SI Table 1: Chromatin-associated proteins identified by SILAC-Proteomics

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
PCNA	1.883	1.852	0.522	+	+
PDIA3	1.589	0.998	0.459		+
CRYAB	1.505	1.441	0.637	+	+
CISD1	1.462	1.957	1.034	+	
CLPP	1.460	1.700	0.820	+	+
HGSNAT	1.297	2.045	1.821	+	+
PGM3	1.285	1.304	0.790	+	+
HSPB1	1.261	1.185	0.747	+	+
PRSS3	1.240	0.265	0.452	+	+
SUCLG1	1.238	1.277	0.834		
FUS	1.232	1.010	0.687		+
TMUB1	1.229	0.879	0.633		+
COL6A3	1.225	1.369	0.925	+	
LEPREL2	1.203	0.901	0.664		+
COL6A2	1.190	1.363	0.983	+	
COPZ1	1.184	1.238	0.885		
APOO	1.181	1.182	0.848		
PTGES2	1.180	1.270	0.917		
HMGN2;HMGN3	1.172	0.629	0.583	+	+
ZC3HAV1	1.170	1.385	1.047	+	
MRPS17	1.166	1.029	0.767		+
CUTA	1.162	1.244	0.925		
COL6A1	1.162	1.293	0.971	+	
HIST1H1E	1.160	0.639	0.595	+	+
DERL2	1.157	0.603	0.584	+	+
LRRC47	1.156	0.912	0.715		+
SSB	1.153	1.197	0.901	+	
EIF2S1	1.147	1.165	0.885		
DDB1	1.144	1.279	0.991	+	
TIMM9	1.140	1.101	0.849		
CTSK	1.134	1.601	1.498	+	+
KDELC2	1.133	1.153	0.898		
EDF1	1.131	1.180	0.924	+	
OLA1	1.131	1.261	0.999		
NAGK	1.130	1.140	0.894		
CHMP1A	1.125	1.278	1.030	+	
ACADVL	1.124	1.196	0.950	+	
TIMM44	1.124	1.207	0.961		
MRPS22	1.123	1.134	0.899		
ATP5L	1.123	0.983	0.792		+
HSPG2	1.123	1.483	1.311	+	+
C2orf47	1.122	1.219	0.976		
YBX3	1.122	0.923	0.757		+
TIMM10	1.121	1.087	0.865		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
EMILIN1	1.121	1.247	1.005	+	
ECH1	1.121	1.139	0.908		
QIL1;C19orf70	1.120	1.109	0.884		
PTCD3	1.119	0.977	0.793		+
PGD	1.119	1.076	0.861		
IDH3A	1.117	0.989	0.803		+
FKBP10	1.116	1.020	0.825		+
PURA	1.114	0.913	0.760		+
MRPS7	1.112	0.944	0.782		+
MT-ND1	1.112	0.772	0.689		+
PDLIM4	1.111	1.058	0.860		+
MAPRE1	1.110	0.971	0.801		+
YARS	1.109	0.906	0.762		+
DLD	1.108	1.082	0.882		
MRPL23	1.107	0.924	0.776		+
LRPPRC	1.105	1.098	0.899		
ROCK2	1.104	0.989	0.821		
PMVK	1.102	1.182	0.978		
LETM1	1.101	1.132	0.934	+	
RPS27L	1.100	1.255	1.058	+	
DLST	1.100	0.933	0.789		+
PNKD	1.099	1.241	1.044		
MRPS28;TPD52	1.099	1.088	0.902		
ALDH18A1	1.098	1.154	0.960		
SDHA	1.097	1.063	0.884		
SRSF7	1.096	1.051	0.875		
PDHA1	1.096	1.081	0.899		
BTF3L4	1.096	0.842	0.740		+
SNX1	1.096	1.170	0.979		
MRPS18A	1.096	0.802	0.720		+
FECH	1.095	0.995	0.837		
KPNA3	1.095	1.050	0.878		
COPG2	1.094	1.120	0.935		
OGDH	1.093	0.993	0.837		+
PCK2	1.093	0.790	0.716	+	+
MRPS34	1.093	1.002	0.845		
MECP2	1.093	1.002	0.845		+
PNPLA6	1.093	1.144	0.960		
EXOC8	1.091	1.231	1.051		
HADHA	1.090	1.038	0.875		
MRPL4	1.090	0.865	0.760		+
PPFIBP1	1.089	1.135	0.960		
SERPINB1	1.088	1.170	0.994		
POTEE;POTEI;POTEK	1.087	0.697	0.677	+	+
RAC2	1.087	1.050	0.890		
TPM1	1.086	0.992	0.847		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
MT-ATP8	1.086	0.815	0.736		+
RAB5A	1.086	1.017	0.865		
ADD1	1.085	1.089	0.925		
SIPA1L1	1.085	1.421	1.337	+	+
CDC42EP2	1.084	0.931	0.808		+
MRPS26	1.084	1.177	1.009		
HIST1H1B	1.084	0.944	0.817		+
GCN1L1	1.084	0.973	0.837		
RANBP2	1.084	1.030	0.879		
EZR	1.083	1.147	0.981		
PDHB	1.083	1.076	0.917		
SLC25A6	1.083	1.173	1.008		
PGM1	1.082	1.075	0.917		
MRPL24	1.082	1.035	0.886		
MYO1E	1.082	1.176	1.012		
ACAT1	1.081	1.104	0.945		
ACTBL2	1.081	0.689	0.679	+	+
TKT	1.081	0.856	0.766		+
MANF	1.081	0.991	0.854		
APC2	1.080	0.812	0.741		+
ANKRD13A	1.080	1.130	0.971		
CCDC50	1.080	1.247	1.096	+	
MTX3	1.080	1.169	1.009		
DLAT	1.079	0.995	0.860		
ITPR3	1.079	1.238	1.087	+	
CCT4	1.079	1.081	0.929		
CTSL1	1.079	1.307	1.176	+	
SLC25A5	1.079	1.073	0.922		
CSRP1	1.078	0.690	0.682	+	+
TAGLN	1.078	0.944	0.826		+
ATP5H	1.077	1.000	0.866		+
PPP2CB;PPP2CA	1.077	1.171	1.017		
NARS	1.076	0.976	0.849		
NDUFA10	1.076	1.167	1.015	+	
DPP3	1.076	1.151	0.999		
ADD3	1.075	1.071	0.926		
UBE2M	1.074	1.053	0.914		
SCCPDH	1.074	0.965	0.846		
PSAT1	1.073	0.800	0.743		+
KIAA1217	1.073	1.311	1.197	+	
APPL2	1.073	1.264	1.134		
MRPL40	1.073	0.874	0.786		+
SPECC1L	1.072	1.105	0.962		
MTHFD1L	1.072	1.089	0.948		
NAA50	1.071	1.153	1.010		
AKR7A2	1.071	1.151	1.009		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
MRPS23	1.071	0.996	0.873		
NDUFA4	1.070	1.081	0.945		
ETHE1	1.070	0.873	0.790		+
LONP1	1.069	0.963	0.851		
ATP6V1F	1.069	1.154	1.016		
NONO	1.069	1.116	0.978		
AGPS	1.069	1.092	0.956		
ACSL3	1.069	1.163	1.025		
GMPS	1.068	1.053	0.922		
SPATS2L	1.068	1.009	0.887		
PMM2	1.068	1.103	0.968		
RPL30	1.068	1.168	1.033		
MTHFD1	1.068	0.993	0.875		
CCT7	1.068	0.901	0.810		+
YBX1	1.068	0.975	0.862		+
TPM3	1.067	0.831	0.767		+
HINT2	1.067	0.940	0.837		
SMARCA1	1.067	1.343	1.263	+	+
PDXK	1.067	1.014	0.893		
DENR	1.067	0.961	0.852		
CARS	1.067	0.908	0.816		+
SCAF11	1.066	1.140	1.007		
LACC1	1.066	1.413	1.389	+	+
SLC25A1	1.066	1.110	0.978		
MTDH	1.066	1.038	0.914		
ALDH1L2	1.065	0.907	0.818		+
EXOG	1.065	1.061	0.936		
P4HA1	1.065	0.946	0.845		
SRP72	1.064	1.130	1.001		
RPS15	1.064	0.883	0.803		+
NIPSNAP1	1.064	0.935	0.838		
FAM129B	1.064	1.173	1.047	+	
RANGAP1	1.063	1.037	0.918		
NPC2	1.063	1.074	0.950		
PGRMC2	1.063	0.906	0.820		+
RPL26L1	1.063	0.998	0.886		
TXNDC17	1.063	1.141	1.015		
ERO1L	1.063	1.031	0.913		
APEX1	1.062	0.954	0.854		
HADHB	1.062	0.995	0.886		
TXNDC12	1.062	0.991	0.884		
HSPA9	1.061	1.088	0.967		
GLS	1.061	1.087	0.967		
MRPL50	1.061	0.872	0.800		+
FKBP9	1.061	1.074	0.955		
MIF	1.061	1.003	0.894		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
BCL2L13	1.060	0.955	0.858		
UBE2N;UBE2NL	1.060	1.015	0.905		
DAP3	1.059	0.915	0.831		
POM121C;POM121	1.059	1.034	0.922		
MRPS36	1.059	0.863	0.797		+
PTPN11	1.058	0.981	0.881		
MRPL48	1.058	1.008	0.903		
RCN3	1.058	0.927	0.842		+
SQRDL	1.058	1.076	0.963		
AKR1C3;AKR1C1	1.058	0.980	0.881		
DPYSL2	1.057	1.049	0.938		
DIABLO	1.057	1.183	1.074		
ANXA6	1.057	1.098	0.984		
TMPO	1.056	0.951	0.860		
TTC29	1.056	1.192	1.087	+	
ARMC10	1.056	1.080	0.969		
UBE2V1;TMEM189	1.056	0.933	0.848		
RPS3	1.056	1.039	0.932		
NUP98	1.056	0.950	0.861		
AIFM1	1.056	1.016	0.913		
HP1BP3	1.055	1.090	0.979		
DNAJC11	1.055	1.105	0.994		
GLUD1;GLUD2	1.055	1.038	0.932		
C22orf28	1.055	1.007	0.907		
BLVRB	1.055	0.886	0.818		+
EHD1	1.054	1.125	1.017		
FSCN1	1.054	0.942	0.858		
G3BP1	1.053	1.048	0.945		
MCU	1.053	1.060	0.955		
COA3	1.053	1.110	1.004		
SMC1A	1.053	1.128	1.023	+	
HSPA4	1.053	1.152	1.048		
TXNL1	1.053	1.049	0.946		
DTYMK	1.053	1.164	1.061		
ESD	1.053	1.040	0.938		
GRN	1.053	1.094	0.989		
UBA1	1.053	1.006	0.910		
MICU1	1.052	1.099	0.995		
COPA	1.052	1.068	0.965		
RABL3	1.052	1.166	1.066		
CAST	1.052	1.088	0.985		
NOC3L	1.052	0.934	0.855		
SYNPO2	1.052	0.969	0.882		
CHMP2A	1.052	1.156	1.055		
GANAB	1.051	0.921	0.846		+
NPEPPS	1.051	1.051	0.951		

