

Interactome Analysis Reveals that Heterochromatin Protein 1 γ (HP1 γ) Is Associated with the DNA Damage Response Pathway

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Supplementary Data

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Supplementary Table 1. List of all identified proteins in the present HP1 γ interactome study

No.	Description	Accession No.	Molecular weight	Unique spectral count		
				G+S	M	Empty
1	Actin, cytoplasmic 1	IPI00021439 (+1)	42 kDa	5	4	43
2	ATP-dependent RNA helicase DDX1	IPI00293655 (+1)	82 kDa	2	1	1
3	Bloom syndrome protein	IPI00004859	159 kDa	2	1	0
4	CASP8-associated protein 2	IPI00100798	223 kDa	0	0	3
5	cDNA FLJ50310, highly similar to Zinc finger protein 198	IPI00941117	43 kDa	2	N.D.	N.D.
6	cDNA FLJ53292, highly similar to Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA	IPI00922213	111 kDa	2	N.D.	N.D.
7	CGI-150 protein	IPI00007102 (+4)	55 kDa	0	0	2
8	Chromobox protein homolog 3	IPI00297579	21 kDa	57	63	4
9	Cubilin	IPI00160130	399 kDa	N.D.	2	N.D.
10	DKFZP586J0619 protein	IPI00740961 (+1)	267 kDa	N.D.	2	N.D.
11	Elongation factor 2	IPI00186290	95 kDa	8	4	4
12	Eukaryotic translation initiation factor 4B	IPI00012079 (+2)	69 kDa	2	N.D.	26
13	fibrous sheath-interacting protein 2	IPI00878236	790 kDa	2	1	2
14	Gamma-aminobutyric acid receptor subunit gamma-1	IPI00166138 (+1)	54 kDa	N.D.	2	N.D.
15	Glucagon-like peptide 2 receptor	IPI00873212 (+1)	63 kDa	N.D.	2	N.D.
16	Heat shock 70 kDa protein 1A/1B	IPI00304925 (+1)	70 kDa	2	4	3
17	Heterogeneous nuclear ribonucleoprotein G	IPI00304692	42 kDa	5	3	10
18	Heterogeneous nuclear ribonucleoprotein L	IPI00027834	64 kDa	1	N.D.	9
19	Histone H1.2	IPI00217465	21 kDa	N.D.	2	3
20	Hypothetical protein LOC643677	IPI00929313	802 kDa	2	2	2
21	Inorganic pyrophosphatase	IPI00015018	33 kDa	1	1	2
22	Isoform 1 of 14-3-3 protein epsilon	IPI00000816	29 kDa	N.D.	1	2
23	Isoform 1 of Bardet-Biedl syndrome 5 protein	IPI00449306 (+1)	39 kDa	N.D.	2	N.D.
24	Isoform 1 of Basic immunoglobulin-like variable motif-containing protein	IPI00158804 (+1)	57 kDa	2	N.D.	N.D.
25	Isoform 1 of Bcl-2-associated transcription factor 1	IPI00006079 (+1)	106 kDa	13	8	21
26	Isoform 1 of Caprin-1	IPI00783872 (+1)	78 kDa	5	3	1
27	Isoform 1 of DNA-binding protein A	IPI00031801	40 kDa	6	8	5
28	Isoform 1 of Drebrin	IPI00003406 (+2)	71 kDa	N.D.	N.D.	13
29	Isoform 1 of Dynein heavy chain 10, axonemal	IPI00784869	515 kDa	N.D.	2	N.D.
30	Isoform 1 of Elongation factor 1-delta	IPI00023048 (+5)	31 kDa	N.D.	N.D.	4
31	Isoform 1 of Far upstream element-binding protein 2	IPI00479786 (+1)	73 kDa	1	1	4
32	Isoform 1 of Gelsolin	IPI00026314 (+5)	86 kDa	N.D.	N.D.	4
33	Isoform 1 of Heat shock cognate 71 kDa protein	IPI00003865	71 kDa	1	6	6
34	Isoform 1 of Hermansky-Pudlak syndrome 5 protein	IPI00010486 (+1)	127 kDa	N.D.	2	N.D.
35	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	40 kDa	2	2	3

Supplementary Table 1. Continued

No.	Description	Accession No.	Molecular weight	Unique spectral count		
				G+S	M	Empty
36	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	IPI00028888 (+1)	38 kDa	2	1	5
37	Isoform 1 of Heterogeneous nuclear ribonucleoprotein K	IPI00216049 (+3)	51 kDa	4	5	10
38	Isoform 1 of Heterogeneous nuclear ribonucleoprotein U-like protein 1	IPI00013070 (+1)	96 kDa	6	3	3
39	Isoform 1 of KH domain-containing, RNA-binding, signal transduction-associated protein 1	IPI00008575 (+2)	48 kDa	N.D.	N.D.	5
40	Isoform 1 of Mitotic checkpoint protein BUB3	IPI00013468 (+2)	37 kDa	2	N.D.	1
41	Isoform 1 of NFX1-type zinc finger-containing protein 1	IPI00165981	220 kDa	2	N.D.	N.D.
42	Isoform 1 of Paraspeckle component 1	IPI00103525 (+2)	59 kDa	2	N.D.	1
43	Isoform 1 of Pogo transposable element with ZNF domain	IPI00410717 (+5)	155 kDa	2	2	N.D.
44	Isoform 1 of Polyadenylate-binding protein 1	IPI00008524 (+3)	71 kDa	2	1	4
45	Isoform 1 of Protein FAM98A	IPI00174442 (+2)	55 kDa	2	3	N.D.
46	Isoform 1 of Proton-coupled amino acid transporter 3	IPI00418819 (+1)	52 kDa	N.D.	2	N.D.
47	Isoform 1 of RNA-binding protein 10	IPI00375731 (+2)	104 kDa	N.D.	N.D.	5
48	Isoform 1 of Regulatory-associated protein of mTOR	IPI00166044 (+1)	149 kDa	N.D.	N.D.	2
49	Isoform 1 of Replication protein A 32 kDa subunit	IPI00013939 (+2)	29 kDa	6	7	4
50	Isoform 1 of Serine/arginine repetitive matrix protein 2	IPI00782992 (+1)	300 kDa	N.D.	N.D.	2
51	Isoform 1 of TBC1 domain family member 9B	IPI00307257 (+1)	141 kDa	N.D.	N.D.	2
52	Isoform 1 of Transcription factor TFIIB component B' homolog	IPI00760877 (+3)	294 kDa	N.D.	2	N.D.
53	Isoform 1 of Transcription intermediary factor 1-beta	IPI00438229	89 kDa	17	8	N.D.
54	Isoform 1 of Transcriptional repressor p66-alpha	IPI00410330 (+3)	68 kDa	N.D.	N.D.	2
55	Isoform 1 of WD repeat-containing protein 33	IPI00106567	146 kDa	1	N.D.	2
56	Isoform 1 of Zinc finger Ran-binding domain-containing protein 2	IPI00029400 (+1)	37 kDa	N.D.	0	5
57	Isoform 2 of AT-rich interactive domain-containing protein 1A	IPI00642705 (+2)	218 kDa	2	N.D.	N.D.
58	Isoform 2 of HMG box transcription factor BBX	IPI00183699 (+3)	102 kDa	2	N.D.	N.D.
59	Isoform 2 of Heterogeneous nuclear ribonucleoprotein A1	IPI00797148	29 kDa	1	3	1
60	Isoform 2 of Microtubule-associated serine/threonine-protein kinase 4	IPI00788168 (+5)	265 kDa	2	N.D.	N.D.
61	Isoform 2 of Mucin-19	IPI00829833 (+1)	564 kDa	2	1	N.D.

