

Supplemental Table S1. Complete list of gene transcripts that are significantly up or down regulated upon PRC silencing in U2OS cells by both shRNAs #1 and #4 relative to a control shRNA.

Gene ID	Gene Symbol	Gene Description	PRC shRNA #1 fold change ^a	PRC shRNA#1 p-value ^b	PRC shRNA#1 FDR p-value ^c	PRC shRNA #4 fold change ^d	PRC shRNA#4 p-value ^e	PRC shRNA#4 FDR p-value ^f
8337	HIST2H2AA3	Histone cluster 2, H2aa3	-45.58	5.02E-10	2.87E-06	-2.88	2.90E-07	3.47E-04
8365	HIST1H4H	Histone cluster 1, H4h	-45.53	5.83E-11	8.79E-07	-3.92	9.96E-08	1.79E-04
8334	HIST1H2AC	Histone cluster 1, H2ac	-26.11	1.25E-09	3.46E-06	-3.21	2.96E-06	8.86E-04
8349	HIST2H2BE	Histone cluster 2, H2be	-18.95	5.32E-08	2.36E-05	-3.15	3.24E-05	2.94E-03
3006	HIST1H1C	histone cluster 1, H1c	-15.45	8.33E-09	1.07E-05	-1.87	2.28E-05	2.54E-03
8970	HIST1H2BJ	Histone cluster 1, H2bj	-14.28	2.57E-09	5.53E-06	-3.35	1.90E-06	8.35E-04
			(-2.86) ^g	(6.63E-07)		(-2.11)	(2.44E-05)	
8338	HIST2H2AC	Histone cluster 2, H2ac	-11.46	1.69E-08	1.21E-05	-2.37	4.32E-06	1.01E-03
3017	HIST1H2BD	histone cluster 1, H2bd	-9.90	9.20E-09	1.07E-05	-1.65	4.29E-04	1.15E-02
8344	HIST1H2BE	Histone cluster 1, H2be	-8.63	1.58E-07	4.87E-05	-2.17	3.62E-05	3.03E-03
8347	HIST1H2BC	Histone cluster 1, H2bc	-8.12	2.83E-07	6.65E-05	-2.25	7.70E-06	1.37E-03
55766	H2AFJ	H2A histone family, member J	-7.67	1.29E-07	4.14E-05	-2.37	3.71E-06	9.01E-04
5118	PCOLCE	procollagen C-endopeptidase enhancer	-6.35	1.03E-06	1.68E-04	-1.71	2.89E-03	3.42E-02
7045	TGFBI	transforming growth factor, beta-induced, 68kDa	-6.25	2.73E-06	3.07E-04	-3.09	5.82E-05	3.92E-03
			(-7.12)	(9.00E-03)		(-3.06)	(2.28E-02)	
8367	HIST1H4E	Histone cluster 1, H4e	-5.79	1.07E-08	1.12E-05	-2.38	8.76E-07	5.42E-04
2791	GNG11	guanine nucleotide binding protein (G protein), gamma 11	-5.01	3.51E-06	3.48E-04	1.53	2.73E-06	8.86E-04
5653	KLK6	kallikrein-related peptidase 6	-4.73	1.14E-05	5.76E-04	2.42	3.56E-04	1.05E-02
1140	CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	-4.70	2.06E-07	5.74E-05	-1.67	3.95E-05	3.22E-03
8351	HIST1H3D	histone cluster 1, H3d	-4.40	9.51E-07	1.62E-04	-1.86	5.36E-07	4.37E-04
9945	GFPT2	Glutamine-fructose-6-phosphate transaminase 2	-4.19	1.88E-06	2.47E-04	-2.15	1.33E-05	1.90E-03
11055	ZBPB	Zona pellucida binding protein	-4.14	1.11E-08	1.12E-05	-2.18	7.38E-08	1.57E-04
4248	MGAT3	Mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	-3.34	5.66E-05	1.42E-03	-2.05	6.05E-06	1.57E-04
9984	THOC1	THO complex 1	-3.18	5.48E-08	2.36E-05	-1.57	3.85E-04	1.08E-02
8764	TNFRSF14	tumor necrosis factor receptor superfamily,	-3.11	2.63E-03	3.46E-03	-1.76	2.48E-03	3.13E-02