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P4HA2	1.051	1.001	0.908		
RAB8A	1.051	1.046	0.947		
SSRP1	1.051	1.097	0.995		
ATP5O	1.051	1.028	0.931		
PSME1	1.051	1.045	0.946		
VPS35	1.051	1.067	0.967		
ACO1;IRP1	1.051	1.100	0.999		
GSN	1.050	1.092	0.992		
DCTD	1.050	1.082	0.982		
EIF4G2	1.050	1.104	1.004		
LARS	1.050	0.968	0.884		
MGMT	1.050	1.105	1.005		
RNPEP	1.050	0.974	0.888		
CALD1	1.049	0.989	0.901		
RMDN2	1.049	1.083	0.985		
RBM39	1.049	1.133	1.035		
TARS	1.049	0.947	0.869		
MDH2	1.049	1.066	0.969		
RBM3	1.049	1.145	1.050	+	
SARS	1.049	1.013	0.922		
HNRNPL	1.049	1.067	0.970		
SDHB	1.049	0.994	0.906		
NANS	1.048	1.055	0.960		
RPS29	1.048	0.996	0.909		
C17orf66	1.048	1.199	1.115	+	+
ARMCX3	1.048	1.199	1.115		
LASP1	1.048	0.949	0.872		
HMGA2	1.048	0.791	0.767		+
IGF2BP2	1.048	0.979	0.895		
IFI16	1.048	0.968	0.887		
CIRBP	1.048	1.171	1.082	+	
LDHA	1.048	1.045	0.952		
COPS6	1.048	1.122	1.028		
HIST1H1C	1.048	1.023	0.933		
SERPINH1	1.047	0.864	0.812		+
NOL6	1.047	0.851	0.804		+
MMGT1	1.047	1.017	0.927		
RIC8A	1.047	1.107	1.013		
ALDH1L1	1.047	0.752	0.745		+
WARS	1.047	0.903	0.840		+
H2AFY2	1.046	1.153	1.064	+	
PRKCSH	1.046	0.966	0.887		
DPYSL3	1.046	1.042	0.952		
CORO1B	1.046	1.039	0.950		
ARL2	1.046	1.231	1.161		
LYPLA2	1.046	1.092	1.000		

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GNPNAT1	1.046	1.139	1.050		
PDZD11	1.046	1.151	1.064		
EIF2AK2	1.046	1.096	1.005		
SPATA5L1	1.045	0.838	0.798		+
FH	1.045	1.044	0.956		
ATP5B	1.045	0.986	0.906		
SFPQ	1.045	0.913	0.850		+
MICU2	1.045	1.158	1.073		
OTUB1	1.045	1.063	0.974		
PTCD1;ATP5J2;ATP5J	1.045	0.946	0.874		
PRDX2	1.045	0.992	0.911		
TBL2	1.044	1.036	0.949		
TUFM	1.044	1.027	0.941		
FAU	1.044	1.019	0.935		
DNAJA1	1.044	1.162	1.081		
XPO1	1.044	1.096	1.009		
ALDOC	1.044	0.959	0.887		
PDCD6IP	1.043	1.091	1.004		
MYO1D	1.043	1.133	1.048		
VPS26A	1.043	1.030	0.946		
PSMC1	1.043	1.029	0.946		
PLS3	1.043	1.049	0.964		
SRSF9	1.043	1.149	1.067		
COPB2	1.043	1.097	1.012		
FHL2	1.043	1.003	0.924		
TUBB6	1.043	0.993	0.915		
TOR1AIP1	1.042	0.867	0.821		
EIF3A	1.042	1.066	0.981		
MEMO1;C2orf4	1.042	1.067	0.983		
DNAJC10	1.042	1.054	0.971		
RMDN3	1.042	0.970	0.897		
USO1	1.042	1.072	0.988		
RPL38	1.042	0.948	0.880		
TMEM109	1.042	0.944	0.878		
MAPK1	1.042	1.032	0.951		
PDAP1	1.041	0.983	0.909		
EPDR1;UCC1	1.041	1.111	1.029		
RAB18	1.041	1.091	1.009		
SMC3	1.041	1.091	1.009		
PLIN3	1.041	1.070	0.988		
ARL8A	1.041	1.039	0.959		
MRPS15	1.041	0.895	0.843		
NCL	1.041	1.110	1.029		
UGGT1	1.041	1.018	0.940		
WDR1	1.041	1.093	1.012		
DECR2	1.041	1.096	1.015		

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MRPL9	1.041	0.920	0.861		
LMCD1	1.041	0.966	0.897		
ACTN1	1.041	1.008	0.932		
PEBP1	1.041	0.981	0.909		
TOMM40	1.040	1.037	0.957		
XRCC6	1.040	1.119	1.040		
ESYT1	1.040	1.035	0.957		
GLB1	1.040	0.947	0.882		
MARCKS	1.040	0.911	0.855		+
AFG3L2	1.040	1.086	1.006		
TPM1	1.040	0.869	0.826		+
H2AFY	1.040	0.972	0.903		
KHDRBS1	1.039	1.027	0.951		
FAM162A	1.039	1.048	0.970		
ARF4	1.039	1.070	0.991		
FAM114A1;DKFZp686F	1.039	1.123	1.047		
GPX1	1.039	0.958	0.893		
IMMT	1.039	1.070	0.992		
TXNDC5	1.039	1.003	0.931		
ARF1;ARF3	1.038	1.059	0.982		
MAVS	1.038	1.000	0.928		
VPS29	1.038	1.008	0.936		
RPS12	1.038	1.084	1.007		
SLC25A13	1.038	0.921	0.866		
ANO10	1.038	1.283	1.261	+	
HSPD1	1.038	1.005	0.934		
MTCH1	1.038	1.206	1.150	+	
QARS	1.037	1.035	0.962		
RPS7	1.037	1.047	0.973		
SEPT7	1.037	1.013	0.943		
PAFAH1B2	1.037	0.919	0.866		
ACAA2	1.037	1.149	1.082		
ACTR2	1.037	0.976	0.911		
GSTK1	1.037	1.050	0.977		
PGK1	1.037	0.991	0.924		
ATP5D	1.037	1.035	0.963		
PRDX3	1.037	1.043	0.970		
NAT14	1.036	0.931	0.876		
ABCF1	1.036	1.026	0.955		
DCTN3	1.036	0.985	0.919		
TUBB	1.036	1.009	0.940		
NME3	1.036	0.971	0.908		
ZYX	1.036	0.839	0.810		+
RPL35A	1.036	1.041	0.970		
HK1	1.036	1.145	1.079	+	
STAT1	1.036	1.048	0.976		

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RPL29	1.036	0.876	0.836		+
VARS	1.036	0.761	0.763		+
PA2G4	1.036	0.996	0.929		
NDUFB6	1.036	0.842	0.813		+
RCN1	1.036	0.948	0.890		
SYNPO	1.036	0.964	0.902		
MOGS	1.036	0.906	0.858		
FAM180A	1.036	1.329	1.346	+	+
SUPT16H	1.036	1.060	0.989		
HSP90B1	1.036	1.006	0.939		
PKM	1.036	1.013	0.945		
GM2A	1.036	1.167	1.106		
P4HB	1.036	0.995	0.930		
BTF3	1.035	1.126	1.058		
CTSD	1.035	1.108	1.039		
CDO1	1.035	1.113	1.044		
PLOD1	1.035	1.036	0.966		
CTSA	1.035	1.146	1.082	+	
SAR1A	1.035	1.103	1.033		
PDIA5	1.035	1.062	0.992		
NIPSNAP3A	1.035	1.139	1.074		
COX20	1.035	0.935	0.881		
CAP1	1.035	1.037	0.968		
ITGAM	1.035	0.864	0.830		+
ANXA1	1.035	1.127	1.061		
RPS19	1.035	1.075	1.006		
PITRM1	1.035	0.974	0.913		
ICT1	1.034	0.913	0.865		
C1QBP	1.034	0.999	0.935		
S100A4	1.034	1.176	1.121	+	+
H1F0	1.034	0.974	0.914		
PPA1	1.034	0.949	0.894		
DDX1	1.034	1.021	0.955		
RHOT2	1.034	1.166	1.109		
ATP5C1	1.034	1.081	1.014		
OSTF1	1.034	1.113	1.047		
VIM	1.034	1.059	0.992		
TIMM21	1.033	1.031	0.966		
DUSP3	1.033	1.046	0.981		
KRAS	1.033	0.991	0.930		
PDIA6	1.033	0.996	0.935		
DCTN5	1.033	1.079	1.014		
UCHL3	1.033	1.047	0.982		
CYB5A	1.032	0.943	0.891		
KPNB1	1.032	1.017	0.954		
FLNC	1.032	1.014	0.952		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
OXA1L	1.032	1.238	1.210	+	
SOD2	1.032	1.049	0.985		
TBCB;CKAP1	1.032	1.143	1.086		
LGALS3	1.032	1.133	1.074	+	
SYNE1	1.032	1.072	1.008		
NDUFB10	1.032	0.873	0.840		+
GHITM	1.032	1.191	1.146		
USP14	1.032	1.008	0.948		
CALR	1.031	0.989	0.931		
HSP90AB1	1.031	1.039	0.977		
APOBEC3C	1.031	1.295	1.302	+	+
TMOD3	1.031	1.103	1.042		
VAT1	1.031	0.882	0.847		+
PSAP	1.031	1.053	0.991		
MRPS25	1.031	0.869	0.838		+
ARPC4;ARPC4-TTLL3	1.031	0.882	0.847		+
DDX3X;DDX3Y	1.031	1.114	1.055		
SCFD1	1.031	1.021	0.961		
CENPB	1.031	1.125	1.067		
SSR3	1.031	0.840	0.819		+
SLC25A12	1.031	1.076	1.015		
EEF1D	1.031	0.977	0.922		
GAA	1.031	0.969	0.915		
EIF3I	1.031	1.137	1.082		
ALDOA	1.031	0.960	0.908		
SRSF1	1.030	0.966	0.913		
CTSB	1.030	1.084	1.024		
RPS5	1.030	1.063	1.002		
ACTR3	1.030	0.938	0.891		
PXDN	1.030	0.951	0.901		
ATXN2L	1.030	0.908	0.868		
RPS8	1.030	0.993	0.937		
MRPL47	1.030	1.005	0.948		
	1.030	0.957	0.907		
NENF	1.030	1.034	0.975		
ATP5F1	1.030	1.057	0.997		
HIST1H1A	1.030	0.669	0.719	+	+
NDUFA7	1.030	1.088	1.030		
SERPINE2	1.030	0.997	0.941		
SND1	1.030	0.974	0.921		
LEPRE1	1.030	0.935	0.889		
NME1-NME2;NME2;NM	1.030	0.926	0.883		
GSTM1;GSTM5;GSTM4	1.029	1.019	0.962		
USP9X	1.029	1.125	1.071		
PARP1	1.029	1.044	0.986		
GBP1	1.029	1.001	0.945		