Supplementary Table 1. Continued

No.	Description	Accession No.	Molecular weight	Unique spectral count		
				G+S	M	Empty
62	Isoform 2 of Protein piccolo	IPI00789624	531 kDa	2	N.D.	2
63	Isoform 2 of Retinoic acid-induced protein 1	IPI00449924 (+2)	198 kDa	N.D.	2	N.D.
64	Isoform 2 of Tropomyosin alpha-3 chain	IPI00218319 (+2)	29 kDa	1	1	4
65	Isoform 2 of Ubiquitin-associated protein 2-like	IPI00029019 (+4)	104 kDa	3	3	3
66	Isoform 2 of Uncharacterized protein C7orf63	IPI00015625 (+2)	101 kDa	N.D.	N.D.	2
67	Isoform 2 of WASH complex subunit FAM21C	IPI00456853 (+6)	144 kDa	N.D.	1	2
68	Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein	IPI00412714 (+1)	42 kDa	7	13	9
69	Isoform 5 of Interleukin enhancer-binding factor 3	IPI00219330 (+6)	75 kDa	N.D.	N.D.	3
70	Isoform 5 of Serine/threonine-protein kinase MRCK alpha	IPI00550263 (+5)	196 kDa	N.D.	2	N.D.
71	Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00396378	37 kDa	1	1	14
72	Isoform Beta of LIM domain and actin-binding protein 1	IPI00008918 (+1)	85 kDa	N.D.	2	N.D.
73	Isoform Beta-1 of Protein phosphatase 1B	IPI00026612 (+4)	53 kDa	N.D.	N.D.	8
74	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	IPI00216592 (+4)	32 kDa	2	1	11
75	Isoform Long of Heterogeneous nuclear ribonucleoprotein U	IPI00883857	91 kDa	24	25	15
76	Isoform Long of Splicing factor, proline- and glutamine-rich	IPI00010740	76 kDa	28	15	21
77	Isoform PLZFA of Zinc finger and BTB domain-containing protein 16	IPI00220823 (+1)	62 kDa	N.D.	2	N.D.
78	Isoform Short of RNA-binding protein FUS	IPI00221354 (+3)	53 kDa	41	35	23
79	Isoform Short of TATA-binding protein-associated factor 2N	IPI00020194 (+1)	62 kDa	10	10	8
80	Krueppel-associated box domain containing protein	IPI00884250	36 kDa	2	N.D.	N.D.
81	LanC-like protein 2	IPI00032995	51 kDa	3	2	7
82	latrophilin-3 precursor	IPI00964226 (+5)	165 kDa	2	N.D.	N.D.
83	Leucine-rich repeat neuronal protein 1	IPI00021485	81 kDa	N.D.	N.D.	2
84	Methylosome protein 50	IPI00012202	37 kDa	N.D.	N.D.	4
85	Methylosome subunit pICln	IPI00004795 (+2)	26 kDa	N.D.	N.D.	4
86	Microsomal triglyceride transfer protein large subunit	IPI00296645 (+1)	99 kDa	N.D.	2	N.D.
87	Microtubule-associated protein 1B	IPI00008868	271 kDa	N.D.	N.D.	2
88	Msx2-interacting protein	IPI00045914	402 kDa	N.D.	2	2
89	Mucin-16	IPI00103552	2,353 kDa	1	3	1
90	Multidrug resistance-associated protein 5	IPI00385383 (+2)	161 kDa	2	N.D.	0
91	Myosin-6	IPI00514201	224 kDa	N.D.	N.D.	2
92	Myristoylated alanine-rich C-kinase substrate	IPI00219301	32 kDa	1	N.D.	2

Supplementary Table 1. Continued

No.	Description	Accession No.	Molecular weight	Unique spectral count		
				G+S	M	Empty
93	Non-POU domain-containing octamer-binding protein	IPI00304596	54 kDa	27	18	29
94	Nuclease-sensitive element-binding protein 1	IPI00031812	36 kDa	29	27	26
95	Peptidyl-prolyl cis-trans isomerase-like 4	IPI00642862	57 kDa	N.D.	N.D.	3
96	Phosphatidylinositol 3-kinase regulatory subunit beta	IPI00011736	82 kDa	N.D.	N.D.	2
97	Poly(rC)-binding protein 1	IPI00016610	37 kDa	1	2	6
98	probable ATP-dependent RNA helicase DDX17 isoform 3	IPI00651653 (+4)	80 kDa	2	1	3
99	Proliferating cell nuclear antigen	IPI00021700	29 kDa	N.D.	1	3
100	protein arginine N-methyltransferase 5 isoform b	IPI00064328 (+1)	71 kDa	N.D.	N.D.	15
101	Protein FAM35B	IPI00749463	94 kDa	2	N.D.	N.D.
102	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	IPI00396435 (+1)	91 kDa	7	8	5
103	RB-associated KRAB zinc finger protein	IPI00302755	83 kDa	2	N.D.	N.D.
104	RING finger protein 219	IPI00465370	81 kDa	N.D.	N.D.	6
105	RNA-binding protein EWS isoform 1	IPI00009841 (+4)	69 kDa	29	24	14
106	Replication protein A 70 kDa DNA-binding subunit	IPI00020127	68 kDa	18	13	17
107	rRNA 2'-O-methyltransferase fibrillarin	IPI00025039	34 kDa	3	4	1
108	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 3	IPI00027423 (+2)	39 kDa	N.D.	N.D.	2
109	SCY1-like protein 2	IPI00396218 (+1)	104 kDa	N.D.	N.D.	2
110	Scaffold attachment factor B1	IPI00300631 (+5)	103 kDa	5	1	N.D.
111	Similar to Potassium voltage-gated channel subfamily V member 2	IPI00742690	9 kDa	2	N.D.	N.D.
112	Src substrate cortactin	IPI00029601 (+1)	62 kDa	4	4	13
113	THO complex subunit 4	IPI00328840 (+1)	28 kDa	5	8	4
114	Thyroid hormone receptor-associated protein 3	IPI00104050	109 kDa	3	1	19
115	Titin, isoform CRA_a	IPI00940872	3,881 kDa	2	3	N.D.
116	Transcriptional repressor protein YY1	IPI00014513	45 kDa	3	3	2
117	Tropomodulin-3	IPI00005087	40 kDa	N.D.	N.D.	5
118	Tubulin beta-2C chain	IPI00007752 (+18)	50 kDa	N.D.	N.D.	2
119	U1 small nuclear ribonucleoprotein A	IPI00012382	31 kDa	1	2	1
120	Uncharacterized protein	IPI00645369	881 kDa	N.D.	2	N.D.
121	Uncharacterized protein	IPI00743873	75 kDa	N.D.	N.D.	2
122	Uncharacterized protein	IPI00966854	30 kDa	N.D.	N.D.	5
123	Uncharacterized protein	IPI00394855	352 kDa	2	N.D.	N.D.
124	Uncharacterized protein	IPI00011986 (+4)	362 kDa	2	N.D.	N.D.
125	WD repeat-containing protein 82	IPI00152695	35 kDa	1	1	2
126	X-ray repair cross-complementing protein 5	IPI00220834	83 kDa	N.D.	2	N.D.
127	Zinc finger protein 106 homolog	IPI00782966	209 kDa	N.D.	2	N.D.
128	33 kDa protein	IPI00413108 (+2)	33 kDa	8	11	5
129	40S ribosomal protein S3a	IPI00419880 (+1)	30 kDa	N.D.	3	3
130	78 kDa glucose-regulated protein	IPI00003362	72 kDa	1	2	N.D.

