Supplementary information

Manuscript title: Chromatin modification by SUMO-1 stimulates the promoters of translation machinery genes

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Supplementary Figure S1: Characterization of HeLa-SUMO cell line. A. Illustration of His6-biotin-tagged SUMO-1 (HBT-SUMO-1) protein used in this study. Protein domains are not drawn to scale. The His6 domain binds to Ni-NTA matrix, and the naturally biotinylated domain binds to streptavidin matrix. **B.** Western blot analysis showing SUMOylated proteins in whole cell lysates from HeLa-SUMO (lane 1) and HeLa (lane 2) cells. The arrow indicates the recombinant SUMO-1 protein and the asterisk indicates the endogenous SUMO-1 protein. Left panel showed biotinylated conjugates detected using streptavidin linked with HRP, whereas the right panel showed the SUMO-1 conjugates detected using SUMO-1 antibody. **C.** Western blot showing the fractionation of SUMOylated chromatin from HeLa-SUMO cells. Chromatin was isolated in the presence of high salt and fragmented by sonication (lane 1). The isolated chromatin was then purified using the Ni-NTA metal ion affinity matrix (lane 2) and subsequently using streptavidin-agarose (lane 3) affinity purification. **D.** Flow cytometry analysis of DNA content of the samples used for ChAP-seq analysis. HeLa-SUMO cells were double blocked in thymidine and released for 13 h (G1), 0 h (S0), 3 h (S3), or 6 h (S6), or the cells were blocked in thymidine and released into nocodazole (M) as described in the Methods section. **E.** FACS analysis of phospho-H3 and propidium iodide stained cells arrested using the thymidine/nocodazole protocol.

Supplementary Figure S2: Binding patterns of tagged-SUMO-1 detected by ChAP-seq are highly similar to the binding patterns of native SUMO-1

detected by ChIP-seq. A. Histogram of the tag densities (bin size =1 kb) of SUMO-1 binding sites on chromosome 1 of the human genome (hg 18) in the S0 sample by using two types of purification strategy, ChIP-seq and ChAP-seq. The frequency of raw reads was plotted along the length of the chromosome 1. Samples were: ChAP-SUMO purified DNAs from HeLa-SUMO cells during S0 (red, panel 1, top), ChIP-SUMO purified DNAs using SUMO-1 specific IgG antibody and chromatin from HeLa cells that do not express tagged SUMO-1 (black, panel 2), ChIP using purified IgG from the matched pre-immune IgG (gray, panel 3). A diagram of chromosome 1 is shown at the bottom. **B.** SUMO-1 binding tracing for a representative stretch of chromosome 1. A ~750 kb multi-gene cluster is shown and detected SUMO-1 tag density is shown for the tagged SUMO-1 (red, top), endogenous SUMO-1 immunoprecipitated using SUMO-1 specific IgG (black, middle), and endogenous chromatin immunoprecipitated using pre-immune IgG (gray, bottom). **C.** *NOSIP* gene as an example of SUMO-1 tracing in IGV genome browser shows the consistency among the ChAP-seq samples and the ChIP-seq samples. Three replicates are shown of the early S phase (S0) ChAP-seq results (S0-1 to -3), ChAP-seq from an untagged cell line (fourth tier), ChIP-seq using SUMO-1 specific IgG (fifth tier) and ChIP-seq using pre-immune IgG (bottom tier). **D.** Scatter plot analysis of the peaks of ChIP-SUMO-1 (x-axis) against those of the double-affinity purified tagged-SUMO-1 (y-axis). The Pearson correlation coefficient (*R)* between these two methods is 0.989.

Supplementary Figure S3: SUMO-1 marks chromatin at active sites on human genome. A. The analysis in Figure 1B is shown with percentages of SUMO-1 reads shown, as opposed to fold-change shown in Figure 1B. Peak annotation depicts the percentage of SUMO-1 binding sites on defined sequence elements in the human genome (hg 18). G1 (blue), early S phase (S0, red), mid S phase (S3, green), late S phase (S6, purple), and mitosis (M, orange), and error bars are SEM from three biological repeats. The black bar represents the frequency of the genetic element in the genome and the expected percentage of the reads if the SUMO-1 locations were random. **B.** Peak annotation depicts of SUMO-1 binding sites on promoter region (5 kb upstream of TSSs as in Panel A; left) and promoters that have no CpG islands (right). **C.** Peak annotation depicts of SUMO-1 binding percentage on exon1 or exon (1+2+3) region (gray) compared to exon distribution in the genome (black).

Supplementary Figure S4: SUMO-1 binding pattern associates with highly transcribed genes in synchronized cells. A histogram is shown of the average gene expression of high SUMO-1-labeled genes (gray) and low SUMO-1-labeled genes (black) from various cell cycle stages using a cell-cycle synchronized HeLa cell mRNA microarray dataset (GSE26922). High SUMO-1-labeled genes are defined as those genes for which the SUMO-1 average tag density at the promoter was the 10% highest, and low SUMO-1 labeled genes are defined as those upstream of genes for which the SUMO-1 average tag density were the

10% least abundant in ChAP-seq datasets. (*, the data of S12 from GSE26922 was used for G1; **, S4 from GSE26922 was used for S3 in this study.

Supplementary Figure S5: RNA-seq showing the high reproducibility of biological replicates. Scatter plot shows the FPKM of each gene from replicate 2 (y-axis) against replicate 1 (x-axis). Pearson correlation coefficient is shown in *R*. Scatter plot for replicates from the control siRNA (*top*) and the SUMO-1 specific siRNA (*bottom*) are shown.

Supplementary Figure S6: Validation of RNA-seq data under SUMO-1 depletion showing an enrichment of genes that encodes protein translation factors. A. Pathway analysis results for genes affected by SUMO-1 depletion are shown. The histogram shows the down regulated (blue) and up regulated genes (red) secondary to SUMO-1 depletion have statistically significant enrichment for the indicated functions. The x-axis is the –log(*p*-value). **B.** Heat map of those genes that significantly changed expression following depletion of SUMO-1 and which are classified as encoding protein translation factors. The expression intensities were row-wise scaled for the specified genes determined to be significantly changed (adj. *p*-value <0.05). Green color indicates lower relative expression and red indicates higher relative expression. **C.** A second siRNA specific for SUMO-1 was used for validation of RNA-seq data shown in Figure 6C. Fold change relative to the control siRNA is represented in $\log_2$ scale for SUMO-1 depletion. The mRNA expression level for each experiment was normalized to

Polr2a (a non-SUMO-1-labeled gene) and to the result with the control siRNA. Four biological replicates were done and error bars reflect the SEM. A western blot is shown to evaluate SUMO-1 protein depletion by the indicated siRNA transfection.

Supplementary Figure S7: SUMO-1 marks on promoter of ribosomal protein genes. Examples of SUMO-1 tracing on specific promoters in G1 phase, mitosis from ChAP-seq data, and S0 phase from ChIP-seq data, are shown above the gene map drawn from the IGV genome browser. Genes shown are *RPL5, RPL7A, RPL10A, RPL26, SLC1A3*, and *PKM2*.

Supplementary Table S1. Overlapping of mapped reads between biological replicates of ChAP-seq experiments

Overlapping among samples (%)			
	S0_091117	S0_100604	S0_100719
S0_091117	100	61	56
S0_100604		100	52
S0_100719			100
	S3_091117	S3_100604	S3_100719
S3_091117	100	91	79
S3_100604		100	78
S3_100719			100
	S6_091221	S6_100604	S6_100812
S6_091221	100	87	77
S6_100604		100	79
S6_100812			100
	M0_100719	M0_100604	M0_100812
M0_100719	100	41	42
M0_100604		100	74
M0_100812			100
	G1_100719	G1_100604	G1_100831
G1_100719	100	89	95
G1_100604		100	79
G1_100831			100

Supplementary Table S2. Ingenuity Pathway Analysis of 127 genes with constant SUMO-1 marks on active promoters during interphase.

Category	*p*-Value	Molecules	# Molecules
Protein Synthesis	6.68E-08	ALG3, DTL, EEF2, MRPL13, MYC, PSMB3, PSMC2, RPL13, RPL18, RPL32, RPL36, RPL38, RPL18A, RPL36A, RPS24, RPS27, RPS29, TNRC6B, WARS	19
Cancer	1.40E-04	ABCD3, AHCYL1, AKAP12, ALG3, ANXA2, BMP6, CD9, CD58, CDKN1C, CNP, CRYZ, CX3CL1, CYR61, DUSP1, ETFA, FTH1, ILF2, JAK1, LASP1, LASS2, LEPR, LRRC8D, MAP1LC3B, MRCL3, MRPL13, MYC, PDCD6, PERP, PHLDA2, PPP1R3C, PRKACB, PRMT1, PSMD4, PTMA, PTPRF, RAE1, S100A2, SLC7A5, SLC9A3R1, STAT3, TMEM106C, TNRC6B, TPD52, TPD52L1, TPM1, TRIP13, USP1, WARS, ZYX	49
Cell Cycle	4.25E-04	AKAP12, ALG3, BMP6, CDKN1C, CREG1, CYR61, DDB1, DTL, DUSP1, GNAI3, MYC, PDCD6, PRMT5, PRPF4, PTPRF, RPS27L, STAT3, TPD52L1, TPM1, TRIP13	20
Other	-	ACADM, AP3D1, BASP1, BHLHB2, BRD9, BRMS1, CCDC72, CLPTM1, CS, DDT, DDX23, DDX27, DDX47, DNASE2, DPP8, DYNC1H1, FAM32A, GGA1, GRPEL1, GTF2IRD1, HMGN4, HSPA9, IARS2, KIAA0100, KIAA0947, LTA4H, M6PRBP1, MAPKAPK3, MARCH6, MLF2, MORF4L2, MRPS12, MTX1, NAPA, NPDC1, NPR3, NPTN, NUP85, OLFML2A, OXCT1, PCBP2, PERP, PH-4, POP5, PPM1J, PSMB7, PSMD1, RAB13, RHOD, S100A10, SEC16A, SEP15, TARS, TEGT, TMED2, TMEM161A, TNRC6B, TOR3A, TPD52, TSC22D3, TTC19, U2AF2, UBE2Q1, UROD, USP13, WDR74, WDR79	67

Supplementary Table S3. Statistics of RNA-seq experiments.