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PRDX6	1.029	0.878	0.847		+
TUBB3	1.029	1.065	1.006		
SPANXB1	1.029	1.294	1.309	+	+
CENPC1	1.029	1.114	1.060		
ARCN1	1.029	1.047	0.989		
SLC25A10;MRPL12	1.029	0.919	0.878		
VASP	1.029	0.849	0.827		
NUTF2	1.029	0.951	0.904		
HSPE1	1.029	1.008	0.953		
TOMM70A	1.029	1.047	0.989		
GSTP1	1.029	0.929	0.887		
NNMT	1.029	0.790	0.789	+	+
DSTN	1.029	1.026	0.970		
RARS	1.028	1.000	0.947		
ARHGAP1	1.028	0.986	0.934		
MTPN	1.028	1.055	0.999		
MINOS1	1.028	0.983	0.932		
AK3	1.028	1.102	1.049		
MRPL49	1.028	0.967	0.919		
MRPL22	1.027	0.990	0.939		
GOT2	1.027	0.976	0.927		
RPS10	1.027	0.986	0.936		
PSIP1	1.027	1.075	1.021		
COMMD3	1.027	1.084	1.031		
RPS23	1.027	1.104	1.052		
RPS9	1.027	1.071	1.017		
PHLDB1	1.027	1.091	1.038		
SUB1	1.027	1.039	0.986		
MFGE8	1.027	1.017	0.965		
ETFB	1.027	1.046	0.993		
PEA15	1.027	1.012	0.960		
FKBP3	1.026	1.062	1.010		
PARK7	1.026	0.931	0.891		
MRPL11	1.026	0.998	0.949		
FLNA	1.026	0.901	0.868		
ATP5A1	1.026	1.014	0.963		
HNRNPK	1.026	1.046	0.994		
FKBP1A;FKBP12-Exip2	1.026	1.041	0.989		
AP3B1	1.026	1.111	1.063		
SERPINB6	1.026	1.020	0.969		
CROCC	1.026	1.021	0.970		
HIST1H1D	1.026	0.694	0.737	+	+
ACTN1	1.026	0.936	0.896		
MRPL13	1.026	0.853	0.834		+
EFTUD1	1.026	1.146	1.104	+	+
YWHAZ	1.026	1.033	0.982		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
CBR1	1.026	1.062	1.011		
MAP4	1.025	0.954	0.912		
AP2A2	1.025	1.001	0.952		
H3F3B;H3F3A;H3F3C	1.025	1.047	0.996		
EMC1	1.025	0.918	0.883		
MRPL19	1.025	0.831	0.820		+
TPM3	1.025	0.979	0.933		
CRABP2	1.025	1.236	1.228		+
RAB2A	1.025	1.133	1.090		
CHCHD3	1.025	1.062	1.012		
CYB5R3	1.025	0.967	0.923		
TLN1	1.025	1.042	0.992		
PHPT1	1.025	1.088	1.040		
PPP1CB	1.025	1.044	0.994		
HSPB7;DKFZp779D09	1.025	1.037	0.987		
KLC1	1.025	1.100	1.053		
TMEM205	1.025	0.712	0.748	+	+
CHCHD6	1.025	1.003	0.956		
SCO1	1.025	0.970	0.927		
SH3BGRL	1.024	1.101	1.054		
FER1L4	1.024	1.050	1.001		
HSP90AA1	1.024	1.016	0.968		
RRP12	1.024	0.863	0.843		
PPIB	1.024	0.966	0.924		
NEXN	1.024	0.996	0.950		
AK4	1.024	0.971	0.928		
TRIOBP	1.024	1.011	0.964		
PARVA	1.024	1.093	1.047		
GBAS	1.024	0.976	0.933		
H2AFV;H2AFZ	1.024	0.998	0.953		
CNPY2	1.024	0.903	0.873		
EWSR1	1.024	0.934	0.898		
RUVBL2	1.024	0.948	0.910		
PYGB	1.024	1.050	1.003		
NSF	1.023	1.015	0.970		
RPL36AL;RPL36A	1.023	0.809	0.808		+
ATAD3A;ATAD3B	1.023	1.017	0.972		
COPE	1.023	1.021	0.975		
GNL3	1.023	0.991	0.948		
HDLBP	1.023	1.012	0.967		
ST13;ST13P4;ST13P5	1.023	1.026	0.980		
CAPZA1	1.023	0.997	0.954		
CNPY4	1.023	1.049	1.004		
EMD	1.023	0.875	0.855		+
HIST1H4A	1.023	1.009	0.965		
CTSC	1.023	1.114	1.074		

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ACTN2	1.022	1.041	0.996		
HNRPDL	1.022	0.995	0.953		
ACLY	1.022	1.003	0.960		
RPS3A	1.022	1.063	1.019		
RPS27A;UBB;UBC;UB	1.022	1.090	1.048		
CSE1L	1.022	0.954	0.917		
MARS	1.022	1.107	1.068		
PTMA	1.022	1.011	0.968		
TUBB2A;TUBB2B	1.022	0.929	0.897		
GPD2	1.022	1.050	1.007		
MP68;C14orf2	1.022	0.949	0.913		
ENO1	1.022	0.971	0.932		
SYNE3	1.022	1.099	1.059		
DSP	1.022	0.977	0.937		
IER3IP1	1.022	1.006	0.964		
AIMP2	1.022	1.085	1.044		
SLC25A11	1.022	1.011	0.969		
EIF5A;EIF5AL1;EIF5A2	1.022	0.965	0.927		
	1.022	1.080	1.038		
FTH1	1.021	1.165	1.138		
RAB7A	1.021	1.087	1.046		
EEF2	1.021	0.970	0.932		
MRPL46	1.021	1.011	0.969		
FGF2	1.021	0.985	0.946		
PLOD3	1.021	1.033	0.991		
ARHGDIA	1.021	0.908	0.882		
NUDT21	1.021	1.033	0.991		
RAB1A	1.021	1.046	1.005		
KANK2	1.021	1.051	1.010		
GPX8	1.021	0.922	0.894		
NR3C1	1.020	1.197	1.184		
MSN	1.020	1.041	1.000		
RHOA;RHOC	1.020	1.027	0.986		
PLEC	1.020	1.034	0.993		
HINT1	1.020	1.040	1.000		
PGAM1	1.020	0.874	0.858		+
SET	1.020	1.046	1.006		
EIF4H	1.020	0.920	0.893		
RAD21	1.020	1.056	1.016		
BCLAF1	1.020	1.123	1.090		
SRI	1.020	1.052	1.012		
EIF5B	1.020	0.986	0.949		
SNX3	1.020	1.149	1.123	+	
SYNCRIP	1.019	1.026	0.987		
VCP	1.019	1.031	0.992		
PISD	1.019	1.124	1.093		

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RPS18	1.019	1.010	0.972		
PDIA3	1.019	0.972	0.937		
ANXA7	1.019	1.028	0.989		
ETFA	1.019	0.976	0.941		
PPP2R1A	1.019	1.074	1.037		
RCN2	1.019	0.885	0.867		
AGK	1.019	1.061	1.023		
MDH1	1.019	1.048	1.010		
GNB2L1	1.019	1.037	0.999		
LGALS1	1.019	1.120	1.090		
ILK	1.019	1.053	1.015		
GLO1	1.019	1.031	0.993		
NACA	1.019	1.032	0.995		
STIP1	1.019	0.996	0.960		
HMGB2	1.019	0.973	0.940		
YWHAH	1.018	1.077	1.042		
VCL	1.018	1.021	0.985		
CANX	1.018	0.866	0.855		+
ABHD14B	1.018	0.962	0.931		
KIF5B	1.018	1.080	1.046		
RPL31	1.018	1.027	0.991		
TOR1AIP1	1.018	0.992	0.958		
HIST1H2AJ;HIST1H2AH	1.018	0.939	0.911		
COMMD8	1.018	1.056	1.021		
TMEM11	1.018	0.895	0.877		
PSMA1	1.018	1.030	0.995		
RDX	1.017	1.063	1.029		
RPS16	1.017	1.006	0.972		
THRAP3	1.017	1.038	1.003		
RPL27A	1.017	0.995	0.963		
EIF3E	1.017	1.045	1.011		
NAPA	1.017	1.103	1.074		
SPTAN1	1.017	1.039	1.005		
VAMP4	1.017	1.216	1.223	+	
DCTN1	1.017	1.072	1.039		
NDUFS1	1.017	1.033	0.999		
PSMB2	1.017	1.022	0.988		
SUN1;UNC84A	1.017	1.109	1.082		
RPS27	1.017	1.029	0.996		
CNN3	1.017	1.022	0.989		
TPI1	1.017	0.958	0.930		
CAPRIN1	1.017	1.136	1.114		
EEF1B2	1.017	0.899	0.882		
TPM4	1.017	0.943	0.917		
TAGLN2	1.016	1.000	0.968		
CALU	1.016	0.984	0.953		

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PRDX4	1.016	0.907	0.889		
TAX1BP3	1.016	1.125	1.101		
GAPDH	1.016	1.053	1.020		
TBCA	1.016	1.065	1.034		
MRPL43	1.016	1.008	0.976		
UGDH	1.016	0.988	0.958		
RPS11	1.016	1.045	1.013		
PABPC1	1.016	1.021	0.989		
RPS21	1.016	1.029	0.997		
SWAP70	1.016	1.023	0.991		
FIS1	1.016	1.108	1.083		
'SEP7	1.016	0.995	0.965		
PTGIS	1.016	0.932	0.910		
RAB1B	1.015	1.069	1.040		
C9orf89	1.015	0.991	0.962		
GNB2	1.015	0.946	0.922		
UBTF	1.015	1.153	1.139	+	+
RAB5C	1.015	1.022	0.991		
LEMD3	1.015	1.068	1.039		
IFIT5	1.015	1.271	1.316		+
SNX9	1.015	1.024	0.994		
TMPO	1.015	0.869	0.861		
AARS	1.015	0.992	0.964		
STOML2	1.015	1.026	0.996		
EIF4A1;EIF4A2	1.015	0.989	0.960		
HNRNPA1;HNRNPA1L	1.015	0.961	0.935		
PPIF	1.015	1.009	0.980		
GPI	1.015	1.030	1.000		
TLDC1;KIAA1609	1.015	1.107	1.084		
SPTBN1	1.015	1.057	1.028		
YWHAQ	1.015	1.072	1.045		
RPS20	1.015	0.934	0.913		
ANKFY1	1.014	0.963	0.938		
RPL3	1.014	1.027	0.998		
C11orf48	1.014	1.034	1.006		
SEC31A	1.014	1.013	0.985		
CNN2	1.014	1.032	1.004		
GBA	1.014	0.954	0.931		
PCBP2	1.014	0.994	0.968		
SAFB2	1.014	1.011	0.984		
PDIA4	1.014	0.934	0.915		
GDI2	1.014	0.993	0.967		
DHCR24	1.014	1.138	1.124		
TPD52L2	1.014	1.055	1.028		
RDH11	1.014	0.946	0.925		
ACTG1	1.014	1.055	1.029		