HP1 γ , heterochromatin protein 1 γ ; N.D., not detected.

Supplementary Table 2. The clustering of proteins that interact with HP1γ

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM_ CC_FAT	GO:0043228	Non-membrane -bounded organelle	44	35.2	6.78E-09	IP100419880, IP100438229, IP100514201, IP100028888, IP100449306, IP100782966, IP100103525, IP100413108, IP100013468, IP100004795, IP100008868, IP100220823, IP100104050, IP100219330, IP100216049, IP100005087, IP100743873, IP100300631, IP100789624, IP100003406, IP100029601, IP100396378, IP100218319, IP100297579, IP100410330, IP100026314, IP100008918, IP100020127, IP100025039, IP100013939, IP100217465, IP100021700, IP100032995, IP100004859, IP100219301, IP100220834, IP100784869, IP100645369, IP100021439, IP100419373, IP100007752, IP100045914, IP100642705, IP100221354	92	2,596	12,782	2.354827	1.60E-06	5.33E-07	8.72E-06
GOTERM_ CC_FAT	GO:0043232	Intracellular non-membrane-bounded organelle	44	35.2	6.78E-09	IP100514201, IP100028888, IP100449306, IP100782966, IP100103525, IP100413108, IP100013468, IP100004795, IP100008868, IP100419880, IP100438229, IP100220823, IP100104050, IP100219330, IP100216049, IP100005087, IP100743873, IP100300631, IP100789624, IP100003406, IP100029601, IP100396378, IP100218319, IP100297579, IP100410330, IP100026314, IP100008918, IP100020127, IP100025039, IP100013939, IP100217465, IP100021700, IP100032995, IP100004859, IP100219301, IP100220834, IP100784869, IP100645369, IP100021439, IP100419373, IP100007752, IP100045914, IP100642705, IP100221354	92	2,596	12,782	2.354827	1.60E-06	5.33E-07	8.72E-06

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM_ CC_FAT	GO:0043233	Organelle lumen	34	27.2	1.27E-07	IP100217465, IP100021700,	92	1,820	12,782	2.595485	2.99E-05	4.99E-06	1.63E-04
						IP100032995, IP100004859,							
						IP100219301, IP100220834,							
						IP100784869, IP100645369,							
						IP100021439, IP100419373,							
						IP100007752, IP100045914,							
						IP100642705, IP100221354							
						IP100514201, IP100014513,							
						IP100782966, IP100103525,							
						IP100010740, IP100922213,							
						IP100013468, IP100027423,							
						IP100027834, IP100419880,							
						IP100438229, IP100104050,							
						IP100220823, IP100782992,							
						IP100219330, IP100216049,							
						IP100941117, IP100300631,							
						IP100396378, IP100410330,							
IP100020127, IP100025039,													
IP100013939, IP100003362,													
IP100021700, IP100004859,													
IP100328840, IP100220834,													
IP100021439, IP100419373,													
IP100045914, IP100740961,													
IP100642705, IP100221354													
GOTERM_ CC_FAT	GO:0031974	Membrane-enclosed lumen	34	27.2	2.03E-07	IP100514201, IP100014513,	92	1,856	12,782	2.545141	4.79E-05	6.84E-06	2.61E-04
						IP100782966, IP100103525,							
						IP100010740, IP100922213,							
						IP100013468, IP100027423,							
						IP100027834, IP100419880,							
						IP100438229, IP100104050,							
						IP100220823, IP100782992,							
						IP100219330, IP100216049,							
						IP100941117, IP100300631,							
						IP100396378, IP100410330,							
						IP100020127, IP100025039,							
						IP100013939, IP100003362,							
						IP100021700, IP100004859,							

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM _CC_FAT	GO:0070013	Intracellular organelle lumen	33	26.4	2.61E-07	IP100328840, IP100220834,	92	1,779	12,782	2.577205	6.15E-05	7.69E-06	3.35E-04
						IP100021439, IP100419373,							
						IP100045914, IP100740961,							
						IP100642705, IP100221354							
						IP100514201, IP100014513,							
						IP100782966, IP100103525,							
						IP100010740, IP100013468,							
						IP100027423, IP100027834,							
						IP100419880, IP100438229,							
						IP100104050, IP100220823,							
						IP100782992, IP100219330,							
						IP100216049, IP100941117,							
						IP100300631, IP100396378,							
						IP100410330, IP100020127,							
IP100025039, IP100013939,													
IP100003362, IP100021700,													
IP100004859, IP100328840,													
IP100220834, IP100021439,													
IP100419373, IP100045914,													
IP100740961, IP100642705,													
IP100221354													
GOTERM _CC_FAT	GO:0031981	Nuclear lumen	32	25.6	7.99E-09	IP100514201, IP100014513,	92	1,450	12,782	3.066147	1.89E-06	4.71E-07	1.03E-05
						IP100782966, IP100103525,							
						IP100010740, IP100013468,							
						IP100027423, IP100027834,							
						IP100419880, IP100438229,							
						IP100104050, IP100220823,							
						IP100782992, IP100219330,							
						IP100216049, IP100941117,							
						IP100300631, IP100396378,							
						IP100410330, IP100020127,							
						IP100025039, IP100013939,							
						IP100021700, IP100004859,							
						IP100328840, IP100220834,							
						IP100021439, IP100419373,							
IP100045914, IP100740961,													
IP100642705, IP100221354													