Replicate	Sample	Reads processed	Unique reads aligned (>1 time) in hg18 (%)	Reads failed to align (%)	Reads suppressed due to aligned >40 locations (%)
1	siCtrl	7,503,876	79.85	19.17	0.98
	siSUMO-1	6,539,732	80.11	18.78	1.11
2	siCtrl	6,295,830	80.24	18.73	1.02
	siSUMO-1	5,225,102	79.72	18.99	1.29
3	siCtrl	9,655,866	79.21	19.57	1.22
	siSUMO-1	5,774,962	80.40	18.33	1.26

Supplementary Table S4. Genes with significant change under SUMO-1 depletion based on RNA-seq experiments (cut off range: FPKM> 1).

RefSeq gene	SUMO-1 peak in promoter in G1 phase	Avg FPKM (Ctrlsi)	Avg FPKM (SUMO1si)	Fold Change	*p*-value	Locus
GAPDH	+	3165.56	2896.61	-1.09285	0.000554101	chr12:6513917-6517797
ACTB	+	2281.17	1923.1	-1.18619	3.48E-08	chr7:5533304-5536758
TMSB10		1617.74	1401.93	-1.15394	8.71E-05	chr2:84986273-84987310
GNB2L1	+	1379.36	1223.64	-1.12726	0.00228591	chr5:180596533-180603512
ENO1		1276.72	987.07	-1.29344	1.27E-09	chr1:8843649-8861367
RPS8		1251.12	933.284	-1.34056	1.23E-11	chr1:45013832-45016999
PKM2	+	1241.43	996.898	-1.24529	2.49E-07	chr15:70278423-70310738
RPL5	+	1161.8	722.933	-1.60706	0	chr1:93070181-93080069
B2M		1154.14	1579.76	1.36878	4.44E-16	chr15:42790976-42797649
HSPA8	+	1090.08	958.194	-1.13764	0.00359087	chr11:122433409-122438054
RPL4		1037.73	755.899	-1.37284	3.35E-11	chr15:64578706-64584238
SLC7A5	+	1031.66	1251.49	1.21308	4.36E-06	chr16:86421129-86460601
TPT1		1023.06	890.409	-1.14898	0.0024451	chr13:44809303-44813297
EEF2	+	992.521	816.635	-1.21538	3.65E-05	chr19:3927053-3936461
PFN1	+	981.316	731.969	-1.34065	1.94E-09	chr17:4789691-4792570
RPL26	+	971.445	391.778	-2.47958	0	chr17:8221558-8227290
CALR	+	951.483	596.969	-1.59386	0	chr19:12910413-12916304
ATP5B		946.618	1171.5	1.23756	1.08E-06	chr12:55318225-55326119
S100A11		920.46	707.935	-1.3002	1.51E-07	chr1:150271605-150276135
FTH1	+	911.095	1395.36	1.53152	0	chr11:61473931-61491708
HSP90AB1	+	907.395	779.016	-1.1648	0.00178944	chr6:44322826-44329592
KRT18	+	872.548	484.695	-1.8002	0	chr12:51628921-51632952
RPS16	+	864.082	736.862	-1.17265	0.00149221	chr19:44615686-44618458
RPL3	+	843.773	491.911	-1.7153	0	chr22:38038832-38045616
RPL23		826.394	671.805	-1.23011	6.70E-05	chr17:34259846-34263579
TUBA1B		776.795	614.691	-1.26372	1.45E-05	chr12:47807832-47811571
VIM		751.623	435.162	-1.72723	0	chr10:17310263-17319598
BSG		693.236	537.081	-1.29075	9.01E-06	chr19:522324-534493
FTL		690.837	1233.29	1.78521	0	chr19:54160377-54161948
KRT7	+	678.338	405.714	-1.67196	2.22E-16	chr12:50913220-50928976
TFRC		670.096	568.355	-1.17901	0.00387978	chr3:197260551-197293429
TUBA1C	+	631.553	471.667	-1.33898	1.61E-06	chr12:47945131-47953380
EEF1A1	+	630.907	519.952	-1.21339	0.00109238	chr6:74282193-74287476
CTSZ		627.842	511.921	-1.22644	0.000608803	chr20:57003637-57015704
NPM1	+	602.972	388.209	-1.55321	1.33E-11	chr5:170747312-170770492
HSP90AA1		594.872	371.225	-1.60246	1.01E-12	chr14:101616827-101675839
MYL6		590.916	449.453	-1.31474	1.25E-05	chr12:54838366-54841633
EIF4G2	+	585.943	453.567	-1.29186	4.23E-05	chr11:10775168-10787158
KRT8	+	531.433	374.041	-1.42079	1.95E-07	chr12:51577237-51585135
RPS19		528.147	689.392	1.3053	4.08E-06	chr19:47055827-47067324

RPL13A		519.182	334.026	-1.55432	3.22E-10	chr19:54682676-54687376
TMSL3	+	502.532	383.565	-1.31016	0.000182186	chrX:12903145-12905267
LGALS1		492.092	255.141	-1.92871	0	chr22:36401558-36405755
ASS1	+	490.189	307.008	-1.59667	1.29E-10	chr9:132309914-132366482
RPL7A	+	483.392	375.321	-1.28794	0.000232661	chr9:135204889-135208101
RPL10A	+	482.116	393.341	-1.22569	0.00274277	chr6:35544155-35546536
CD55	+	468.155	361.557	-1.29483	0.000223919	chr1:205561439-205600934
RPS9		460.391	376.197	-1.2238	0.00366156	chr19:59396537-59403327
SCD	+	444.112	279.021	-1.59168	1.17E-09	chr10:102096761-102114578
RPS25		435.905	337.471	-1.29168	0.000302572	chr11:118374061-118394267
S100P		431.097	236.341	-1.82405	1.12E-13	chr4:6746466-6749798
ANXA2P2		425.74	314.374	-1.35425	4.54E-05	chr9:33614222-33615532
SLC3A2	+	423.742	546.605	1.28995	8.47E-05	chr11:62380093-62412929
PRDX6	+	416.744	328.344	-1.26923	0.00123412	chr1:171713108-171724569
HNRNPA2B1		415.326	321.44	-1.29208	0.000561805	chr7:26196080-26206938
HDGF	+	410.071	281.867	-1.45484	1.29E-06	chr1:154978522-154988864
TAGLN2		379.476	205.769	-1.84418	1.55E-12	chr1:158154526-158161908
SPINK4		375.621	142.765	-2.63104	0	chr9:33209069-33501047
PSMA5	+	365.415	251.668	-1.45197	5.30E-06	chr1:109745994-109770560
TM4SF1	+	359.869	446.112	1.23965	0.0024295	chr3:150569494-150578258
UQCRH		355.619	454.048	1.27678	0.000559426	chr1:46541966-46555034
DBI		355.054	263.45	-1.34771	0.000243507	chr2:119840973-119846592
PTMA	+	353.498	265.704	-1.33042	0.000437733	chr2:232281478-232286494
COX4I1		348.771	429.39	1.23115	0.00391642	chr16:84390696-84398108
GPX4		340.213	252.518	-1.34728	0.000332962	chr19:1054935-1057787
MYL12B		334.074	435.61	1.30393	0.000269197	chr18:3252110-3268280
ANXA2	+	333.349	251.976	-1.32294	0.000802544	chr15:58426641-58477477
H19		310.893	185.012	-1.68039	2.27E-08	chr11:1972981-1975641
RBBP7		307.388	236.869	-1.29771	0.00257628	chrX:16772697-16798455
H2AFZ		302.823	212.105	-1.4277	6.99E-05	chr4:101088266-101090535
IFITM3		286.446	478.899	1.67186	5.96E-12	chr11:309672-310914
MGST3	+	285.35	216.446	-1.31834	0.00216804	chr1:163867073-163891479
PCBP1		284.363	199.675	-1.42413	0.000128487	chr2:70168088-70169836
IFI30		284.226	383.45	1.3491	0.000130394	chr19:18145578-18149927
PHB2	+	266.602	187.825	-1.41942	0.000214442	chr12:6944777-6950177
ECEL1		261.868	386.232	1.47491	1.21E-06	chr2:233052780-233060776
ANXA1	+	260.209	144.685	-1.79845	1.52E-08	chr9:74956600-74975127
CYBA		258.076	179.378	-1.43873	0.000182553	chr16:87237197-87244958
SERPINB6	+	250.202	181.426	-1.37909	0.000980085	chr6:2893391-2917089
HSPB1		247.495	164.468	-1.50482	4.86E-05	chr7:75769810-75771549
COX6C		246.976	343.455	1.39064	7.73E-05	chr8:100959547-100975071
SQSTM1		246.643	189.497	-1.30157	0.00153201	chr5:179157204-179218446
EIF3E	+	246.062	183.465	-1.34119	0.00261675	chr8:109283147-109330135
FKBP10		243.292	170.559	-1.42644	0.000375776	chr17:37222487-37232995
ID1		240.035	180.711	-1.32828	0.00399233	chr20:29656752-29657974
ILF2	+	237.655	146.588	-1.62124	4.21E-06	chr1:151901137-151910103
TXNRD1		236.811	104.429	-2.26767	3.04E-12	chr12:103133688-103268192
EIF2S3	+	232.8	298.778	1.28341	0.00431443	chrX:23982985-24006851
COX6A1		232.64	308.797	1.32736	0.00110618	chr12:119360286-119362912
CRIP1		229.783	114.976	-1.99853	1.35E-09	chr14:105024301-105026169
CLU	+	226.454	149.459	-1.51516	8.06E-05	chr8:27510367-27528244