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HEXB	1.013	1.059	1.033		
FLNB	1.013	0.880	0.872		
ANXA2;ANXA2P2	1.013	0.986	0.961		
CAPZB	1.013	1.014	0.987		
SYNM	1.013	1.073	1.048		
RPLP0;RPLP0P6	1.013	1.003	0.977		
HSPA8	1.013	1.006	0.981		
ARL3	1.013	1.015	0.990		
EIF1AX;EIF1AY	1.013	1.049	1.024		
YWHAE	1.013	1.036	1.011		
TIMM50	1.013	0.947	0.928		
LEMD2	1.013	0.837	0.841		+
PDLIM1	1.013	0.925	0.908		
EEF1A1P5;EEF1A1;EE	1.013	0.954	0.934		
PIGS	1.013	0.983	0.959		
FKBP7	1.013	1.063	1.039		
ASPH	1.012	1.053	1.029		
RPL10	1.012	1.024	0.999		
USMG5	1.012	1.033	1.009		
TPT1	1.012	1.042	1.018		
SOD1	1.012	0.939	0.921		
EIF4G1	1.012	1.053	1.030		
EEA1	1.012	1.120	1.106		
LDHB	1.012	0.997	0.973		
ACIN1	1.012	1.007	0.984		
NME1	1.012	1.047	1.024		
PRKAR1A	1.012	1.207	1.224	+	
PCBP1	1.012	1.053	1.030		
FKBP8	1.012	1.198	1.212		
MT-ATP6	1.012	1.040	1.018		
CPNE1	1.011	0.911	0.899		
SRSF2;SFRS2;SRSF8	1.011	0.920	0.907		
HYOU1	1.011	0.961	0.943		
PRPS2;PRPS1	1.011	0.934	0.919		
ACTN4	1.011	1.017	0.995		
BANF1	1.011	0.813	0.827	+	+
STX2	1.011	0.994	0.973		
C1orf123	1.011	0.921	0.909		
PNPO	1.011	1.097	1.082		
AKAP2	1.011	1.107	1.093		
SFXN1	1.011	0.888	0.882		
MRPL1	1.011	1.009	0.988		
HNRNPH1	1.011	0.949	0.933		
TCP1	1.010	1.002	0.981		
RPS25	1.010	1.081	1.064		
EIF1	1.010	1.124	1.115		

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COX7A2	1.010	0.997	0.977		
NDUFS7	1.010	0.999	0.979		
RPL19	1.010	1.028	1.008		
RSU1	1.010	0.991	0.972		
MT-CO3	1.010	0.926	0.914		
PTPLAD1	1.010	0.762	0.795	+	+
PTMS	1.010	0.926	0.914		
PPIA	1.010	0.995	0.977		
RPS17L;RPS17	1.010	1.025	1.005		
AK2	1.010	0.903	0.896		
LPP	1.010	0.843	0.850		
HEBP1	1.010	1.012	0.993		
EXOC3	1.010	0.888	0.884		
COPZ2	1.010	1.023	1.004		
HIST2H3A;HIST3H3	1.009	0.998	0.980		
PGLS	1.009	0.761	0.795		+
RAI14	1.009	1.024	1.005		
SRSF10	1.009	1.022	1.004		
TSN	1.009	0.977	0.960		
CDC42	1.009	0.947	0.934		
CAPNS1	1.009	1.142	1.141		
DBN1	1.009	0.940	0.928		
ATAD1	1.009	1.195	1.215		+
IKBIP	1.009	0.973	0.958		
AKAP9	1.009	1.034	1.017		
RPL6	1.009	0.990	0.974		
ANXA4	1.009	1.110	1.102		+
MGAT1	1.009	1.134	1.132		
DEGS1	1.009	1.131	1.129		
STAU1	1.008	1.136	1.136		
GPX4	1.008	0.949	0.937		
MRPS11	1.008	1.034	1.018		
NDUFA2	1.008	0.936	0.926		
HSPA5	1.008	0.941	0.930		
NDUFS2	1.008	0.991	0.975		
NEK7	1.008	1.024	1.008		
MCFD2	1.008	0.936	0.926		
HSD17B10	1.008	0.928	0.919		
TFAM	1.008	0.972	0.958		
HIST1H3A	1.008	1.072	1.060		
AFAP1	1.008	1.070	1.057		
NDUFB11	1.008	0.720	0.772	+	+
MYO1C	1.008	0.982	0.967		
RAB11B	1.008	1.087	1.077		
HIST2H2BE;HIST1H2B	1.008	0.974	0.960		
RDH14	1.007	1.019	1.004		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
RPS4X;RPS4Y2;RPS4Y	1.007	0.985	0.971		
HIST1H2BM;HIST1H2B	1.007	1.050	1.037		
HNRNPD	1.007	1.077	1.067		
MRPL18	1.007	0.986	0.973		
COPG1	1.007	0.948	0.938		
CNP	1.007	1.100	1.093		
MGST3	1.007	1.070	1.059		
PHGDH	1.007	0.857	0.864		+
FASN	1.007	1.028	1.015		
HDGFRP2	1.007	0.911	0.907		
ECHS1	1.007	0.995	0.981		
CAPN2	1.007	1.087	1.079		
SRRT	1.007	0.948	0.938		
PYCR1	1.007	0.919	0.914		
CALM1;CALM2;CALM3	1.006	1.021	1.008		
HSPA1A	1.006	1.019	1.007		
CHMP6	1.006	0.992	0.980		
LUZP1	1.006	0.919	0.914		
RPS26;RPS26P11	1.006	1.032	1.020		
SYNJ2BP	1.006	1.120	1.121		
NAP1L1	1.006	0.962	0.952		
UBAP2L	1.006	1.005	0.993		
ARPC1B	1.006	1.071	1.062		
HIBADH	1.006	1.001	0.989		
ACTC1;ACTA1;ACTA2;	1.006	0.944	0.937		
PSMB3	1.006	1.019	1.007		
TMEM173	1.006	1.011	0.999		
RPS28	1.006	1.014	1.002		
PFDN2	1.006	1.063	1.053		
HSP90AB2P	1.006	0.982	0.971		
PFN1	1.006	1.029	1.017		
SRP19	1.006	1.017	1.006		
CTTN	1.006	1.029	1.018		
DAD1	1.006	0.850	0.861		
MLEC	1.006	0.913	0.911		
COX7A2L	1.006	1.034	1.023		
RAB9A	1.005	1.111	1.111		
HLA-A	1.005	0.968	0.959		
GNL2	1.005	0.870	0.877		
CFL2	1.005	1.005	0.994		
MYH9	1.005	0.972	0.962		
MRPL44	1.005	1.068	1.061		
CRYZ	1.005	1.116	1.118		
RAB23	1.005	1.085	1.080		
ANXA5	1.005	1.041	1.031		
RPS15A	1.005	1.045	1.035		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
PSMB1	1.005	0.944	0.938		
TUBB4B	1.005	0.900	0.901		
IMP4	1.005	1.076	1.071		
NDUFB8	1.005	0.776	0.811		+
RPS14	1.005	0.874	0.880		
S100A6	1.005	1.042	1.034		
VPS8	1.005	1.076	1.071		
SMARCA5	1.005	1.095	1.094		
CCDC90B;MDS025	1.005	1.072	1.067		
NDUFS3	1.005	0.962	0.955		
NDUFS4	1.005	1.119	1.124		
RAC1;RAC3	1.004	0.892	0.896		
MAP1B	1.004	1.020	1.011		
CYB5B	1.004	0.916	0.915		
HMGA1	1.004	0.845	0.859		
MPRIP	1.004	1.019	1.010		
IARS2	1.004	1.038	1.030		
SUMF2	1.004	0.890	0.894		
DBI	1.004	0.980	0.973		
PRDX1	1.004	1.004	0.996		
RAB5B	1.004	1.125	1.133		
SEPT2	1.004	1.009	1.001		
NQO1	1.004	0.962	0.956		
RPL39P5;RPL39	1.004	0.714	0.773	+	+
PSMD5	1.003	1.001	0.994		
RPSA;RPSAP58	1.003	0.996	0.989		
EXOC4	1.003	0.997	0.990		
AGA	1.003	0.997	0.990		
DERL1	1.003	0.804	0.831		
AP3S1	1.003	0.939	0.937		
AK1	1.003	1.035	1.029		
PDCD6	1.003	0.996	0.989		
NDUFB3	1.003	0.948	0.945		
DEK	1.003	1.026	1.020		
ARPC3	1.003	0.907	0.910		
NDUFC2;NDUFC2-KCT	1.003	0.976	0.971		
PIN1	1.003	1.042	1.037		
PSMB8	1.003	0.948	0.945		
BAX	1.003	1.008	1.002		
SURF1	1.003	0.935	0.934		
RIN1	1.003	1.224	1.280		
CAMK2D	1.003	1.041	1.037		
DDRGK1	1.003	0.928	0.928		
RPL9	1.003	0.997	0.991		
DST	1.003	1.175	1.204	+	+
MYL9	1.003	1.105	1.111		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
CYB5R1	1.003	1.007	1.002		
GNS	1.002	1.136	1.150		
DYNC1H1	1.002	1.021	1.016		
RAP1B	1.002	1.032	1.027		
BCAP29	1.002	1.126	1.138		
GSTO1	1.002	1.012	1.007		
TMEM256	1.002	0.963	0.960		
ABAT	1.002	0.976	0.973		
TIMM17B	1.002	0.985	0.981		
SLC25A22	1.002	0.994	0.990		
HNRNPA2B1	1.002	0.966	0.963		
RHOG	1.002	0.891	0.899		
SDF2	1.002	1.005	1.001		
RAB10	1.002	1.030	1.027		
HIST1H2BJ	1.002	0.987	0.984		
RPS13	1.002	0.936	0.937		
SEC23A	1.001	0.908	0.913		
SEPT11	1.001	0.954	0.954		
SEC22B	1.001	1.002	0.999		
FKBP4	1.001	0.924	0.927		
PSMA6	1.001	1.022	1.019		
CSNK2B	1.001	0.936	0.937		
IQGAP1	1.001	0.996	0.993		
ERP29	1.001	0.889	0.898		
PFN2	1.001	1.072	1.076		
SH3BGRL3	1.001	1.069	1.072		
RPL8	1.001	1.021	1.019		
ATP2A2	1.001	0.967	0.967		
ECI1;DCI	1.001	1.016	1.015		
GLIPR2	1.001	0.876	0.889		
HNRNPA0	1.000	1.020	1.019		
CAPN1	1.000	1.057	1.060		
NDRG1	1.000	1.080	1.086		
BAZ1B	1.000	1.090	1.097		
CMPK1	1.000	1.008	1.007		
DBNL	1.000	0.896	0.905		
COMT	1.000	0.985	0.985		
SAFB	1.000	0.954	0.956		
GMFB	1.000	1.014	1.014		
UROD	1.000	1.057	1.060		
C14orf166	1.000	0.993	0.993		
DGKA	1.000	0.990	0.990		
RYBP	1.000	1.034	1.036		
SRSF3	1.000	0.889	0.901		
ARPC5	1.000	1.012	1.013		
VDAC2	1.000	1.020	1.021		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
INA;NEFM;NEFL	0.999	0.960	0.963		
ARF6	0.999	1.011	1.013		
PSMD2	0.999	0.999	1.001		
GNB1	0.999	0.987	0.989		
HIST1H2AC;HIST3H2A;	0.999	1.005	1.007		
MTCH2	0.999	0.984	0.986		
SPR	0.999	1.023	1.026		
IQGAP2	0.999	0.995	0.997		
CFL1	0.999	0.983	0.985		
PCMT1	0.999	0.934	0.941		
EMC3	0.999	0.984	0.987		
CYC1	0.999	0.887	0.901		
RPL4	0.999	0.958	0.963		
PFDN5	0.999	1.130	1.153		
WIBG	0.999	0.907	0.917		
OPA1	0.998	1.121	1.142		
S100A13	0.998	1.023	1.027		
ITPA	0.998	0.999	1.002		
MACF1	0.998	1.011	1.015		
S100A11	0.998	1.080	1.091		
CUL4B	0.998	0.905	0.916		
CORO1C	0.998	0.962	0.967		
ERGIC1	0.998	1.028	1.033		
CBR3	0.998	1.015	1.020		
TMED5	0.998	1.007	1.011		
HNRNPH3	0.998	0.946	0.952		
NDUFB9	0.997	0.974	0.980		
ANXA11	0.997	1.066	1.077		
CBX5	0.997	1.109	1.130		
TOP1	0.997	0.977	0.983		
ZMPSTE24	0.997	1.014	1.020		
MRPL15	0.997	0.854	0.877		
CAND1	0.997	0.941	0.949		
SRM	0.997	0.983	0.988		
TALDO1	0.997	0.987	0.993		
SLAIN2	0.997	0.961	0.968		
ATP6V1D	0.997	1.125	1.150		
TMTC3	0.997	0.949	0.958		
DCTN2	0.997	1.038	1.047		
SSR4	0.997	1.035	1.043		
OSBPL8	0.997	0.861	0.883		
TEX10	0.997	0.850	0.875		
EPRS	0.997	0.934	0.944		
MYO6	0.996	1.075	1.090		
SSR1	0.996	0.921	0.933		
VDAC1	0.996	1.058	1.070		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
RPS6	0.996	1.018	1.026		
RAB14	0.996	1.003	1.011		
G6PD	0.996	0.935	0.946		
MT-CO2	0.996	0.990	0.998		
MAP1LC3A	0.996	1.081	1.098		
RPL24	0.996	1.054	1.067		
UBE2V2	0.996	1.017	1.026		
MBNL1;MBLL;MBNL2	0.996	0.998	1.007		
TMEM43	0.996	0.934	0.946		
PGRMC1	0.995	0.844	0.872		
COX5B	0.995	0.854	0.880		
TPP1	0.995	1.121	1.150		
ACP1	0.995	0.941	0.952		
CPNE3	0.995	0.957	0.967		
LMAN2	0.995	1.003	1.012		
PSMD8	0.995	1.018	1.028		
TSPO	0.995	1.072	1.089		
GNAQ	0.995	0.901	0.918		
RPL15	0.995	1.006	1.016		
HNRNPUL1	0.995	0.997	1.007		
GRHPR	0.995	1.028	1.040		
SNRPA	0.995	1.008	1.019		
UFC1	0.995	1.051	1.065		
PC	0.995	0.789	0.833		
NBAS	0.995	0.949	0.961		
RPS2	0.994	0.989	1.000		
NDUFA12	0.994	1.063	1.081		
PSMB7	0.994	0.894	0.914		
GOSR1	0.994	1.112	1.141		
MYL1;MYL3	0.994	0.995	1.007		
SBDS	0.994	1.040	1.054		
UQCRFS1;UQCRFS1P1	0.994	1.047	1.062		
RAP1A	0.994	1.111	1.140		
UACA	0.994	1.095	1.119		
SFXN3	0.994	0.963	0.975		
MYH10	0.994	0.949	0.962		
NDUFAB1	0.994	0.917	0.934		
ARPC5L	0.994	0.912	0.930		
PRKAR2A	0.994	0.996	1.008		
RALB	0.994	1.033	1.048		
TMSB4X;TMSB4XP4	0.994	0.897	0.917		
MCM2	0.994	1.146	1.189		
TOMM20	0.994	1.065	1.084		
AP2A1	0.994	0.963	0.976		
C9orf63	0.994	0.980	0.993		
MBOAT7	0.994	0.962	0.976		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
RNF170	0.993	0.804	0.845		
CCDC127	0.993	1.021	1.036		
STX5	0.993	1.028	1.043		
MRPL14	0.993	0.960	0.975		
SURF4	0.993	0.869	0.896		
RANBP1	0.993	1.008	1.023		
COX6B1	0.993	0.952	0.967		
GARS	0.993	0.867	0.894		
PSMD7	0.993	0.997	1.012		
RRBP1	0.993	0.984	0.999		
SRPRB	0.993	1.046	1.065		
ANP32B	0.992	0.923	0.942		
PSMA5	0.992	1.037	1.055		
COX4I1	0.992	0.956	0.972		
MYL12A;MYL12B	0.992	1.043	1.062		
RER1	0.992	0.873	0.900		
CYCS	0.992	0.985	1.000		
SARNP;CIP29	0.992	1.021	1.038		
NDUFB5	0.992	1.001	1.018		
CLIC4	0.992	1.002	1.018		
PPP1R12A	0.992	1.004	1.021		
GOSR2	0.992	1.003	1.019		
FTL	0.992	1.080	1.107		
RPL35	0.992	1.010	1.027		
CKAP4	0.992	0.949	0.967		
HNRNPAB	0.992	1.010	1.027		
CBFB	0.992	1.007	1.024		
RPS24	0.991	1.009	1.026		
SLC25A3	0.991	0.944	0.963		
LAMP2	0.991	0.967	0.985		
CLIC1	0.991	1.017	1.036		
IDH1	0.991	1.009	1.027		
NNT	0.991	0.962	0.980		
UQCRB	0.991	0.988	1.005		
SCP2	0.991	1.072	1.098		
ATP13A1	0.991	1.000	1.018		
RALA	0.991	1.096	1.129		+
HMGB1;HMGB1P1	0.991	0.927	0.948		
SNX12	0.991	0.936	0.956		
ATP6V1A	0.990	1.028	1.050		
NDUFB7	0.990	0.978	0.997		
RMND1	0.990	1.012	1.033		
INF2	0.990	1.077	1.107		
S100A10	0.990	1.024	1.046		
RAB6A	0.990	1.023	1.045		
PPP1R9B	0.990	0.944	0.966		

