 polypeptide	RRM1	1/2	0/2	3/4	3/4
6282	S100 calcium binding protein A11	S100A11	1/2	1/2	2/4	2/4
23256	sec1 family domain containing 1	SCFD1	1/3	1/3	3/4	2/4
4735	septin 2	SEPT2	1/3	1/3	3/4	1/4
83852	SET domain, bifurcated 2	SETDB2	0/2	2/2	1/4	2/4
50485	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	SMARCAL1	1/1	0/1	2/4	1/4
23626	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)	SPO11	1/3	1/3	1/4	2/4
258010	small VCP/p97-interacting protein	SVIP	1/3	2/3	0/4	4/4
50945	T-box 22	TBX22	1/3	1/3	2/4	1/4
221400	tudor domain containing 6	TDRD6	0/3	2/3	3/4	1/4
7398	ubiquitin specific peptidase 1	USP1	0/3	1/3	2/4	2/4
8237	ubiquitin specific peptidase 11	USP11	0/2	1/2	2/4	2/4
151525	WD repeat, sterile alpha motif and U-box domain containing 1	WDSUB1	0/2	1/2	1/4	2/4
7465	WEE1 homolog (S. pombe)	WEE1	3/3	3/3	2/4	4/4
7486	Werner syndrome	WRN	0/4	1/4	2/4	1/4
56897	Werner helicase interacting protein 1	WRNIP1	0/4	1/4	2/4	2/4
56949	XPA binding protein 2	XAB2	1/3	1/3	2/4	1/4
7507	xeroderma pigmentosum, complementation group A	XPA	0/3	1/3	2/4	2/4
7709	zinc finger and BTB domain containing 17	ZBTB17	0/3	1/3	2/4	1/4

**Table 2. Mean  $\gamma$ H2AX foci in U2OS cells with and without aphidicolin treatment following siRNA silencing.** The data represents four cell counts from two independent transfections. The  $p$  value was calculated for each siRNA in comparison to the non-targeting control using an unpaired, two-tailed t-test. A False Discovery Rate (FDR) controlled  $p$ -value with a cut-off value of 0.05 was also calculated. NA, data is unavailable.

Entrez ID	GeneSymbol	OligoName	OligoSequence	Untreated				Aphidicolin-treated (0.1mM)			
				Mean	Std Dev	$p$ value	FDR $p$ value	Mean	Std Dev	$p$ value	FDR $p$ value
29882	ANAPC2	Hs_ANAPC2_1	GAGAGTCTATATGCAGAGTAA	4.75	1.89	0.0227	0.0700	5.75	2.22	0.0244	0.0707
29882	ANAPC2	Hs_ANAPC2_6	CTCACTGGATCGTATCTACAA	2.96	1.68	0.1440	0.2796	14.63	4.51	0.0350	0.0828
29882	ANAPC2	Hs_ANAPC2_5	AAGGTTCTTCTACCCGCTCTA	2.15	0.47	0.0205	0.0653	5.37	2.37	0.0893	0.1691
29882	ANAPC2	Hs_ANAPC2_3	CAGCGGTGCAGTCCCGCCAAA	0.75	0.96	0.9328	0.9392	2.00	0.82	0.1277	0.2071
51433	ANAPC5	Hs_ANAPC5_7	CAGAATCAAAGTATGGCTGA	0.27	0.47	0.2415	0.3716	5.08	0.52	0.0013	0.0148
51433	ANAPC5	Hs_ANAPC5_4	AGCGGTTGTATTACAAGCTCA	0.00	0.00	0.0075	0.0334	0.00	0.00	0.0044	0.0244
51433	ANAPC5	Hs_ANAPC5_6	ACCCTTGATAAACCATCTCTA	7.54	0.93	0.0047	0.0334	5.08	1.03	0.0176	0.0587
51433	ANAPC5	Hs_ANAPC5_3	CGCATTATCTCAGCTACTTAA	4.50	1.91	0.0278	0.0819	3.00	2.16	0.1858	0.2782
648	BMI1	Hs_PCGF4_3	CAGAGTTCCGACCTACTTGTA	25.59	3.36	0.0059	0.0334	19.41	3.39	0.0110	0.0450
648	BMI1	Hs_PCGF4_1	TTGGATCGGAAAGTAAACAAA	5.39	1.87	0.0478	0.1184	9.85	1.79	0.0125	0.0473
648	BMI1	Hs_BMI1_2	CAAGACCAGACCCTACTGAA	1.00	1.41	0.7070	0.7929	0.25	0.50	0.0274	0.0707
648	BMI1	Hs_BMI1_1	ATGGGTCTATGGTCAACAATA	3.00	0.82	0.0086	0.0375	2.75	1.50	0.1216	0.2011
9577	BRE	Hs_BRE_6	TAGCGTGGTCCGGAATGGAAA	0.00	0.00	0.0075	0.0334	0.00	0.00	0.0044	0.0244
9577	BRE	Hs_BRE_3	AAGGTGCAGTACGTGATTCAA	8.08	1.62	0.0147	0.0533	7.17	0.90	0.0045	0.0244
9577	BRE	Hs_BRE_2	CCGCCTCATGTTTGAATACCA	18.58	2.14	0.0045	0.0334	5.37	1.79	0.0525	0.1141
9577	BRE	Hs_BRE_7	TGCCCGTAGATTCAGCAATA	0.75	0.96	0.9328	0.9392	1.00	1.15	0.8101	0.8522
83990	BRIP1	Hs_BRIP1_1	TAGCATGGCAACAACTCTTAA	6.46	3.52	0.1049	0.2242	14.03	1.86	0.0061	0.0306
83990	BRIP1	Hs_BRIP1_5	ACAGTCAAGAGTCAATCGAATA	1.25	1.89	0.6066	0.7316	10.25	3.59	0.0145	0.0522
83990	BRIP1	Hs_BRIP1_2	AAGATAAACAGTCCAATCAA	37.98	7.18	0.0121	0.0462	22.99	6.78	0.0305	0.0767
83990	BRIP1	Hs_BRIP1_6	TAGATAGTATGGTCAACAATA	1.00	1.15	0.6484	0.7627	5.75	6.60	0.2582	0.3574
55143	CDCA8	Hs_CDCA8_2	ACGAAAGGTAATACAGGTAGA	11.58	1.23	0.0036	0.0297	6.57	1.86	0.0352	0.0830
55143	CDCA8	Hs_CDCA8_3	CTGGTACCTACTTCAATAAA	4.31	0.47	0.0020	0.0222	5.67	2.25	0.0271	0.1464
55143	CDCA8	Hs_CDCA8_7	TGAAAAGACTTCGACCGTGA	3.00	0.82	0.0086	0.0375	2.00	1.41	0.3204	0.4198
55143	CDCA8	Hs_CDCA8_6	CAGCAGCATACGGACCACAAA	NA	NA	NA	NA	0.75	0.96	0.4697	0.5514
9744	CENTB1	Hs_CENTB1_2	ACGGGCCAGCAACGCAITTTAA	0.00	0.00	0.0075	0.0334	5.97	1.37	0.0227	0.0707
9744	CENTB1	Hs_CENTB1_1	CACCGTGAGCTGAACCACAA	NA	NA	NA	NA	11.35	3.62	0.0390	0.0906
9744	CENTB1	Hs_CENTB1_6	CCGGTGTCCCAGTATCGAAA	1.50	1.91	0.4687	0.6504	0.50	0.58	0.1063	0.1797
9744	CENTB1	Hs_CENTB1_5	GAGGCCTGGATTACAGCTAAA	0.25	0.50	0.1685	0.2860	1.50	1.29	0.6351	0.7074
1111	CHK1	Hs_CHEK1_9	AAGAAAGAGATCTGTATCAAT	58.75	1.71	0.0000	0.0008	69.75	7.37	0.0003	0.0061
1111	CHK1	Hs_CHEK1_8	CCCGCACAGGCTTCTTCCAT	7.27	1.40	0.0136	0.0503	54.04	2.88	0.0009	0.0111
1111	CHK1	Hs_CHEK1_7	AACTGAAGAAGACCTCCAGT	31.51	4.04	0.0056	0.0334	18.51	1.86	0.0033	0.0244
1111	CHK1	Hs_CHEK1_13	TTGGAATAACTCACAGGGATA	6.75	5.85	0.1307	0.2579	15.00	5.10	0.0121	0.0467
11200	CHK2	Hs_CHEK2_9	ACGCCGTCTTCGAGACTATA	4.31	1.23	0.0344	0.0932	21.20	3.15	0.0078	0.0359
11200	CHK2	Hs_CHEK2_10	AGGACTGTCTTATAAAGATTA	0.54	0.93	0.7883	0.8720	8.36	1.37	0.0098	0.0416
11200	CHK2	Hs_CHEK2_14	CAGGATGGATTTGCCAATCTT	1.00	1.41	0.7070	0.7929	1.75	1.71	0.5390	0.6216
11200	CHK2	Hs_CHEK2_15	CTCCGTGGTTTGAAACGAAA	0.50	0.58	0.5435	0.6711	1.00	1.41	0.8431	0.8728
51550	CINP	Hs_CINP-1	AAACCTGTCTTATCTGTCAAT	5.66	0.00	0.0000	0.0014	11.05	2.25	0.0159	0.0550
51550	CINP	Hs_CINP_8	ATGCGGTGATGGCACAAATT	2.75	1.26	0.0454	0.1159	6.50	2.52	0.0230	0.0707
51550	CINP	Hs_CINP_6	GCGGCTGATGGCACAAITTA	6.25	6.24	0.1735	0.2928	5.75	5.32	0.1822	0.2739
51550	CINP	Hs_CINP-3	TTCCTTGGTAGTTGAAGACAGCTT	10.77	1.68	0.0085	0.0375	6.27	4.74	0.2022	0.3012
23122	CLASP2	Hs_CLASP2_6	TCCACGCTCTCGAGACTATA	0.75	0.96	0.9328	0.9392	0.00	0.00	0.0044	0.0244
23122	CLASP2	Hs_CLASP2_3	AAGAAGCAGTATTAACATCAA	3.50	2.03	0.1390	0.2712	5.97	1.03	0.0112	0.0451
23122	CLASP2	Hs_CLASP2_1	CTGGTTAAGATACTGTCTTAA	1.08	1.23	0.6552	0.7662	8.36	1.86	0.0200	0.0648
23122	CLASP2	Hs_CLASP2_8	TTCAAGGTTCTGACCTATAA	0.50	1.00	0.7128	0.7929	1.00	2.00	0.8876	0.9006
152330	CNTN4	Hs_CNTN4_2	CACATCTGTCAATGAAACAAA	17.78	1.40	0.0019	0.0218	4.18	0.52	0.0029	0.0240
152330	CNTN4	Hs_CNTN4_8	AAGACACCCAGTACTAAGTAA	1.25	0.50	0.1148	0.2343	1.75	1.26	0.4189	0.5196
152330	CNTN4	Hs_CNTN4_1	CAGTTGGAAATCAGACATCAA	5.39	0.93	0.0106	0.0427	0.90	0.90	0.6717	0.7453
152330	CNTN4	Hs_CNTN4_6	CAAATTCGAATCCAAAGATA	0.00	0.00	0.0075	0.0334	1.00	0.82	0.7406	0.7948
22818	COPZ1	Hs_COPZ1_2	TTGGCTGTGGATGAAATGTGA	NA	NA	NA	NA	40.91	2.88	0.0016	0.0176
22818	COPZ1	Hs_COPZ1_6	AGCCATCCTGATTCTGGACAA	4.50	2.89	0.0780	0.1761	12.00	3.56	0.0086	0.0383
22818	COPZ1	Hs_COPZ1_8	CCCATCGGACTGACAGTGAAA	6.00	4.69	0.1090	0.2313	9.75	3.40	0.0146	0.0522
22818	COPZ1	Hs_COPZ1_1	AGCGATTAAATGTATTGAA	0.27	0.47	0.2415	0.3716	1.49	1.86	0.7842	0.8384
1642	DDB1	Hs_DDB1_1	TCGCGATAATAAAGAACTCAA	8.75	6.90	0.1019	0.2200	6.25	1.50	0.0054	0.0286
1642	DDB1	Hs_DDB1_2	ATGCAAGATCGACTCAATAAA	22.50	10.60	0.0260	0.0769	11.25	3.30	0.0085	0.0381
1642	DDB1	Hs_DDB1_7	AAGCTCAACGTTGACAGTAAT	20.50	14.62	0.0732	0.1667	12.75	4.03	0.0102	0.0422
1642	DDB1	Hs_DDB1_6	CCACTAGATCGCGATAATAAA	17.50	2.89	0.0013	0.0176	5.00	2.83	0.0718	0.1464
9077	DIRAS3	Hs_ARHI_1	CAGAGAATCAAATGTGTTAAA	5.93	1.23	0.0163	0.0568	37.62	9.97	0.0240	0.0707
9077	DIRAS3	Hs_ARHI_2	ACAGCTTATTGACTTAATAAA	0.27	0.47	0.2415	0.3716	17.02	6.46	0.0509	0.1118
9077	DIRAS3	Hs_DIRAS3_2	TGTGCGCAAGTCGGAATATAA	0.50	1.00	0.7128	0.7929	0.50	1.00	0.2861	0.3791
9077	DIRAS3	Hs_DIRAS3_4	CAGCAAGAGTGGCGACGGCAA	2.00	0.82	0.0461	0.1159	2.00	1.83	0.4251	0.5242
1775	DNASE1L2	Hs_DNASE1L2_1	CCGGCAGATGTCTGCTCAATA	5.12	1.23	0.0230	0.0700	21.20	4.93	0.0194	0.0632
1775	DNASE1L2	Hs_DNASE1L2_2	TCCAGTGGAGGTGACCCTCAA	1.89	0.47	0.0337	0.0932	6.87	1.86	0.0317	0.0785
1775	DNASE1L2	Hs_DNASE1L2_3	CGCGCTCATGGAGCAGATCAA	1.75	1.50	0.2585	0.3937	4.00	4.32	0.2795	0.3791
1775	DNASE1L2	Hs_DNASE1L2_4	CCGCGAGCCCTGCTGGTCAA	0.00	0.00	0.0075	0.0334	0.75	0.96	0.4697	0.5514
1775	DNASE1L2	Hs_DNASE1L2_6	CACGTGATGTGCTGCTCTGTA	0.50	0.58	0.5435	0.6711	1.50	1.73	0.7193	0.7907

**Table 2 (continued). Mean  $\gamma$ H2AX foci in U2OS cells with and without aphidicolin treatment following siRNA silencing.** The data represents four cell counts from two independent transfections. The *p* value was calculated for each siRNA in comparison to the non-targeting control using an unpaired, two-tailed t-test. A False Discovery Rate (FDR) controlled *p*-value with a cut-off value of 0.05 was also calculated. NA, data is unavailable.