PON2		225.835	299.728	1.3272	0.00131628	chr7:94872109-94902320
FDPS	+	222.012	157.956	-1.40553	0.000138641	chr1:153545162-153567533
PTMS	+	221.692	137.342	-1.61416	1.04E-05	chr12:6745801-6750379
ACADVL		213.496	141.459	-1.50924	0.000115705	chr17:7033933-7069309
LMNA	+	212.428	153.635	-1.38268	0.00269446	chr1:154351084-154376502
PTGES3	+	207.434	141.212	-1.46895	0.000423797	chr12:55343391-55368345
ATP1B3		206.665	342.083	1.65525	1.06E-08	chr3:143078159-143128072
EIF3H		206.603	98.3222	-2.10129	1.36E-09	chr8:117726235-117837243
ECH1		204.159	105.608	-1.93318	3.81E-08	chr19:43997901-44014337
LGALS3		203.47	140.024	-1.45311	0.000668302	chr14:54665624-54681901
DSTN	+	203.197	127.685	-1.59139	3.89E-05	chr20:17498598-17536652
S100A10	+	199.891	107.045	-1.86735	1.84E-07	chr1:150222009-150233338
STMN1		198.924	121.174	-1.64164	1.70E-05	chr1:26083264-26105955
LAPTM4B		198.369	263.426	1.32796	0.00255049	chr8:98856984-98934006
PSMA7		196.165	120.468	-1.62836	2.53E-05	chr20:60145185-60151869
AP2M1		190.846	269.025	1.40964	0.00028586	chr3:185375327-185384573
EIF3D	+	190.716	120.965	-1.57662	8.97E-05	chr22:35236842-35255223
COTL1	+	190.633	81.226	-2.34695	1.21E-10	chr16:83156704-83209170
ATP6V0C		190.103	270.033	1.42046	0.000209575	chr16:2503953-2510220
CBX3		187.39	122.597	-1.5285	0.000260417	chr7:26207623-26219501
GSTM1		186.907	69.7136	-2.68107	2.10E-12	chr1:110031940-110037889
MYC	+	186.51	135.464	-1.37682	0.00461513	chr8:128817496-128822860
ANP32B	+	185.238	112.767	-1.64266	3.25E-05	chr9:99785309-99818045
PEBP1		184.565	266.711	1.44508	0.000120479	chr12:117058252-117067773
JUP	+	182.595	242.119	1.32599	0.00400442	chr17:37164384-37196490
NPTX1		180.415	115.154	-1.56673	0.000167017	chr17:76055227-76064999
TMEM106C	+	179.06	98.3703	-1.82026	1.82E-06	chr12:46643596-46648927
FASN		177.218	124.116	-1.42784	0.00234278	chr17:77629502-77649395
LAMA1		177.009	291.775	1.64836	1.56E-07	chr18:6931885-7107813
PDHA1		171.12	89.3322	-1.91555	6.24E-07	chrX:19271931-19410315
GLO1		168.203	116.297	-1.44632	0.00221368	chr6:38751679-38778930
LAMP1	+	166.428	251.769	1.51278	3.42E-05	chr13:112999469-113025742
SEPP1	+	166.237	251.2	1.5111	3.39E-05	chr5:42792676-42847781
DEGS1		163.54	326.7	1.99768	6.26E-13	chr1:222437550-222447765
BCAP31		163.118	228.042	1.39802	0.00110101	chrX:152619140-152643395
CTSC	+	161.843	76.6107	-2.11254	1.30E-07	chr11:87666407-87710589
PRSS23		161.249	239.394	1.48462	0.000104956	chr11:86189138-86199921
CSRP1	+	158.203	245.658	1.5528	1.58E-05	chr1:199719282-199743010
RPL17		153.241	105.196	-1.45672	0.00307936	chr18:45268853-45272904
SF3B4		145.382	99.5702	-1.4601	0.00361797	chr1:148161834-148166326
NOLC1		141.839	64.63	-2.19463	1.63E-07	chr10:103901922-103913617
PA2G4		140.067	91.3182	-1.53383	0.00147036	chr12:54784369-54793961
TMED9		139.846	93.2077	-1.50037	0.00241195	chr5:176951818-176955705
TNFSF9		139.447	195.16	1.39953	0.00243392	chr19:6482009-6486939
TOB1		138.59	81.5237	-1.7	0.000143724	chr17:46294585-46296412
NDUFA13		137.914	222.521	1.61348	1.01E-05	chr19:19488018-19500013
SEC61A1		137.644	222.097	1.61356	1.03E-05	chr3:129253901-129273216
CDK4		136.978	89.296	-1.53398	0.00113387	chr12:56425050-56432431
EIF4A2	+	136.418	196.482	1.44029	0.000190722	chr3:187984054-188007178
PTP4A2	+	133.386	199.179	1.49325	0.000341518	chr1:32146379-32176575
MYBL2		131.828	54.7774	-2.40661	4.68E-08	chr20:41729122-41778536

SF3B2		130.052	79.7287	-1.63118	0.000581607	chr11:65576391-65592958
MOSC1	+	128.663	83.7188	-1.53685	0.00221052	chr1:219026661-219054363
PPT1		127.465	67.5144	-1.88797	2.48E-05	chr1:40310968-40335729
SLC1A3	+	125.652	209.534	1.66757	6.02E-06	chr5:36642213-36724193
PLOD2	+	123.48	71.3675	-1.7302	0.000227066	chr3:147269917-147361972
PRR13		119.754	56.6394	-2.11432	3.73E-06	chr12:52121699-52126694
ATP6V0B		119.548	190.993	1.59763	5.91E-05	chr1:44213188-44216559
C19orf53	+	118.008	76.9435	-1.5337	0.00351422	chr19:13746256-13750586
CHCHD10		117.264	76.5987	-1.53089	0.00374757	chr22:22435207-22440141
GNG11		117.082	49.8139	-2.35039	4.38E-07	chr7:93388951-93393762
NAP1L1		116.945	62.7968	-1.86228	7.12E-05	chr12:74724938-74765005
HEXB		112.645	168.612	1.49684	5.00E-05	chr5:74016724-74098798
MST4		112.526	68.6696	-1.63866	0.00128021	chrX:130984925-131037652
C19orf33	+	111.15	48.4217	-2.29546	0	chr19:43486039-43498446
RBM3		110.887	63.4101	-1.74873	0.000385613	chrX:48317779-48321748
ITGB5		108.699	59.2342	-1.83507	0.000170556	chr3:125964484-126088834
ADIPOR1	+	107.962	66.8477	-1.61504	0.00206937	chr1:201176583-201194323
CTNNB1	+	105.613	173.743	1.64509	5.53E-05	chr3:41215945-41256943
UBE2T	+	105.121	67.4103	-1.55942	0.00440647	chr1:200567408-200577717
LASS2	+	104.532	161.113	1.54128	0.00057195	chr1:149204272-149214064
CS		104.091	161.047	1.54718	0.000520046	chr12:54951749-54980442
C20orf199		102.885	128.036	1.24446	0.00283344	chr20:47295845-47339202
TMEM147		99.2532	160.971	1.62182	0.000151308	chr19:40728384-40730268
TMEM59		98.8622	162.825	1.64699	9.10E-05	chr1:54269936-54291699
GABARAPL1	+	98.8065	172.888	1.74976	9.15E-06	chr12:10256755-10266991
TPX2		98.4896	55.8945	-1.76206	0.000717693	chr20:29790564-29853264
PPIF		96.5749	160.304	1.65989	8.35E-05	chr10:80777225-80785095
AKR1B1		96.5109	197.005	2.04127	9.29E-09	chr7:133777646-133794428
LITAF		95.8435	151.113	1.57666	0.000488827	chr16:11549082-11588823
RNASEH2A		95.5401	48.3685	-1.97525	0.000114639	chr19:12778427-12785462
WBP11		95.4644	56.026	-1.70393	0.00154206	chr12:14830678-14847668
BAG1		95.0599	128.435	1.3511	0.000411526	chr9:33209069-33501047
ADAM9		94.2488	37.0207	-2.54584	1.45E-06	chr8:38973661-39081936
GSTM3		93.7458	42.9839	-2.18095	2.30E-05	chr1:110078076-110085183
CDK2AP1		93.3409	55.2333	-1.68994	0.00199624	chr12:122311492-122322640
EID1		91.1688	154.638	1.69617	6.01E-05	chr15:46903226-47042933
IMPDH2		91.0115	50.3116	-1.80896	0.0007408	chr3:49036765-49041879
MAZ		90.1238	54.7056	-1.64743	0.00359638	chr16:29725355-29730005
KIAA0100	+	89.8762	134.494	1.49644	0.00309037	chr17:23965584-23996300
UGP2		87.7553	32.9111	-2.66643	1.60E-06	chr2:63921601-63972200
C19orf10		87.3189	39.1076	-2.23279	2.98E-05	chr19:4608556-4621415
SEC13		86.9742	44.091	-1.97261	0.000238159	chr3:10317614-10337858
BZW1		86.1074	163.471	1.89845	3.00E-08	chr2:201384891-201396805
PSIP1	+	85.9316	51.1011	-1.6816	0.00340465	chr9:15454064-15501003
CPA4		85.1551	250.81	2.94533	0	chr7:129720209-129751255
VCL		84.9801	20.7938	-4.0868	8.72E-09	chr10:75427877-75549920
TOP2A		83.1094	49.8408	-1.6675	0.00431588	chr17:35798321-35827695
GALNT2		83.1042	264.266	3.17994	0	chr1:228269578-228484498
ITM2B		81.4877	126.546	1.55295	0.00194256	chr13:47705274-47734233
MCAM	+	81.0242	155.128	1.91459	2.15E-06	chr11:118684443-118693050
SNX2		80.7277	130.759	1.61975	0.000656259	chr5:122138648-122193701