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM _CC_FAT	GO:0030529	Ribonucleoprotein complex	25	20	9.52E-14	IP100003865, IP100028888, IP100413108, IP100304692, IP100012382, IP100883857, IP100419880, IP100027834, IP100782992, IP100219330, IP100216049, IP100016610, IP100008524, IP100396378, IP100186290, IP100293655, IP100025039, IP100216592, IP100328840, IP100021439, IP100419373, IP1000031812, IP100396435, IP100013070, IP100304925	92	515	12,782	6.744407	2.25E-11	2.25E-11	1.22E-10
GOTERM _CC_FAT	GO:005829	Cytosol	23	18.4	1.22E-04	IP100783872, IP100015018, IP100012079, IP100166044, IP100028888, IP100003865, IP100026314, IP100782966, IP100413108, IP100027423, IP100003362, IP100013468, IP100032995, IP100004795, IP100000816, IP100008868, IP100419880, IP100021439, IP100220823, IP100023048, IP100007752, IP100011736, IP100008524	92	1,330	12,782	2.402632	0.028359	0.002612	0.156803
GOTERM _CC_FAT	GO:0005654	Nucleoplasm	20	16	1.13E-05	IP100396378, IP100410330, IP100020127, IP100014513, IP100013939, IP100103525, IP100027423, IP100021700, IP100328840, IP100004859, IP100220834, IP100027834, IP100021439, IP100438229, IP100104050, IP100220823, IP100782992, IP100216049, IP100941117, IP100740961	92	882	12,782	3.150449	0.002657	2.66E-04	0.014512
GOTERM _CC_FAT	GO:0005856	Cytoskeleton	20	16	0.003494	IP100514201, IP100029601, IP100218319, IP100297579,	92	1,381	12,782	2.01209	0.562173	0.042539	4.405239

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM _CC_FAT	GO:005730	Nucleolus	18	14.4	7.22E-06	IP100008918, IP100026314,	92	698	12,782	3.582845	0.001703	1.89E-04	0.009297
						IP100020127, IP100449306,							
						IP100032995, IP100004795,							
						IP100219301, IP100008868,							
						IP100645369, IP100784869,							
						IP100021439, IP100743873,							
						IP100005087, IP100007752,							
						IP100789624, IP100003406							
						IP100514201, IP100396378,							
						IP100410330, IP100025039,							
						IP100782966, IP100103525,							
						IP100013468, IP100004859,							
						IP100419880, IP100104050,							
IP100220823, IP100419373,													
IP100216049, IP100219330,													
IP100045914, IP100642705,													
IP100221354, IP100300631													
GOTERM _CC_FAT	GO:004451	Nucleoplasm part	13	10.4	5.48E-04	IP100410330, IP100014513,	92	555	12,782	3.254328	0.121448	0.009911	0.703788
						IP100020127, IP100103525,							
						IP100027423, IP100328840,							
						IP100004859, IP100021439,							
						IP100220823, IP100104050,							
						IP100782992, IP100941117,							
						IP100740961							
						IP100514201, IP100032995,							
						IP100219301, IP100008868,							
						IP100218319, IP100297579,							
						IP100008918, IP100784869,							
						IP100007752, IP100449306,							
						IP100743873, IP100003406							
GOTERM _CC_FAT	GO:004430	Cytoskeletal part	12	9.6	0.074781	IP100514201, IP100032995,	92	952	12,782	1.751279	1	0.416962	63.23272
						IP100219301, IP100008868,							
						IP100218319, IP100297579,							
						IP100008918, IP100784869,							
						IP100007752, IP100449306,							
						IP100743873, IP100003406							
						IP100012382, IP100396378,							
						IP100328840, IP100883857,							
						IP100782992, IP100419373,							
						IP100216049, IP100396435,							
						IP100216592, IP100008524,							
						IP100304692							
						GOTERM _CC_FAT							
IP100328840, IP100883857,													
IP100782992, IP100419373,													
IP100216049, IP100396435,													
IP100216592, IP100008524,													
IP100304692													

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM _CC_FAT	GO:0005694	Chromosome	10	8	0.005387	IP100217465, IP100013468, IP100021700, IP100004859, IP100297579, IP100028888, IP100220834, IP100438229, IP100020127, IP100013939	92	460	12,782	3.020321	0.72053	0.058902	6.71771
GOTERM _CC_FAT	GO:0042995	Cell projection	10	8	0.059574	IP100783872, IP100027423, IP100029601, IP100008868, IP100026314, IP100784869, IP100021439, IP100449306, IP100160130, IP100003406	92	697	12,782	1.993325	0.999999	0.355489	54.64719
GOTERM _CC_FAT	GO:0044427	Chromosomal part	9	7.2	0.006169	IP100217465, IP100013468, IP100021700, IP100004859, IP100297579, IP100220834, IP100438229, IP100020127, IP100013939	92	386	12,782	3.239412	0.767852	0.061521	7.656929
GOTERM _CC_FAT	GO:0016604	Nuclear body	8	6.4	1.92E-04	IP100004859, IP100328840, IP100410330, IP100020127, IP100220823, IP100782992, IP100103525, IP100941117	92	168	12,782	6.615942	0.044208	0.003761	0.246333
GOTERM _CC_FAT	GO:0015629	Actin cytoskeleton	8	6.4	0.003042	IP100514201, IP100032995, IP100219301, IP100218319, IP100026314, IP100008918, IP100645369, IP100003406	92	269	12,782	4.131889	0.51271	0.039152	3.845476
GOTERM _CC_FAT	GO:0015630	Microtubule cytoskeleton	8	6.4	0.096029	IP100219301, IP100008868, IP100297579, IP100645369, IP100784869, IP100007752, IP100449306, IP100743873	92	549	12,782	2.024551	1	0.457151	72.73703
GOTERM _CC_FAT	GO:0016023	Cytoplasmic membrane-bounded vesicle	8	6.4	0.096726	IP100003362, IP100000816, IP100003865, IP100645369, IP100789624, IP100160130, IP100396218, IP100922213	92	550	12,782	2.02087	1	0.451301	73.00656
GOTERM _CC_FAT	GO:0030530	Heterogeneous nuclear ribonucleoprotein complex	7	5.6	1.28E-09	IP100396378, IP100883857, IP100028888, IP100027834, IP100216049, IP100013070, IP100304692	92	17	12,782	57.20844	3.02E-07	1.51E-07	1.65E-06
GOTERM _CC_FAT	GO:0048471	Perinuclear region of cytoplasm	7	5.6	0.016773	IP100514201, IP100412714, IP100003362, IP100008868,	92	288	12,782	3.376887	0.981538	0.142333	19.56765