Entrez ID	GeneSymbol	OligoName	OligoSequence	Untreated				Aphidicolin-treated (0.1mM)			
				Mean	Std Dev	<i>p</i> value	FDR <i>p</i> value	Mean	Std Dev	<i>p</i> value	FDR <i>p</i> value
161829	EXDL1	Hs EXDL1_2	CAGAAGTTTGGTGCTGCGATA	0.50	1.00	0.7128	0.7929	0.25	0.50	0.0274	0.0707
161829	EXDL1	Hs MGC33637_1	TCAGATGATACTAGAAGACAA	4.58	0.47	0.0016	0.0195	8.36	2.88	0.0483	0.1078
161829	EXDL1	Hs EXDL1_4	CCCTGGTGGATGGTTACCTAA	2.25	1.50	0.1306	0.2579	1.50	1.29	0.6351	0.7074
55120	FANCL	Hs FANCL_5	CACTCTCAAGTTGAAGGCAAA	15.89	4.59	0.0290	0.0845	16.12	4.74	0.0315	0.0785
55120	FANCL	Hs FANCL_8	TCAGAGCTCCTTAATAAGCAT	0.50	1.00	0.7128	0.7929	1.75	0.50	0.0974	0.1797
55120	FANCL	Hs FANCL_1	CAGAATTGCATTAGGTAATAA	2.96	0.93	0.0475	0.1184	4.18	3.15	0.2371	0.3354
55120	FANCL	Hs FANCL_9	ATGCGGATACCTGCTTCAGTA	1.50	2.38	0.5530	0.6815	0.50	1.00	0.2861	0.3791
55120	FANCL	Hs FANCL_6	TAGACGTGAGTTATCCAAGTA	0.25	0.50	0.1685	0.2860	2.50	2.38	0.3415	0.4370
6468	FBXW4	Hs SHFM3_2	TGGGAAGATTGGCATTCTATA	14.01	1.68	0.0049	0.0334	8.06	0.90	0.0032	0.0244
6468	FBXW4	Hs SHFM3_1	CAGCACCTTCACTGTCAAGTA	5.93	1.23	0.0163	0.0568	11.65	3.90	0.0427	0.0971
6468	FBXW4	Hs FBXW4_1	TCCATTGCTATCAGCCCTATA	1.00	1.15	0.6484	0.7627	2.00	0.82	0.1277	0.2071
6468	FBXW4	Hs FBXW4_2	TCGCATATTGTTAGTGCAAGTA	1.00	0.82	0.5301	0.6711	2.25	1.50	0.2411	0.3395
56776	FMN2	Hs FMN2_8	CTGGACCAGGATCAACTACA	0.00	0.00	0.0075	0.0334	4.25	2.50	0.0886	0.1691
56776	FMN2	Hs FMN2_7	CTGATACTATCTCAAAGACGA	3.77	0.93	0.0256	0.0761	3.88	2.59	0.2083	0.3096
56776	FMN2	Hs FMN2_6	CCAGCGCTGTTTCAAGCCCTA	9.16	1.23	0.0061	0.0334	2.09	1.03	0.2544	0.3547
56776	FMN2	Hs FMN2_12	CACAGTCAGACCAACTCGAAA	0.25	0.50	0.1685	0.2860	1.00	0.82	0.7406	0.7948
26130	GAPVD1	Hs GAPVD1_4	ATGGATGAAATAACTCAGGAT	0.50	0.58	0.5435	0.6711	0.00	0.00	0.0044	0.0244
26130	GAPVD1	Hs DKFZP434C212_1	TTGATTGAAATTTGAACCTAAA	1.35	0.47	0.1257	0.2506	4.18	1.03	0.0306	0.0767
26130	GAPVD1	Hs DKFZP434C212_2	AAGCAATTAATTTACAAGATA	3.77	1.87	0.1030	0.2218	5.08	1.37	0.0344	0.0818
26130	GAPVD1	Hs GAPVD1_2	AAGGTTTCACTATGCTAGGCCA	0.50	0.58	0.5435	0.6711	2.50	1.73	0.2183	0.3196
26354	GNL3	Hs GNL3_8	GAGTATTGTGGTAGACATGAA	3.75	1.71	0.0365	0.0973	2.50	0.58	0.1133	0.0451
26354	GNL3	Hs GNL3_2	AAAGCTGGTACTTATAITAAA	3.77	0.93	0.0256	0.0761	1.79	0.00	0.0234	0.0707
26354	GNL3	Hs GNL3_3	CAGCATTATCAATAGCTTAAA	0.81	1.40	0.9110	0.9392	3.28	2.25	0.2424	0.3404
26354	GNL3	Hs GNL3_4	CAGCAGGTGAACAGCTCACA	0.25	0.50	0.1685	0.2860	0.50	1.00	0.2861	0.3791
51512	GTSE1	Hs GTSE1_7	CAAGTTCTAAGCGAACCAAAA	9.16	1.68	0.0121	0.0462	22.39	2.37	0.0038	0.0244
51512	GTSE1	Hs GTSE1_6	TTCCGACCCCTTTGGACATAAA	1.62	0.00	0.0036	0.0297	5.67	2.25	0.0721	0.1464
51512	GTSE1	Hs GTSE1_9	CCTCGAGATCTTTACCCTAAA	1.50	0.58	0.0642	0.1490	0.75	0.50	0.2241	0.3201
51512	GTSE1	Hs GTSE1_8	GACGGCGAGATCTCTGTCTAA	1.25	1.26	0.4531	0.6319	1.25	1.26	0.8914	0.9006
9555	H2AFY	Hs H2AFY_1	AAGGCTTTGGTTCCAGTTTAA	1.62	0.81	0.1850	0.3035	24.48	4.60	0.0125	0.0473
9555	H2AFY	Hs H2AFY_3	CAAGTTTGTGATCCACTGTAA	0.75	1.50	0.9566	0.9566	3.25	0.96	0.0176	0.0587
9555	H2AFY	Hs H2AFY_2	CTGGCTGTGGCCAAATGATGAA	8.35	1.68	0.0148	0.0533	2.39	0.52	0.0344	0.0818
9555	H2AFY	Hs H2AFY_6	ATGCTGCGGTACATCAAGAAA	0.25	0.50	0.1685	0.2860	1.75	1.71	0.5390	0.6216
57520	HECW2	Hs HECW2_2	ACGGTCTACTATCATCAGTAA	8.89	3.23	0.0478	0.1184	16.12	0.90	0.0005	0.0084
57520	HECW2	Hs HECW2_1	AAGCGGGATTTGGAAGCCAAA	5.93	0.47	0.0007	0.0139	14.63	2.74	0.0129	0.0481
57520	HECW2	Hs HECW2_4	CTCCATCACTTGAGAAAGTATA	0.50	0.58	0.5435	0.6711	0.50	1.00	0.2861	0.3791
57520	HECW2	Hs HECW2_3	CAGGATTGGTGGCCTTTTCAA	2.50	1.29	0.0670	0.1537	1.25	1.26	0.8914	0.9006
8924	HERC2	Hs HERC2_3	CCAGAGGATATTAAACAAAA	7.27	1.40	0.0136	0.0503	8.06	0.90	0.0032	0.0244
8924	HERC2	Hs HERC2_8	CAGCGACGATTCAGATAACGA	0.00	0.00	0.0075	0.0334	0.50	0.58	0.1063	0.1797
8924	HERC2	Hs HERC2_2	CGGGATGATCATGAAGAGTTA	5.12	0.93	0.0120	0.0462	0.90	0.00	0.1801	0.2717
8924	HERC2	Hs HERC2_4	CAACGTTTGGTTATTAGTAAA	0.25	0.50	0.1685	0.2860	0.75	0.96	0.4697	0.5514
221613	HIST1H2AA	Hs HIST1H2AA_2	CTGCTTCGTAAGGGGAAACTAT	4.31	0.93	0.0183	0.0612	5.37	0.90	0.0100	0.0416
221613	HIST1H2AA	Hs HIST1H2AA_1	AAGCCAAAGCAAGTAACTTA	8.35	2.47	0.0324	0.0921	12.84	3.15	0.0227	0.0707
221613	HIST1H2AA	Hs HIST1H2AA_3	CAGGCAATGGCTCTCGCGATA	1.00	1.15	0.6484	0.7627	0.25	0.50	0.0274	0.0707
221613	HIST1H2AA	Hs HIST1H2AA_5	TTAGAGTATCTCACAGCAGAA	3.00	2.16	0.1231	0.2479	3.50	2.38	0.1428	0.2235
3305	HSPA1L	Hs HSPA1L_1	CTGGATGCTGAGAAATATAAA	8.89	1.40	0.0087	0.0375	13.44	2.37	0.0115	0.0451
3305	HSPA1L	Hs HSPA1L_2	ATCAGTAAATTTGTTTCGTAAA	7.27	0.81	0.0034	0.0297	9.55	2.59	0.0291	0.0744
3305	HSPA1L	Hs HSPA1L_6	CTCTTCGATGGTATTGACTAA	0.50	0.58	0.5435	0.6711	2.75	2.06	0.2195	0.3201
3305	HSPA1L	Hs HSPA1L_8	AAAGAATGCCTTAGAATCCTA	0.00	0.00	0.0075	0.0334	1.25	0.96	0.8597	0.8822
3306	HSPA2	Hs HSPA2_3	TAGAAGCTTGGAACAGTAAA	0.81	0.81	0.8485	0.9231	6.27	0.00	0.0001	0.0024
3306	HSPA2	Hs HSPA2_7	ACAGTCGAGTCGGATATGAAA	0.75	0.96	0.9328	0.9392	2.25	0.50	0.0137	0.0501
3306	HSPA2	Hs HSPA2_2	ATGCATAAATGCAAATGATAA	2.69	0.47	0.0093	0.0388	4.78	1.86	0.0754	0.1517
3306	HSPA2	Hs HSPA2_8	CCCGTTGTGCTGGGACATCGA	0.00	0.00	0.0075	0.0334	0.75	0.50	0.2241	0.3201
3576	IL8	Hs IL8_9	CAAGGAGTGCTAAAGCACTTA	1.00	1.41	0.7070	0.7929	0.00	0.00	0.0044	0.0244
3576	IL8	Hs IL8_5	AAGAGGGCTGAGAATTCATAA	6.19	1.87	0.0353	0.0946	6.57	1.03	0.0087	0.0384
3576	IL8	Hs IL8_6	ATCAGTGAAGATGCCAGTGAA	13.20	3.27	0.0217	0.0683	33.44	5.96	0.0111	0.0451
3576	IL8	Hs IL8_4	AACAATTGGGTACCCAGTTAA	1.25	1.50	0.5224	0.6711	0.75	1.50	0.6307	0.7074
3659	IRF1	Hs IRF1_1	CAGCCGAGATGCTAAGAGCAA	42.02	2.14	0.0008	0.0148	11.05	1.03	0.0023	0.0219
3659	IRF1	Hs IRF1_4	CTGGCTAGAGATGCAGATTA	0.00	0.00	0.0075	0.0334	0.00	0.00	0.0044	0.0244
3659	IRF1	Hs IRF1_2	AGCGCCTTGGTATGACTTAAA	12.12	3.70	0.0330	0.0932	9.85	1.55	0.0090	0.0386
3659	IRF1	Hs IRF1_5	CAAGCATGGCTGGGACATCAA	3.00	1.83	0.0857	0.1898	2.50	2.38	0.3415	0.4370
51438	MAGEC2	Hs MAGEC2_2	TAGCTTCAGAGTGTAAATTTA	1.35	1.68	0.5776	0.7060	8.66	1.37	0.0090	0.0386
51438	MAGEC2	Hs MAGEC2_1	CAGGGTAGTGTGGTATTGTAA	2.69	2.60	0.3159	0.4588	3.58	0.90	0.0341	0.0818
51438	MAGEC2	Hs MAGEC2_5	AACAGGGCAGTTTAGGTTCTA	0.50	1.00	0.7128	0.7929	3.50	3.11	0.2286	0.3249
51438	MAGEC2	Hs MAGEC2_7	CCGACCTCAGTTGAGTTAGA	0.25	0.50	0.1685	0.2860	1.50	1.29	0.6351	0.7074
23389	MED13L	Hs THRAP2_6	CAGCCTATTGATACCACCTAA	5.93	2.47	0.0663	0.1527	4.48	0.90	0.0171	0.0584
23389	MED13L	Hs THRAP2_5	ATGGCTTAAATGGGACGCTAA	9.16	2.03	0.0181	0.0609	13.44	4.48	0.0412	0.0941

**Table 2 (continued). Mean  $\gamma$ H2AX foci in U2OS cells with and without aphidicolin treatment following siRNA silencing.** The data represents four cell counts from two independent transfections. The *p* value was calculated for each siRNA in comparison to the non-targeting control using an unpaired, two-tailed t-test. A False Discovery Rate (FDR) controlled *p*-value with a cut-off value of 0.05 was also calculated. NA, data is unavailable.