EIF5B	+	80.3231	37.1475	-2.16227	0.000101677	chr2:99320265-99383160
IFITM1		79.9484	235.693	2.94806	0	chr11:303990-305272
LXN		79.2776	40.7719	-1.94442	2.76E-10	chr3:159845010-159893054
C19orf28		79.0613	135.413	1.71276	0.000116645	chr19:3489262-3508571
VAT1		78.3046	135.974	1.73648	0.00010022	chr17:38420147-38427985
CUL4A		76.3783	118.659	1.55357	0.00267249	chr13:112911086-112967393
TAF10	+	75.1144	40.2543	-1.866	6.85E-12	chr11:6581539-6590021
CD59		72.7482	118.198	1.62475	0.00112573	chr11:33681131-33714601
CREG1		72.596	112.244	1.54615	0.00381191	chr1:165776874-165789680
SERPINB5		72.0739	123.307	1.71084	0.000292741	chr18:59295123-59323298
WDR34	+	71.6006	51.8272	-1.38153	3.22E-07	chr9:130354686-130458950
GSR		69.6607	36.2617	-1.92105	0.00143132	chr8:30655976-30704985
INPPL1		69.2457	125.663	1.81474	6.84E-05	chr11:71613529-71632868
TGFBR1	+	68.4929	164.316	2.39902	1.17E-09	chr9:100907232-100956294
CHTF8		66.0538	32.9347	-2.0056	0.000931795	chr16:67697660-67723985
ENO3		65.1649	23.4806	-2.77527	2.23E-05	chr17:4795130-4801148
MGAT4B		64.5175	99.976	1.5496	1.37E-08	chr5:179157204-179218446
PLAC8		64.3183	34.9234	-1.8417	0.00380109	chr4:84230234-84254935
AIMP2		61.9627	45.056	-1.37524	9.70E-06	chr7:6015407-6065386
ACSL4		61.8122	30.4337	-2.03104	0.00137657	chrX:108771219-108863277
OSMR	+	61.2465	136.918	2.23552	1.67E-07	chr5:38881892-38970159
DPH5	+	61.1415	27.7375	-2.20429	0.000555182	chr1:101227768-101263950
SDF4		61.0433	103.459	1.69485	0.00107957	chr1:1142150-1157310
SLC39A6		60.9557	143.498	2.35414	2.72E-08	chr18:31942491-31963355
CCNG1		59.5776	133.896	2.24742	2.01E-07	chr5:162797154-162804600
FAM127A		58.3637	95.9345	1.64374	0.00275607	chrX:133993998-133995241
PCSK9		57.9063	27.754	-2.08641	0.00144467	chr1:55277807-55303111
ACAT2		57.2357	43.6153	-1.31228	0.00304108	chr6:160102978-160130725
NUP210		56.2593	27.8854	-2.01752	0.00244081	chr3:13332736-13436809
SUPT16H		55.8378	28.4818	-1.96047	0.00345997	chr14:20889471-20922265
TMEM2	+	55.558	108.087	1.94548	5.54E-05	chr9:73488101-73573620
NMRAL1	+	55.5213	20.6061	-2.69441	3.55E-13	chr16:4451695-4500349
PDE2A		55.3447	117.378	2.12085	4.01E-06	chr11:71964833-72063142
C6orf176		54.9793	96.3171	1.75188	0.000877378	chr6:166257525-166323093
RGS2	+	54.8423	140.469	2.56133	3.49E-09	chr1:191044791-191048029
DUSP16	+	54.8157	91.026	1.66058	0.00301194	chr12:12520097-12606584
SUMO1		54.5937	15.0985	-3.61584	9.94E-06	chr2:202779147-202811567
TAF6		53.9202	28.6359	-1.88296	4.08E-09	chr7:99528339-99554915
HIBADH		53.2536	24.1791	-2.20246	0.00128283	chr7:27531585-27669127
CEP55		52.4588	25.6568	-2.04464	0.00299841	chr10:95246358-95278839
WARS	+	51.9951	110.668	2.12843	7.14E-06	chr14:99869877-99912433
NNMT		51.9196	115.132	2.21751	1.90E-06	chr11:113671744-113688448
SERINC3		51.0097	85.0008	1.66637	0.00410761	chr20:42558277-42584140
SLC20A1	+	50.5805	92.2513	1.82385	0.000592955	chr2:113119997-113137871
ALDH3B1		50.1812	22.8196	-2.19904	0.00181032	chr11:67532623-67553319
TM7SF3	+	49.7401	123.522	2.48335	6.07E-08	chr12:27015774-27058606
RECQL		48.8933	26.4788	-1.84651	0.00299045	chr12:21481804-21545870
SLC12A3		48.5445	13.3464	-3.63727	2.94E-05	chr16:55456619-55507263
TWF1		47.7225	21.7257	-2.19659	0.00236201	chr12:42473792-42486445
DDAH1	+	47.6282	87.4272	1.83562	0.000744696	chr1:85556756-85816634
CDKN1A		47.5873	223.052	4.68722	0	chr6:36754436-36763087

CPNE1		46.0701	84.5303	1.83482	2.59E-06	chr20:33677379-33716262
DAB2	+	45.9759	87.5991	1.90533	0.000400434	chr5:39407536-39461092
ORMDL2		45.5432	27.0253	-1.68521	0.00138497	chr12:54498072-54509687
GDA		44.5292	78.5331	1.76363	0.00249032	chr9:73954112-74056960
TLCD1	+	44.3445	26.4232	-1.67824	1.69E-08	chr17:24071126-24078076
CALD1		43.9971	15.6236	-2.81607	0.000441386	chr7:134114703-134306019
ANKRD52	+	43.9409	79.0264	1.79847	0.00181459	chr12:54910086-54938410
LYPD3	+	42.5219	73.9633	1.73942	0.00402359	chr19:48656785-48661671
ITFG3		42.3167	18.1372	-2.33314	0.00253842	chr16:224801-256119
EPHX1		42.0285	87.8987	2.09141	3.88E-07	chr1:224064419-224136671
SERPINE2	+	41.7538	85.9276	2.05796	0.00013048	chr2:224548008-224612280
C1QTNF6		41.7514	106.882	2.55996	2.72E-07	chr22:35906151-35914276
STRA6	+	41.6114	18.252	-2.27983	0.00334441	chr15:72258862-72288424
DARS2	+	40.6674	19.7801	-2.05598	0.00160188	chr1:172035310-172094305
PPP2R1B		40.6551	99.7106	2.4526	5.83E-11	chr11:110978379-111142379
PLK2	+	39.7453	79.6388	2.00373	0.00034534	chr5:57785566-57791670
PHLDA3		39.4351	87.2682	2.21296	3.48E-05	chr1:199701244-199704922
DPP7	+	39.2716	70.104	1.78511	0.00364576	chr9:139124812-139129016
FBLN2		39.0498	16.5137	-2.36469	0.00336794	chr3:13565624-13654923
LSMD1		38.4845	24.9111	-1.54487	0.00242442	chr17:7700727-7706325
RPL18AP3		37.3588	73.0774	1.9561	5.43E-05	chr19:17831726-17835124
RASSF8		37.2068	67.6568	1.8184	0.00340213	chr12:26003230-26124091
PIK3R2	+	34.6606	77.0857	2.22402	9.29E-05	chr19:18125015-18142343
BZW1L1		32.7759	68.371	2.08601	1.55E-11	chr2:201384891-201396805
ERCC1	+	32.4645	17.7627	-1.82768	0.00164414	chr19:50574732-50619017
IGFBP3	+	31.9295	71.2642	2.23192	0.000163242	chr7:45918368-45927396
STAT3	+	31.9061	61.7416	1.9351	0.00246729	chr17:37718868-37794039
EPAS1	+	31.2381	87.672	2.80657	7.33E-07	chr2:46378044-46467346
C3	+	29.2586	72.041	2.46222	3.95E-05	chr19:6628845-6671662
DUSP3		28.8184	56.3714	1.95609	0.0033902	chr17:39199014-39211894
LRFN4		28.0421	43.0792	1.53623	0.00184424	chr11:66372572-66482423
KDELR3		27.2026	10.6988	-2.54258	0	chr22:37194028-37232291
SYNC		26.7377	4.93784	-5.41486	0	chr1:32889335-32940948
SAMD11		26.1827	15.6739	-1.67046	0.00134136	chr1:850983-884542
CUTC		24.5774	14.6735	-1.67495	5.58E-06	chr10:101409252-101505884
VWA5A		23.9336	67.0193	2.80022	1.61E-05	chr11:123491320-123522828
SCARNA12		22.9644	17.3226	-1.32569	1.28E-13	chr12:6944777-6950177
SUMO1P3		22.4883	4.87028	-4.61746	0	chr1:158525000-158595366
RAVER2	+	22.3907	37.2057	1.66166	3.13E-09	chr1:64983365-65204775
GDF15	+	22.1827	240.699	10.8508	0	chr19:18357967-18360986
PEG10		21.8543	46.3892	2.12266	0.00371946	chr7:94123572-94136942
SAT2	+	21.4619	33.9234	1.58063	0.000129845	chr17:7435271-7477425
TGFBR3		20.9234	54.1558	2.58829	0.000220305	chr1:91918489-92124375
C1S	+	20.7275	47.8957	2.31073	0.00144645	chr12:7038240-7048594
ACOT13		19.8932	8.1734	-2.4339	8.81E-06	chr6:24775241-24827382
ADCY3		19.2447	6.78757	-2.83529	0.00400527	chr2:24869836-24995559
POLG	+	19.0758	44.8	2.34853	7.92E-09	chr15:87588197-87679030
NR1H3	+	18.8129	9.23537	-2.03705	0.00106626	chr11:47217428-47246977
XPR1		18.5026	41.5556	2.24593	0.00379084	chr1:178867768-179126036
FAS	+	18.4876	45.5618	2.46445	0.00103333	chr10:90684812-90765522
HNRPA1L-2		18.3169	2.30226	-7.95605	0	chr12:52960754-52965297