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MYL6	0.990	1.014	1.036		
RPL21	0.990	0.940	0.963		
ANP32A	0.990	0.955	0.976		
RBPMS	0.989	1.063	1.092		
SUN2	0.989	1.014	1.037		
AP2B1	0.989	1.006	1.029		
BCAP31	0.989	0.979	1.001		
RPN2	0.989	0.919	0.944		
CAPZA2	0.989	0.957	0.979		
ARPC2	0.989	0.988	1.011		
RPL13A	0.988	0.994	1.017		
TMED10	0.988	1.003	1.027		
PSMA4	0.988	1.020	1.045		
EEF1G	0.988	0.981	1.005		
CACNA1A	0.988	0.927	0.953		
COPB1	0.988	0.894	0.924		
SMARCAD1	0.988	1.020	1.046		
OCIAD1	0.988	1.088	1.126		+
SNAP29	0.988	1.037	1.065		
CDK5	0.988	1.096	1.136		
PPIH	0.988	1.007	1.032		
PSMD11	0.988	1.077	1.112		
PPP1CA	0.988	0.946	0.972		
IPO5	0.988	1.033	1.061		
EMC8	0.988	0.931	0.958		
DDAH2	0.988	0.930	0.957		
MYH14	0.987	0.957	0.982		
ERLIN1	0.987	0.925	0.953		
TRA2B	0.987	0.953	0.979		
NDUFA9	0.987	0.994	1.020		
UQCRH	0.987	0.942	0.968		
COL5A2	0.987	0.800	0.852		
HEXA	0.987	1.061	1.095		
PSMC3	0.987	0.922	0.951		
DPM1	0.987	1.008	1.036		
PRDX5	0.987	0.960	0.987		
RPL23	0.987	0.942	0.969		
HDGF	0.987	0.900	0.932		
RAD23B	0.986	0.986	1.013		
FAM120A	0.986	0.916	0.947		
HNRNPA3	0.986	0.955	0.983		
CCT3	0.986	0.951	0.979		
RAB27B	0.986	1.158	1.229		
MAP1LC3B;MAP1LC3B	0.986	1.120	1.174		
API5	0.986	0.925	0.956		
LACTB	0.986	0.952	0.981		

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COX5A	0.986	0.887	0.922		
FAM98A	0.986	1.023	1.054		
PSMA2	0.985	0.974	1.004		
VAPA	0.985	0.884	0.921		
XPOT	0.985	0.889	0.925		
ABCF2	0.985	1.052	1.089		
KPNA1	0.985	0.994	1.025		
RPN1	0.985	0.884	0.921		
TCEB2	0.985	1.001	1.033		
IARS	0.985	0.911	0.945		
MYLK	0.985	1.053	1.092		
STMN1	0.985	1.012	1.044		
OSTC	0.985	0.795	0.852		
PHB2	0.985	1.005	1.037		
UQCR10	0.984	1.068	1.110		
ATP5I	0.984	0.959	0.990		
RAB21	0.984	1.032	1.069		
CSTB	0.984	1.022	1.057		
MYO18A	0.984	1.014	1.048		
PRKRA	0.984	0.920	0.954		
PLGRKT	0.984	1.056	1.097		
LPXN	0.984	1.176	1.264	+	+
RPL22	0.984	0.987	1.020		
RPL23A	0.984	0.937	0.970		
COX6A1P2;COX6A1	0.984	0.764	0.831	+	+
PEX14	0.984	1.029	1.066		
UFL1	0.983	0.950	0.983		
C6orf120	0.983	0.880	0.920		
RIN3	0.983	1.027	1.064		
KIAA2013	0.983	1.028	1.066		
RPL17	0.983	1.024	1.062		
VDAC3	0.983	1.011	1.047		
GNG12	0.983	0.940	0.975		
DUT	0.983	1.060	1.104		
UQCRC1	0.983	1.045	1.087		
EIF4B	0.983	0.850	0.896		
RNH1	0.983	0.970	1.005		
RRAS2	0.983	1.003	1.039		
TNKS1BP1	0.983	0.955	0.990		
EFHD2	0.983	1.006	1.043		
LRRC59	0.983	0.899	0.938		
SEC11A;SEC11L1	0.982	0.946	0.982		
RPLP2	0.982	0.966	1.002		
DNAJC7	0.982	1.048	1.092		
LAMTOR3	0.982	0.747	0.822	+	+
SLC12A9	0.982	0.975	1.012		