Entrez ID	GeneSymbol	OligoName	OligoSequence	Untreated				Aphidicolin-treated (0.1mM)			
				Mean	Std Dev	<i>p</i> value	FDR <i>p</i> value	Mean	Std Dev	<i>p</i> value	FDR <i>p</i> value
284382	MGC33407	Hs_MGC33407_5	TGGACCTAGTGGAGAACATTA	1.50	1.73	0.4279	0.6037	1.50	1.00	0.5488	0.6317
9221	NOLC1	Hs_NOLC1_8	CACCAAGAATTCTTCAAATAA	4.04	2.14	0.1129	0.2343	12.84	2.25	0.0114	0.0451
9221	NOLC1	Hs_NOLC1_9	AAGGTGGATTCCACAGATAA	0.50	1.00	0.7128	0.7929	2.25	0.50	0.0137	0.0501
9221	NOLC1	Hs_NOLC1_7	CAGGTCAATTCTATTAAGTTT	4.04	0.81	0.0151	0.0533	20.30	8.13	0.0550	0.1187
9221	NOLC1	Hs_NOLC1_6	CTGGCGGATAACCAACTCTCA	1.00	0.82	0.5301	0.6711	1.25	1.50	0.9082	0.9098
	NON-TARGETING		ATGAACGTGAATTGCTCAA	0.46	0.68			0.70	0.88		
4897	NRCAM	Hs_NRCAM_7	ATACCCGTGTATGTTATGAAA	1.75	0.50	0.0178	0.0603	0.25	0.50	0.0274	0.0707
4897	NRCAM	Hs_NRCAM_5	AGCCGGCTGAAGGAACGAAA	0.81	0.81	0.8485	0.9231	2.39	0.50	0.0344	0.0818
4897	NRCAM	Hs_NRCAM_8	CTCCGTAGGCTTCTTAATCTT	0.75	0.96	0.9328	0.9392	1.75	0.96	0.3080	0.4062
4897	NRCAM	Hs_NRCAM_6	AGCCTAGTTGACTATGGAGAA	7.27	1.40	0.0136	0.0503	1.79	0.90	0.3432	0.4370
9381	OTOF	Hs_OTOF_2	CCGGTACAAGTGCTCATCAT	15.35	2.91	0.0127	0.0479	17.02	2.69	0.0089	0.0386
9381	OTOF	Hs_OTOF_1	CAGGATTGAAGCTTATGTA	1.35	1.68	0.5776	0.7060	9.55	2.25	0.0220	0.0694
9381	OTOF	Hs_OTOF_4	AAGGAGCAACTTCGACAACAA	0.25	0.50	0.1685	0.2860	0.75	0.96	0.4697	0.5514
9381	OTOF	Hs_OTOF_3	TCCGCCATCATTTGTCATTGA	1.00	1.41	0.7070	0.7929	1.00	0.82	0.7406	0.7948
80301	PLEKHO2	Hs_pp9099_2	AACAAGGCTAGCGACATCAA	5.39	0.47	0.0010	0.0160	17.02	1.55	0.0026	0.0228
80301	PLEKHO2	Hs_PLEKHQ1_2	ACCAACGAGAGTCCACCTGAA	0.25	0.50	0.1685	0.2860	0.00	0.00	0.0044	0.0244
80301	PLEKHO2	Hs_pp9099_3	GACGGAGAACTGTGAACAA	4.58	1.23	0.0298	0.0859	2.39	0.52	0.0344	0.0818
80301	PLEKHO2	Hs_PLEKHQ1_1	AACAAGGCTTTCGATGAGGTA	0.50	1.00	0.7128	0.7929	0.75	1.50	0.6307	0.7074
5422	POLA1	Hs_POLA_3	CTGCATGAAAGCTACACTCA	72.50	6.56	0.0002	0.0061	76.25	3.40	0.0000	0.0023
5422	POLA1	Hs_POLA_4	CTGGAGAACTTACTACCGAT	46.25	7.41	0.0012	0.0165	64.75	5.50	0.0002	0.0046
5422	POLA1	Hs_POLA_1	CAGGTGAGAGTACAGAAGAA	35.96	1.71	0.0209	0.0659	63.00	6.36	0.0035	0.0244
5422	POLA1	Hs_POLA_2	CAGGATCTTAACATGACATTA	36.90	6.17	0.0095	0.0392	54.64	7.00	0.0056	0.0291
5423	POLB	Hs_POLB_7	TACGAGTTCATCCATCAATTT	5.12	0.47	0.0012	0.0165	4.78	0.52	0.0017	0.0180
5423	POLB	Hs_POLB_2	CCGGAGCGAATGAGCGCTGTA	4.85	1.40	0.0340	0.0932	3.88	0.52	0.0039	0.0244
5423	POLB	Hs_POLB_8	CAGGTTGATACCCAAAGATCA	0.75	0.50	0.8779	0.9378	0.00	0.00	0.0044	0.0244
5423	POLB	Hs_POLB_9	CAGGTTGTGGAGCAGTTACAA	0.00	0.00	0.0075	0.0334	1.00	0.82	0.7406	0.7948
5424	POLD1	Hs_POLD1_3	CAGTTGGAGATGACCAITAT	11.00	8.16	0.0860	0.1898	12.75	2.87	0.0037	0.0244
5424	POLD1	Hs_POLD1_5	CCGAGAGAGCATGTTTGGGTA	4.58	0.47	0.0016	0.0195	47.18	7.18	0.0080	0.0362
5424	POLD1	Hs_POLD1_2	CGGGACCAGGAGAAATTAATA	2.69	1.68	0.1758	0.2934	36.13	9.87	0.0255	0.0707
5424	POLD1	Hs_POLD1_6	CTGGTCCACCTTCATCCGTAT	1.75	1.71	0.3093	0.4503	2.00	0.82	0.1277	0.2071
5426	POLE	Hs_POLE_7	ACAGATCGGAATATCCGGAA	11.50	6.76	0.0495	0.1219	62.00	4.32	0.0001	0.0034
5426	POLE	Hs_POLE_2	CCGCATCATCCTCTGTATCAA	22.62	1.62	0.0016	0.0195	56.43	4.10	0.0018	0.0185
5426	POLE	Hs_POLE_3	CTGGATGGATCCATCTAATA	1.62	0.00	0.0036	0.0297	20.60	2.37	0.0045	0.0246
5426	POLE	Hs_POLE_6	AACCGTATTTCTACATTCGGA	19.75	14.52	0.0788	0.1773	57.75	17.35	0.0073	0.0349
5427	POLE2	Hs_POLE2_1	CAGTCTGTTGATGAAACTATA	0.81	0.00	0.4159	0.5889	38.82	3.39	0.0026	0.0228
5427	POLE2	Hs_POLE2_4	CCCGATCTACTTGTCAATTGCA	12.25	12.04	0.1509	0.2860	13.25	2.99	0.0037	0.0244
5427	POLE2	Hs_POLE2_2	CCGTGAAGACTTGGATAATAA	5.39	1.23	0.0204	0.0653	25.08	6.21	0.0215	0.0687
5427	POLE2	Hs_POLE2_5	CCCAAGTATTTGGACATATGA	2.75	2.36	0.1818	0.2999	1.00	0.00	0.3746	0.4729
54776	PPP1R12C	Hs_PPP1R12C_7	CGGAGGCTTTAGGACCGTCTA	1.00	0.82	0.5301	0.6711	4.25	0.50	0.0001	0.0041
54776	PPP1R12C	Hs_PPP1R12C_5	CAGGAGGACCTTCGGAACCAA	10.50	3.23	0.0340	0.0932	12.84	1.37	0.0035	0.0244
54776	PPP1R12C	Hs_PPP1R12C_2	CAGCGGACCTCAACCCAGAA	0.00	0.00	0.0075	0.0334	8.36	6.10	0.1771	0.2686
54776	PPP1R12C	Hs_PPP1R12C_4	TTGGAGGAACCTGGCCCGAAA	0.50	1.00	0.7128	0.7929	1.75	1.71	0.5390	0.6216
5518	PPP2R1A	Hs_PPP2R1A_5	CTGGTGTCCGATGCCAACCAA	NA	NA	NA	NA	10.15	1.37	0.0061	0.0306
5518	PPP2R1A	Hs_PPP2R1A_7	GACCAGGATGTGGACGTCAAA	0.50	1.00	0.7128	0.7929	0.25	0.50	0.0274	0.0707
5518	PPP2R1A	Hs_PPP2R1A_6	ACGGCTGAACATCATCTCTAA	9.16	1.23	0.0061	0.0334	10.15	3.62	0.0493	0.1096
5518	PPP2R1A	Hs_PPP2R1A_1	TCCCATCTTGGGCAAGACAA	0.75	0.96	0.9328	0.9392	1.00	1.41	0.8431	0.8728
5557	PRIM1	Hs_PRIM1_2	AAGGGTGGTCAAGACGTTAAA	12.12	2.14	0.0110	0.0436	58.52	7.83	0.0061	0.0306
5557	PRIM1	Hs_PRIM1_3	CTGGGATAGTTGAGTATTGTA	4.58	0.47	0.0016	0.0195	51.95	7.96	0.0080	0.0363
5557	PRIM1	Hs_PRIM1_4	AGCCTTGTAAGGGTGGTCAA	2.25	3.20	0.4061	0.5771	3.00	1.63	0.1071	0.1797
5557	PRIM1	Hs_PRIM1_5	CTGAATCTGATGTCAAACATA	3.25	1.26	0.0254	0.0761	1.50	1.91	0.7442	0.7972
5714	PSMD8	Hs_PSMD8_3	CTGCAGGGTTTCGCCAATAA	13.50	3.87	0.0070	0.0334	25.25	10.08	0.0173	0.0587
5714	PSMD8	Hs_PSMD8_2	AAGGGCGAGTGAACCCGTAAA	10.77	1.87	0.0107	0.0428	20.30	4.93	0.0212	0.0679
5714	PSMD8	Hs_PSMD8_5	CAGCTGGAGATGATCGTCTGA	6.25	2.87	0.0303	0.0870	3.50	2.52	0.1588	0.2446
5714	PSMD8	Hs_PSMD8_1	TCCAACCTGACATGTTCAATA	3.23	1.40	0.0863	0.1898	2.69	1.79	0.2754	0.3791
5929	RBBP5	Hs_RBBP5_1	CAGGTGTCTCTCAACAGCTA	14.54	3.70	0.0228	0.0700	10.45	1.37	0.0057	0.0295
5929	RBBP5	Hs_RBBP5_3	ACGGCAGATCGAATAATCAGA	5.93	1.23	0.0163	0.0568	12.24	3.15	0.0251	0.0707
5929	RBBP5	Hs_RBBP5_6	AAGATTCTCCATTAAACCGCA	1.50	1.29	0.3074	0.4503	0.25	0.50	0.0274	0.0707
5929	RBBP5	Hs_RBBP5_7	TGGAGCCGAGATGGTCATAAA	0.50	1.00	0.7128	0.7929	1.25	0.96	0.8597	0.8822
5937	RBMS1	Hs_RBMS1_7	CTGGTGAAGCTCTGTCAACCA	2.00	2.00	0.2865	0.4320	0.25	0.50	0.0274	0.0707
5937	RBMS1	Hs_RBMS1_2	CTGGTCTATTATGCTTGTATA	16.43	2.60	0.0087	0.0375	8.06	2.37	0.0357	0.0839
5937	RBMS1	Hs_RBMS1_1	AACGAACAAATGCAAAAGGTTA	8.35	2.03	0.0220	0.0684	13.44	6.27	0.0767	0.1537
5937	RBMS1	Hs_RBMS1_5	TACGTGATTCAGTGGTACAA	0.50	0.58	0.5435	0.6711	0.75	0.96	0.4697	0.5514
5937	RBMS1	Hs_RBMS1_4	ACCTTTCAACCTAATAAGTAA	0.75	0.50	0.8779	0.9378	1.50	1.29	0.6351	0.7074
23186	RCOR1	Hs_RCOR1_8	ATCAGATGTAATTTGGTATA	0.50	0.58	0.5435	0.6711	0.00	0.00	0.0044	0.0244
23186	RCOR1	Hs_RCOR1_3	AACGACAGATCCAGAATATTA	0.00	0.00	0.0075	0.0334	5.67	1.37	0.0258	0.0707
23186	RCOR1	Hs_RCOR1_1	CCCAATAATGGCCAGAATAAA	2.15	1.23	0.1763	0.2934	9.55	2.74	0.0326	0.0801

**Table 2 (continued). Mean  $\gamma$ H2AX foci in U2OS cells with and without aphidicolin treatment following siRNA silencing.** The data represents four cell counts from two independent transfections. The *p* value was calculated for each siRNA in comparison to the non-targeting control using an unpaired, two-tailed *t*-test. A False Discovery Rate (FDR) controlled *p*-value with a cut-off value of 0.05 was also calculated. NA, data is unavailable.