LOC100270710		17.764	25.3435	1.42668	0.0019143	chr10:99463470-99467895
CFI		17.7457	47.8752	2.69785	0.000355605	chr4:110881296-110942784
HDDC3	+	16.9076	11.5681	-1.46157	0.00115782	chr15:89274413-89298327
CCDC18	+	16.0444	8.65494	-1.85379	0.00189955	chr1:93389996-93516856
CTU2		15.9992	13.5779	-1.17833	0.00125302	chr16:87300391-87378873
KRT17		15.278	97.9417	6.41064	1.43E-11	chr17:37029217-37034408
GBA2		14.373	35.346	2.45919	0	chr9:35687333-35742871
CHAC2		14.3552	8.53411	-1.6821	0.000100251	chr2:53750621-53940674
TRIM14		13.995	33.4725	2.39175	0.000102236	chr9:99858779-99921309
NME7		13.8901	27.1006	1.95107	4.44E-16	chr1:167342570-167603810
PBXIP1		13.6996	33.9256	2.47639	0.00461449	chr1:153183179-153195191
HTRA2		13.4761	7.66007	-1.75927	0.000741462	chr2:74607282-74634570
FAM120AOS		12.6614	7.08997	-1.78582	7.44E-08	chr9:95248602-95368218
SMAGP		12.4986	31.3078	2.5049	0	chr12:49918774-49950469
ATF5		12.4888	22.22	1.77919	0.000848645	chr19:55084722-55129004
MMACHC	+	12.2308	6.6743	-1.83252	1.54E-12	chr1:45738442-45760196
C16orf53		12.0514	3.96318	-3.04084	4.85E-05	chr16:29735028-29766842
PPAP2A		11.9033	18.9682	1.59352	0.000366191	chr5:54639332-54866630
KDELC1		10.6857	22.4204	2.09817	0.000775213	chr13:102234631-102291888
TMEM183A	+	10.0768	23.5762	2.33965	0.000312304	chr1:201243156-201259820
DDIT3		10.0762	14.6834	1.45724	2.39E-05	chr12:56168117-56200567
PLEKHA9		9.68312	5.31114	-1.82317	1.45E-05	chr12:43853113-44120454
TSPAN31		9.58298	5.06361	-1.89252	1.05E-05	chr12:56425050-56432431
CREB3L4	+	7.22463	4.13405	-1.74759	5.09E-07	chr1:152207020-152217075
HCCA2		5.91069	8.69964	1.47185	2.05E-06	chr11:1447268-1742077
LOC100302652		5.6682	9.91736	1.74965	0.000920715	chr2:53750621-53940674
MXD3		5.56056	2.26063	-2.45974	7.79E-08	chr5:176663440-176671898
FAM158A		5.36166	3.54	-1.51459	0.00451339	chr14:23675217-23680637
PIH1D2		5.27113	0.500478	-10.5322	0	chr11:111400747-111450105
YY2		5.26432	9.02292	1.71398	2.41E-05	chrX:21767576-21813461
LENG9	+	5.12877	2.53373	-2.0242	2.10E-05	chr19:59651876-59666706
FTHL3P		4.68882	8.02649	1.71184	1.32E-08	chr2:27457564-27486000
EIF3CL_dup2		3.84277	7.44152	1.9365	1.42E-05	chr16:28630282-28654554
CCDC24		3.19833	1.86549	-1.71447	0.00273831	chr1:44229866-44269721
C5orf45		3.1876	5.25934	1.64994	0	chr5:179157204-179218446
SUGT1P		3.12756	8.63422	2.76069	0	chr9:33209069-33501047
DUSP8		3.08337	6.63625	2.15227	1.23E-07	chr11:1447268-1742077
C18orf56		2.93561	5.53287	1.88474	0	chr18:586997-702662
EFCAB5		2.82826	0.95332	-2.96675	0.00325526	chr17:24977090-25459595
IQCG		2.6985	1.27731	-2.11264	3.39E-12	chr3:199100343-199171283
RPL23AP64		2.34397	3.83666	1.63682	1.11E-09	chr11:118374061-118394267
DNASE1		2.26202	3.65263	1.61476	5.07E-05	chr16:3642940-3707599
PPAN-P2RY11		2.18561	0.816961	-2.67529	1.99E-08	chr19:10077964-10091599
GPR75		2.16913	3.67753	1.69539	0.00229248	chr2:53750621-53940674
PART1		2.07086	4.20706	2.03155	3.72E-06	chr5:58300622-59879241
TYRO3P		1.91505	3.98377	2.08024	3.33E-15	chr15:74295683-74390865
C1orf182	+	1.87327	2.14174	1.14332	0.000388905	chr1:154545375-154583409
PLTP		1.82496	0	-18249.6	0	chr20:43950673-43974193
INE1		1.47898	3.00734	2.03339	0	chrX:46935142-46959471

LNP1	+	1.18628	0.547498	-2.16673	6.52E-07	chr3:101564996-101657860
DGCR11		1.00754	2.01666	2.00157	0.001946	chr22:17403794-17489967
TIAF1		0.989095	1.7083	1.72713	0.00309614	chr17:24424653-24531533
SLC15A3		0.827363	2.26874	2.74213	3.85E-07	chr11:60448488-60475833
HSN2		0.794177	2.17633	2.74036	0	chr12:732485-890879
CCDC152		0.756597	1.28685	1.70084	4.09E-05	chr5:42792676-42847781
LOC29034		0.542746	3.67656	6.774	0	chr2:211050653-211252076
PLAC4		0.147533	3.60753	24.4524	0	chr21:41461597-41570394
LOC338651		0	1.23633	12363.3	0	chr11:1447268-1742077
CCRL1		0	1.27969	12796.9	0	chr3:133759671-133879634
LPAR6		0	2.57967	25796.7	0	chr13:47775883-47954027
KRTAP5-1		0	2.67247	26724.7	0	chr11:1447268-1742077
SCARNA9		0	4.54132	45413.2	0	chr11:93034463-93103170

The 357 genes with significantly changing RNA abundance following SUMO-1 depletion are shown. Whether a gene had SUMO-1 present at its promoter during G1 is indicated, and the average expression for cells transfected with the control siRNA or the SUMO-1 specific siRNA are shown. The genes are ordered according to the expression levels (high to low) in the control transfected cells.

Supplementary Table S5. Comparison between Ubiquitin and SUMO-1 mark during M or G1 phase

	Total peaks	Overlap w/ SUMO-1 (G1) (%)
Ub-G1	7531	2816 (38%)
Ub-M	3446	1829 (53%)

Supplementary Table S6. Primers and siRNAs used in this paper.

Primers for RT-qPCR

Gene name (Refseq)	Sequence (5’ to 3’)
RPL3	TTCTCTGTGGCACGCGCTGG
	CCAGCAAGGACTTGCGGAGGG
RPL5	GGCCCGCAGGCTTCTCAATAGG
	GTGAAGGCACCTGGCTGACCA
RPL7A	ACGTGGATCCCATCGAGCTGGT
	CCACCCCAGTGACGGCGGAT
RPL10A	TTAGCGCGGCGTGAGAAGCC
	TCCAGGAACTTGCGGCGCTT
RPL17	GGTGATCTGTGAAAATGGTTCGC
	ATGCTGAATTTACTCCCGTGC
RPL23	GGTGGGCGGGGCGTTAAAGT
	CCCACCACGTCCTCGCTTCG
RPL26	AGCGGGAGCGGCCAAAATGA
	TTCCCGCTGCACCCGTTCAA
SLC1A3	TGGCAAAACCATTCCACCCAACA
	ACCGTGTCCGGGATTTGGGTCT
Polr2a	ATCTCTCCTGCCATGACACC
	AGACCAGGCAGGGGAGTAAC

Primers for ChIP-qPCR

Gene name (Refseq)	Sequence (5’ to 3’)
IL2	TCTGCCTGCTTTCTGTGAAACTCAA
	GGACAAGCCTCATCCCAAACTCCA
EIF3F	GTTTCTCTTCGAACGCCGT
	GAGCACTGAAATAGTCCCGC
RPS27	CAGGATTTCCGCTTTCGCTC
	ACAGAACAGCGAGATCTCCG
RPL26	GACCTATGTCTCTCGGAGCG
	GTTTTGCAATCCCTCGCAGT
RPL38	TGATCCTCGGCAGGCACCGT
	CAGCAAGCAGCAACCGGGGA
RPL5	CGTCACTGGCGTGACCGTCC
	CTGCGGAACAGAGACCGGCG
RPL7A	CCGCCGCCCAAGATGGTGAG

	GGCAGCGGATACAGCCGGAA
RPL10A	GGCGCTCAGGACTGCGACAA
	GCTCCTCGGTCCTACCCGCA
RPL3	CCTTCGGAGTGCACCAGCGG
	TTGCTTTAGGGGCACGGGCG
RPL23	AATCCGCCAGCCACTGCACG
	TTGCTCCGGCCACGTGAGGA

siRNAs

Gene name	Sequence
SUMO-1	
siRNA-1	CAAAAAAUCCCGAUGGCAC
	GUGCCAUCGGGAUUUUUUG
siRNA-2	GGACAGGAUAGCAGUGAGA
	UCUCACUGCUAUCCUGUCC
UBC9	CUGGGAAUGGAGGAAGAAG
	CUUCUUCCUCCAUUCCCAG