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
						IP100026314, IP100385383, IP100396218							
GOTERM	GO:0044454	Nuclear chromosome part	6	4.8	0.001764	IP100004859, IP100297579, IP100220834, IP100438229, IP100020127, IP100013939	92	122	12,782	6.832858	0.340764	0.024212	2.247202
GOTERM	GO:0000228	Nuclear chromosome	6	4.8	0.005957	IP100004859, IP100297579, IP100220834, IP100438229, IP100020127, IP100013939	92	162	12,782	5.145733	0.755871	0.062083	7.403115
GOTERM	GO:0034399	Nuclear periphery	5	4	9.20E-04	IP100021700, IP100004859, IP100014513, IP100103525, IP100010740	92	61	12,782	11.3881	0.195314	0.015402	1.178326
GOTERM	GO:0005657	Replication fork	4	3.2	0.001491	IP100021700, IP100004859, IP100020127, IP100013939	92	32	12,782	17.36685	0.296835	0.023204	1.90262
GOTERM	GO:0016605	PML body	4	3.2	0.001632	IP100004859, IP100020127, IP100220823, IP1000941117	92	33	12,782	16.84058	0.319838	0.023801	2.080429
GOTERM	GO:0016363	Nuclear matrix	4	3.2	0.00737	IP100004859, IP100014513, IP100103525, IP100010740	92	56	12,782	9.923913	0.825506	0.070161	9.083778
GOTERM	GO:0032993	Protein-DNA complex	4	3.2	0.02337	IP100217465, IP100220834, IP100020127, IP100013939	92	86	12,782	6.462083	0.99623	0.180705	26.24427
GOTERM	GO:0016607	Nuclear speck	4	3.2	0.037073	IP100328840, IP100410330, IP100220823, IP100782992	92	103	12,782	5.395526	0.999866	0.257091	38.51098
GOTERM	GO:0005938	Cell cortex	4	3.2	0.085974	IP100029601, IP100032995, IP100219301, IP100021439	92	146	12,782	3.806432	1	0.454556	68.56477
GOTERM	GO:0044445	Cytosolic part	4	3.2	0.094261	IP100003362, IP100419880, IP100011736, IP100413108	92	152	12,782	3.656178	1	0.468198	72.04264
GOTERM	GO:0045120	Pronucleus	3	2.4	0.003716	IP100004859, IP100027834, IP100216592	92	13	12,782	32.06187	0.584612	0.042976	4.679182
GOTERM	GO:0043073	Germ cell nucleus	3	2.4	0.008763	IP100004859, IP100219301, IP100020127	92	20	12,782	20.84022	0.874722	0.07973	10.71227
GOTERM	GO:0016585	Chromatin remodeling complex	3	2.4	0.0909	IP100410330, IP100375731, IP100642705	92	71	12,782	5.870484	1	0.464602	70.67736
GOTERM	GO:0005719	Nuclear Euchromatin	2	1.6	0.021208	IP100297579, IP100438229	92	3	12,782	92.62319	0.993648	0.170862	24.115
GOTERM	GO:0000791	Euchromatin	2	1.6	0.028178	IP100297579, IP100438229	92	4	12,782	69.46739	0.998824	0.207533	30.78477

Supplementary Table 2. Continued

Category	GO	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM _CC_FAT	GO:0005662	DNA replication factor A complex	2	1.6	0.041971	IP100020127, IP100013939	92	6	12,782	46.31159	0.99996	0.2785	42.41841
GOTERM _CC_FAT	GO:0070688	MLL5-L complex	2	1.6	0.055571	IP100027423, IP100021439	92	8	12,782	34.7337	0.999999	0.344044	52.09806
GOTERM _CC_FAT	GO:0043601	Nuclear replisome	2	1.6	0.095234	IP100020127, IP100013939	92	14	12,782	19.84783	1	0.462885	72.42687
GOTERM _CC_FAT	GO:0030894	Replisome	2	1.6	0.095234	IP100020127, IP100013939	92	14	12,782	19.84783	1	0.462885	72.42687

HP1 γ , heterochromatin protein 1 γ ; FDR, false discovery rate.

Supplementary Table 3. Functional annotation of proteins that interact with HP1 γ

Category	Term	Count	%	p-value	Genes	List total	Pop his	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	Pre-mRNA splicing	2	1.6	0.043219	IP100012382, IP100010740	122	7	19,235	45.04684	0.999914	0.218453	42.82394
SP_PIR_KEYWORDS	Molecular chaperone	2	1.6	0.078785	IP100003865, IP100304925	122	13	19,235	24.25599	1	0.339143	64.59688
SP_PIR_KEYWORDS	Methylated amino acid	3	2.4	0.006924	IP100514201, IP100021439, IP100025039	122	20	19,235	23.64959	0.770779	0.05722	8.416762
SP_PIR_KEYWORDS	DNA recombination	3	2.4	0.022645	IP100220834, IP100010740, IP100304596	122	37	19,235	12.78356	0.992218	0.136834	25.16092
SP_PIR_KEYWORDS	Tandem repeat	3	2.4	0.080974	IP100514201, IP100743873, IP100221354	122	75	19,235	6.306557	1	0.340526	65.64666
SP_PIR_KEYWORDS	Actin binding	4	3.2	0.002024	IP100514201, IP100219301, IP100218319, IP100026314	122	40	19,235	15.76639	0.349244	0.021252	2.531646
SP_PIR_KEYWORDS	DNA replication	4	3.2	0.018087	IP100021700, IP100004859, IP100020127, IP100019399	122	88	19,235	7.166542	0.979134	0.11735	20.62318
SP_PIR_KEYWORDS	Viral nucleoprotein	5	4	3.13E-05	IP100883857, IP100027834, IP100216049, IP100013070, IP100304692	122	29	19,235	27.18344	0.00662	5.11E-04	0.039637
SP_PIR_KEYWORDS	Nucleotide binding	5	4	0.004672	IP100514201, IP100186290, IP100883857, IP100651653, IP100385383	122	107	19,235	7.367474	0.629456	0.046175	5.753405
SP_PIR_KEYWORDS	P-loop	5	4	0.006209	IP100514201, IP100186290, IP100883857, IP100651653, IP100385383	122	116	19,235	6.795859	0.732969	0.058252	7.578378
SP_PIR_KEYWORDS	Helicase	5	4	0.010218	IP100004859, IP100293655, IP100220834, IP100651653, IP100396435	122	134	19,235	5.882983	0.88665	0.080331	12.18636
SP_PIR_KEYWORDS	Protein biosynthesis	5	4	0.03105	IP100186290, IP100012079, IP100419880, IP100023048, IP100413108	122	188	19,235	4.19319	0.998753	0.173915	32.90918
SP_PIR_KEYWORDS	Proto-oncogene	5	4	0.057456	IP100218319, IP100020194, IP100220823, IP100009841, IP100221354	122	230	19,235	3.427477	0.999996	0.269202	52.70412
SP_PIR_KEYWORDS	ATP	6	4.8	0.016799	IP100514201, IP100883857, IP100003865, IP100651653, IP100385383, IP100304925	122	236	19,235	4.008405	0.972445	0.116485	19.2948