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		member 14 (herpesvirus entry mediator)						
5521	PPP2R2B	Protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	-3.06 (-4.44)	6.52E-03 (8.95E-04)	3.02E-02	-2.06 (-4.07)	3.37E-06 (5.89E-04)	8.86E-04
79822	ARHGAP28	Rho GTPase activating protein 28	-3.06	1.87E-03	1.26E-02	-1.51	4.58E-04	1.19E-02
968	CD68	CD68 molecule	-2.84	5.48E-04	5.65E-03	-1.52	1.10E-03	1.96E-02
2192	FBLN1	fibulin 1	-2.75	1.22E-04	2.14E-03	-1.80	4.30E-04	1.15E-02
58191	CXCL16	chemokine (C-X-C motif) ligand 16	-2.72	1.70E-06	2.37E-04	-1.59	4.98E-06	1.05E-03
8357	HIST1H3H	histone cluster 1, H3h	-2.68	3.56E-06	3.51E-04	-1.73	8.36E-05	4.75E-03
6578	SLCO2A1	Solute carrier organic anion transporter family, member 2A1	-2.65	1.81E-03	1.24E-02	-2.83	9.32E-09	8.36E-05
5243	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	-2.58	8.93E-06	5.17E-04	-1.71	8.78E-06	1.49E-03
11211	FZD10	frizzled homolog 10 (Drosophila)	-2.56	2.86E-05	9.18E-04	-1.51	6.31E-06	1.18E-03
120	ADD3	adducin 3 (gamma)	-2.55	1.81E-05	7.34E-04	-1.78	9.23E-05	4.99E-03
7781	SLC30A3	solute carrier family 30 (zinc transporter), member 3	-2.39	1.57E-05	6.75E-04	-1.52	1.28E-04	5.99E-03
5266	PI3	peptidase inhibitor 3, skin-derived (SKALP)	-2.38	2.45E-03	1.52E-02	-1.66	1.18E-04	5.73E-03
26277	TINF2	TERF1 (TRF1)-interacting nuclear factor 2	-2.32	2.26E-03	1.44E-02	-1.50	6.13E-04	1.40E-02
23416	KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member 3	-2.26	1.98E-05	7.65E-04	1.52	1.41E-04	6.34E-03
3394	IRF8	interferon regulatory factor 8	-2.21	3.50E-06	3.48E-04	-1.81	8.85E-06	1.49E-03
401472	FLJ45248	FLJ45248 protein	-2.20	7.92E-03	3.49E-02	-1.91	1.10E-04	5.49E-03
3490	IGFBP7	insulin-like growth factor binding protein 7	-2.17	7.10E-04	6.63E-03	2.42	8.33E-04	1.66E-02
284217	LAMA1	laminin, alpha 1	-2.17	2.16E-04	3.11E-03	-1.56	9.08E-05	4.98E-03
3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	-2.15	3.50E-06	3.48E-04	-1.58	7.64E-06	1.37E-03
4747	NEFL	neurofilament, light polypeptide 68kDa	-2.14	7.11E-05	1.58E-03	-2.06	4.07E-04	1.12E-02
84767	SPRYD5	SPRY domain containing 5	-2.13	1.09E-05	5.65E-04	-1.61	4.71E-05	3.48E-03
8774	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	-2.12	5.80E-06	4.23E-04	-1.82	2.24E-04	8.08E-03
2948	GSTM4	glutathione S-transferase M4	-2.07	8.41E-05	1.74E-03	1.66	7.22E-04	1.55E-02