Figure S1

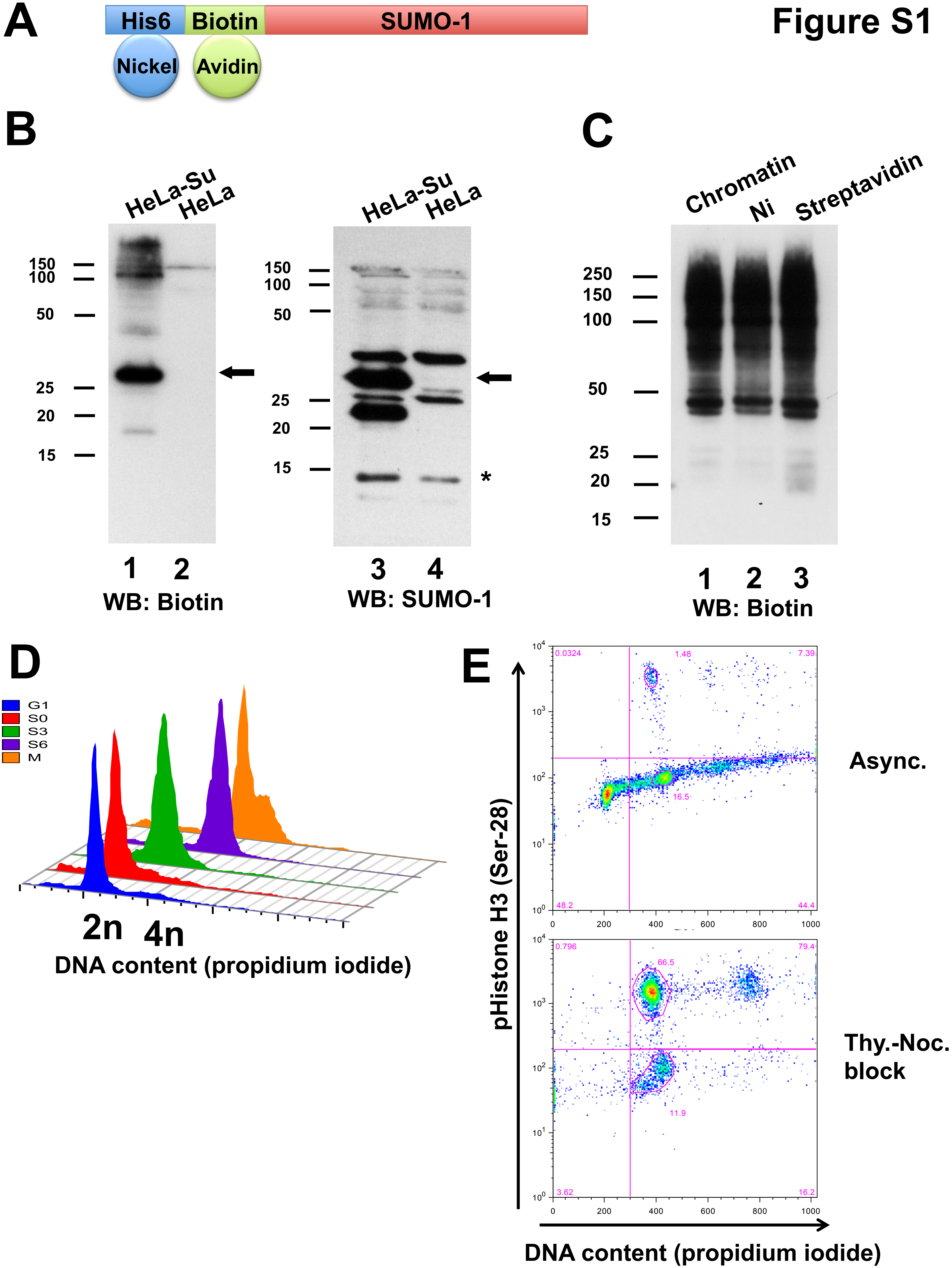

A
His6
Biotin
SUMO-1
Nickel
Avidin
B
HeLa-Su
HeLa
150
100
50
25
20
15
1
2
WB: Biotin
HeLa-Su
HeLa
150
100
50
25
20
15
*
3
4
WB: SUMO-1
C
Chromatin
Ni
Streptavidin
250
150
100
50
25
20
15
1
2
3
WB: Biotin
D
G1
S0
S3
S6
M
2n
4n
DNA content (propidium iodide)
E
pHistone H3 (Ser-28)
0.0324
1.48
7.39
16.5
48.2
44.4
Async.
0.796
66.5
79.4
11.9
3.62
16.2
Thy.-Noc. block
0
200
400
600
800
1000
DNA content (propidium iodide)

Figure S2

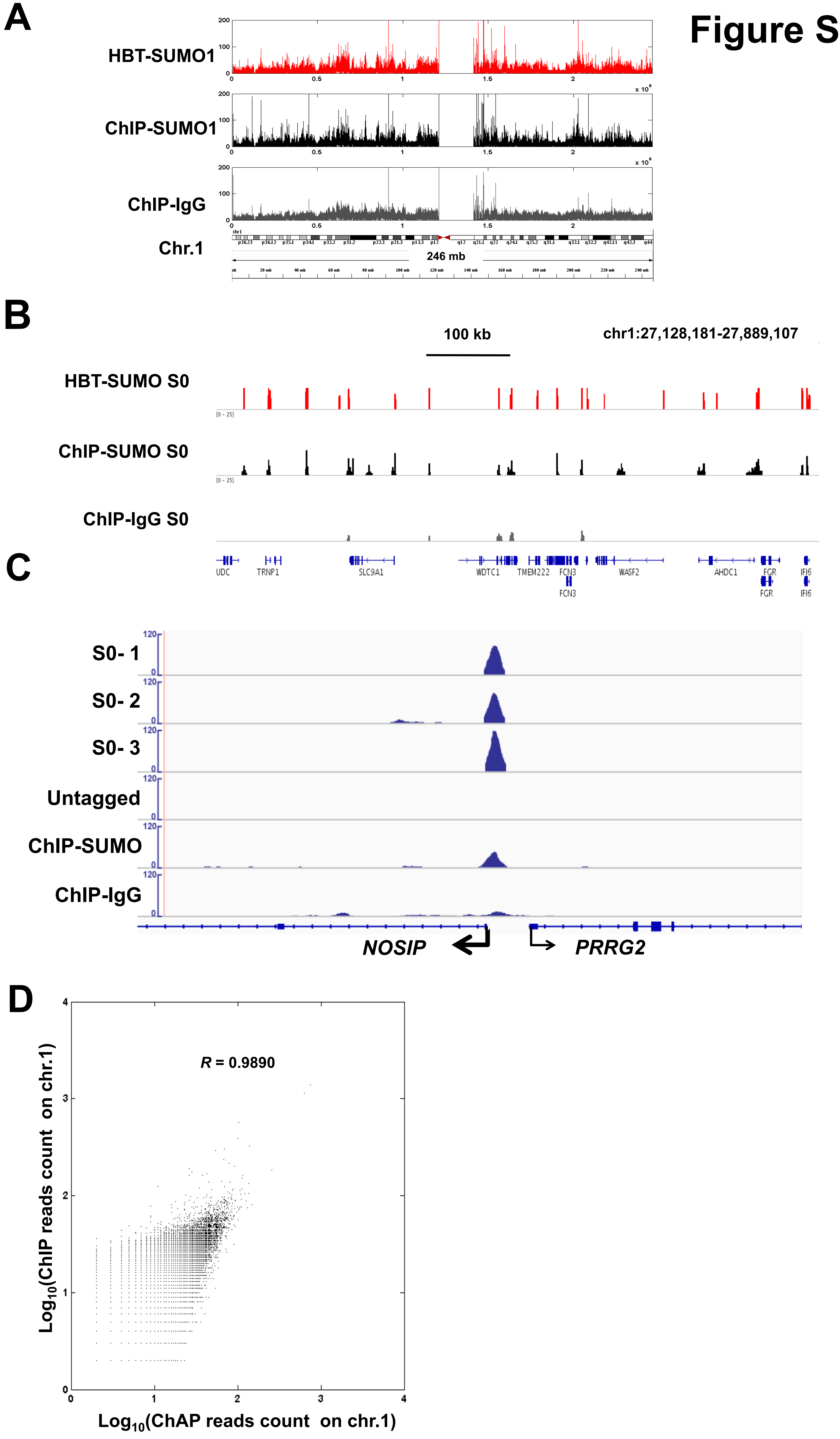

A
HBT-SUMO1
ChIP-SUMO1
ChIP-IgG
Chr.1
200
100
0
0
0.5
1
1.5
2
x 10^8
chr1
p36.23
p36.12
p35.1
p34.1
p32.2
p31.2
p22.3
p21.3
p13.3
p12
q12
q21.1
q22
q24.1
q25.2
q31.1
q32.1
q32.3
q42.11
q42.3
q44
246 mb
20 mb
40 mb
60 mb
80 mb
100 mb
120 mb
140 mb
160 mb
180 mb
200 mb
220 mb
240 mb
B
100 kb
chr1:27,128,181-27,889,107
HBT-SUMO S0
ChIP-SUMO S0
ChIP-IgG S0
[0 - 25]
[0 - 25]
UDC
TRNP1
SLC9A1
WDTC1
TMEM222
FCN3
FCN3
WASF2
AHDC1
FGR
FGR
IFI6
IFI6
C
S0- 1
S0- 2
S0- 3
Untagged
ChIP-SUMO
ChIP-IgG
120
0
NOSIP
PRRG2
D
R = 0.9890
Log10(ChIP reads count on chr.1)
Log10(ChAP reads count on chr.1)
0
1
2
3
4

Figure S3

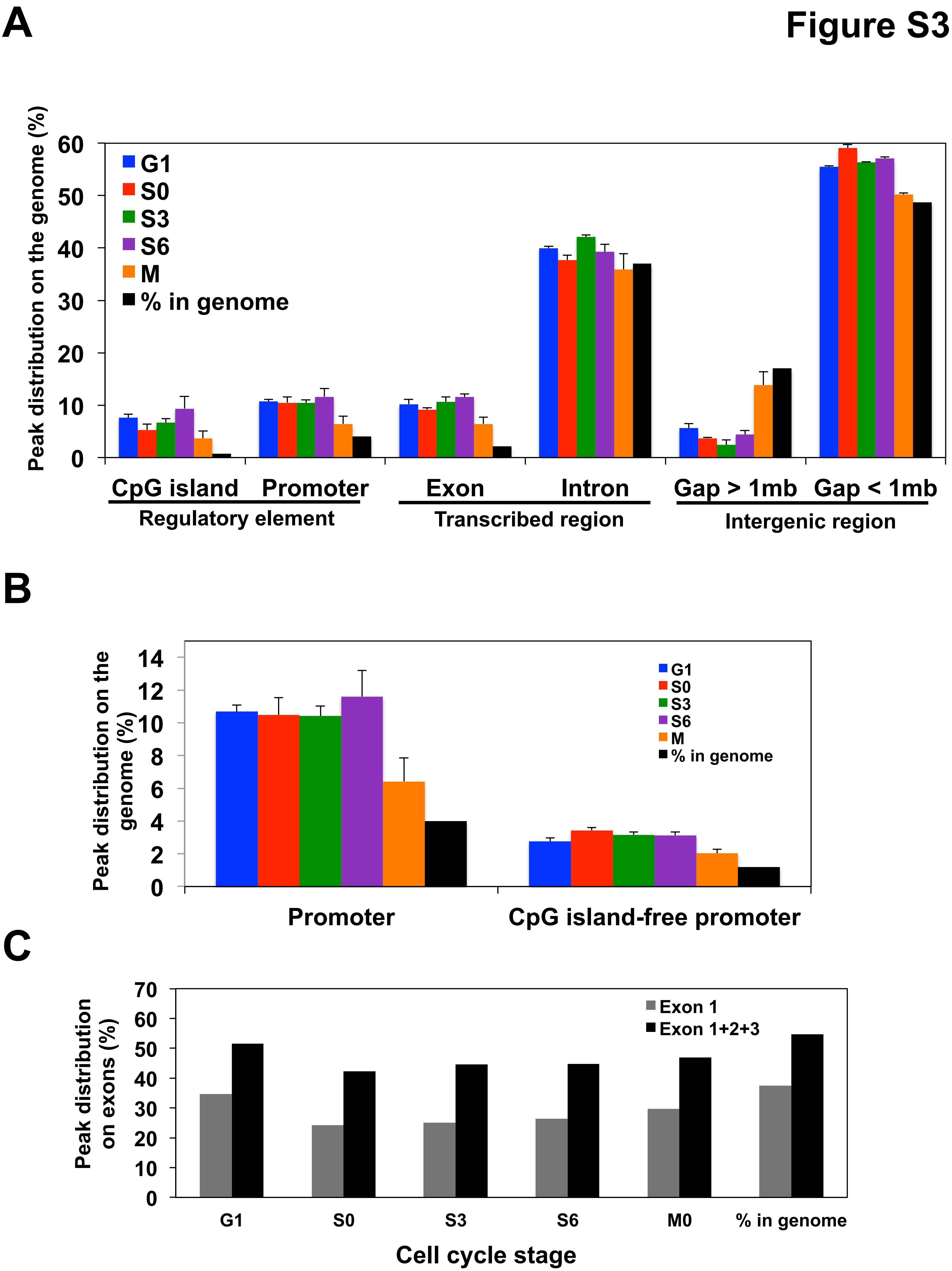

A
Peak distribution on the genome (%)
60
50
40
30
20
10
0
G1
S0
S3
S6
M
% in genome
CpG island
Promoter
Regulatory element
Exon
Intron
Transcribed region
Gap > 1mb
Gap < 1mb
Intergenic region
B
Peak distribution on the genome (%)
14
12
10
8
6
4
2
0
G1
S0
S3
S6
M
% in genome
Promoter
CpG island-free promoter
C
Peak distribution on exons (%)
70
60
50
40
30
20
10
0
Exon 1
Exon 1+2+3
G1
S0
S3
S6
M0
% in genome
Cell cycle stage