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	wd repeat	6	4.8	0.030418	IP100013468, IP100152695, IP100166044, IP100782966, IP100106567, IP100012202	122	276	19,235	3.427477	0.998568	0.175197	32.35328
SP_PIR_KEYWORDS	DNA binding	6	4.8	0.063737	IP100028888, IP100031801, IP100220834, IP100031812, IP100216049, IP100010740	122	340	19,235	2.782305	0.999999	0.288612	56.54055
SP_PIR_KEYWORDS	RNA binding	8	6.4	3.47E-10	IP100012382, IP100396378, IP100012079, IP100020194, IP100008575, IP100651653, IP100216049, IP100221354	122	28	19,235	45.04684	7.36E-08	9.20E-09	4.39E-07
SP_PIR_KEYWORDS	Actin-binding	8	6.4	9.65E-04	IP100514201, IP100219301, IP100218319, IP100026314, IP100008918, IP100645369, IP100005087, IP100003406	122	247	19,235	5.106524	0.185084	0.011306	1.214166
SP_PIR_KEYWORDS	Chromosomal rearrangement	8	6.4	0.00194	IP100218319, IP100020194, IP100220823, IP100009841, IP100941117, IP100221354, IP100010740, IP100304596	122	279	19,235	4.52083	0.337459	0.021434	2.427178
SP_PIR_KEYWORDS	Activator	9	7.2	0.01704	IP100302755, IP100014513, IP100104050, IP100760877, IP100100798, IP100013070, IP100103525, IP100010740, IP100304596	122	520	19,235	2.728799	0.973844	0.11437	19.54546
SP_PIR_KEYWORDS	Spliceosome	10	8	6.65E-08	IP100012382, IP100396378, IP100328840, IP100883857, IP100782992, IP100419373, IP100216049, IP100216592, IP100008524, IP100304692	122	120	19,235	13.13866	1.41E-05	1.28E-06	8.41E-05
SP_PIR_KEYWORDS	Isopeptide bond	10	8	1.88E-04	IP100514201, IP100217465, IP100013468, IP100021700, IP100645369, IP100031812, IP100216049, IP100100798, IP100216592, IP100922213	122	319	19,235	4.942443	0.039166	0.002494	0.238181
SP_PIR_KEYWORDS	ubl conjugation	10	8	0.01201	IP100514201, IP100217465, IP100013468, IP100021700, IP100220834, IP100645369, IP100031812, IP100216049, IP100100798, IP100216592	122	588	19,235	2.681359	0.922821	0.087426	14.17792

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	Cytoskeleton	11	8.8	0.006886	IP100029601, IP1000219301, IP100004795, IP1000218319, IP100026314, IP1000008918, IP1000645369, IP1000784869, IP100021439, IP1000005087, IP100449306	122	636	19,235	2.726892	0.768904	0.059213	8.372229
SP_PIR_KEYWORDS	Ribonucleoprotein	14	11.2	2.31E-08	IP100396378, IP100028888, IP100025039, IP1000216592, IP100413108, IP1000304692, IP100012382, IP100883857, IP100027834, IP100419880, IP100419373, IP1000216049, IP100016610, IP100013070	122	279	19,235	7.911452	4.90E-06	4.90E-07	2.93E-05
SP_PIR_KEYWORDS	Repressor	14	11.2	3.63E-06	IP100302755, IP100297579, IP100410330, IP100031801, IP100014513, IP100006079, IP100100798, IP100010740, IP100438229, IP100031812, IP100009841, IP100045914, IP100013070, IP1000300631	122	435	19,235	5.074242	7.69E-04	6.41E-05	0.00459
SP_PIR_KEYWORDS	ATP-binding	16	12.8	0.019301	IP100514201, IP100293655, IP100003865, IP100651653, IP100385383, IP100788168, IP100550263, IP100003362, IP100004859, IP100883857, IP100784869, IP100220834, IP100021439, IP100104050, IP100396435, IP100304925	122	1,326	19,235	1.902431	0.983947	0.121132	21.85584
SP_PIR_KEYWORDS	mRNA splicing	17	13.6	2.78E-13	IP100396378, IP100375731, IP100479786, IP100216592, IP100010740, IP100304692, IP100012382, IP100328840, IP100883857, IP100029400, IP100782992, IP100419373, IP100031812, IP1000216049, IP100396435, IP100008524, IP100304596	122	209	19,235	12.82434	5.89E-11	9.82E-12	3.52E-10

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	mRNA processing	17	13.6	7.90E-12	IP100396378, IP100375731, IP100479786, IP100216592, IP100010740, IP100304692, IP100012382, IP100328840, IP100883857, IP100029400, IP100782992, IP100419373, IP100031812, IP100216049, IP100396435, IP100008524, IP100304596	122	260	19,235	10.3088	1.67E-09	2.39E-10	9.99E-09
SP_PIR_KEYWORDS	Nucleotide-binding	18	14.4	0.035014	IP100514201, IP100186290, IP100293655, IP100003865, IP100651653, IP100385383, IP100788168, IP100550263, IP100003362, IP100004859, IP100883857, IP100784869, IP100220834, IP100021439, IP100104050, IP100396435, IP100007752, IP100304925	122	1,686	19,235	1.683245	0.999477	0.184714	36.30018
SP_PIR_KEYWORDS	Methylation	20	16	8.04E-16	IP100514201, IP100396378, IP100020194, IP100028888, IP100025039, IP100008575, IP100010740, IP100304692, IP100217465, IP100328840, IP100883857, IP100021439, IP100104050, IP100419373, IP100009841, IP100216049, IP100219330, IP100013070, IP100221354, IP100008524	122	242	19,235	13.03008	1.65E-13	3.30E-14	9.88E-13
SP_PIR_KEYWORDS	Zinc-finger	20	16	0.010866	IP100302755, IP100449924, IP100020194, IP100410330, IP100020127, IP100014513, IP100884250, IP100375731, IP100782966, IP100410717, IP100550263, IP100029400, IP100438229, IP100220823, IP100465370, IP100009841, IP100941117, IP100165981, IP100221354, IP100789624	122	1,718	19,235	1.835436	0.90135	0.082208	12.91138

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR												
SP_PIR_KEYWORDS	Coiled coil	20	16	0.048022	IP100514201, IP100783872,	122	2,019	19,235	1.561802	0.999971	0.234722	46.35145												
					IP100183699, IP100218319,																			
					IP100410330, IP100394855,																			
					IP100103525, IP100396218,																			
					IP100011986, IP100410717,																			
					IP100550263, IP100929313,																			
					IP100784869, IP100645369,																			
					IP100782992, IP100465370,																			
					IP100760877, IP100045914,																			
					IP100165981, IP100304596																			
					SP_PIR_KEYWORDS								Zinc	22	17.6	0.031959	IP100302755, IP100449924,	122	2,189	19,235	1.584562	0.998978	0.174097	33.7013
																	IP100020194, IP100410330,							
																	IP100008918, IP100020127,							
IP100014513, IP100884250,																								
IP100375731, IP100782966,																								
IP100410717, IP100027423,																								
IP100550263, IP100029400,																								
IP100438229, IP100220823,																								
IP100465370, IP100009841,																								
IP100941117, IP100165981,																								
IP100221354, IP100789624																								
SP_PIR_KEYWORDS	DNA-binding	26	20.8	2.16E-04		IP100020194, IP100028888,	122	1,868	19,235	2.194466	0.044702	0.002686					0.272584							
						IP100031801, IP100014513,																		
					IP100479786, IP100010740,																			
					IP100888857, IP100220823,																			
					IP100219330, IP100216049,																			
					IP100016610, IP100300631,																			
					IP100304596, IP100183699,																			
					IP100020127, IP100884250,																			
					IP100006079, IP100021700,																			
					IP100217465, IP100004859,																			
					IP100220834, IP100031812,																			
					IP100009841, IP100045914,																			
					IP100642705, IP100221354																			
SP_PIR_KEYWORDS	Transcription regulation	28	22.4	1.22E-04	IP100028888, IP100031801,	122	2,026	19,235	2.178968	0.025576	0.001849	0.154519												
					IP100014513, IP100008575,																			
					IP100479786, IP100103525,																			