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NSUN2	0.981	0.971	1.008		
TMEM126A	0.981	0.965	1.002		
NDUFS8	0.981	0.987	1.025		
H1FX	0.981	0.925	0.964		
COX6C	0.981	0.973	1.011		
ERLIN2	0.981	0.979	1.017		
RPL26;KRBA2	0.981	0.949	0.988		
HM13	0.981	0.976	1.015		
EMC4	0.980	0.934	0.974		
HIST2H2AB	0.980	0.968	1.007		
ALYREF	0.980	0.909	0.951		
CTSZ	0.980	1.047	1.095		
AP2M1	0.980	1.019	1.063		
CLTB	0.980	0.947	0.988		
MCUR1	0.980	1.032	1.079		
PSMA3	0.980	1.048	1.098		
XRCC5	0.979	0.993	1.035		
COPS8	0.979	0.936	0.978		
BDH2;SLC9B2	0.979	1.103	1.169		
MPC2	0.979	0.965	1.007		
COL12A1	0.979	0.956	0.998		
DECR1	0.979	0.993	1.036		
CEP170	0.979	0.951	0.993		
PAPSS2	0.979	1.095	1.160		
TRIM25	0.979	0.912	0.957		
HNRNPR	0.978	0.976	1.020		
DYNLRB1	0.978	1.040	1.091		
PDLIM2	0.978	0.906	0.952		
RFTN1	0.978	0.792	0.859	+	
NDUFA1	0.978	1.011	1.059		
RPL11	0.978	0.949	0.993		
UQCRQ	0.978	0.967	1.012		
MYOF	0.978	0.953	0.997		
TUBA4A	0.978	0.846	0.902		
CUL5	0.978	0.911	0.958		
RPL27	0.978	0.926	0.972		
AIMP1	0.978	0.901	0.949		
DNM2	0.977	1.066	1.126		
ATP5J	0.977	0.820	0.881		
SAMM50	0.977	0.973	1.018		
KIAA1715;LNP	0.977	0.835	0.894		
LMAN1	0.976	0.900	0.950		
G3BP2	0.976	0.935	0.983		
ARHGEF2	0.976	0.987	1.036		
GNB4	0.976	0.903	0.953		
PSMC5	0.976	0.949	0.996		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
HRAS;NRAS	0.976	0.947	0.996		
TMED9	0.976	0.948	0.997		
PDCD11	0.976	0.938	0.987		
MAN2A1	0.976	0.990	1.040		
SRP68	0.975	0.895	0.947		
RRP1	0.975	1.062	1.126		
RPL13	0.975	0.940	0.989		
MEST	0.975	0.942	0.991		
MT-ND4	0.975	0.988	1.039		
ACO2	0.975	0.881	0.935		
NDUFA13;YJEFN3	0.975	0.869	0.925		
RPL18A	0.975	1.035	1.093		
C5orf24	0.975	1.120	1.205		
NDUFV2	0.975	0.919	0.970		
UBR5	0.975	0.853	0.912		
STX7	0.974	0.944	0.995		
PDCD10	0.974	0.859	0.918		
SPCS3	0.974	0.948	1.000		
NDUFS5	0.974	0.916	0.969		
NDUFA6	0.974	1.093	1.169		+
KHSRP	0.974	0.883	0.939		
PHB	0.974	0.976	1.029		
TOP2A	0.974	1.158	1.267		+
HMG20A	0.974	1.038	1.100		
U2AF2	0.974	0.932	0.985		
CEBPZ	0.974	1.083	1.157		
RAB35	0.973	1.028	1.088		
PSMC2	0.973	1.045	1.109		
SLTM	0.973	0.978	1.032		
TMED1	0.973	0.938	0.992		
UQCRC2	0.973	1.018	1.078		
EMC2	0.973	0.937	0.991		
SLC16A7	0.973	0.748	0.835		
CD99	0.973	0.903	0.959		
NUMA1	0.973	1.060	1.130		+
KDELR1;KDELR2	0.972	0.934	0.990		
SOAT1	0.972	1.073	1.147		
LAMP1	0.972	1.126	1.222		+
PSMB6	0.972	0.927	0.983		
SERBP1	0.972	0.946	1.003		
FKBP11	0.971	0.860	0.923		
PRKACA;PRKACB	0.971	1.008	1.070		
RPL14	0.971	0.968	1.027		
SRP14	0.971	1.077	1.155		+
MVP	0.971	0.930	0.988		
RPL28	0.971	1.010	1.074		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
PSMD9	0.971	0.844	0.912		
TMED7;TIRAP3	0.970	0.984	1.045		
SERPINB2	0.970	1.127	1.229		+
VAPB	0.970	0.911	0.971		
MGST1	0.970	0.825	0.896		
TNPO1	0.970	0.986	1.048		
MRC2	0.970	0.984	1.046		
MAGT1	0.970	0.953	1.014		
RPRD1B	0.970	1.017	1.084		
CCT5	0.970	0.975	1.037		
FNDC3B	0.970	1.008	1.074		
RPL32	0.970	0.943	1.003		
EIF4E	0.970	1.005	1.070		
H6PD	0.969	1.006	1.072		
SLIRP	0.969	1.047	1.121		
RAN	0.969	0.868	0.935		
SYNE2	0.969	1.014	1.082		
SLC39A7	0.969	0.695	0.805	+	+
ZNF148	0.969	1.125	1.230		
LAMTOR5	0.969	1.033	1.106		
VAMP5	0.968	1.039	1.114		
PPP1CC	0.967	0.988	1.056		
TRAM1	0.967	0.937	1.002		
YWHAG	0.967	0.905	0.971		
DDOST	0.967	0.891	0.959		
TMED2	0.967	0.937	1.003		
SLC25A24	0.967	0.980	1.049		
FARP1	0.967	0.694	0.807	+	+
LMNB2	0.967	0.910	0.978		
B2M	0.966	1.065	1.153		+
STT3A	0.966	0.880	0.950		
RPL10A	0.966	0.935	1.003		
PDLIM7	0.966	0.896	0.965		
GREM1	0.966	0.829	0.907		
SNX18	0.966	0.680	0.799	+	+
RPL37A	0.966	0.991	1.064		
INTS1;DKFZP586J061	0.965	1.067	1.157		
PFDN4	0.965	1.035	1.116		
PCOLCE	0.965	1.057	1.144		
PNO1	0.965	0.997	1.071		
NDUFV1	0.965	0.979	1.052		
RPL36	0.965	0.903	0.973		
REEP5	0.965	1.062	1.153		
SLC25A20	0.964	1.002	1.079		
TMOD2	0.964	0.991	1.067		
GNAS	0.964	0.970	1.044		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B ($p \leq 0.05$)	Reverse Significance B ($p \leq 0.05$)
EMC7	0.964	1.015	1.095		
S100A16	0.964	0.982	1.057		
MYO1B	0.964	0.967	1.041		
EMC10	0.964	0.996	1.074		
EIF2S2	0.964	0.992	1.069		
EBP	0.964	0.952	1.026		
RPL18	0.964	0.925	0.998		
RPL5	0.963	0.982	1.059		
TOMM22	0.963	0.847	0.926		
GPNMB	0.963	0.986	1.064		
RPL12	0.963	0.966	1.041		
IPO7	0.963	0.978	1.056		
LMNB1	0.963	0.912	0.987		
ITGB6	0.962	1.180	1.344	+	+
PGAM5	0.962	0.951	1.027		
LIMA1	0.962	0.871	0.950		
RPL7	0.962	0.915	0.991		
LAMTOR2	0.962	0.998	1.080		
ATP6V1E1;ATP6V1E2	0.962	1.023	1.111		
CCT6A	0.961	0.954	1.032		
TXN	0.961	1.001	1.086		
ADA	0.961	1.116	1.242		
YME1L1	0.961	1.061	1.162		
LAMTOR1	0.961	0.933	1.012		
SDCBP	0.961	1.047	1.143		
TP53BP1	0.960	0.910	0.989		
EIF2S3;EIF2S3L	0.960	0.880	0.960		
TUBA1A;TUBA3C;TUB	0.960	1.043	1.140		
SPCS2	0.960	0.890	0.971		
UBE2I	0.960	0.900	0.980		
SART1	0.960	1.015	1.105		
APRT	0.960	0.978	1.062		
CSNK2A1;CSNK2A3	0.960	0.927	1.008		
PTBP1	0.960	0.928	1.009		
FTSJ3	0.959	0.935	1.016		
PSMB5	0.959	0.927	1.009		
GTPBP4	0.959	0.953	1.036		
FUBP3	0.959	0.925	1.007		
DDX5	0.959	1.047	1.149		+
MCM7	0.959	1.072	1.182		
ATP6V1G1	0.958	1.050	1.154		
FAM129A	0.958	1.117	1.251		+
RAB22A	0.958	1.004	1.096		
ILF3	0.958	0.889	0.973		
PSMA7;PSMA8	0.958	0.922	1.006		
SKP1	0.958	1.008	1.100		

Protein name	**Average fold change in chromatin abundance (SILAC ratio UV vs no UV)**	**Forward L(no UV) / H(UV)**	**Reverse L(UV) / H(no UV)**	**Forward Significance B (p ≤0.05)**	**Reverse Significance B (p ≤0.05)**
AHCTF1	0.958	1.062	1.171		
KTN1	0.958	0.939	1.024		
MRPL17	0.958	0.886	0.971		
FAM3C	0.958	1.162	1.328	+	+
DDT;DDTL	0.957	0.889	0.975		
CD63	0.957	1.002	1.096		+
HIST2H2BD;HIST2H2B	0.957	0.988	1.081		
SNAP23	0.956	1.024	1.125		
SCAMP3	0.956	0.991	1.086		
DYNC1I2	0.956	0.914	1.002		
UGP2	0.956	0.952	1.042		
DDX17	0.956	1.003	1.101		+
KRTCAP2	0.955	0.847	0.941		
LAMTOR4	0.955	1.057	1.173		+
U2AF1	0.955	0.850	0.944		
BAG2	0.954	0.842	0.938		
GNAI2	0.954	1.000	1.101		+
TOP2B	0.954	1.071	1.194		+
RRAS	0.954	0.944	1.037		
LOX	0.953	1.083	1.214		
CCT8	0.953	0.983	1.083		
MYCBP	0.953	0.839	0.937		
PPP1R18	0.953	0.877	0.972		
HSPA6;HSPA7	0.953	0.920	1.014		
MTX2	0.953	0.967	1.066		
TM9SF4	0.952	0.982	1.083		
HDAC1;HDAC2	0.952	1.040	1.157		
CHD2;CHD1	0.952	0.979	1.081		
DYNLL1	0.952	0.987	1.090		
CTNNA1	0.952	1.000	1.107		
EIF6	0.952	0.910	1.007		
VAMP2;VAMP3	0.951	0.994	1.100		
ITGA4	0.951	1.022	1.135		
GPR107	0.951	0.972	1.075		
STIM1	0.951	1.000	1.109		
GOLGB1	0.950	1.004	1.116		
CD81	0.950	0.996	1.106		
COTL1	0.950	1.034	1.154		
POR	0.950	1.004	1.116		
LRRN4CL	0.950	0.828	0.933		
CAD	0.950	0.966	1.071		
STT3B	0.950	0.896	0.996		
CHCHD2;CHCHD2P9	0.949	0.981	1.089		
EHD2	0.949	1.041	1.167		+
FAF2	0.949	0.926	1.028		
SEC61A1;SEC61A2	0.949	0.843	0.948		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
RPL7A	0.949	0.906	1.009		
NDUFS6	0.949	1.046	1.176		+
STX4	0.948	0.902	1.005		
TPM1	0.948	0.935	1.040		
CLDN11	0.948	1.052	1.186		
NDUFB4	0.948	0.726	0.855	+	+
TMCO1	0.947	0.985	1.100		
SNRNP70	0.947	1.001	1.119		
PLCD3	0.947	0.917	1.024		
TJP1	0.946	0.904	1.012		
STX8	0.945	1.018	1.146		
HEATR1	0.945	0.945	1.057		
ILF2	0.945	0.933	1.045		
SSFA2	0.945	1.018	1.147		
GADD45GIP1	0.944	0.804	0.922		
RBMX;RBMXL1	0.944	0.898	1.010		
SSBP1	0.944	1.011	1.140		+
MAP7D1	0.943	0.933	1.049		
MOXD1	0.943	0.962	1.082		
HSD17B12	0.943	0.910	1.025		
NOP56	0.943	0.890	1.005		
ELAVL1	0.942	0.933	1.051		
NPM1	0.942	0.852	0.970		
SLC12A4	0.941	0.968	1.094		
SLC3A2	0.941	0.796	0.921	+	
CLTC	0.941	0.891	1.009		
THY1	0.941	0.909	1.028		
CTNND1	0.940	0.859	0.978		
HDGFRP3	0.940	0.788	0.915		
CLTA	0.940	0.919	1.041		
STX12	0.939	1.010	1.152		
PRAF2	0.939	0.949	1.077		
FAP	0.939	1.003	1.144		
ITGB1	0.938	0.992	1.131		+
AIDA	0.938	0.891	1.016		
MAP9	0.937	0.981	1.121		
PEX11B	0.937	1.002	1.148		
PSMD10	0.936	0.978	1.118		
NDUFA5;DKFZp781K13	0.936	0.982	1.122		
VAMP3	0.936	0.939	1.071		
SLC1A5	0.936	0.822	0.952		
NOP58	0.936	0.885	1.014		
GNA13	0.935	0.950	1.086		
SEC13	0.935	1.052	1.222		+
TIMM13	0.935	0.929	1.062		
TMEM55B	0.935	0.716	0.867	+	