Figure S4

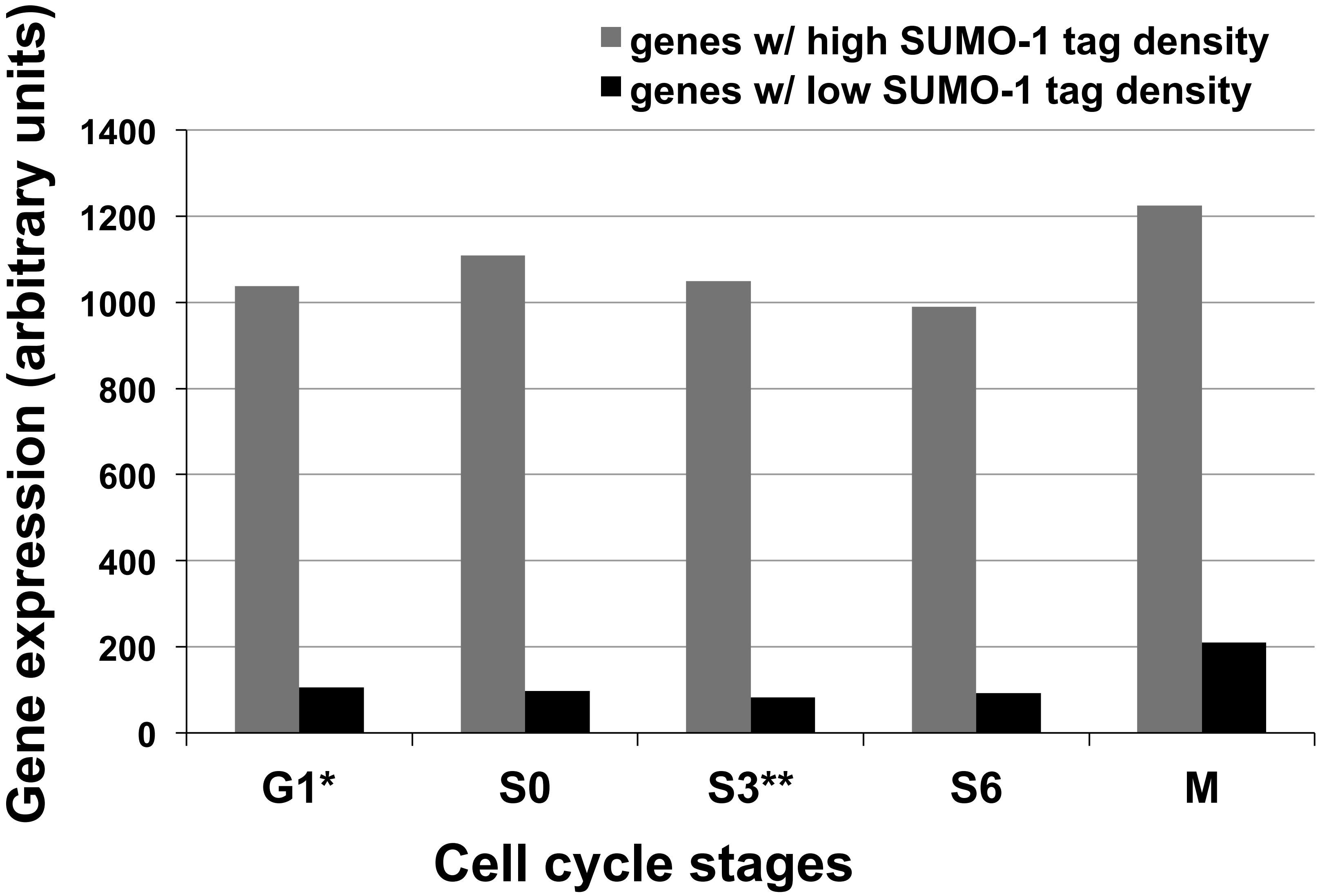
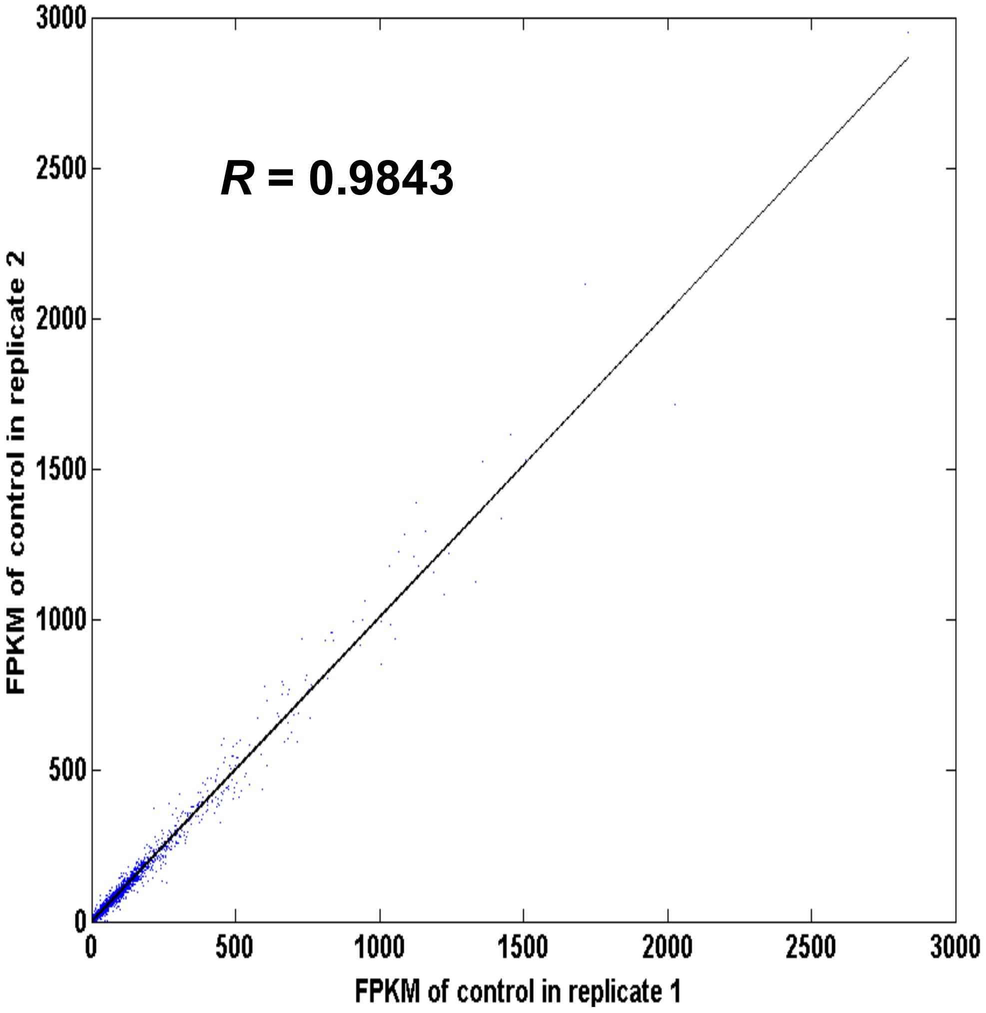
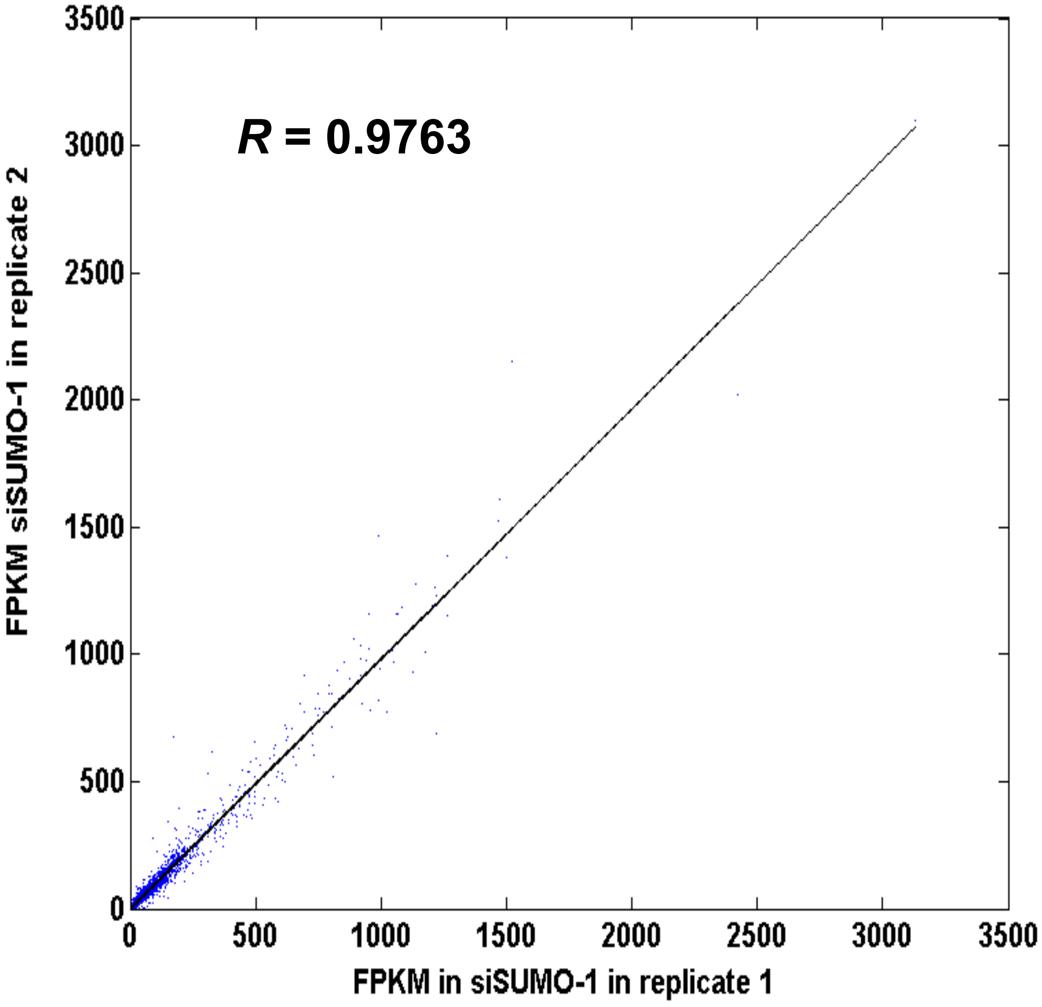

genes w/ high SUMO-1 tag density
genes w/ low SUMO-1 tag density
Gene expression (arbitrary units)
1400
1200
1000
800
600
400
200
0
G1*
S0
S3**
S6
M
Cell cycle stages