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
					IP100456853, IP100165981, IP100008524, IP100183699, IP100166044, IP100410330, IP100008918, IP100006079, IP100013939, IP100216592, IP100010486, IP100410717, IP100412714, IP100009841, IP100023048, IP100013070, IP100221354, IP100783872, IP100449924, IP100020194, IP100003865, IP100418819, IP100103525, IP100010740, IP100922213, IP100027423, IP100029400, IP100158804, IP100220823, IP100782992, IP100216049, IP100219330, IP100743873, IP100789624, IP100003406, IP100396378, IP100218319, IP100026314, IP100015625, IP100011986, IP100784869, IP100645369, IP100419373, IP100642705, IP100026612, IP100064328	122	2,635	19,235	4.008912	4.64E-24	4.64E-24	2.77E-23
SP_PIR_KEYWORDS	Acetylation	67	53.6	2.19E-26	IP100015018, IP100012079, IP100028888, IP100375731, IP100029019, IP100008575, IP100479786, IP100304692, IP100413108, IP100012382, IP100013468, IP100000816, IP100004795, IP100883857, IP100438229, IP100104050, IP100007102, IP100008524, IP100304596, IP100293655, IP100020127, IP100006079, IP100216592, IP100013939, IP100410717, IP100412714, IP100003362, IP100021700,	67	53.6	2.19E-26				

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR				
					IP100152695, IP100023048, IP100740961, IP100013070, IP100304925, IP100449924, IP100020194, IP100003865, IP100103525, IP100010740, IP100027423, IP100008868, IP100029400, IP100027834, IP100419880, IP100782992, IP100216049, IP100219330, IP100743873, IP100300631, IP100003406, IP100029601, IP100396378, IP100186290, IP100218319, IP100297579, IP100025039, IP100217465, IP100004859, IP100328840, IP100220834, IP100021439, IP100419373, IP100031812, IP100396435, IP100007752, IP100642705, IP100106567, IP100064328	122	4,283	19,235	2.539998	1.18E-13	2.94E-14	6.99E-13				
SP_PIR_KEYWORDS	Nucleus	69	55.2	5.26E-16	IP100028888, IP100031801, IP100014513, IP100375731, IP100651653, IP100008575, IP100479786, IP100304692, IP100413108, IP100012382, IP100013468, IP100004795, IP100883857, IP100438229, IP100104050, IP100016610, IP100760877, IP100008524, IP100304596, IP100183699, IP100410330, IP100020127, IP100884250, IP100006079, IP100216592, IP100013939, IP100410717, IP100412714, IP100021700, IP100152695, IP100642862, IP100009841, IP100045914, IP100740961,	69	55.2	5.26E-16								

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR			
					IP100013070, IP100221354, IP10044924, IP100020194, IP100103525, IP100782966, IP100010740, IP100027423, IP100029400, IP100419880, IP100027834, IP100158804, IP100220823, IP100782992, IP100216049, IP100219330, IP100941117, IP100300631, IP100012202, IP100396378, IP100302755, IP100297579, IP100025039, IP100100798, IP100217465, IP100032995, IP100004859, IP100328840, IP100220834, IP100419373, IP100031812, IP100396435, IP100642705, IP100106567, IP100064328	122	7,263	19,235	2.170783	4.71E-21	1.57E-21	2.81E-20			
SP_PIR_KEYWORDS	Phosphoprotein	100	80	2.22E-23	IP100012079, IP100028888, IP100031801, IP100014513, IP100008575, IP100651653, IP100413108, IP100550263, IP100013468, IP100000816, IP10088857, IP100307257, IP100104050, IP100016610, IP100304596, IP100183699, IP100166044, IP100410330, IP100293655, IP100006079, IP100013939, IP100216592, IP100010486, IP100412714, IP100003362, IP100152695, IP100103552, IP100642862, IP100023048, IP100013070, IP100011736, IP100221354, IP100020194, IP100003865, IP100418819, IP100385383, IP100782992, IP100219330,	100	80	2.22E-23							

Supplementary Table 3. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
					IP100789624, IP100003406,							
					IP100012202, IP100396378,							
					IP100218319, IP100297579,							
					IP100025039, IP100100798,							
					IP100217465, IP100004859,							
					IP100021439, IP100396435,							
					IP100642705, IP100375731,							
					IP100029019, IP100479786,							
					IP100304692, IP100788168,							
					IP100012382, IP100004795,							
					IP100438229, IP100760877,							
					IP100005087, IP100456853,							
					IP100008524, IP100008918,							
					IP100020127, IP100396218,							
					IP100410717, IP100219301,							
					IP100009841, IP100045914,							
					IP100740961, IP100304925,							
					IP100783872, IP100449924,							
					IP100103525, IP100782966,							
					IP100010740, IP100922213,							
					IP100027423, IP100008868,							
					IP100029400, IP100027834,							
					IP100419880, IP100220823,							
					IP100465370, IP100216049,							
					IP100743873, IP100941117,							
					IP100300631, IP100029601,							
					IP100186290, IP100026314,							
					IP100032995, IP100328840,							
					IP100220834, IP100645369,							
					IP100031812, IP100419373,							
					IP100007752, IP100106567							

HP1 γ , heterochromatin protein 1 γ ; FDR, false discovery rate.