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84978	FRMD5	FERM domain containing 5	-2.06	2.20E-05	8.04E-04	1.64	7.60E-05	4.51E-03
23492	CBX7	chromobox homolog 7	-2.05	1.99E-03	1.32E-02	-1.71	6.80E-07	4.69E-04
27147	DENND2A	DENN/MADD domain containing 2A	-2.04	3.24E-03	1.85E-02	2.64	1.61E-05	2.09E-03
9212	AURKB	aurora kinase B	-2.04	5.42E-04	5.61E-03	-1.93	5.26E-06	1.05E-03
1075	CTSC	cathepsin C	-2.04	1.20E-04	2.12E-03	1.70	3.35E-04	1.02E-02
29887	SNX10	sorting nexin 10	-2.03	2.12E-04	3.07E-03	-1.71	6.65E-07	4.69E-04
649970	LOC649970	similar to creatine kinase, mitochondrial 1B precursor	-2.03	1.20E-06	1.88E-04	-1.73	2.82E-06	8.86E-04
197021	LCTL	lactase-like	-2.02	8.24E-06	4.94E-04	1.51	2.70E-04	8.93E-03
10063	COX17	COX17 cytochrome c oxidase assembly homolog	-1.97 (-2.76)	1.29E-03 (1.94E-03)	9.80E-03	-1.59 (-2.50)	3.87E-04 (3.85E-03)	1.09E-02
9929	JOSD1	Josephin domain containing 1	-1.94	1.62E-05	6.89E-04	-1.86	2.17E-06	8.86E-04
306	ANXA3	annexin A3	-1.91	3.85E-05	1.09E-03	1.52	2.03E-06	8.48E-04
84953	MICALCL	MICAL C-terminal like	-1.90	8.23E-04	7.28E-03	-1.63	3.20E-05	2.94E-03
1854	DUT	dUTP pyrophosphatase	-1.89	2.48E-04	3.36E-03	-1.91	4.88E-07	4.37E-04
22995	CEP152	centrosomal protein 152kDa	-1.88	6.56E-04	6.33E-03	-1.61	4.04E-03	4.20E-02
8685	MARCO	macrophage receptor with collagenous structure	-1.87	1.35E-03	1.01E-02	-1.65	6.02E-04	1.38E-02
376267	RAB15	RAB15, member RAS oncogene family	-1.87	2.91E-05	9.24E-04	-1.60	3.20E-03	3.63E-02
54471	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	-1.87	2.81E-05	9.15E-04	-1.53	2.99E-04	9.41E-03
56993	TOMM22	translocase of outer mitochondrial membrane 22	-1.84	5.14E-04	5.44E-03	-1.59	2.49E-05	2.71E-03
8195	MKKS	McKusick-Kaufman syndrome	-1.84	7.18E-06	4.68E-04	-1.97	2.35E-07	3.01E-04
23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	-1.83	4.65E-05	1.24E-03	-1.58	1.94E-04	7.52E-03
6000	RGS7	regulator of G-protein signaling 7	-1.82	8.30E-05	1.74E-03	1.69	2.57E-03	3.18E-02
11019	LIAS	lipoic acid synthetase	-1.80	6.40E-05	1.50E-03	-1.65	6.82E-05	4.28E-03
26258	PLDN	pallidin homolog (mouse)	-1.77	2.27E-04	3.21E-03	-1.64	2.65E-04	8.83E-03
256586	LYSMD2	LysM, putative peptidoglycan-binding, domain containing 2	-1.77	1.25E-03	9.56E-03	-1.89	2.77E-05	2.81E-03
8536	CAMK1	calcium/calmodulin-dependent protein	-1.75	3.32E-03	1.88E-02	-1.54	1.62E-04	6.94E-03

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		kinase I						
132299	OCIAD2	OCIA domain containing 2	-1.74	7.56E-03	3.37E-02	1.90	1.35E-05	1.90E-03
1809	DPYSL3	Dihydropyrimidinase-like 3	-1.74	2.83E-03	1.69E-02	-3.60	1.23E-07	2.00E-04
51087	YBX2	Y box binding protein 2	-1.72	4.63E-03	2.38E-02	-2.18	3.39E-08	1.01E-04
22837	COBLL1	COBL-like 1	-1.72	6.52E-04	6.31E-03	-1.54	2.31E-03	3.01E-02
93273	LEMD1	LEM domain containing 1	-1.71	9.65E-03	4.00E-02	-1.50	7.18E-05	4.37E-03
5216	PFN1	profilin 1	-1.70	6.39E-05	1.50E-03	-1.63	1.43E-04	6.37E-03
708	C1QBP	complement component 1, q subcomponent binding protein	-1.69	3.60E-03	1.99E-02	-1.71	1.03E-04	5.32E-03
460	ASTN1	astrotactin 1	-1.69	2.81E-05	9.15E-04	-1.52	1.23E-05	1.83E-03
2944	GSTM1	glutathione S-transferase M1	-1.66	3.45E-04	4.18E-03	1.80	1.04E-03	1.89E-02
10463	SLC30A9	solute carrier family 30 (zinc transporter), member 9	-1.66	2.52E-05	8.60E-04	-1.51	8.63E-05	4.82E-03
4927	NUP88	nucleoporin 88kDa	-1.65	7.85E-05	1.69E-03	-1.70	1.87E-06	8.35E-04
79083	MLPH	melanophilin	-1.64	1.60E-03	1.14E-02	-1.84	4.03E-06	9.63E-04
10762	NUP50	nucleoporin 50kDa	-1.63	2.49E-03	1.54E-02	-1.90	3.23E-04	9.91E-03
11249	NXPH2	neurexophilin 2	-1.62	4.99E-04	5.34E-03	-1.77	1.59E-05	2.08E-03
63979	FIGNL1	fidgetin-like 1	-1.62	8.82E-04	7.58E-03	-1.67	3.41E-05	2.98E-03
9582	APOBEC3B	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	-1.61	5.49E-03	2.68E-02	-2.63	2.20E-07	3.01E-04
7139	TNNT2	troponin T type 2 (cardiac)	-1.61	3.54E-03	1.97E-02	1.73	1.12E-03	1.98E-02
23466	CBX6	chromobox homolog 6	-1.58	5.39E-04	5.60E-03	-1.73	2.91E-06	8.86E-04
174	AFP	alpha-fetoprotein	-1.55	1.15E-03	9.02E-03	-1.79	2.29E-05	2.54E-03
9022	CLIC3	chloride intracellular channel 3	-1.54	3.62E-03	1.99E02	1.74	4.92E-04	1.24E-02
84888	SPPL2A	signal peptide peptidase-like 2A	-1.50	2.75E-04	3.58E-03	-1.62	1.53E-05	2.05E-03
5986	RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	1.50	3.79E-03	2.06E-02	1.59	4.51E-06	1.03E-03
389860	PAGE2B	P antigen family, member 2B	1.50	2.45E-04	3.34E-03	-1.91	9.62E-06	1.57E-03
4072	TACSTD1	Tumor-associated calcium signal transducer 1	1.55	6.05E-04	6.03E-03	2.49	5.35E-08	1.37E-04
5217	PFN2	profilin 2	1.56	3.63E-05	1.05E-03	-1.57	2.49E-03	3.14E-02
29085	PHPT1	phosphohistidine phosphatase 1	1.56	1.20E-03	9.29E-03	1.57	1.17E-03	2.04E-02