Figure S5



Control si



SUMO-1 si

Figure S6

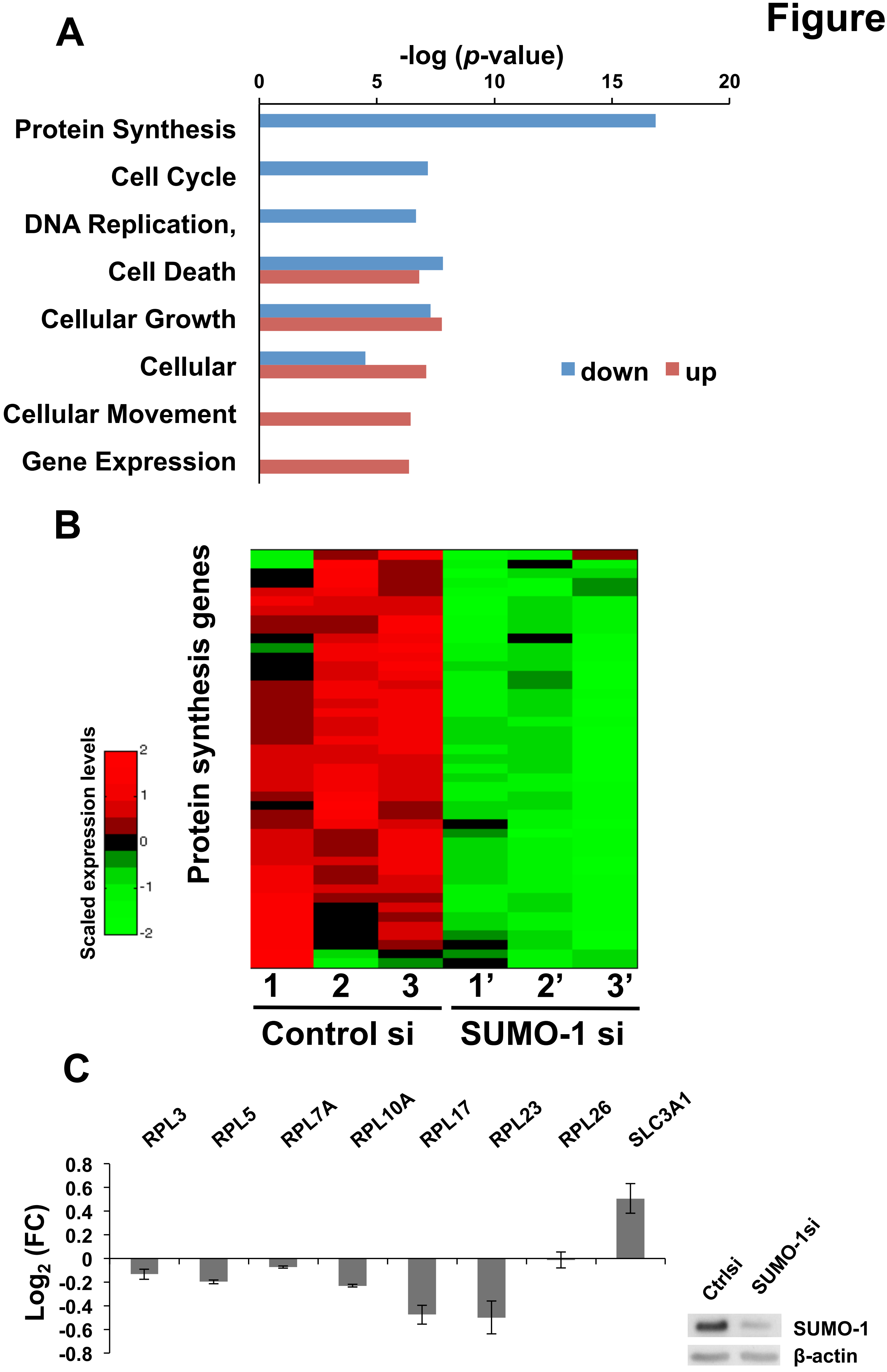
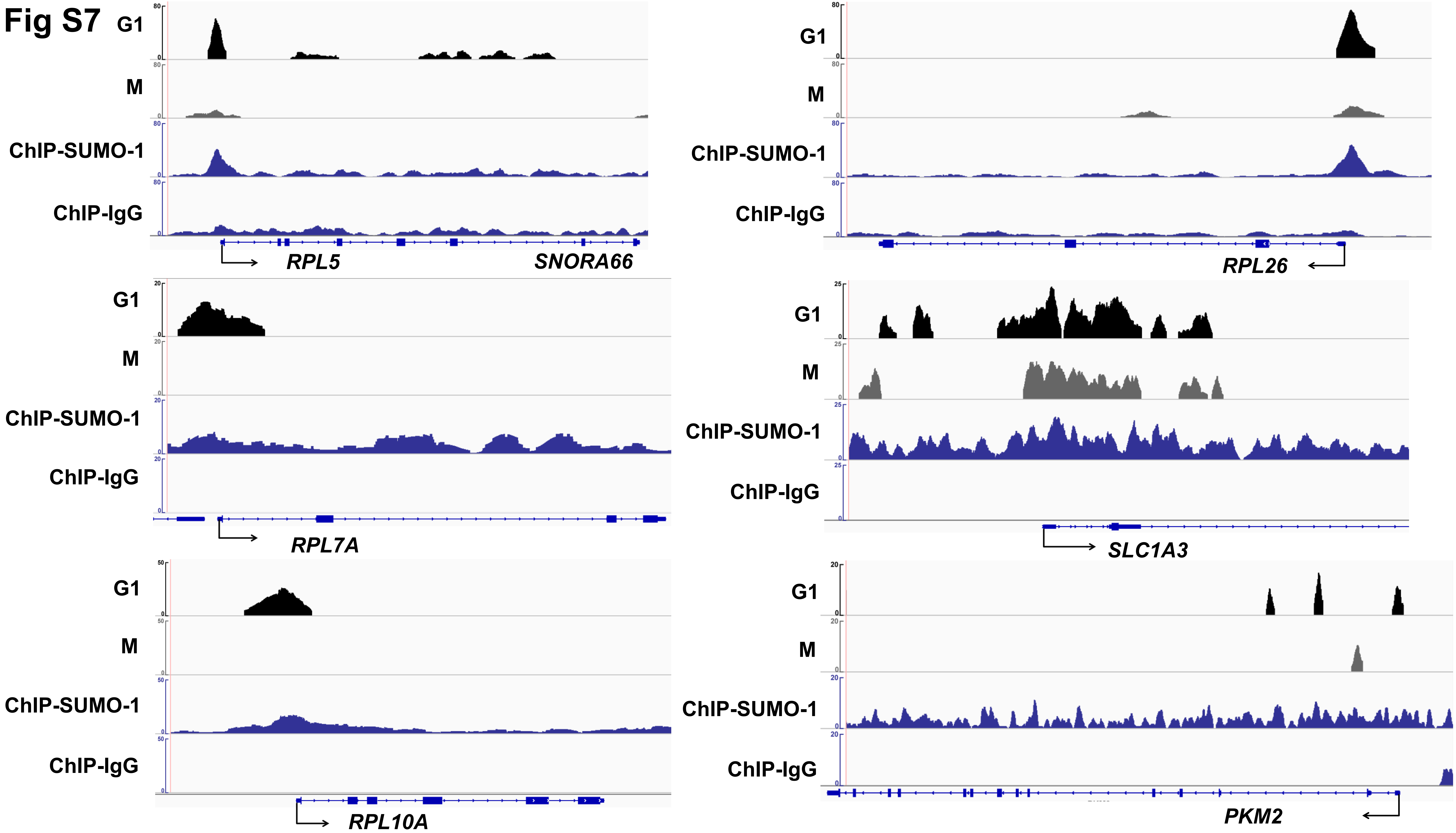

A
-log (p-value)
0
5
10
15
20
Protein Synthesis
Cell Cycle
DNA Replication,
Cell Death
Cellular Growth
Cellular
Cellular Movement
Gene Expression
down
up
B
Protein synthesis genes
Scaled expression levels
2
1
0
-1
-2
1
2
3
1'
2'
3'
Control si
SUMO-1 si
C
RPL3
RPL5
RPL7A
RPL10A
RPL17
RPL23
RPL26
SLC3A1
Log2 (FC)
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
Ctrlsi
SUMO-1si
SUMO-1
β-actin

Fig S7


G1
M
ChIP-SUMO-1
ChIP-IgG
80
0
RPL5
SNORA66
G1
M
ChIP-SUMO-1
ChIP-IgG
80
0
RPL26
G1
M
ChIP-SUMO-1
ChIP-IgG
20
0
RPL7A
G1
M
ChIP-SUMO-1
ChIP-IgG
25
0
SLC1A3
G1
M
ChIP-SUMO-1
ChIP-IgG
50
0
RPL10A
G1
M
ChIP-SUMO-1
ChIP-IgG
20
0
PKM2