Entrez ID	GeneSymbol	OligoName	OligoSequence	Untreated				Aphidicolin-treated (0.1mM)			
				Mean	Std Dev	<i>p</i> value	FDR <i>p</i> value	Mean	Std Dev	<i>p</i> value	FDR <i>p</i> value
117584	RFFL	Hs_RFFL_1	ATCGGTTTCTCAGTGCCTTA	3.23	1.62	0.1117	0.2343	9.26	1.03	0.0036	0.0244
117584	RFFL	Hs_RFFL_3	TCGCAACTTTGTCAACTACAA	1.89	1.23	0.2378	0.3716	17.02	3.90	0.0192	0.0631
117584	RFFL	Hs_RFFL_4	CCGGCTATACAAGGATCAGAA	2.00	1.83	0.2514	0.3849	1.75	0.50	0.0974	0.1797
117584	RFFL	Hs_RFFL_5	CTCCATGACATCTTACCAGAA	0.25	0.50	0.1685	0.2860	0.50	0.58	0.1063	0.1797
6117	RPA1	Hs_RPA1CONTROL	AACACTCTATCTCTTTCATG	63.30	8.09	0.0000	0.0008	73.03	7.74	0.0000	0.0001
6117	RPA1	Hs_RPA1_5	CAGGAATTATGTCGTAAGTCA	72.50	6.45	0.0002	0.0061	74.00	4.97	0.0001	0.0032
6117	RPA1	Hs_RPA1_6	CCGTGTGACAGTCCCATGTTA	74.50	2.65	0.0000	0.0011	78.75	5.91	0.0001	0.0036
6117	RPA1	Hs_RPA1_3	ACCGCATGATCCTGTCAGTAA	70.00	2.16	0.0000	0.0008	65.00	8.16	0.0006	0.0084
6117	RPA1	Hs_RPA1_2	GAGGTGCTACATAGTTGGTAA	59.50	9.33	0.0011	0.0165	68.75	9.18	0.0007	0.0093
6118	RPA2	Hs_RPA2_5	AACAGTGGATTGCGAAAGCTAT	36.00	8.52	0.0037	0.0299	65.50	8.85	0.0007	0.0093
6118	RPA2	Hs_RPA2_1	TACCAGGAGAGTACTTACATA	11.00	4.08	0.0149	0.0533	29.75	4.79	0.0012	0.0144
6118	RPA2	Hs_RPA2_3	CCAGGTGTTGAATTTGATTAA	22.25	13.67	0.0512	0.1246	45.25	11.32	0.0044	0.0244
6118	RPA2	Hs_RPA2_4	AAGGCTTGTCGAAGCTGAA	16.25	8.46	0.0348	0.0941	16.50	5.69	0.0123	0.0473
6240	RRM1	Hs_RRM1_6	CAGCTACATTGCTGGGACTAA	86.50	3.51	0.0000	0.0014	81.75	4.35	0.0000	0.0024
6240	RRM1	Hs_RRM1_1	AACGGATATATTGAAATCAA	53.06	2.03	0.0005	0.0109	73.15	5.96	0.0022	0.0219
6240	RRM1	Hs_RRM1_5	ATCGCCTGAATTCGCTATTA	56.29	4.59	0.0022	0.0237	54.04	4.51	0.0023	0.0219
6240	RRM1	Hs_RRM1_7	CAGGGCCATACGAAACCTAT	4.75	4.92	0.1990	0.3247	2.00	1.41	0.3204	0.4198
6282	S100A11	Hs_S100A11_1	CTGCCAATAGTAATAAAGCAA	6.19	2.47	0.0605	0.1442	7.76	0.52	0.0003	0.0056
6282	S100A11	Hs_S100A11_6	CAGAACTAGCTGCCTCACAA	9.00	4.55	0.0353	0.0946	19.50	2.65	0.0007	0.0093
6282	S100A11	Hs_S100A11_3	ACCAACAGTGATGGTCAGCTA	1.89	0.47	0.0337	0.0932	4.78	3.62	0.2247	0.3202
6282	S100A11	Hs_S100A11_8	CCACCTGCCAATAGTAATAAA	0.75	0.96	0.9328	0.9392	2.00	1.15	0.2412	0.3395
23256	SCFD1	Hs_SCFD1_1	CAGAATCTTGTGACTACATA	4.85	0.81	0.0094	0.0392	11.05	1.37	0.0050	0.0268
23256	SCFD1	Hs_SCFD1_3	CTGGAAGATATTGCAAAATGCA	8.62	2.03	0.0206	0.0653	3.28	0.52	0.0078	0.0359
23256	SCFD1	Hs_SCFD1_8	CACGATGTACTGGATTCCAT	4.00	1.41	0.0174	0.0597	3.75	2.36	0.1147	0.1907
23256	SCFD1	Hs_SCFD1_7	CTGATGCAGGATGCAACCTTA	1.00	0.82	0.5301	0.6711	2.50	1.91	0.2552	0.3550
4735	SEPT2	Hs_SEPT2_2	GAGATATATCTTATACTTAA	2.15	0.47	0.0205	0.0653	8.36	0.52	0.0002	0.0052
4735	SEPT2	Hs_SEPT2_3	ACCCAGGACCTTCATTATGAA	1.89	0.93	0.1551	0.2860	3.88	1.37	0.0699	0.1435
4735	SEPT2	Hs_SEPT2_7	ATAGTTAATGAAGGTGTGCTA	2.25	0.96	0.0450	0.1159	1.75	1.71	0.5390	0.6216
4735	SEPT2	Hs_SEPT2_8	AAGAATCGGCATGTATCTTA	2.00	0.82	0.0461	0.1159	1.00	0.82	0.7406	0.7948
83852	SETDB2	Hs_SETDB2_2	CCAGTGATATTCGCAACTCAA	8.35	1.68	0.0148	0.0533	10.45	1.03	0.0026	0.0230
83852	SETDB2	Hs_SETDB2_4	CCGAGAGCATCTGAACTCTAA	1.00	0.82	0.5301	0.6711	0.25	0.50	0.0274	0.0707
83852	SETDB2	Hs_SETDB2_3	TACCAGGTTTAGAATGGTATA	1.08	0.93	0.5637	0.6918	3.58	0.90	0.0341	0.0818
83852	SETDB2	Hs_SETDB2_5	TCGGCCGCTTCCTTAACTATA	1.25	1.50	0.5224	0.6711	0.75	1.50	0.6307	0.7074
50485	SMARCAL1	Hs_SMARCAL1_1	CAGCTTGCACCTTCTTAGCAA	17.24	6.12	0.0426	0.1120	14.63	5.17	0.0454	0.1022
50485	SMARCAL1	Hs_SMARCAL1_3	TTGAGTTATGAGTTAGGTCAA	4.31	1.23	0.0344	0.0932	11.35	4.51	0.0590	0.1265
50485	SMARCAL1	Hs_SMARCAL1_4	CAGAACAGCATCAGAGGACTA	0.75	0.96	0.9328	0.9392	2.75	1.26	0.0818	0.1617
50485	SMARCAL1	Hs_SMARCAL1_5	TTGATTGGTACAATTGCGGAA	0.50	1.00	0.7128	0.7929	0.75	0.50	0.2241	0.3201
23626	SPO11	Hs_SPO11_1	CAGAGTGACTTACCTAACAA	18.31	1.68	0.0027	0.0271	43.59	3.73	0.0025	0.0226
23626	SPO11	Hs_SPO11_2	ACAACCTAATGTAAACGCATA	0.00	0.00	0.0075	0.0334	4.78	1.37	0.0403	0.0924
23626	SPO11	Hs_SPO11_4	TACCTTCTACGATAACAATA	0.00	0.00	0.0075	0.0334	0.50	0.58	0.1063	0.1797
23626	SPO11	Hs_SPO11_6	TTGCATCATGATTACGGGAAA	1.00	2.00	0.7883	0.8720	0.75	0.96	0.4697	0.5514
258010	SVIP	Hs_DKFZp313A2432_2	GAGGCTGCAGAGAGAAGACAA	0.00	0.00	0.0075	0.0334	7.46	1.37	0.0130	0.0481
258010	SVIP	Hs_DKFZp313A2432_4	TTAGATGTTCAATCTGTGCAA	0.75	0.96	0.9328	0.9392	3.50	1.29	0.0326	0.0801
258010	SVIP	Hs_DKFZp313A2432_1	ATGGACATGAACCTTTGAATTT	0.54	0.47	0.6109	0.7316	3.58	0.90	0.0341	0.0818
258010	SVIP	Hs_SVIP_3	CACGCCGACCTGGAAGAGAA	5.00	4.55	0.1552	0.2860	3.00	1.15	0.0453	0.1022
50945	TBX22	Hs_TBX22_8	GCCGGTGGATCCAAACGCTA	0.75	0.50	0.8779	0.9378	0.00	0.00	0.0044	0.0244
50945	TBX22	Hs_TBX22_1	CTGGAAGAGAAAGATATCTAA	10.77	0.93	0.0021	0.0226	8.66	2.25	0.0275	0.0707
50945	TBX22	Hs_TBX22_2	ATGGATGTAATCTCATGAAA	2.96	0.47	0.0067	0.0334	5.08	1.86	0.0652	0.1367
50945	TBX22	Hs_TBX22_7	TTCATTGGTATCCAGCAATTA	1.00	0.82	0.5301	0.6711	1.75	2.06	0.6062	0.6909
221400	TDRD6	Hs_TDRD6_3	TTGAATAAAGTTTATCTTAA	1.89	0.47	0.0337	0.0932	5.08	0.52	0.0013	0.0148
221400	TDRD6	Hs_TDRD6_8	CTTGACCTTGTAAATGCAATA	0.00	0.00	0.0075	0.0334	0.25	0.50	0.0274	0.0707
221400	TDRD6	Hs_TDRD6_1	AACACTGATTATAGAACTATA	3.77	0.47	0.0030	0.0295	8.96	3.90	0.0737	0.1491
221400	TDRD6	Hs_TDRD6_7	TAGGGTACAAGTTACCTAATA	3.25	0.96	0.0109	0.0434	2.50	1.73	0.2183	0.3196
7398	USP1	Hs_USP1_6	ATGTGGCAGAATTACCTACTA	19.66	2.03	0.0036	0.0297	8.36	0.52	0.0002	0.0052
7398	USP1	Hs_USP1_5	AGCAGATTATGAGCTATACAA	12.12	2.80	0.0191	0.0630	5.67	1.37	0.0258	0.0707
7398	USP1	Hs_USP1_9	CTGGGACCCATGAATCTGATA	1.75	0.96	0.1148	0.2343	5.50	4.36	0.1400	0.2215
7398	USP1	Hs_USP1_10	ACAGGCATTAATATTAGTGGGA	4.25	3.30	0.1210	0.2452	2.25	1.89	0.3324	0.4336
8237	USP11	Hs_USP11_6	ACCGATTCTATTGGCCTAGTA	8.62	0.93	0.0034	0.0297	9.55	1.86	0.0147	0.0522
8237	USP11	Hs_USP11_5	CTGCGTCGGGTACGTGATGAA	23.97	2.03	0.0024	0.0242	11.65	2.37	0.0157	0.0550
8237	USP11	Hs_USP11_3	AAGGTGCAAGTGTACCAGTA	3.00	3.16	0.2427	0.3725	3.00	1.63	0.1071	0.1797
8237	USP11	Hs_USP11_4	CCCATTTGAACGTAAGTGCATA	1.00	0.82	0.5301	0.6711	1.25	1.50	0.9082	0.9098
151525	WDSUB1	Hs_WDSAM1_1	TCCATTGAAGTTTACATACCTA	2.42	1.40	0.1651	0.2860	4.48	0.00	0.0002	0.0050
151525	WDSUB1	Hs_WDSAM1_3	TCGCATCAGATGGCTATTTCAT	11.31	4.28	0.0499	0.1224	17.02	2.37	0.0068	0.0334
151525	WDSUB1	Hs_WDSUB1_1	TCGCCTGTACTCGTTACGTGA	1.00	1.15	0.6484	0.7627	3.75	2.50	0.1288	0.2082
151525	WDSUB1	Hs_WDSAM1_4	AACATCAGCTGAAGCAATTTA	0.50	1.00	0.7128	0.7929	0.75	0.96	0.4697	0.5514
7465	WEE1	Hs_WEE1_3	CAGGGTAGATTACCTCGGATA	31.25	5.12	0.0013	0.0173	55.00	4.24	0.0001	0.0037

**Table 2 (continued). Mean  $\gamma$ H2AX foci in U2OS cells with and without aphidicolin treatment following siRNA silencing.** The data represents four cell counts from two independent transfections. The  $p$  value was calculated for each siRNA in comparison to the non-targeting control using an unpaired, two-tailed t-test. A False Discovery Rate (FDR) controlled  $p$ -value with a cut-off value of 0.05 was also calculated. NA, data is unavailable.

Entrez ID	GeneSymbol	OligoName	OligoSequence	Untreated				Aphidicolin-treated (0.1mM)			
				Mean	Std Dev	$p$ value	FDR $p$ value	Mean	Std Dev	$p$ value	FDR $p$ value
7486	WRN	Hs_WRN_7	CCACGGAGGGTTTCTATCTTA	8.89	0.81	0.0021	0.0229	3.58	2.37	0.2168	0.3196
7486	WRN	Hs_WRN_8	CTACGTGACITTTGATATCAAA	4.00	1.41	0.0174	0.0597	1.75	1.26	0.4189	0.5196
56897	WRNIP1	Hs_WRNIP1_1	CGCCATGTTTCATAGAGGATAA	2.69	0.47	0.0093	0.0388	7.76	0.52	0.0003	0.0056
56897	WRNIP1	Hs_WRNIP1_5	ATGAATTAATGTTATAAGGAA	5.39	0.47	0.0010	0.0160	21.20	5.96	0.0281	0.0720
56897	WRNIP1	Hs_WRNIP1_9	TGCAGCGTATTGCTTATGAA	1.00	0.82	0.5301	0.6711	1.75	1.26	0.4189	0.5196
56897	WRNIP1	Hs_WRNIP1_8	GAGGCGCAGTCTTTCGAATA	1.25	1.50	0.5224	0.6711	1.50	1.73	0.7193	0.7907
56949	XAB2	Hs_XAB2_6	CCGCGTGTACAAGTCACTGAA	28.28	4.91	0.0103	0.0421	9.55	1.37	0.0071	0.0342
56949	XAB2	Hs_XAB2_3	CAGCTACGTTTGATACATCAAA	2.50	1.00	0.0340	0.0932	0.25	0.50	0.0274	0.0707
56949	XAB2	Hs_XAB2_5	CACGTACAACACGCAGGTCAA	6.06	1.71	0.1393	0.2712	9.26	3.39	0.0530	0.1148
56949	XAB2	Hs_XAB2_7	CCGGCATGCCATGGCCGTGTA	1.00	1.15	0.6484	0.7627	0.75	0.50	0.2241	0.3201
7507	XPA	Hs_XPA_5	AGGGAGACGATTGTTTCATCAA	6.46	3.23	0.0904	0.1974	6.27	0.00	0.0001	0.0024
7507	XPA	Hs_XPA_6	CTGCAGAGATGCTGATGATAA	7.54	1.68	0.0186	0.0616	9.55	3.15	0.0429	0.0972
7507	XPA	Hs_XPA_3	TTGAGTTGTACGAGTCTGAAA	1.75	2.22	0.4164	0.5889	0.75	0.96	0.4697	0.5514
7507	XPA	Hs_XPA_8	TGGGAGCTGAGTCTAGAGTA	2.25	0.96	0.0450	0.1159	0.75	0.96	0.4697	0.5514
7709	ZBTB17	Hs_ZBTB17_2	CCGCCTCATCAGCCTGTGAA	2.69	1.68	0.1758	0.2934	6.27	0.00	0.0001	0.0024
7709	ZBTB17	Hs_ZBTB17_1	CCCTTCTGACTGTTTATTTAA	12.39	3.64	0.0306	0.0875	3.88	1.37	0.0699	0.1435
7709	ZBTB17	Hs_ZBTB17_8	TGGCTTCAACCCGGTAGACAA	1.75	0.50	0.0178	0.0603	2.75	1.71	0.1577	0.2436
7709	ZBTB17	Hs_ZBTB17_6	CACCACCTCAGGAACCTGAA	1.00	1.41	0.7070	0.7929	1.25	1.50	0.9082	0.9098