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56675	NRIP3	nuclear receptor interacting protein 3	1.59	1.86E-03	1.26E-02	-1.57	8.45E-05	4.77E-03
79850	FAM57A	family with sequence similarity 57, member A	1.59	3.12E-04	3.91E-03	1.73	6.84E-07	4.69E-04
1508	CTSB	cathepsin B	1.61	8.44E-04	7.40E-03	2.08	5.80E-06	1.12E-03
205	AK3L1	adenylate kinase 3-like 1	1.62	3.34E-04	4.07E-03	-1.77	5.94E-05	3.98E-03
6238	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	1.62	6.82E-04	6.47E-03	-2.38	6.68E-06	1.21E-03
51206	GP6	glycoprotein VI (platelet)	1.63	9.59E-03	3.99E-02	1.78	3.94E-04	1.10E-02
140885	SIRPA	signal-regulatory protein alpha	1.65	4.86E-05	1.28E-03	1.81	3.75E-04	1.07E-02
3799	KIF5B	kinesin family member 5B	1.68	8.32E-05	1.74E-02	-1.51	2.33E-03	3.01E-02
9772	KIAA0195	KIAA0195	1.70	6.95E-03	3.17E-02	1.55	2.54E-05	2.72E-03
7077	TIMP2	TIMP metalloproteinase inhibitor 2	1.70	1.09E-03	8.68E-03	1.64	8.04E-05	4.65E-03
6453	ITSN1	intersectin 1 (SH3 domain protein)	1.72	1.97E-03	1.31E-02	1.74	5.23E-04	1.28E-02
116225	ZMYND19	zinc finger, MYND-type containing 19	1.73	6.08E-04	6.05E-03	1.50	2.86E-04	9.19E-03
55178	RNMTL1	RNA methyltransferase like 1	1.73	1.21E-03	9.35E-03	1.50	1.18E-03	2.04E-02
64975	MRPL41	mitochondrial ribosomal protein L41	1.74	2.79E-04	3.61E-03	1.73	2.27E-05	2.54E-03
65992	C20orf116	chromosome 20 open reading frame 116	1.75	1.14E-05	5.76E-04	1.66	2.35E-05	2.57E-03
875	CBS	cystathionine-beta-synthase	1.77	4.92E-04	5.30E-03	-1.57	2.17E-05	2.47E-03
11253	MAN1B1	mannosidase, alpha, class 1B, member 1	1.78	6.00E-04	6.01E-03	1.63	3.76E-04	1.07E-02
10439	OLFM1	olfactomedin 1	1.86	1.93E-05	7.51E-04	-2.56	1.66E-06	8.35E-04
25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	1.89	3.44E-03	1.93E-03	1.72	7.49E-05	4.47E-03
92285	ZNF585B	zinc finger protein 585B	1.89	3.12E-05	9.75E-04	1.63	2.89E-06	8.87E-04
50863	HNT	Neurotrimin	1.89	9.21E-03	3.89E-02	3.12	1.90E-05	2.29E-03
55684	C9orf86	chromosome 9 open reading frame 86	1.89	5.34E-06	4.09E-04	1.57	9.45E-05	5.00E-03
5157	PDGFRL	Platelet-derived growth factor receptor-like	1.97	6.70E-04	6.41E-03	2.48	2.73E-05	2.80E-03
2889	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	2.01	2.18E-05	8.03E-04	1.60	3.61E-06	8.99E-04
7991	TUSC3	Tumor suppressor candidate 3	2.02	7.42E-06	4.74E-04	2.66	3.84E-07	3.93E-04
221061	C10orf38	chromosome 10 open reading frame 38	2.05	1.24E-05	5.97E-04	1.88	2.72E-04	8.94E-03
1398	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	2.06	3.26E-06	3.34E-04	1.82	4.74E-06	1.05E-03