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ERH	0.934	0.935	1.071		
PDGFRB	0.934	0.977	1.122		
C12orf23	0.934	0.981	1.128		
CRTAP	0.934	0.973	1.119		
MLLT4	0.933	0.864	0.997		
PTGES3	0.933	0.924	1.061		
CSPG4	0.933	1.081	1.273		
FBLL1	0.933	0.759	0.904	+	
PSMD13	0.933	0.989	1.141		
GALNT2	0.932	1.005	1.163		
DHX9	0.932	0.867	1.002		
NOC2L	0.932	0.787	0.928		
PRNP	0.931	0.905	1.043		
NOP10	0.931	0.749	0.898	+	
SLC39A9	0.930	1.064	1.255		
VTI1B	0.930	1.000	1.162		
DNTTIP2	0.930	0.990	1.149		
RBM4;RBM4B	0.930	0.982	1.138		
TMED4	0.930	0.929	1.075		
RBM14	0.930	0.800	0.944		
HLA-A	0.929	0.993	1.155		
DKC1	0.929	0.829	0.972		
PSMB4	0.929	0.952	1.104		
SEC61B	0.928	0.859	1.003		
FBL	0.928	0.776	0.926	+	
NSA2	0.928	0.995	1.163		
TM9SF3	0.927	1.020	1.198		
PPP3R1	0.927	1.102	1.329		+
AHNAK	0.927	0.966	1.127		+
CCDC47	0.926	0.943	1.099		
DPP4	0.926	1.146	1.418		+
NCSTN	0.925	0.919	1.074		
COL3A1	0.925	0.879	1.030		
NPC1	0.925	0.859	1.010		
CCT2	0.925	0.931	1.089		
MAK16	0.924	0.949	1.111		
GBE1	0.924	0.847	0.998		
POLR2M;GCOM1	0.924	0.598	0.800	+	+
SUMO1	0.924	0.958	1.124		
EPB41L2	0.923	0.868	1.022		
RAP2B	0.923	0.964	1.134		
SON	0.922	0.991	1.173		
NHP2	0.922	0.708	0.880	+	
JAG1	0.922	0.864	1.021		
SCARB2	0.922	0.870	1.027		
SYPL1	0.921	0.850	1.008		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
SEC62	0.921	0.967	1.142		
NDUFA8	0.921	0.657	0.844	+	+
GLYR1	0.921	0.960	1.134		
ITGAV	0.921	0.910	1.075		
ITGB5	0.920	0.908	1.072		
HLA-A	0.920	1.021	1.221		+
GALK1	0.920	0.761	0.927	+	
HNRNPUL2;hCG_2044	0.920	0.894	1.058		
CD59	0.920	0.970	1.150		+
HLA-B	0.920	1.035	1.243		+
BSG	0.919	0.841	1.003		
CD47	0.919	1.014	1.212		
FAS	0.919	1.015	1.216		
NUP107	0.919	0.802	0.966		
FLOT2	0.918	0.894	1.061		
LMO7	0.918	1.003	1.201		+
LIN7C	0.918	0.911	1.082		
MAN2C1	0.917	0.774	0.943	+	
MACROD1	0.917	0.926	1.102		
DLG1	0.916	0.893	1.064		
FSTL1	0.916	0.986	1.182		
RPL34	0.916	1.045	1.270		
HMGN1	0.916	0.873	1.044		
RUVBL1	0.916	0.874	1.045		
SPPL2A	0.915	0.977	1.170		
DDX21	0.915	0.933	1.114		
MYADM	0.915	0.715	0.896	+	
AHNAK2	0.914	1.023	1.242		+
IFITM2;IFITM3;IFITM1	0.913	0.913	1.095		
CHP1	0.913	0.908	1.090		
OCC1;C12orf75	0.913	0.937	1.126		
BLVRA	0.912	0.874	1.051		
ADAR	0.912	0.953	1.148		
DSE	0.912	0.903	1.087		
CBX3	0.912	0.896	1.079		
HLA-C;HLA-B	0.912	0.992	1.203		+
CYBRD1	0.910	0.894	1.079		
NT5E	0.910	0.954	1.155		+
FLOT1	0.909	0.906	1.096		
CDKN2A;CDKN2B	0.909	1.036	1.279		
CACNA2D1	0.909	0.901	1.091		
ANPEP	0.908	0.855	1.040		
DNAJC13	0.908	0.813	0.997		
TFRC	0.908	0.858	1.044		
NPTN;DKFZp566H1924	0.907	0.904	1.099		
DDR2	0.907	0.892	1.086		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B ($p \leq 0.05$)	Reverse Significance B ($p \leq 0.05$)
LMNA	0.907	0.803	0.990	+	
LARP1	0.907	0.935	1.138		
TCIRG1	0.906	0.896	1.091		
SAP18	0.906	1.012	1.249		+
PTK7	0.905	0.854	1.045		
STOM	0.904	0.961	1.180		+
ATP2B4	0.904	0.924	1.130		
COL1A2	0.904	0.741	0.937	+	
PCDHGA3;PCDHGB5;	0.904	0.960	1.179		
AATF	0.904	0.950	1.167		
GNA11	0.903	0.850	1.045		
HNRNPF	0.903	0.895	1.097		+
COL1A1	0.903	0.747	0.944	+	
UTP14A	0.903	0.925	1.136		
ATP6V0A1	0.903	0.951	1.170		
CDIPT	0.902	0.941	1.159		
UTP11L	0.902	0.967	1.195		
NUP153	0.901	0.904	1.113		
SLC16A3	0.901	0.877	1.082		
RND3;ARHE	0.901	1.035	1.304		+
HNRNPU	0.901	0.898	1.107		+
ATP1A1	0.900	0.871	1.076		
PLP2	0.900	0.871	1.077		
IMP3	0.899	1.012	1.272		+
MPHOSPH10	0.898	0.883	1.095		
POLR2C	0.896	0.877	1.093		
DDX27	0.896	0.976	1.225		+
AKAP8L	0.896	0.994	1.254		
LMNA	0.895	0.889	1.111		+
NHP2L1	0.894	0.811	1.025		
ATP6V0D1	0.893	0.892	1.118		+
RTN4	0.893	0.655	0.884	+	
ITGA5	0.891	0.875	1.103		
TARDBP	0.891	0.870	1.097		
UTRN	0.891	0.874	1.102		
SGCD	0.890	0.858	1.084		
MAPK3	0.890	0.935	1.183		
TMEM165	0.890	0.718	0.942	+	
CD44	0.889	0.939	1.191		+
ZFR	0.889	0.915	1.159		
SNTB2	0.888	0.830	1.056		
ABCD3	0.888	0.852	1.082		
PPAP2A	0.888	0.914	1.160		
LRP1	0.888	0.989	1.271		+
PROSC	0.888	0.778	1.003		
SUMO2;SUMO4;SUMO	0.887	0.835	1.065		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
CAV2	0.886	0.766	0.994	+	
CTNNA2	0.885	0.982	1.268		+
ATP1B3	0.885	0.807	1.040		
PEAK1	0.884	0.940	1.206		
RRS1	0.884	0.883	1.132		
TRIP12	0.881	0.951	1.234		
POLR2H	0.880	0.901	1.164		
NUCB1	0.880	0.867	1.120		
TCOF1	0.878	0.820	1.068		
NOP16	0.877	0.818	1.067		
MRTO4	0.875	0.819	1.073		
MFI2	0.874	0.717	0.969	+	
WDR43	0.874	0.882	1.155		
RPF2	0.873	0.890	1.168		+
XRN2	0.873	0.848	1.113		
HNRNPC	0.873	0.887	1.163		+
LSM6	0.873	0.783	1.039		
CACYBP	0.872	1.015	1.371		+
MKI67IP	0.870	0.882	1.164		
HNRNPM	0.870	0.824	1.091		
MYBBP1A	0.870	0.875	1.157		
MME	0.870	0.886	1.172		+
MMP14	0.870	1.001	1.356		+
SPARC	0.869	0.854	1.131		
DDX50	0.869	0.920	1.223		
TPR	0.869	0.844	1.119		
DDX39B;DDX39A	0.869	0.847	1.124		+
RPL7L1	0.867	0.933	1.247		+
MRE11A	0.867	0.930	1.244		+
PES1	0.866	0.918	1.228		+
PPAP2B	0.866	0.997	1.361		+
SDPR	0.864	0.929	1.251		+
ALCAM	0.864	0.894	1.199		+
PTRF	0.863	0.857	1.150		+
RSL1D1	0.863	0.824	1.108		
SART3	0.863	0.754	1.030	+	
GOLIM4	0.860	0.963	1.322		+
CAV1	0.859	0.836	1.135		+
GAR1	0.857	0.826	1.126		
PRRX2	0.857	0.761	1.050		
GLG1	0.856	1.002	1.406		+
PPIL3	0.855	0.771	1.064		
PRKCDBP	0.855	0.863	1.182		+
LAS1L	0.854	0.796	1.096		
TECR	0.854	1.074	1.579		+
ELMSAN1	0.854	0.857	1.176		

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
NOP2	0.851	0.810	1.121		
MT-ND5	0.848	0.745	1.053		
DDX24	0.847	0.951	1.344		+
LSM2	0.847	0.779	1.094		
HNRNPH2	0.846	0.796	1.117		
WDR74	0.846	0.838	1.172		
RALY	0.846	0.832	1.164		+
KIAA0020	0.845	0.865	1.212		
RAD50	0.843	0.852	1.199		
SGCB	0.841	0.773	1.100	+	
PRKDC	0.839	0.819	1.164	+	
KIAA1967	0.835	0.739	1.073	+	
BRIX1	0.835	0.753	1.091	+	
CHTOP	0.833	0.829	1.195		+
KIRREL	0.833	0.909	1.322		+
POLR2E	0.832	0.824	1.191		
TNS1	0.831	0.856	1.239		
NIP7	0.831	0.794	1.152		
RBM28	0.830	0.943	1.396		+
SLC12A2	0.828	0.834	1.215		
TMEM119	0.826	0.933	1.392		+
DNAH7	0.824	1.326	3.107	+	+
KRR1	0.822	0.788	1.169		
TRIM28	0.819	0.823	1.227		+
SNRPD2	0.819	0.787	1.176		+
SNRPN;SNRPB	0.816	0.831	1.249		+
MATR3	0.813	0.793	1.200	+	+
EBNA1BP2	0.812	0.794	1.206		+
DDX18	0.811	0.830	1.262		+
EIF4A3	0.806	0.852	1.315		+
MLF2	0.805	0.830	1.282		+
RECK	0.802	0.829	1.291		+
POLR2B	0.799	0.803	1.256		+
ENPP1	0.796	0.841	1.332		+
SNRPE	0.796	0.785	1.240		+
SUGP2	0.789	0.886	1.447		+
SF3B1	0.786	0.822	1.333		+
SNRPD1	0.786	0.768	1.245	+	+
MAGOHB;MAGOH	0.786	0.722	1.177	+	+
SMARCC2	0.783	0.889	1.477		+
CDC5L	0.782	0.785	1.282		+
PRPF19	0.782	0.673	1.123	+	
KM-PA-2;BOP1	0.779	0.642	1.093	+	
BCAS2	0.778	0.765	1.263		
GJA1	0.777	0.905	1.542		+
RBM8A	0.775	0.784	1.305		+