<b>Table 3. Genes with genome maintenance defects and tumor suppressor phenotypes.</b>					
Entrez ID	Gene Name	Gene Symbol	chromosome location	Cancer Types	Example references
83990	BRCA1 interacting protein C-terminal helicase 1	BRIP1	17q22-q24	breast	PMID: 11301010
150274	CHK2 checkpoint homolog ( <i>S. pombe</i> )	CHK2	22q12.1	breast	PMID: 16998506
152330	contactin 4	CNTN4	3p26-p25	colon	PMID: 17932254
9077	DIRAS family, GTP-binding RAS-like 3	DIRAS3	1p31	breast, ovarian, oligodendroglial	PMID: 9874798
2074	excision repair cross-complementing rodent repair deficiency, complementation group 6	ERCC6	8p23	colon, lung	PMID: 17932254, PMID: 17854076
55120	Fanconi anemia, complementation group L	FANCL	2p16.1	leukemia, head and neck	PMID: 16998502
3659	interferon regulatory factor 1	IRF1	5q31.1	breast, leukemia, gastric	PMID: 8438156, PMID: 11846974
284382	hypothetical protein MGC33407	MGC33407	19p13.2	colon	PMID: 16959974
4897	neuronal cell adhesion molecule	NRCAM	7q31.1-q31.2	breast	PMID: 16959974
9381	otoferlin	OTOF	2p23.1	breast	PMID: 17932254
5423	polymerase (DNA directed), beta	POLB	8p11.2	bladder	PMID: 17203305
5424	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	POLD1	19q13.3	several in mice, not clear for humans	PMID: 17785453
5518	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	PPP2R1A	19q13.33	breast, lung and skin	PMID: 10713707
6282	S100 calcium binding protein A11	S100A11	1q21	bladder and renal	PMID: 17566693
221400	tudor domain containing 6	TDRD6	6p12.3	breast	PMID: 17932254
7486	Werner syndrome	WRN	8p12-p11.2	muscle, connective tissue, mesenchymal tumors	PMID: 18006573
7507	xeroderma pigmentosum, complementation group A	XPA	9q22.3	skin	PMID: 16069818

**Table 4. Sensitivity to hydroxyurea following siRNA silencing in U2OS cells.** HU sensitivity was determined by calculating the viability ratio (treated/untreated) and the sensitivity index (SI) for each siRNA. P values were determined by comparison to the non-targeting control using an unpaired, two-tailed t-test. Values highlighted in pink were sensitive ( $p < 0.05$ ) to HU treatment (dark pink =  $\text{Log}_2 < -0.3$  or  $\text{SI} > 0.1$ , light pink =  $\text{Log}_2$  between  $-0.1$  and  $-0.3$  or  $\text{SI}$  between  $0$  and  $0.1$ ). Those highlighted in blue were resistant ( $p < 0.05$ ) to HU treatment (dark blue =  $\text{Log}_2 > 0.3$  or  $\text{SI} < -0.1$ , light blue =  $\text{Log}_2$  between  $0.1$  and  $0.3$  or  $\text{SI}$  between  $0$  and  $-0.1$ ). Gene symbols highlighted in dark pink had 2 or more siRNAs that were sensitive to HU treatment in both statistical tests; those highlighted in light pink had 2 or more siRNAs that were sensitive by a single statistical test. Gene symbols highlighted in dark blue had 2 or more siRNAs that were resistant to HU treatment in both statistical tests; those highlighted in light blue had 2 or more siRNAs that were resistant by a single statistical test.

Entrez ID	Gene Symbol	Oligo Name	Oligo sequence	HU Sensitivity			
				Mean $\text{Log}_2$ Ratio	p Value $\text{Log}_2$ Ratio	Mean SI	p Value SI
29882	ANAPC2	Hs ANAPC2_5	AAGGTTCTTCTACCGCATCTA	-0.085596173	0.840772005	-0.0475827	0.99852282
29882	ANAPC2	Hs ANAPC2_6	CTCACTGGATCGTATCTACAA	0.710214039	0.470888073	-0.0220619	0.65329857
29882	ANAPC2	Hs ANAPC2_1	GAGAGTCTATATGCAGAGTAA	0.011476764	0.891186732	0.01479705	0.590092
29882	ANAPC2	Hs ANAPC2_3	CAGCGGTGTCAGTCCCAGCCAAA	-0.531058969	0.00030347	0.08218847	0.00530934
51433	ANAPC5	Hs ANAPC5_4	AGCGGTTGATTACCAAGCTCA	0.213994514	0.155565405	-0.0453513	0.21340279
51433	ANAPC5	Hs ANAPC5_3	CGCATTATCTCAGCTACTTAA	0.347108868	0.054773003	-0.024952	0.58309821
51433	ANAPC5	Hs ANAPC5_6	ACCCTTGATAAACCATCTCTA	-0.180864244	0.299058082	0.02540368	0.45461079
51433	ANAPC5	Hs ANAPC5_7	CAGAATCAAACTGGTCTGA	-0.259758939	0.147344845	0.03237586	0.14630324
545	ATR		AACCTCCGTGATGTTGCTTGA	-2.7430198	1.82697E-05	0.38916	0.00064363
84126	ATRP		AAGGTCCACAGATTATAGTA	-1.0378538	0.003948926	0.20095	0.00563251
648	BMI1	Hs BMI1_1	ATGGGTCTATCAGCAACTTCTT	-0.027892411	0.84766532	0.00942585	0.75764754
648	BMI1	Hs PCGF4_1	TTGGATCGGAAAGTAAACAAA	-0.367298914	0.257192658	0.08880184	0.22205756
648	BMI1	Hs PCGF4_3	CAGAGTTGACACTTGTGAA	-0.149370147	0.525681219	0.08903181	0.2652965
648	BMI1	Hs BMI1_2	CAAGACCAGACCACACTGAA	-0.696747565	2.03052E-07	0.11762686	1.6906E-06
9577	BRE	Hs BRE_7	TGCCCGTAGATTTCAGCAATA	0.235281208	0.044541584	-0.0614196	0.06395522
9577	BRE	Hs BRE_3	AAGGTGTCAGTACGTGATCTCA	0.393665468	0.152701408	-0.0410069	0.35178433
9577	BRE	Hs BRE_2	CGGCCTCATGTTGAATACCA	-2.33949471	0.116987661	0.03176296	0.39139919
9577	BRE	Hs BRE_6	TAGCGTGGTCCGGAATGGAAA	-0.389866444	0.014242702	0.12496999	0.00758548
83990	BRIP1	Hs BRIP1_5	ACAGTCAAGAGTCAATGAATA	0.408985632	0.002207858	-0.1391643	0.00503507
83990	BRIP1	Hs BRIP1_6	TAGATAGTATGGTCAACAATA	-0.175799422	0.366508104	0.04144772	0.08804521
83990	BRIP1	Hs BRIP1_2	AAGATAAACAGTCCACTTCAA	-0.761989056	0.015077098	0.06448106	0.08542021
83990	BRIP1	Hs BRIP1_1	TAGCATGGCAACAAATCTCTTA	0.020831749	0.877491206	0.10348353	0.49594771
55143	CDC8	Hs CDC8_6	CAGCAGCATACGGACCACAA	0.090043194	0.272621491	-0.0332235	0.10347595
55143	CDC8	Hs CDC8_7	CTGAAAAGACTTGGACCGTGAA	-0.021700067	0.848241662	0.0031467	0.87111988
55143	CDC8	Hs CDC8_2	ACGAAAAGGTAATACAGGTAGA	-0.069506173	0.795715796	0.00330084	0.93576377
55143	CDC8	Hs CDC8_3	CTGGTACCTACTTTCATGAAA	0.098135399	0.567215265	0.00688459	0.23530594
9744	CENTB1	Hs CENTB1_5	GAGGCCTGGATTACCGCTAAA	0.036072678	0.696104918	0.01207569	0.71388699
9744	CENTB1	Hs CENTB1_1	CACCGTGTGCGTCAACACAAA	-1.076069448	0.294831916	0.016694	0.23029349
9744	CENTB1	Hs CENTB1_6	CGGCTGTGCCATATCGAAA	-0.178134893	0.028325019	0.08202064	0.0206657
9744	CENTB1	Hs CENTB1_2	ACGGGGCAGCAACGCATTTAA	-0.742153898	0.001612168	0.10074455	0.02106104
1111	CHK1	Hs CHEK1_9	AAGAAAGAGATCTGTATCAAT	-1.145244991	2.72196E-05	0.13420879	0.00227154
1111	CHK1	Hs CHEK1_13	TTGGAATAACTACAGGGGATA	-0.549983867	0.000228256	0.16192439	0.00096975
1111	CHK1	Hs CHEK1_7	AACTGAAGAAGCAGTCCGAGT	-2.213141371	9.63771E-05	0.21097324	0.00021288
1111	CHK1	Hs CHEK1_8	CCGCACAGGCTTCTCTTAT	-1.553947722	7.95412E-06	0.23575805	0.00574243
11200	CHK2	Hs CHEK2_15	CTCCGTGGTTGAACACGAAA	0.299194072	0.003095387	-0.0794216	0.00045592
11200	CHK2	Hs CHEK2_14	CAGGATGGATTGCCAAATCTT	-0.035069531	0.71495342	0.00618589	0.70676191
11200	CHK2	Hs CHEK2_10	AGGACTGTCTTATAAAGATTA	0.064909947	0.767618967	0.01310368	0.85852118
11200	CHK2	Hs CHEK2_9	ACGCCGTCCTTGAATAACAA	-2.300231551	0.085343006	0.05114409	0.11147481
51550	CINP	Hs CINP_1	AAACCTGTCTTATCTGTCAIT	-0.735610755	0.000609939	0.19725232	0.00018613
51550	CINP	Hs CINP_3	TTCCCTTGGTATGTGGAAGCAGCTT	-0.849513016	0.00046293	0.18034141	0.00018613
51550	CINP	Hs CINP_6	GGGGCTGATGGCAAAATTA	-0.281952545	0.054876261	0.1105562	0.03820755
51550	CINP	Hs CINP_8	ATGCGGCTGATGGCAAAIT	-0.421996711	0.000657558	0.11795285	0.00054963
23122	CLASP2	Hs CLASP2_3	AAGAAGCAGTATTAACATCAA	-0.196934681	0.614509079	0.02214806	0.85243358
23122	CLASP2	Hs CLASP2_6	CTCCACGCTCTCGAGACTATA	-0.167437081	0.389706591	0.03712102	0.114733
23122	CLASP2	Hs CLASP2_8	TTCAAGGTTCTCGACCTAAA	-0.261668739	0.011228697	0.07164734	0.00794412
23122	CLASP2	Hs CLASP2_1	CTGGTTAAGATACTGCTTTA	-0.678530581	0.004446177	0.26866304	0.03192165
152330	CNTN4	Hs CNTN4_8	AAGACACCCAGTCAATAAGTAA	0.126198917	0.376973057	-0.0672953	0.08011211
152330	CNTN4	Hs CNTN4_6	CAAATTGCAATTCCAAGAATA	0.127100011	0.191744747	-0.0419185	0.07662936
152330	CNTN4	Hs CNTN4_2	CACATCTGTCATGAAACAAA	-0.593138405	0.355732613	0.02299208	0.6149943
152330	CNTN4	Hs CNTN4_1	CAGTTGGAAATCAGACATCAA	-0.749113375	0.139835677	0.0414026	0.16013614
22818	COPZ1	Hs COPZ1_8	CCCATCGGACTGACAGTGAAA	-0.836183143	0.00241842	0.01256093	0.63150189
22818	COPZ1	Hs COPZ1_6	AGCCATCTGATTCTGGGCAA	-0.008564107	0.991257212	0.01389012	0.59703345
22818	COPZ1	Hs COPZ1_2	TTGGCTGTGGATGAAATGTA	0.245779755	0.528904141	0.02387624	0.56948572
22818	COPZ1	Hs COPZ1_1	AGCGATTAAATTTGATTGAA	0.157620347	0.648083529	0.10333796	0.6780526
1642	DDB1	Hs DDB1_1	TCGGGATAATAAAGAACTCAA	-0.00102064	0.956110079	-0.0038276	0.89016361
1642	DDB1	Hs DDB1_7	AAGCTCAACGTTGACAGTAAT	-0.057004193	0.628954274	0.00266672	0.92578046
1642	DDB1	Hs DDB1_6	CCACTAGATCGGATAATAAA	0.000732611	0.976603043	0.00270472	0.77737038
1642	DDB1	Hs DDB1_2	ATGCAGAATCGACTCAATAAA	-0.09182996	0.443383555	0.01458965	0.59667491
9077	DIRAS3	Hs DIRAS3_2	TGTGCGCAAGTCGGAATATA	0.513928853	0.001320338	-0.2034872	0.00033445
9077	DIRAS3	Hs ARHI_1	CAGAGAATTCAAATTTGTTAA	0.318937563	0.300916847	-0.0910678	0.67699004
9077	DIRAS3	Hs DIRAS3_4	CAGCAAGAGTGGCGACGGCAA	-0.478994688	0.019964404	0.01919565	0.07649809
9077	DIRAS3	Hs ARHI_2	ACAGCTTATTGACTTAATAAA	0.079929452	0.745561568	0.03817323	0.81140411
1775	DNASE1L2	Hs DNASE1L2_6	CACGTGATGTGCTGCTCTGTA	0.466716684	3.84534E-05	-0.1460679	3.5623E-06
1775	DNASE1L2	Hs DNASE1L2_4	CCGGAGCCTTCTGCTGCCAA	0.382909911	0.002020543	-0.1344456	0.00074113
1775	DNASE1L2	Hs DNASE1L2_1	CCGGCAGATGTCTGTCTAATA	0.042832743	0.624703723	-0.0949655	0.4117783
1775	DNASE1L2	Hs DNASE1L2_3	CGCGCTCATGGAGCACATCAA	0.02768565	0.755251394	0.00099696	0.71701153
1775	DNASE1L2	Hs DNASE1L2_2	TCCAGTGGAGGTGACCTCAA	-0.584074036	0.012087516	0.08048839	0.04647818
2074	ERCC6	Hs ERCC6_6	CAGGACTCGTGGTTCAAATTA	0.455737966	0.00010344	-0.1379059	1.2381E-05
2074	ERCC6	Hs ERCC6_7	CAGGATGACATTAGCAGGTA	0.219551683	0.050529497	-0.0544313	0.03797295
2074	ERCC6	Hs ERCC6_5	CAGAGCGTTTGAAGAGTGAAA	-0.009430593	0.957648256	-0.0307796	0.57012471
2074	ERCC6	Hs ERCC6_2	ATGGATGGTACCACTACAATA	-0.710900071	0.014115588	0.18772392	0.00580652
161829	EXDL1	Hs EXDL1_4	CCCTGGTGGATGGTTACTTAA	0.468618424	4.83364E-05	-0.1504845	2.2489E-06
161829	EXDL1	Hs EXDL1_2	CAGAAGTTTGGTGTGCGGATA	0.007258743	0.881808132	-0.0025918	0.85196372
161829	EXDL1	Hs MGC33637_1	TCAGATGATCACTAGAAGCAA	-1.451473169	0.00897913	0.05789743	0.11866643
161829	EXDL1	Hs MGC33637_2	AAGAAGTATAATTTCTGATTA	0.094462511	0.701085723	0.06702223	0.5526051

**Table 4 (continued). Sensitivity to hydroxyurea following siRNA silencing in U2OS cells.** HU sensitivity was determined by calculating the viability ratio (treated/untreated) and the sensitivity index (SI) for each siRNA. *P* values were determined by comparison to the non-targeting control using an unpaired, two-tailed *t*-test. Values highlighted in pink (*p*<0.05) to HU treatment (dark pink = Log<sub>2</sub> < -0.3 or SI > 0.1, light pink = Log<sub>2</sub> between -0.1 and -0.3 or SI between 0 and 0.1). Those highlighted in blue were resistant (*p*<0.05) to HU treatment (dark blue = Log<sub>2</sub> > 0.3 or SI < -0.1, light blue = Log<sub>2</sub> between 0.1 and 0.3 or SI between 0 and -0.1). Gene symbols highlighted in dark pink had 2 or more siRNAs that were sensitive to HU treatment in both statistical tests; those highlighted in light pink had 2 or more siRNAs that were sensitive by a single statistical test. Gene symbols highlighted in dark blue had 2 or more siRNAs that were resistant to HU treatment in both statistical tests; those highlighted in light blue had 2 or more siRNAs that were resistant by a single statistical test.