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83700	JAM3	junctional adhesion molecule 3	2.07	7.78E-04	7.03E-03	-1.99	1.06E-05	1.67E-03
6836	SURF4	surfeit 4	2.09	8.80E-05	1.79E-03	1.54	5.66E-04	1.34E-02
285761	DCBLD1	discoidin, CUB and LCCL domain containing 1	2.10	1.50E-05	6.70E-04	1.76	1.29E-05	1.86E-03
26012	NELF	nasal embryonic LHRH factor	2.12	1.75E-05	7.19E-04	1.61	3.41E-04	1.02E-02
84660	CCDC62	coiled-coil domain containing 62	2.16	9.59E-05	1.89E-03	1.59	5.15E-05	3.64E-03
50628	GEMIN4	gem (nuclear organelle) associated protein 4	2.17	1.22E-04	2.13E-03	1.62	2.38E-06	8.87E-04
7531	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2.20	7.97E-06	4.87E-04	1.63	6.18E-06	1.17E-03
55174	INTS10	Integrator complex subunit 10	2.22	4.76E-06	4.09E-04	2.22	7.05E-07	4.69E-04
51031	GLOD4	glyoxalase domain containing 4	2.29	8.59E-07	1.50E-04	1.70	1.72E-06	8.35E-04
5033	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	2.29	7.93E-05	1.71E-03	1.53	2.91E-03	3.43E-02
252969	NEIL2	Nei-like 2 (E. Coli)	2.30	2.26E-05	8.11E-04	2.05	3.66E-05	3.05E-03
2022	ENG	endoglin (Osler-Rendu-Weber syndrome 1)	2.31	4.84E-03	2.45E-02	1.59	1.38E-06	7.56E-04
55326	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	2.34	1.46E-04	2.40E-03	1.70	2.77E-05	2.81E-03
29928	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast)	2.34	8.19E-07	1.47E-04	1.55	1.70E-05	2.14E-03
29883	CNOT7	CCR4-NOT transcription complex, subunit 7	2.35	1.50E-06	2.26E-04	2.49	1.03E-05	1.65E-03
2280	FKBP1A	FK506 binding protein 1A, 12kDa	2.50	7.68E-06	4.84E-04	1.77	2.84E-05	2.82E-03
23362	PSD3	Pleckstrin and Sec7 domain containing 3	2.59	5.06E-06	4.09E04	2.45	2.16E-04	7.92E-03
			(2.63)	(4.87E-02)		(3.09)	(4.54E-02)	
871	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	2.60	2.20E-07	5.92E-05	1.84	1.45E-06	7.68E-04

Gene ID	Gene Symbol	Gene Description	PRC shRNA #1 fold change ^a	PRC shRNA#1 p-value ^b	PRC shRNA#1 FDR p-value ^c	PRC shRNA #4 fold change ^d	PRC shRNA#4 p-value ^e	PRC shRNA#4 FDR p-value ^f
2222	FDFT1	Farnesyl-diphosphate farnesyltransferase 1	2.61	2.02E-04	2.98E-03	2.64	3.15E-06	8.86E-04
5108	PCM1	Pericentriolar material 1	2.67 (2.02)	4.00E-07 (2.85E-06)	8.62E-05	2.49 (3.55)	9.28E-05 (5.45E-02)	4.99E-03
29	ABR	active BCR-related gene	2.68	1.43E-05	6.52E-04	1.83	5.44E-06	1.07E-03
9639	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	2.90	5.32E-08	2.36E-05	1.86	2.63E-06	8.87E-04
8076	MFAP5	microfibrillar associated protein 5	2.95	2.48E-06	2.87E-04	-1.57	4.61E-05	3.46E-03
56952	PRTFDC1	phosphoribosyl transferase domain containing 1	3.05	3.95E-06	3.61E-04	-1.73	1.91E-06	8.35E-04
1404	HAPLN1	hyaluronan and proteoglycan link protein 1	3.38	3.84E-03	2.08E-02	1.75	7.62E-05	4.51E-03
2151	F2RL2	Coagulation factor II (thrombin) receptor-like 2	4.59	5.45E-05	1.39E-03	2.08	6.60E-05	4.19E-03
284406	ZNF545	Zinc finger protein 545	4.80	3.42E-09	6.30E-06	2.74	7.85E-08	1.57E-04
51316	PLAC8	Placenta-specific 8	17.78 (17.85)	4.11E-05 (8.56E-04)	1.15E-03	5.74 (7.36)	1.65E-07 (3.81E-04)	2.47E-04

^aMean fold changes in mRNA levels for a subset of genes whose expression is altered in both shRNA #1 and #4 transductants as assessed by Illumina microarray. Values are for those genes whose expression was significantly up or down regulated ($p < 0.01$, FDR $p < 0.05$) by at least 1.5-fold in response to shRNA#1-mediated silencing of PRC in U2OS cells relative to a negative control shRNA.