Supplementary Table 4. Analysis of domains in proteins that interact with HP1 γ

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000504	RNA recognition motif, RNP-1	20	16	1.31E-16	IP100396378, IP100012079, IP100020194, IP100028888, IP100375731, IP100216592, IP100103525, IP100010740, IP100304692, IP100012382, IP100328840, IP100027834, IP100642862, IP100419373, IP100009841, IP100045914, IP100221354, IP100300631, IP100008524, IP100304596	111	211	16,659	14.22569	2.89E-14	2.89E-14
INTERPRO	IPR012677	Nucleotide-binding, alpha-beta plait	20	16	1.56E-16	IP100396378, IP100012079, IP100020194, IP100028888, IP100375731, IP100216592, IP100103525, IP100010740, IP100304692, IP100012382, IP100328840, IP100027834, IP100642862, IP100419373, IP100009841, IP100045914, IP100221354, IP100300631, IP100008524, IP100304596	111	213	16,659	14.09212	2.89E-14	1.44E-14
INTERPRO	IPR015943	WD40/YVTN repeat-like	7	5.6	0.014599	IP100013468, IP100152695, IP100166044, IP100782966, IP100106567, IP100010486, IP100012202	111	300	16,659	3.501892	0.978154	0.293628
INTERPRO	IPR017986	WD40 repeat, region	6	4.8	0.020816	IP100013468, IP100152695, IP100166044, IP100782966, IP100106567, IP100012202	111	238	16,659	3.783557	0.995785	0.366039
INTERPRO	IPR019781	WD40 repeat, subgroup	6	4.8	0.022182	IP100013468, IP100152695, IP100166044, IP100782966, IP100106567, IP100012202	111	242	16,659	3.721019	0.997069	0.361504
INTERPRO	IPR001680	WD40 repeat	6	4.8	0.031608	IP100013468, IP100152695, IP100166044, IP100782966, IP100106567, IP100012202	111	266	16,659	3.385288	0.999764	0.426908
INTERPRO	IPR019775	WD40 repeat, conserved site	6	4.8	0.036655	IP100013468, IP100152695, IP100166044, IP100782966, IP100106567, IP100012202	111	277	16,659	3.250854	0.999939	0.416904

Supplementary Table 4. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001876	Zinc finger, RanBP2-type	5	4	1.73E-05	IP100020194, IP100029400, IP100375731, IP100009841, IP100221354	111	24	16,659	31.26689	0.00448	0.001496
INTERPRO	IPR019782	WD40 repeat 2	5	4	0.062771	IP100013468, IP100152695, IP100782966, IP100106567, IP100012202	111	226	16,659	3.320378	1	0.519455
INTERPRO	IPR004088	K Homology, type 1	4	3.2	0.001323	IP100008575, IP100216049, IP100016610, IP100479786	111	33	16,659	18.19165	0.291229	0.066528
INTERPRO	IPR018111	K Homology, type 1, subgroup	4	3.2	0.001572	IP100008575, IP100216049, IP100016610, IP100479786	111	35	16,659	17.15212	0.335714	0.065902
INTERPRO	IPR012340	Nucleic acid-binding, OB-fold	4	3.2	0.005163	IP100031801, IP100020127, IP100031812, IP100013939	111	53	16,659	11.32687	0.739699	0.138901
INTERPRO	IPR001650	DNA/RNA helicase, C-terminal	4	3.2	0.033901	IP100004859, IP100293655, IP100651653, IP100396435	111	107	16,659	5.610508	0.999872	0.429048
INTERPRO	IPR014021	Helicase, superfamily 1 and 2, ATP-binding	4	3.2	0.033901	IP100004859, IP100293655, IP100651653, IP100396435	111	107	16,659	5.610508	0.999872	0.429048
INTERPRO	IPR014001	DEAD-like helicase, N-terminal	4	3.2	0.035523	IP100004859, IP100293655, IP100651653, IP100396435	111	109	16,659	5.507563	0.999918	0.424878
INTERPRO	IPR012975	NOPS	3	2.4	1.29E-04	IP100103525, IP100010740, IP100304596	111	3	16,659	150.0811	0.033001	0.008354
INTERPRO	IPR013126	Heat shock protein 70	3	2.4	0.002731	IP100003362, IP100003865, IP100304925	111	12	16,659	37.52027	0.508862	0.096587
INTERPRO	IPR001023	Heat shock protein Hsp70	3	2.4	0.002731	IP100003362, IP100003865, IP100304925	111	12	16,659	37.52027	0.508862	0.096587
INTERPRO	IPR018181	Heat shock protein 70, conserved site	3	2.4	0.004289	IP100003362, IP100003865, IP100304925	111	15	16,659	30.01622	0.672914	0.130373
INTERPRO	IPR003034	DNA-binding SAP	3	2.4	0.009985	IP100883857, IP100013070, IP100300631	111	23	16,659	19.57579	0.926408	0.229658
INTERPRO	IPR004087	K Homology	3	2.4	0.024759	IP100008575, IP100216049, IP100479786	111	37	16,659	12.16874	0.998524	0.372246
INTERPRO	IPR018355	SPla/Ryanodine receptor subgroup	3	2.4	0.051154	IP100883857, IP100293655, IP100013070	111	55	16,659	8.186241	0.999999	0.494708
INTERPRO	IPR011545	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	3	2.4	0.061467	IP100004859, IP100293655, IP100651653	111	61	16,659	7.381037	1	0.527498

Supplementary Table 4. Continued

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR019844	Cold-shock conserved site	2	1.6	0.038976	IP100031801, IP100031812	111	6	16,659	50.02703	0.999968	0.419592
INTERPRO	IPR011129	Cold shock protein	2	1.6	0.05163	IP100031801, IP100031812	111	8	16,659	37.52027	0.999999	0.481244
INTERPRO	IPR002059	Cold-shock protein, DNA-binding	2	1.6	0.05163	IP100031801, IP100031812	111	8	16,659	37.52027	0.999999	0.481244
INTERPRO	IPR004365	Nucleic acid binding, OB-fold, tRNA /helicase-type	2	1.6	0.076446	IP100020127, IP100013939	111	12	16,659	25.01351	1	0.577484

HP1 γ ; heterochromatin protein 1 γ ; FDR, false discovery rate.

Supplementary Table 5. Gene ontology analysis of DNA damage response-related genes that interact with HP1 γ

Category	Term	Count	%	p-value	Genes	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006281 DNA repair	8	8	0.456100342	0.005651094	BLM, XRCC5, RPA2, SFPQ, PCNA	103	284	13.528	3.69971	0.99036	0.1983
GOTERM_BP_FAT	GO:0006310 DNA recombination	5	5	0.285062714	0.008141841	BLM, SVPQ, RPA1, XRCC5	103	105	13.528	6.25428	0.99876	0.24344
GOTERM_BP_FAT	GO:0006974 Response to DNA damage stimulus	8	8	0.456100342	0.02262858	BLM XRCC5, RPA2, PLZF, SFPQ, PCNA	103	373	13.528	2.81694	1	0.43337
GOTERM_BP_FAT	GO:0051276 Chromosome organization	9	9	0.513112885	0.030032507	BLM, XRCC5, SAFB, CBX3, ARID1A BUB3	103	485	13.528	2.43723	1	0.47289
GOTERM_BP_FAT	GO:0006259 DNA metabolic process	9	9	0.513112885	0.037197279	BLM, SFPQ, POGZ, XRCC5, RPA2, PCNA	103	506	13.528	2.33608	1	0.5225
GOTERM_BP_FAT	GO:0006289 Nucleotide -excision repair	3	3	0.171037628	0.06459413	RPA2, PCNA	103	55	13.528	7.16399	1	0.66505
GOTERM_BP_FAT	GO:0006302 Double-strand break repair	3	3	0.171037628	0.079548154	BLM, XRCC5	103	62	13.528	6.35515	1	0.71554

HP1 γ , heterochromatin protein 1 γ ; FDR, false discovery rate.