Entrez ID	Gene Symbol	Oligo Name	Oligo sequence	HU Sensitivity			
				Mean Log <sub>2</sub> Ratio	<i>p</i> Value Log <sub>2</sub> Ratio	Mean SI	<i>p</i> Value SI
55120	FANCL	Hs FANCL 8	TCAGAGCTCCTTAATAAGCAT	0.552248917	5.24304E-06	-0.1769185	4.6207E-09
55120	FANCL	Hs FANCL 9	ATGGCGGATACCTGCTTCAGTA	0.367247459	0.00322777	-0.1148314	0.00228422
55120	FANCL	Hs FANCL 5	CACTCTCAAGTGAAGGCAAA	0.024917422	0.903141976	-0.0452339	0.97020075
55120	FANCL	Hs FANCL 6	TAGACGTGAGTTATCCAAGTA	0.047600906	0.717747916	-0.0161643	0.81855397
55120	FANCL	Hs FANCL 1	CAGAATTGCATTAGGTAATAA	-1.402195512	0.06899787	0.08490316	0.00516269
6468	FBXW4	Hs SHFM3 2	TGGGAAGATGGCATTCAATA	0.420786606	0.001378644	-0.1471261	0.00051194
6468	FBXW4	Hs SHFM3 1	CAGCACCTTCACTGTCAGTA	0.23448769	0.011704477	-0.0720371	0.00215227
6468	FBXW4	Hs FBXW4 1	TCCATTGCTATCAAGCCATTA	0.121097567	0.416514183	-0.0099439	0.82366294
6468	FBXW4	Hs SHFM3 1	CAGCACCTTCACTGTCAGTA	-0.432431726	0.401219373	-0.000912	0.97095099
6468	FBXW4	Hs SHFM3 2	TGGGAAGATGGCATTCAATA	-0.244166645	0.268286677	0.04365082	0.31336265
6468	FBXW4	Hs FBXW4 2	TCGCATATTGTTAGTGCAGGA	-0.244114816	0.236322004	0.05220592	0.0818698
56776	FMN2	Hs FMN2 12	CACAGTCAGACGAACTCGAAA	-0.269198179	0.064242091	0.0623944	0.14255077
56776	FMN2	Hs FMN2 8	CTGGACCAGTCCAACTGACA	-0.558331764	0.004699029	0.07385405	0.00972403
56776	FMN2	Hs FMN2 6	CCAGCGCTGTTCAAGCCCTA	-1.098858391	0.001716164	0.13962296	0.00382325
56776	FMN2	Hs FMN2 7	CTGATACTATCCTCAAGCGA	-0.609638234	0.000995432	0.18991983	4.9238E-06
26130	GAPVD1	Hs GAPVD1 2	AAGGTTTCAATCTCAAGGCCA	0.224028899	0.050811796	-0.0503221	0.12014743
26130	GAPVD1	Hs DKFZP434C212 2	AAGCAATTAATTTACAAGATA	-0.116671823	0.710282562	0.06632705	0.36575329
26130	GAPVD1	Hs GAPVD1 4	TTGGATGAATAACACACGAT	-0.258343734	0.008569471	0.00928873	0.01054285
26130	GAPVD1	Hs DKFZP434C212 1	TTCGATTGAATTTGAACCTAAA	0.033365275	0.885628588	0.09282883	0.50349563
26354	GNL3	Hs GNL3 4	CAGCAGGTGAACAGTCTACAA	0.427542008	0.022448359	-0.0199848	0.7041573
26354	GNL3	Hs GNL3 2	AAAGTGTGGTACTTATATAAA	-0.683011554	0.316855356	0.01173726	0.90062873
26354	GNL3	Hs GNL3 3	CAGCATTATCAATAGCTTAAA	-0.923039099	0.030289171	0.08767882	0.01176595
26354	GNL3	Hs GNL3 8	GAGTATTGTGGTAGACATGAA	-0.591836537	0.01689042	0.13534566	0.01869776
51512	GTSE1	Hs GTSE1 9	CCTCGAGATCTTACCCCTAAA	0.447815356	6.88185E-05	-0.1492188	1.7164E-05
51512	GTSE1	Hs GTSE1 8	GACCGCGAGATTCCGTGTCTAA	0.080522242	0.42583347	-0.0233627	0.27183753
51512	GTSE1	Hs GTSE1 7	CAAGTTCTAAGCCGAACCAAA	-0.184508887	0.054063619	0.02296091	0.18045502
51512	GTSE1	Hs GTSE1 6	TTCGGACCTTTGGACATAAA	-0.707711516	0.097670992	0.05645781	0.08932766
9555	H2AFY	Hs H2AFY 3	CAAGTTTGTGATCCACTGTAA	0.127039863	0.209720067	-0.0507453	0.140503
9555	H2AFY	Hs H2AFY 2	CTGGCTGTGGCCAAATGATGAA	0.082548169	0.500527105	0.04103072	0.23517758
9555	H2AFY	Hs H2AFY 6	ATGCTGCGGTACATCAAGAAA	-0.370152279	0.016055081	0.07999503	0.01991126
9555	H2AFY	Hs H2AFY 1	AAGGCTTTGGTTTCCAGTTA	-1.519584134	0.024611255	0.20172936	0.00144778
57520	HECW2	Hs HECW2 4	CTCCATCATTTGAGAAGTATA	0.454079723	6.30155E-05	-0.1331061	7.7102E-07
57520	HECW2	Hs HECW2 3	CAGGATTTGGTGGCCTTTCAA	0.356249877	0.000459238	-0.0997698	5.2306E-05
57520	HECW2	Hs HECW2 1	AAGCGGATTTGCAAGCCAAA	0.129573586	0.393549025	-0.0661968	0.23153333
57520	HECW2	Hs HECW2 2	ACGGTCTACTATCATCAGTAA	-0.910156611	0.000626345	0.07302593	0.0319822
8924	HERC2	Hs HERC2 8	CAGCGCAGATTCAGATAACGA	0.166054329	0.038625711	-0.0294643	0.11112339
8924	HERC2	Hs HERC2 2	CGGGATGATCATGAAGAGTTA	-0.371429476	0.271621051	0.03093939	0.4406686
8924	HERC2	Hs HERC2 3	CCAGAGGATATTTAAACCAAA	-0.153209542	0.341478079	0.03702032	0.44791376
8924	HERC2	Hs HERC2 4	CAACGTTTGGTATTATGATAA	-0.178631476	0.420994789	0.06013975	0.0954301
221613	HIST1H2AA	Hs HIST1H2AA 1	AAGCCCAAAGCAAGTAACCTA	0.175154184	0.314386979	-0.0763763	0.63367696
221613	HIST1H2AA	Hs HIST1H2AA 5	TTAGAGTATCTACAGCAGAA	0.06155066	0.594934152	-0.0169499	0.55073213
221613	HIST1H2AA	Hs HIST1H2AA 2	CTGTCTCGTAAGGGAAACTAT	-0.160267505	0.295054458	0.02448802	0.21009822
221613	HIST1H2AA	Hs HIST1H2AA 3	CAGGCAATGCGTCTCGGATA	-0.146486237	0.153222498	0.05829071	0.05519084
3305	HSPA1L	Hs HSPA1L 8	AAAGAAATGCCTTAGAATCCTA	0.423833339	0.000820505	-0.1185125	0.00016879
3305	HSPA1L	Hs HSPA1L 6	CTCTTCGATGGTATGACTAAA	-0.126625117	0.286469884	0.04589645	0.18608143
3305	HSPA1L	Hs HSPA1L 1	CTGGATGCTGAGAAAATATAA	-1.198158979	0.032455429	0.10839345	0.01191861
3305	HSPA1L	Hs HSPA1L 2	ATCAGTAAATTGTTCTGTA	-0.691762679	0.063910512	0.28133575	0.07306331
3306	HSPA2	Hs HSPA2 2	ATGCATAAATGCAAAATGATAA	0.142593753	0.667174918	0.00870683	0.97280786
3306	HSPA2	Hs HSPA2 7	ACAGTGCAGTCGGATGATAA	-0.287152964	0.033082899	0.06219993	0.0461227
3306	HSPA2	Hs HSPA2 3	TAGAAGCTTGGAAACAGTAAA	-0.257300964	0.332784275	0.08562791	0.19706911
3306	HSPA2	Hs HSPA2 8	CCCGTTGCTGGGATCGA	-0.47249751	0.000265519	0.14380637	6.7287E-05
3576	IL8	Hs IL8 4	AACAATTTGGGTACCAGTAA	0.331365323	0.001419988	-0.0883931	0.00028408
3576	IL8	Hs IL8 9	CAAGAGGTGCTAAAGACTTCA	0.016807431	0.784302348	-0.004068	0.75420257
3576	IL8	Hs IL8 6	ATCAGTGAAGATGCCAGTAA	-0.195089949	0.015966478	0.00879115	0.25516364
3576	IL8	Hs IL8 5	AAGAGGGCTGAGAATTCATAA	-0.866635598	6.95015E-05	0.10968863	0.01308374
3659	IRF1	Hs IRF1 1	CAGCCGAGATGCTAAGAGCAA	0.370974491	0.141214229	-0.0847294	0.16925601
3659	IRF1	Hs IRF1 4	CTGGCTAGAGATGCAGATTA	0.02609313	0.767871831	0.00250754	0.89461829
3659	IRF1	Hs IRF1 5	CAAGCATGGCTGGGACATAA	-0.063735676	0.415074533	0.01882629	0.42039201
3659	IRF1	Hs IRF1 2	AGCCCTTTGGTATGACTAAA	-0.353886391	0.057812862	0.14967227	0.05362966
51438	MAGEC2	Hs MAGEC2 7	CCCAGCTCAGTTGAGTTAGA	0.431928601	0.000210204	-0.1367102	4.5227E-05
51438	MAGEC2	Hs MAGEC2 5	AACAGGGCAGTTTGGTTCTA	0.300189521	0.006654553	-0.082988	0.0023269
51438	MAGEC2	Hs MAGEC2 1	CAGGGTATGGTGTGTAITGTA	-1.515207484	0.017788044	0.05330142	0.15654385
51438	MAGEC2	Hs MAGEC2 2	TAGCTTCAGAGTGTTAATTTA	-0.883013348	0.052429464	0.33542496	0.06226871
23389	MED13L	Hs THRAP2 8	AAGCATTAAATGGCTAATTGAA	0.322290466	0.009021495	-0.0629575	0.01487053
23389	MED13L	Hs THRAP2 6	CAGCCTATTGATCAACTTAA	-1.929489475	0.125851975	0.02304047	0.54292332
23389	MED13L	Hs THRAP2 7	AACCAATTAATAGTACCTGA	-0.22811474	0.278527579	0.04413902	0.11655765
23389	MED13L	Hs THRAP2 5	ATGGCTTAAATGGGACGCTAA	-0.969077942	0.002130698	0.15539601	0.00886849
284382	MGC33407	Hs MGC33407 3	CCGGCCGAGCAGGAGTACAA	0.437254979	0.008250892	-0.0728694	0.03894917
284382	MGC33407	Hs MGC33407 2	TCCCTATATCTGCTAGCCGAA	-0.014846784	0.958051717	-0.0349029	0.83494007
284382	MGC33407	Hs MGC33407 5	TGGACCTAGTGGAAGAACATTA	-0.170366028	0.166339282	0.00402922	0.75133957
284382	MGC33407	Hs MGC33407 1	CAGGAATTCTCCGATGATGAT	-0.480996406	0.05403989	0.1586583	0.03683908
9221	NOLC1	Hs NOLC1 7	CAGGTCAATTCTATTAAGTTT	0.119298294	0.410741503	-0.1155039	0.38529867
9221	NOLC1	Hs NOLC1 8	CACCAAGAATTTCAAAATAA	-0.296751722	0.158617109	0.02250932	0.201158
9221	NOLC1	Hs NOLC1 6	CTGGCGATACTTCAACTTCA	-0.124553451	0.432719415	0.03232883	0.38951761
9221	NOLC1	Hs NOLC1 9	AAGGTGGATTTCCACGATAA	-0.323892526	0.011743858	0.08301487	0.01541029
4897	NRCAM	Hs NRCAM 7	ATACCCGTGATGCTTATGAAA	-0.220554597	0.171141627	0.00919526	0.78009463
4897	NRCAM	Hs NRCAM 8	CTCCGTAGGCTTCTTAATCTT	-0.097191368	0.332487889	0.02952007	0.27710731

**Table 4 (continued). Sensitivity to hydroxyurea following siRNA silencing in U2OS cells.** HU sensitivity was determined by calculating the viability ratio (treated/untreated) and the sensitivity index (SI) for each siRNA. *P* values were determined by comparison to the non-targeting control using an unpaired, two-tailed *t*-test. Values highlighted in pink were sensitive ( $p < 0.05$ ) to HU treatment (dark pink =  $\text{Log}_2 < -0.3$  or  $\text{SI} > 0.1$ , light pink =  $\text{Log}_2$  between  $-0.1$  and  $-0.3$  or  $\text{SI}$  between  $0$  and  $0.1$ ). Those highlighted in blue were resistant ( $p < 0.05$ ) to HU treatment (dark blue =  $\text{Log}_2 > 0.3$  or  $\text{SI} < -0.1$ , light blue =  $\text{Log}_2$  between  $0.1$  and  $0.3$  or  $\text{SI}$  between  $0$  and  $-0.1$ ). Gene symbols highlighted in dark pink had 2 or more siRNAs that were sensitive to HU treatment in both statistical tests; those highlighted in light pink had 2 or more siRNAs that were sensitive by a single statistical test. Gene symbols highlighted in dark blue had 2 or more siRNAs that were resistant to HU treatment in both statistical tests; those highlighted in light blue had 2 or more siRNAs that were resistant by a single statistical test.