^bCorresponding p-values of gene expression changes in ^a

^cCorresponding FDR adjusted p-values of gene expression changes in ^a

^dMean fold changes in mRNA levels for a subset of genes whose expression is altered in both shRNA #1 and #4 transductants as assessed by Illumina microarray. Values are for those genes whose expression was significantly up or down regulated ($p < 0.01$, FDR $p < 0.05$) by at least 1.5-fold in response to shRNA#4-mediated silencing of PRC in U2OS cells relative to a negative control shRNA.

^eCorresponding p-values of gene expression changes in ^d

^fCorresponding FDR adjusted p-values of gene expression changes in ^d

[§]Numbers in parentheses are derived from the independent validation of gene expression as determined by quantitative real time RT-PCR for seven different genes. Values represent the average fold changes in mRNA expression for three separate determinations along with the corresponding p-values for PRC shRNA#1- or PRC shRNA#4-expressing cells relative to control shRNA-expressing cells.

Supplemental Table S2. Effects of PRC silencing by shRNAs #1 or #4 on the expression of mitochondrion-related genes in U2OS cells.

Gene ID	Gene symbol	Gene description	PRC shRNA #1 fold change ^a	PRC shRNA#1 p-value ^b	PRC shRNA#1 FDR p-value ^c	PRC shRNA #4 fold change ^d	PRC shRNA#4 p-value ^e	PRC shRNA#4 FDR p-value ^f
Mitochondrial respiratory chain								
4726	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	-1.29	2.71E-03	1.63E-02			
374291	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	-1.38	3.60E-03	1.99E-02			
51103	NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex	-1.40	1.85E-03	1.26E-02			
4729	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	-1.51	3.80E-04	4.47E-03	-1.25	8.11E-04	1.64E-02
4696	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex	-1.64	1.18E-04	2.10E-03			
4701	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7	-1.76	7.99E-06	4.87E-04			
6389	SDHA	succinate dehydrogenase complex, subunit A	-2.45	3.60E-05	1.05E-03	-1.31	4.04E-04	1.11E-02
517	ATP5G2	ATP synthase, H+ transporting, mitochondrial F0 C2	-1.43	7.32E-04	6.77E-03			
9551	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 F2	-2.01	4.40E-06	3.83E-04			
2110	ETFDH	electron-transferring-flavoprotein dehydrogenase	-1.48	3.96E-03	2.13E-02			
80777	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	-1.38	2.25E-04	3.20E-03			
Mitochondrial protein import and assembly								
1352	COX10	COX10 homolog, cytochrome c oxidase assembly protein	-1.35	2.55E-03	1.57E-02	-1.30	1.85E-04	7.38E-03
1355	COX15	COX15 homolog, cytochrome c oxidase assembly protein	-1.19	9.61E-03	4.00E-02			
10063	COX17	COX17 cytochrome c oxidase assembly homolog	-1.97	1.29E-03	9.80E-03	-1.59	3.87E-04	1.09E-02
90639	COX19	COX19 cytochrome c oxidase assembly	-1.59	1.36E-04	2.30E-03			