Entrez ID	Gene Symbol	Oligo Name	Oligo sequence	HU Sensitivity			
				Mean $\text{Log}_2$ Ratio	<i>p</i> Value $\text{Log}_2$ Ratio	Mean SI	<i>p</i> Value SI
4897	NRCAM	Hs NRCAM_6	AGCCTAGTGTGACTATGGAGAA	-0.544438006	0.131292559	0.05752293	0.09640931
4897	NRCAM	Hs NRCAM_5	AGCCGGCTGAAGGAAACGAAA	-0.891764159	0.00589431	0.20634763	0.00019301
	NON-TARGETING		ATGAACTGTAATGGCTCAA	-0.0092975	0.459535796	-0.0035981	0.43526988
9381	OTOF	Hs OTOF_3	TCCGCCATCATTGTCATTGA	0.504705735	2.27555E-05	-0.1666649	1.608E-06
9381	OTOF	Hs OTOF_4	AAGGAGCAACTTCGACAAACA	0.119297077	0.325732158	-0.0350201	0.15839012
9381	OTOF	Hs OTOF_3	TCCGCCATCATTGTCATTGA	0.018602415	0.799324897	0.01042899	0.51995666
9381	OTOF	Hs OTOF_2	CCGGTACAAGTGCTCATCAT	-1.130163962	1.911E-05	0.08561837	0.02305137
9381	OTOF	Hs OTOF_1	CAGGATTGAAGCTTGTAGTGAA	-0.51625013	6.19965E-05	0.14169141	0.00440351
80301	PLEKH02	Hs PLEKH01_1	AACAAGGCTTCGATGAGGTA	0.373132898	0.011105148	-0.1277768	0.00577816
80301	PLEKH02	Hs PLEKH01_2	ACCAACGAGACTCCACTGAA	0.33496235	0.045033082	-0.0740828	0.05403823
80301	PLEKH02	Hs pp9099_2	AACAAGGTCAGCGACATCAAA	-0.132562574	0.622644459	0.00897454	0.91003674
80301	PLEKH02	Hs pp9099_3	GACGGGAAACTGTTGAACAA	-0.607327765	0.071682267	0.13129549	0.06589783
5422	POLA1	Hs POLA_3	CTGCATGAAAGTGCACATCA	1.045551757	0.000172525	-0.0768311	0.00366232
5422	POLA1	Hs POLA_4	CTGGAGAACTTACTACCGAT	0.468412382	0.006756837	-0.0683321	0.01495093
5422	POLA1	Hs POLA_2	CAGGATCTTAACTACCTGAGACA	-0.563524492	0.553320327	-0.006477	0.89606786
5422	POLA1	Hs POLA_1	CAGGTCGAGAGTACAGAAAGA	0.712190155	0.250145349	0.02369977	0.54339112
5423	POLB	Hs POLB_8	CAGGTTGATACCCAAAGATCA	-0.150402817	0.461517624	0.02659487	0.2282872
5423	POLB	Hs POLB_2	CCGGAGCGAATGAGGCTGTGA	-0.958467309	0.032021581	0.0312722	0.4188239
5423	POLB	Hs POLB_7	TACGAGTTCATCATCAATTT	-0.256469378	0.018577825	0.06112982	0.00785629
5423	POLB	Hs POLB_9	CAGGTTGTGGGAGCAGTACAA	-0.380000164	0.023445176	0.18754881	0.02229406
5424	POLD1	Hs POLD1_3	CAGTTGGAGATTGACCAATTA	0.501167491	0.000116532	-0.1199494	0.0002347
5424	POLD1	Hs POLD1_6	CTGTGCCACCTTCATCCGTAT	0.262585069	0.002868964	-0.0728879	8.3392E-05
5424	POLD1	Hs POLD1_2	CGGGACCGAGGAAATAATA	0.030521729	0.791971753	-0.064226	0.80768208
5424	POLD1	Hs POLD1_5	CCGAGAGAGCATGTTGGGTA	-0.456765862	0.001547866	0.10331964	0.01637008
5426	POLE	Hs POLE_3	CTGGATGGATCCATCTAACTA	0.589528558	0.020147093	-0.1212368	0.00638706
5426	POLE	Hs POLE_2	CCGCATCATCTGTATGACAAA	0.215884516	0.210547707	-0.0404125	0.27275368
5426	POLE	Hs POLE_6	AACCGTATTCTACATTTGCGA	0.080801877	0.471996018	-0.0295567	0.42145384
5426	POLE	Hs POLE_7	ACAGATCGGAATATCCGGAA	-0.339710879	0.005537892	0.12704555	0.00567117
5427	POLE2	Hs POLE2_5	CCCAGTGTAATGGCCATATGA	0.503051592	1.43815E-05	-0.1334849	1.8857E-07
5427	POLE2	Hs POLE2_1	CAGTCTGTTGATGAAACTATA	0.289078682	0.173817001	-0.0727233	0.34217476
5427	POLE2	Hs POLE2_4	CCCGATCTACTTGCTACTGCA	0.059640562	0.562622996	-0.0154452	0.52374271
5427	POLE2	Hs POLE2_2	CCGTGAAGACTTAGTAAATAA	-0.435886562	0.026620592	0.06215303	0.1213476
54776	PPP1R12C	Hs PPP1R12C_4	TTGGAGAACTGGCCGGGAAA	-0.141002057	0.167423934	0.03910661	0.03817024
54776	PPP1R12C	Hs PPP1R12C_5	CAGGAGGACCTCGGAACCAA	-0.712137779	0.01195162	0.07347782	0.0322901
54776	PPP1R12C	Hs PPP1R12C_2	CAGCCGGACCTCAACCCAGAA	-1.916586499	0.024283435	0.08224542	0.02698725
54776	PPP1R12C	Hs PPP1R12C_7	CGGAGGCTTAGGACGCTGTA	-0.37575812	0.000875427	0.09525613	0.00154225
5518	PPP2R1A	Hs PPP2R1A_6	ACGGCTGAACATCTATCTAA	-0.265072831	0.441750503	0.00342493	0.9376948
5518	PPP2R1A	Hs PPP2R1A_1	TCCCATCTGGGCAAAAGACAA	-0.390780047	5.98903E-06	0.04671932	0.00032895
5518	PPP2R1A	Hs PPP2R1A_5	CTGGTGTCCGATGCCAACCAA	-1.762494615	0.005562934	0.11706856	0.01289521
5518	PPP2R1A	Hs PPP2R1A_7	GACCAGGATGTGGACGTCAAA	-0.382658718	0.000506163	0.11740745	0.00073662
5557	PRIM1	Hs PRIM1_5	CTGAATCTGTATGCAAACTAA	0.378885403	0.0010975	-0.1203543	0.00106035
5557	PRIM1	Hs PRIM1_4	AGCCTTGTAAAGGTGGTCCAA	0.424267154	0.000119261	-0.1084184	7.0429E-06
5557	PRIM1	Hs PRIM1_3	CTGGGATAGTTGAGTATTTGA	0.244598281	0.218546835	-0.1021816	0.31209248
5557	PRIM1	Hs PRIM1_2	AAGGGTGGTCAAGACGTTAAA	-0.514857007	0.032529255	0.17119632	0.03518814
5714	PSMD8	Hs PSMD8_1	TCCAACGTACATGCTTAAATA	0.003926183	0.969440335	-0.0542453	0.89560524
5714	PSMD8	Hs PSMD8_5	CAGCTGGAGATGATGCTGTGA	0.612454399	0.047290891	-0.0132749	0.25304785
5714	PSMD8	Hs PSMD8_3	CTGCAGGGTTCGCCAACTAAA	0.414394673	0.01995429	-0.0027276	0.64696567
5714	PSMD8	Hs PSMD8_2	AAGGGCGAGTGGAAACCGTAAA	-0.567773721	0.385346385	0.02200665	0.19550486
5929	RBBP5	Hs RBBP5_3	ACGGCAGATCGAATAATACAGA	0.346909955	0.172455376	-0.1390017	0.25721304
5929	RBBP5	Hs RBBP5_6	AAGATTCTCCATTTAAACCGA	0.21764025	0.027975703	-0.0579974	0.01110402
5929	RBBP5	Hs RBBP5_7	TGGAGCCGAGATGGTCAATAA	0.099062649	0.463365847	-0.036242	0.33793406
5929	RBBP5	Hs RBBP5_1	CAGGTGTCTCTCAACAAAGTCA	-0.446959802	0.103212875	0.07342567	0.21110325
5937	RBMS1	Hs RBMS1_7	CTGGTGAAGCTGTGCAACCCA	0.440560383	0.00022049	-0.1310454	6.4105E-05
5937	RBMS1	Hs RBMS1_5	TACGTGATTCAGATGGTACAAA	0.273763255	0.012334458	-0.0753067	0.00465489
5937	RBMS1	Hs RBMS1_2	CTGGTCTATAGCTTGTAAATA	-0.123858333	0.417948393	0.0097494	0.8679051
5937	RBMS1	Hs RBMS1_4	ACCTTTCAACCTAATAAGTAA	-0.322910693	0.090114844	0.04458997	0.07344861
5937	RBMS1	Hs RBMS1_1	AACGAACAATGCAAGAGGTTA	-1.178744307	0.015749725	0.11179335	0.01594326
23186	RCOR1	Hs RCOR1_6	TAGCCTGTTCTAAACCGAAT	-0.079451957	0.60007644	0.02236281	0.33745575
23186	RCOR1	Hs RCOR1_3	AACGACAGATCCAGAATATTA	0.261884813	0.344148904	0.02362184	0.85622704
23186	RCOR1	Hs RCOR1_8	ATCAGATGTACTATTGGTATA	-0.052398984	0.687845173	0.03182301	0.43024553
23186	RCOR1	Hs RCOR1_1	CCCAATAATGGCCAGAAATAA	-0.359505473	0.238143474	0.24850175	0.1804897
5985	RFC5	Hs RFC5_6	TGGGTGGCAGAGCCTGTATAA	-0.008947807	0.9885314	-0.0201873	0.55656608
5985	RFC5	Hs RFC5_3	TAGCACAAAGGACCAATTTAA	-0.569696495	0.064632901	0.15350476	0.01708492
5985	RFC5	Hs RFC5_7	CTGTGCGAAACAGCTATATAA	-0.84166068	3.30473E-05	0.18047352	9.983E-05
5985	RFC5	Hs RFC5_1	ACAGAAGACTTCAAATTTAA	-1.453575586	0.000799459	0.29672207	0.0108168
117584	RFFL	Hs RFFL_5	CTCCATGACATCTTACCGAA	-0.067432433	0.655118039	-0.0051746	0.8811206
117584	RFFL	Hs RFFL_3	TGCAACTTGTCAACTACAA	-1.622942729	0.171220448	0.01391429	0.72450691
117584	RFFL	Hs RFFL_1	ATCCGTTTCTTACAGTGCCTTA	-2.753353498	0.000239629	0.02677144	0.48525859
117584	RFFL	Hs RFFL_4	CCGGTATACAAGGATCGAGAA	-0.389507707	0.002553081	0.07875764	0.01151735
6117	RPA1	Hs RPA1_5	CAGGAATATGTCGTAAGTCA	0.624747434	2.7391E-05	-0.0325731	0.00739082
6117	RPA1	Hs RPA1_3	ACCGATGATCCCTGCAAGTAA	0.519782253	0.005613307	-0.0189889	0.01189172
6117	RPA1	Hs RPA1_2	GAGGTGCTACATAGTTGGTAA	0.436359703	0.034203913	-0.018784	0.24606089
6117	RPA1	Hs RPA1_6	CCGTGTGACGATCCCAATGTTA	0.204736011	0.049818824	-0.0113699	0.63352246
6118	RPA2	Hs RPA2_5	AACAGTGGATCCGAAGCTAT	-0.145848439	0.322493411	0.0275531	0.2311487
6118	RPA2	Hs RPA2_4	AAGGCTTGCCAAAGACCTGAA	-0.4040565	4.20556E-06	0.07940484	5.567E-05
6118	RPA2	Hs RPA2_3	CCAGGTGTGAATTTGATGATA	-0.254892786	0.078904781	0.08065047	0.02245665
6118	RPA2	Hs RPA2_1	TACCAGGAGATCTTACATA	-0.244808685	0.070015684	0.10178122	0.0202069

**Table 4 (continued). Sensitivity to hydroxyurea following siRNA silencing in U2OS cells.** HU sensitivity was determined by calculating the viability ratio (treated/untreated) and the sensitivity index (SI) for each siRNA. *P* values were determined by comparison to the non-targeting control using an unpaired, two-tailed *t*-test. Values highlighted in pink were sensitive ( $p < 0.05$ ) to HU treatment (dark pink =  $\text{Log}_2 < -0.3$  or  $\text{SI} > 0.1$ , light pink =  $\text{Log}_2$  between  $-0.1$  and  $-0.3$  or  $\text{SI}$  between  $0$  and  $0.1$ ). Those highlighted in blue were resistant ( $p < 0.05$ ) to HU treatment (dark blue =  $\text{Log}_2 > 0.3$  or  $\text{SI} < -0.1$ , light blue =  $\text{Log}_2$  between  $0.1$  and  $0.3$  or  $\text{SI}$  between  $0$  and  $-0.1$ ). Gene symbols highlighted in dark pink had 2 or more siRNAs that were sensitive to HU treatment in both statistical tests; those highlighted in light pink had 2 or more siRNAs that were sensitive by a single statistical test. Gene symbols highlighted in dark blue had 2 or more siRNAs that were resistant to HU treatment in both statistical tests; those highlighted in light blue had 2 or more siRNAs that were resistant by a single statistical test.

Entrez ID	Gene Symbol	Oligo Name	Oligo sequence	HU Sensitivity			
				Mean Log <sub>2</sub> Ratio	p Value Log <sub>2</sub> Ratio	Mean SI	p Value SI
6240	RRM1	Hs_RRM1_1	AACGGATATATTGAGAATCAA	0.120962118	0.485186489	-0.0358199	0.82797505
6240	RRM1	Hs_RRM1_6	CAGCTACATTGGCTGGACTAA	0.245835366	0.224563043	-0.0047375	0.69275142
6240	RRM1	Hs_RRM1_5	ATCCGCTGAATCTCTGTATTA	0.731167824	0.507607778	-0.0043488	0.90041005
6240	RRM1	Hs_RRM1_7	CAGGGCCATACGAAACCTAT	-0.418591769	0.002625459	0.12334966	0.00700524
6282	S100A11	Hs_S100A11_6	CAGAACTAGTCGCCTCACAA	1.06869801	1.92152E-06	-0.1721043	3.4385E-06
6282	S100A11	Hs_S100A11_1	CTGCCAATAGTAATAAGCAA	-1.274784961	0.01981472	0.03369226	0.33454701
6282	S100A11	Hs_S100A11_3	ACCAACAGTGAATGGCTAGCTA	-0.949825923	0.156692821	0.04609655	0.16183622
6282	S100A11	Hs_S100A11_8	CCACCTGCCAATAGTAATAAAA	-0.345894066	0.07706256	0.11132702	0.05795941
23256	SCFD1	Hs_SCFD1_7	CTGATGCAGGATGCAACCTTA	-0.393132754	0.000340389	0.02745035	0.27485901
23256	SCFD1	Hs_SCFD1_3	CTGGAAGATATGCAAAATGCA	-1.278535961	0.056499569	0.06650455	0.04727565
23256	SCFD1	Hs_SCFD1_8	CACGATGTACTGGATTCCAT	-0.235766439	0.024507884	0.07045069	0.0163642
23256	SCFD1	Hs_SCFD1_1	CAGAATCTTGTGTACTACATA	-0.610755698	0.001106798	0.09120843	0.00513738
4735	SEPT2	Hs_SEPT2_7	ATAGTTAATGAAGGTGTGCTA	-0.044432513	0.763885527	-0.005927	0.84211016
4735	SEPT2	Hs_SEPT2_8	AAGAATCGGATGTATACTTA	-0.031368992	0.811296909	0.00807395	0.78390664
4735	SEPT2	Hs_SEPT2_3	ACCAAGCCTTCCATATGAA	-1.253825753	0.073678858	0.02507484	0.76056253
4735	SEPT2	Hs_SEPT2_2	GAGATATATCTTTATCTTAA	-0.661778585	3.16192E-05	0.14262274	0.00458698
83852	SETDB2	Hs_SETDB2_2	CCAATGATATTGCAATCAA	0.226089229	0.360979861	-0.1276427	0.32655941
83852	SETDB2	Hs_SETDB2_3	TCCAGGTTAGATAAGTGATA	-0.035606248	0.821914614	-0.0252682	0.75047925
83852	SETDB2	Hs_SETDB2_5	TGGCCGCTTCCTTAATCATA	0.085391632	0.429665776	-0.0066786	0.86314344
83852	SETDB2	Hs_SETDB2_4	CCGAGAGCATCTGAACTCTAA	-0.412411308	0.036267088	0.09571575	0.00588025
50485	SMARCAL1	Hs_SMARCAL1_4	CAGAACAGCATCAGAGACTA	-0.095783259	0.529138491	-0.0103831	0.69375751
50485	SMARCAL1	Hs_SMARCAL1_5	TTGATTGGGTACAATGCGGAA	-0.121100147	0.225790188	0.04538315	0.11035888
50485	SMARCAL1	Hs_SMARCAL1_1	CAGCTTGTGACCTTCTTAGCAA	-1.255736767	0.004322969	0.06580061	0.04152355
50485	SMARCAL1	Hs_SMARCAL1_3	TTGAGTTATGAGTTAGTCAA	-1.467825702	0.00072814	0.07527991	0.03228197
23626	SPO11	Hs_SPO11_4	TACCTTCTACGATAAAGTAA	-0.032263657	0.827448336	0.00722697	0.81672241
23626	SPO11	Hs_SPO11_1	CAGAGTGACTACCTAACAA	-0.751680361	0.0084982	0.09903737	0.04986491
23626	SPO11	Hs_SPO11_6	TTGCATCATGATTACGGGAAA	-0.347228647	0.003575532	0.1186979	0.00070667
23626	SPO11	Hs_SPO11_2	ACAACATGTTAAACGCATAA	-0.915375123	0.008531773	0.14117165	0.04330952
258010	SVIP	Hs_DKFZp313A2432_4	TTAGATGTTCAATCTGTGCAA	0.035841926	0.718031818	-0.0054796	0.89682504
258010	SVIP	Hs_SVIP_3	CACGCCGACTGGAAGAGAA	-0.002931352	0.974815456	0.00916117	0.74706576
258010	SVIP	Hs_DKFZp313A2432_1	ATGGACATGACCTTGAATTT	-0.0674709	0.756548653	0.0189577	0.36088429
258010	SVIP	Hs_DKFZp313A2432_2	GAGGCTGCAAGAGAAAGACAA	-0.809622959	0.000534013	0.13760354	0.00930353
50945	TBX22	Hs_TBX22_7	TTTATTGGTATCCAAAGTAA	0.341460295	0.001529306	-0.1039502	0.00074036
50945	TBX22	Hs_TBX22_8	GCCGGTGGATCCAAACGCTA	0.372497933	0.011552295	-0.090464	0.00529483
50945	TBX22	Hs_TBX22_2	ATGGATGTAATCTCATGAA	-0.13757392	0.274097946	0.0519558	0.27502461
50945	TBX22	Hs_TBX22_1	CTGGAAGAGAAAGATATCCAA	-0.363872064	0.038309016	0.13269444	0.02778666
221400	TDRD6	Hs_TDRD6_7	TAGGGTACAAGTTACCTAATA	0.453480808	0.001361111	-0.092859	0.00801044
221400	TDRD6	Hs_TDRD6_8	CTTGACCTTGTAAATGCAATA	-0.018446595	0.918069674	-0.0015701	0.95897181
221400	TDRD6	Hs_TDRD6_3	TTGAATAAAGTTATCTCTAA	-0.145202864	0.097180153	0.03592235	0.10272608
221400	TDRD6	Hs_TDRD6_1	AACACTGATTATAGAAGTAA	-0.281745848	0.002109815	0.12928482	0.00015555
7398	USP1	Hs_USP1_10	ACAGGCATTAATATTAGTGGG	-0.153557025	0.168776481	0.042133	0.17444393
7398	USP1	Hs_USP1_9	CTGGGACCCATGATCTGATA	-0.337890157	0.001790786	0.05597499	0.03195572
7398	USP1	Hs_USP1_6	ATGTGGCAGAATTACCTACTA	-1.15708075	0.127746014	0.05855848	0.0921394
7398	USP1	Hs_USP1_5	AGCAGATTAAGTACTAACA	-0.964632576	0.019353196	0.12007729	0.0014837
8237	USP11	Hs_USP11_4	CCCATGGAACGCAAGTCATA	0.016962274	0.840335025	0.00694902	0.79370912
8237	USP11	Hs_USP11_6	ACCGATTCTATTGGCCTAGTA	-0.719898808	0.0103534	0.05395699	0.06024106
8237	USP11	Hs_USP11_3	AAGTTCGAAGTGTACCAGTA	-0.297318123	0.084429513	0.0886866	0.06084911
8237	USP11	Hs_USP11_5	CTGGCTGCGGTACGTGATGAA	-0.468989553	0.000170324	0.09220168	0.02671176
151525	WDSUB1	Hs_WDSAM1_1	TCCATTGAAGTTTCACTACTA	0.040877055	0.800981781	-0.0461286	0.98034194
151525	WDSUB1	Hs_WDSAM1_4	AACATCAGCTGAAGCAATTTA	0.14392966	0.142190794	0.0373961	0.2302422
151525	WDSUB1	Hs_WDSAM1_3	TGCGATCAGATGGCTATTCAT	-0.3120947	0.126990473	0.04968563	0.1091155
151525	WDSUB1	Hs_WDSUB1_1	TGCCTGTACTCGTTACGTGA	-0.221029267	0.044250086	0.06467974	0.03157688
7465	WEE1	Hs_WEE1_3	CAGGGTAGATTACTCCGATA	-0.050423047	0.65685663	0.00264778	0.92262623
7465	WEE1	Hs_WEE1_9	ACAATTACGAATAGAATTGAA	-0.438336722	0.00078906	0.10149441	0.00121021
7465	WEE1	Hs_WEE1_5	CACCTGGTAAAGCATTAGAT	-1.869866687	0.001152659	0.11857303	0.01030829
7465	WEE1	Hs_WEE1_8	CAAGACCTGCCTAAGAGATTA	ND	ND	ND	ND
7486	WRN	Hs_WRN_5	ATGGAGATGCTTAAGCATTA	0.243770918	0.094557703	-0.0719565	0.06332694
7486	WRN	Hs_WRN_8	TACATGACTTGTATACATA	0.067928717	0.512314314	-0.0243055	0.35867914
7486	WRN	Hs_WRN_7	CCACGGAGGGTTTCTATCTTA	-0.112092473	0.694455881	0.12042869	0.33191944
7486	WRN	Hs_WRN_6	CGGATTGTATACGTAACCTCA	-0.961869461	0.000105249	0.18595647	0.00868468
56897	WRNIP1	Hs_WRNIP1_8	GAGGCGCAGTTCTTTCGAATA	-0.053617726	0.683857104	0.00828047	0.8271014
56897	WRNIP1	Hs_WRNIP1_9	TGCAGCGTATTGCTTATGAA	-0.169241987	0.203025499	0.02381516	0.51221713
56897	WRNIP1	Hs_WRNIP1_1	GCCTATGTTTCATAGAGATAA	-1.807413429	0.062612488	0.08637752	0.00375376
56897	WRNIP1	Hs_WRNIP1_5	ATGAAATAATGTTATAAGGAA	-0.281470668	0.085254948	0.08698445	0.06468247
56949	XAB2	Hs_XAB2_7	CCGGCATCCGATCGCGCTGTA	0.543951319	1.0035E-05	-0.1877711	4.2249E-07
56949	XAB2	Hs_XAB2_3	CAGCTACGTTGTACATCAA	0.188223041	0.185169682	-0.0543882	0.13906824
56949	XAB2	Hs_XAB2_6	CCGCTGTACAGTCTACGAA	-1.267963826	0.106677788	0.02323128	0.18401092
56949	XAB2	Hs_XAB2_5	CACGTACAACCGCAGTCAA	-1.594730587	0.045343863	0.02491076	0.17768615
7507	XPA	Hs_XPA_8	TGGAGCTGAGTGCTAGAGTA	0.48619151	6.8338E-05	-0.147644	1.3272E-05
7507	XPA	Hs_XPA_3	TTGAGTTGACGAGTCTGAAA	0.439343312	0.000302163	-0.1088758	0.00013705
7507	XPA	Hs_XPA_6	CTGCAGAGATGCTGATGATA	-0.496343135	0.042808775	0.03263942	0.36693335
7507	XPA	Hs_XPA_5	AGGGAGACGATTGTCAACAA	-0.042071099	0.939027822	0.08951586	0.05032855
7709	ZBTB17	Hs_ZBTB17_1	CCCTTCTGAAGTTTATTAA	-0.049755117	0.716818933	0.0083812	0.88409379
7709	ZBTB17	Hs_ZBTB17_8	TGGCTTCAACCCGGTAGACAA	-0.0785376	0.466076544	0.01693697	0.52017132
7709	ZBTB17	Hs_ZBTB17_2	CCGCTCATCAGCCTGCTGAA	-1.022059288	0.313318587	0.02358297	0.54065767
7709	ZBTB17	Hs_ZBTB17_6	CACCACCTCAGGGAACCTGAA	-0.415868858	0.000797056	0.13230629	0.0004806

**Table 5. Cell cycle analysis after release from hydroxyurea block.** The percentage of U2OS cells with phosphorylated H3 staining following silencing of the genome maintenance genes was normalized to the value of the non-targeting siRNA included within each experimental set. The *P* value was calculated using a unpaired, two-tailed *t*-test (*n*=3). Only siRNAs yielding significant differences from the non-targeting siRNA are shown. The percent of BrdU incorporation was determined from a single siRNA transfection and compared to the non-targeting siRNA.

Entrez ID	Gene Symbol	siRNA target sequence	Phospho-H3				>2-fold increase in BrdU incorporation
			Mean	Std Dev	Std Error	<i>P</i> value	
1642	DDB1	GCAAGGACCTGCTGTTTAT	0.0967	0.0351	0.0203	0.0005	Yes
545	ATR	AACCTCCGTGATGTTGCTTGA	0.1270	0.0115	0.0067	0.0001	Yes
6117	RPA1	AACACTCTATCCTCTTTTCATG	0.1330	0.0153	0.0088	0.0001	Yes
23626	SPO11	CAGAGTGTACTTACCTAACAA	0.2700	0.0700	0.0404	0.0031	Yes
84307	ZNF397	AAGCAGAATGGGAGTACTCAA	0.3300	0.0624	0.0361	0.0029	Yes
55734	ZFP64	AAGGACATGGAGCGGCATTTA	0.3730	0.0379	0.0219	0.0012	Yes
56949	XAB2	CACGTACAACACGCAGGTCAA	0.3830	0.1210	0.0698	0.0126	Yes
84126	ATRIP	AAGGTCCACAGATTATTAGAT	0.4230	0.1360	0.0784	0.0180	Yes
4605	MYBL2	TCAGAAGTACTCCATGGACAA	0.4830	0.1630	0.0940	0.0316	No
57520	HECW2	ACGGTCTACTATCATCAGTAA	0.5050	0.0071	0.0050	0.0064	Yes
51438	MAGEC2	CAGGGTAGTGTGGTATTGTAA	0.5400	0.1230	0.0709	0.0230	No
9555	H2AFY	AAGGCTTTGGTTCCAGTTA	0.5470	0.1420	0.0819	0.0311	No
23626	SPO11	ACAATAATGTTAACGCATAA	0.6000	0.1040	0.0603	0.0220	No
83990	BRIP1	AAGATAAACAGTCCACTTCAA	0.6030	0.1330	0.0767	0.0354	No
23389	MED13L	ATGGCTTAAATGGGACGCTAA	0.6730	0.1060	0.0612	0.0333	No
1111	CHK1	AACTGAAGAAGCAGTCGCAGT	0.7200	0.0854	0.0493	0.0297	No
56165	TDRD1	CTGGTGGAGCTTATTGATAAA	0.7430	0.0379	0.0219	0.0072	No
	Non-targeting	ATGAACGTGAATTGCTCAA	1.0000	0.0000	0.0000		No

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