Gene ID	Gene symbol	Gene description	PRC shRNA #1 fold change ^a	PRC shRNA#1 p-value ^b	PRC shRNA#1 FDR p-value ^c	PRC shRNA #4 fold change ^d	PRC shRNA#4 p-value ^e	PRC shRNA#4 FDR p-value ^f
55245	UQCC	homolog ubiquinol-cytochrome c reductase complex chaperone	-1.57	2.44E-03	1.52E-02			
5188	PET112L	PET112-like (yeast)	-2.17	2.26E-06	2.79E-04			
6341	SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	-1.67	3.18E-05	9.77E-04	-1.45	2.35E-05	2.57E-03
10431	TIMM23	translocase of inner mitochondrial membrane 23	-1.34	1.22E-03	9.36E-03	-1.21	1.88E-03	2.67E-02
54543	TOMM7	translocase of outer mitochondrial membrane 7	-1.25	1.02E-02	4.18E-02			
9804	TOMM20	translocase of outer mitochondrial membrane 20	-1.57	2.61E-05	8.76E-03			
56993	TOMM22	translocase of outer mitochondrial membrane 22	-1.84	5.14E-04	5.44E-03	-1.59	2.49E-05	2.71E-03
9868	TOMM70A	translocase of outer mitochondrial membrane 70	-1.48	4.97E-04	5.33E-03			
9512	PMPCB	peptidase (mitochondrial processing) beta	-2.16	1.72E-05	7.11E-04			
Mitochondrial translation								
55052	MRPL20	mitochondrial ribosomal protein L20	-1.50	1.02E-04	1.94E-03			
10573	MRPL28	mitochondrial ribosomal protein L28	-1.45	2.87E-04	3.68E-03			
9553	MRPL33	mitochondrial ribosomal protein L33	-1.94	4.57E-05	1.24E-03	-1.19	3.63E-03	3.93E-02
64979	MRPL36	mitochondrial ribosomal protein L36	-1.64	4.33E-05	1.19E-03			
64976	MRPL40	mitochondrial ribosomal protein L40	-1.45	9.07E-04	7.71E-03			
116540	MRPL53	mitochondrial ribosomal protein L53	-1.83	9.28E-06	5.30E-04			
128308	MRPL55	mitochondrial ribosomal protein L55	-1.79	4.95E-05	1.30E-03			
64951	MRPS24	mitochondrial ribosomal protein S24	-1.56	7.69E-04	7.00E-03			
65993	MRPS34	mitochondrial ribosomal protein S34	-1.30	8.54E-03	3.70E-02			
55157	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	-2.02	5.48E-05	1.39E-03			
79587	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	-1.37	1.83E-04	2.82E-03			
55699	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial	-1.66	7.29E-05	1.61E-03			
10102	TSFM	Ts translation elongation factor, mitochondrial	-1.72	8.22E-05	1.73E-03			

^aMean fold reduction in mRNA expression assessed by Illumina microarray of genes required for mitochondrial respiratory function including respiratory chain subunits, mitochondrial protein import and assembly factors, and components of the mitochondrial translation machinery. Values are for those genes that were significantly down regulated ($p < 0.01$, FDR $p < 0.05$) in response to shRNA#1-mediated silencing of PRC in U2OS cells relative to a negative control shRNA.

^bCorresponding p-values for gene expression changes in ^a

^cCorresponding FDR adjusted p-values for gene expression changes in ^a

^dMean fold reduction in mRNA expression assessed by Illumina microarray of genes required for mitochondrial respiratory function including respiratory chain subunits, mitochondrial protein import and assembly factors, and components of the mitochondrial translation machinery. Values are for those genes that were significantly down regulated ($p < 0.01$, FDR $p < 0.05$) in response to shRNA#4-mediated silencing of PRC in U2OS cells relative to a negative control shRNA.

^eCorresponding p-values for gene expression changes in ^d

^fCorresponding FDR adjusted p-values for gene expression changes in ^d

Supplemental Table S3. Effects of PRC silencing by shRNAs #1 or #4 on the expression of histone genes in U2OS cells.

Gene ID	Gene Symbol	Gene Description	PRC shRNA#1 fold change ^a	PRC shRNA#1 p-value ^b	PRC shRNA#1 FDR p- value ^c	PRC shRNA#4 fold change ^d	PRC shRNA#4 p-value ^e	PRC shRNA#4 FDR p- value ^f
8337	HIST2H2AA3	Histone cluster 2, H2aa3	-45.58	5.02E-10	2.87E-06	-2.88	2.90E-07	3.47E-04
8365	HIST1H4H	Histone cluster 1, H4h	-45.53	5.83E-11	8.79E-07	-3.92	9.96E-08	1.79E-04
8364	HIST1H4C	histone cluster 1, H4c	-26.20	1.94E-07	5.52E-05			
8334	HIST1H2AC	Histone cluster 1, H2ac	-26.11	1.25E-09	3.46E-06	-3.21	2.96E-06	8.86E-04
8349	HIST2H2BE	Histone cluster 2, H2be	-18.95	5.32E-08	2.36E-05	-3.15	3.24E-05	2.94E-03
3006	HIST1H1C	histone cluster 1, H1c	-15.45	8.33E-09	1.07E-05	-1.87	2.28E-05	2.54E-03
8970	HIST1H2BJ	Histone cluster 1, H2bj	-14.28	2.57E-09	5.53E-06	-3.35	1.90E-06	8.35E-04
8370	HIST2H4A	histone cluster 2, H4a	-12.95	6.55E-07	1.23E-04			
54145	H2BFS	H2B histone family, member S	-12.69	1.38E-09	3.46E-06			
8338	HIST2H2AC	Histone cluster 2, H2ac	-11.46	1.69E-08	1.21E-05	-2.37	4.32E-06	1.01E-03
3017	HIST1H2BD	histone cluster 1, H2bd	-9.90	9.20E-09	1.07E-05	-1.65	4.29E-04	1.15E-02
8344	HIST1H2BE	Histone cluster 1, H2be	-8.63	1.58E-07	4.87E-05	-2.17	3.62E-05	3.03E-03
8347	HIST1H2BC	Histone cluster 1, H2bc	-8.12	2.83E-07	6.65E-05	-2.25	7.70E-06	1.37E-03
55766	H2AFJ	H2A histone family, member J	-7.67	1.29E-07	4.14E-05	-2.37	3.71E-06	9.01E-04
8367	HIST1H4E	Histone cluster 1, H4e	-5.79	1.07E-08	1.12E-05	-2.38	8.76E-07	5.42E-04
8351	HIST1H3D	histone cluster 1, H3d	-4.40	9.51E-07	1.62E-04	-1.86	5.36E-07	4.37E-04
8362	HIST1H4K	histone cluster 1, H4k	-3.01	6.70E-07	1.25E-04	-1.21	3.43E-04	1.02E-02
8357	HIST1H3H	histone cluster 1, H3h	-2.68	3.56E-06	3.51E-04	-1.73	8.36E-05	4.75E-03
8353	HIST1H3E	histone cluster 1, H3e	-2.26	3.44E-05	1.03E-03	-1.36	4.25E-05	3.30E-03
8969	HIST1H2AG	histone cluster 1, H2ag	-2.12	4.03E-05	1.13E-03	-1.43	3.82E-04	1.08E-02
317772	HIST2H2AB	histone cluster 2, H2ab	-2.01	6.60E-06	4.60E-04	-1.43	3.47E-05	3.01E-03
85236	HIST1H2BK	histone cluster 1, H2bk	-1.99	2.28E-05	8.14E-04	-1.24	2.11E-04	7.81E-03
8350	HIST1H3A	histone cluster 1, H3a	-1.79	9.51E-06	5.32E-04	-1.20	3.62E-03	3.93E-02
3013	HIST1H2AD	histone cluster 1, H2ad	-1.77	6.62E-05	1.52E-03	-1.48	7.12E-04	1.54E-02
8335	HIST1H2AB	histone cluster 1, H2ab	-1.75	4.25E-06	3.76E-04			
8343	HIST1H2BF	histone cluster 1, H2bf	-1.73	5.98E-05	1.45E-03	-1.18	3.71E-03	3.97E-02
8968	HIST1H3F	histone cluster 1, H3f	-1.57	3.90E-04	4.53E-03	-1.31	9.19E-05	4.98E-03
9555	H2AFY	H2A histone family, member Y	-1.41	1.95E-04	2.92E-03			
126961	HIST2H3C	histone cluster 2, H3c	-1.40	6.70E-04	6.41E-03	-1.26	7.42E-04	1.57E-02
8366	HIST1H4B	histone cluster 1, H4b	-1.34	3.93E-04	4.56E-03	-1.16	4.37E-03	4.41E-02

Gene ID	Gene Symbol	Gene Description	PRC shRNA#1 fold change ^a	PRC shRNA#1 p-value ^b	PRC shRNA#1 FDR p- value ^c	PRC shRNA#4 fold change ^d	PRC shRNA#4 p-value ^e	PRC shRNA#4 FDR p- value ^f
8358	HIST1H3B	histone cluster 1, H3b	-1.33	1.24E-03	9.52E-03			
8345	HIST1H2BH	histone cluster 1, H2bh	-1.28	8.54E-04	7.42E-03			
8341	HIST1H2BN	histone cluster 1, H2bn	-1.26	3.01E-03	1.75E-02			
8339	HIST1H2BG	histone cluster 1, H2bg	-1.23	2.09E-03	1.36E-02	-1.15	4.18E-03	4.30E-02
8360	HIST1H4D	histone cluster 1, H4d	-1.23	2.97E-03	1.74E-02			
554313	HIST2H4B	histone cluster 2, H4b				-2.60	4.65E-06	1.04E-03
3024	HIST1H1A	histone cluster 1, H1a				-1.34	1.20E-03	2.05E-02
3015	H2AFZ	H2A histone family, member Z				-1.22	4.43E-04	1.16E-02

^aMean fold reduction in expression assessed by Illumina microarray of histone gene transcripts. Values are for those genes that were significantly down regulated ($p < 0.01$, FDR $p < 0.05$) in response to shRNA#1-mediated silencing of PRC in U2OS cells relative to a negative control shRNA.

^bCorresponding p-values of gene expression changes in ^a

^cCorresponding FDR adjusted p-values of gene expression changes in ^a

^dMean fold reduction in expression assessed by Illumina microarray of histone gene transcripts. Values are for those genes that were significantly down regulated ($p < 0.01$, FDR $p < 0.05$) in response to shRNA#4-mediated silencing of PRC in U2OS cells relative to a negative control shRNA.

^eCorresponding p-values for gene expression changes in ^d

^fCorresponding FDR adjusted p-values for gene expression changes in ^d