Protein name	Average fold change in chromatin abundance (SILAC ratio UV vs no UV)	Forward L(no UV) / H(UV)	Reverse L(UV) / H(no UV)	Forward Significance B (p ≤0.05)	Reverse Significance B (p ≤0.05)
PRPF6	0.771	0.873	1.494		+
SNRPD3	0.770	0.788	1.328		+
DDX56	0.758	0.855	1.515		+
SNW1	0.751	0.802	1.428		+
POLR2A	0.748	0.867	1.592		+
FN1	0.746	0.826	1.502		+
SF3B2	0.744	0.715	1.292	+	+
PPIL1	0.741	0.633	1.178	+	
SNRNP40	0.731	0.726	1.360	+	+
SNRPA1	0.724	0.681	1.304	+	+
SF3A1	0.718	0.765	1.489		+
SNRPF	0.711	0.513	1.100	+	
SNRNP200	0.709	0.771	1.547		+
XPC	0.705	0.782	1.591	+	+
EFTUD2	0.704	0.641	1.302	+	+
PRPF8	0.697	0.780	1.626		+
USP5	0.692	0.893	2.036		+
SNRPB2	0.687	0.740	1.576	+	+
SF3B5	0.643	0.558	1.374	+	+
TTN	0.642	0.395	1.124	+	
BUD31	0.642	0.694	1.694	+	+
CPSF6	0.639	0.960	3.146		

Chromatin was isolated from mock-treated or UV irradiated HDFs (20 J/m^2, 1hr post-irradiation) that were grown in media containing light [12C^6]-lysine and [12C^6,14N^4]-arginine or heavy [13C^6]-lysine and [13C^6,15N^4]-arginine. Nanoflow liquid chromatography tandem mass spectrometry (LC-MS/MS) and data analysis was performed as described in the Methods. In the forward SILAC experiment, cells grown in Light media (L) were mock-treated and cells grown in Heavy media (H) were UV-irradiated. Conversely, in the reverse experiment the mock-treated cells were those metabolically labeled with heavy amino-acids. Ratio Significance B[17] was calculated by estimating the variance of the distribution of all protein ratios, taking into account the dependency of the distribution on the summed protein intensity. Proteins

SI Table 2: UV-triggered and ATM-dependent alternative splicing events

SKIPPED EXONS

Gene ID	exon Start (0 base)	exon End	chr.(x)	no UV vs UV p Value	no UV vs UV Inc.Level Dif.	UV vs ATMi+UV Inc.Level Dif.
ABCA1	107566906	107567001	chr9	0.032	0.16	-0.16
ACAD10	112167609	112167760	chr12	0.019	0.17	-0.13
ACLY	40052872	40052902	chr17	0.009	0.14	-0.16
ACTN1	69345174	69345240	chr14	0.016	0.14	-0.15
AFTPH	64778576	64780543	chr2	0.003	0.25	-0.25
AGAP1	236626200	236626288	chr2	0.043	0.13	-0.13
AGFG1	228384663	228384779	chr2	0.000	0.11	-0.11
AGO1	36372535	36372720	chr1	0.002	0.19	-0.22
AKAP10	19835117	19835291	chr17	0.020	0.15	-0.19
ALS2CR8	203839056	203839219	chr2	0.022	0.45	-0.40
ANAPC1	112631189	112631241	chr2	0.002	0.13	-0.13
ANAPC10	146002811	146002902	chr4	0.012	0.15	-0.15
ANKRD17	73956383	73958017	chr4	0.010	0.11	-0.11
ANKRD28	15793256	15793327	chr3	0.012	0.12	-0.17
AP4M1	99700297	99700404	chr7	0.017	0.18	-0.11
ARFGEF2	47591302	47591411	chr20	0.015	0.14	-0.17
ARHGAP12	32106715	32106814	chr10	0.009	0.21	-0.16
ARHGEF11	156908209	156908305	chr1	0.000	0.39	-0.21
ARID1A	27088642	27088810	chr1	0.000	0.20	-0.20
ARIH1	72837160	72837305	chr15	0.000	0.11	-0.11
ARV1	231125855	231126009	chr1	0.001	0.27	-0.28
ASPM	197069560	197074315	chr1	0.003	0.51	-0.20
ATF7	53910798	53911138	chr12	0.009	0.24	-0.24
ATG10	81460217	81460356	chr5	0.045	0.28	-0.48
ATG16L1	234164747	234164841	chr2	0.003	0.20	-0.20
ATP5S	50790662	50790834	chr14	0.017	0.13	-0.13
ATXN7	63976413	63976535	chr3	0.019	0.10	-0.10
BAG4	38065029	38065284	chr8	0.043	0.20	-0.20
BFAR	14742244	14742449	chr16	0.000	0.11	-0.12
BLZF1	169351299	169351519	chr1	0.000	0.25	-0.25
BOC	112991915	112992188	chr3	0.008	0.19	-0.14
BPNT1	220236098	220236296	chr1	0.007	0.11	-0.12
BRAP	112098403	112098479	chr12	0.016	0.22	-0.22
BRAP	112103442	112103591	chr12	0.015	0.10	-0.10
C12orf52	113623989	113624121	chr12	0.010	0.10	-0.10
C2orf47	200826503	200826651	chr2	0.000	0.60	-0.49
C6orf136	30617334	30617736	chr6	0.000	0.77	-0.38
C6orf136	30617334	30617736	chr6	0.020	0.37	-0.19
CAD	27448998	27449187	chr2	0.021	0.18	-0.11
CAMLG	134076752	134077213	chr5	0.000	0.37	-0.23
CAMLG	134076752	134077213	chr5	0.000	0.47	-0.22
CAMTA2	4884972	4885126	chr17	0.030	0.16	-0.16
CBFA2T2	32207322	32207412	chr20	0.040	0.29	-0.33
CCDC58	122087022	122087169	chr3	0.001	0.12	-0.12

Gene ID	**exon Start (0 base)**	**exon End**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
CDAN1	43023817	43024023	chr15	0.040	0.16	-0.16
CDK17	96728496	96728643	chr12	0.000	0.12	-0.13
CDK19	111067328	111067404	chr6	0.000	0.29	-0.29
CDK5RAP2	123169289	123169526	chr9	0.014	0.16	-0.18
CDYL2	80718434	80719026	chr16	0.002	0.24	-0.27
CEP164	117257918	117258128	chr11	0.005	0.13	-0.13
CEP164	117233119	117233254	chr11	0.016	0.12	-0.12
CEP63	134214137	134214206	chr3	0.004	0.28	-0.30
CEP78	80880774	80880822	chr9	0.028	0.43	-0.22
CFLAR	202005079	202005162	chr2	0.003	0.15	-0.15
CHTOP	153614721	153614905	chr1	0.000	0.42	-0.13
CKAP2L	113518289	113518341	chr2	0.039	0.21	-0.16
CMC1	28304781	28304871	chr3	0.028	0.11	-0.22
CNTNAP3B	43844143	43844315	chr9	0.035	0.22	-0.20
COL6A3	238250707	238250804	chr2	0.040	0.13	-0.13
CPT1C	50195077	50195146	chr19	0.003	0.36	-0.18
CROCCP3	16802893	16802999	chr1	0.016	0.23	-0.26
CSRP2BP	18143020	18143589	chr20	0.003	0.25	-0.25
CSTF3	33112077	33112273	chr11	0.006	0.13	-0.13
CUL2	35318415	35318568	chr10	0.003	0.16	-0.16
CYP20A1	204111477	204111644	chr2	0.004	0.56	-0.39
CYTH1	76688498	76688575	chr17	0.041	0.24	-0.24
DAG1	49508397	49508482	chr3	0.042	0.78	-0.29
DCAF10	37857237	37857348	chr9	0.013	0.23	-0.33
DCAF5	69542061	69542128	chr14	0.002	0.14	-0.14
DCAF8	160231074	160231148	chr1	0.012	0.11	-0.13
DDX58	32485172	32485277	chr9	0.045	0.11	-0.11
DDX6	118635916	118636063	chr11	0.000	0.22	-0.13
DENND4B	153915031	153915101	chr1	0.014	0.23	-0.31
DET1	89070829	89071017	chr15	0.027	0.30	-0.20
DHX35	37653872	37654002	chr20	0.012	0.36	-0.36
DHX57	39033700	39033835	chr2	0.015	0.11	-0.11
DIABLO	122702812	122702944	chr12	0.000	0.11	-0.10
DLGAP5	55615311	55615402	chr14	0.046	0.18	-0.27
DNAJC16	15888636	15888820	chr1	0.003	0.18	-0.18
DNMT3A	25459804	25459874	chr2	0.013	0.43	-0.43
DPP8	65746600	65746753	chr15	0.039	0.20	-0.37
DRAM1	102313886	102313979	chr12	0.005	0.16	-0.15
DRAM1	102313886	102313979	chr12	0.007	0.12	-0.12
DSTYK	205128674	205128807	chr1	0.005	0.18	-0.18
DUS4L	107211589	107211711	chr7	0.002	0.17	-0.17
EHMT1	140685299	140685422	chr9	0.001	0.13	-0.13
EI24	125452241	125452315	chr11	0.000	0.64	-0.31
EI24	125451106	125451218	chr11	0.000	0.21	-0.11
ELK4	205592803	205593019	chr1	0.027	0.13	-0.13
EML4	42531623	42531691	chr2	0.005	0.11	-0.12
ENTPD6	25187157	25187226	chr20	0.018	0.23	-0.33
ENTPD6	25187711	25188033	chr20	0.015	0.15	-0.24

Gene ID	**exon Start (0 base)**	**exon End**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
ERI3	44818521	44818597	chr1	0.029	0.13	-0.11
ESF1	13753160	13753261	chr20	0.024	0.25	-0.25
ETV4	41622925	41623036	chr17	0.020	0.27	-0.17
FAM102A	130716083	130716204	chr9	0.021	0.16	-0.16
FAM72D	143906011	143906136	chr1	0.015	0.49	-0.56
FAM86DP	75478286	75478388	chr3	0.008	0.24	-0.57
FBXO11	48045917	48046003	chr2	0.000	0.11	-0.11
FBXO27	39521668	39521764	chr19	0.039	0.22	-0.22
FBXO28	224321775	224321914	chr1	0.000	0.14	-0.10
FGF5	81196062	81196166	chr4	0.000	0.19	-0.12
FKBP15	115973756	115973872	chr9	0.037	0.17	-0.23
FUT10	33246480	33247316	chr8	0.045	0.27	-0.33
GABPA	27117520	27117665	chr21	0.013	0.11	-0.12
GMEB1	29016615	29016698	chr1	0.030	0.19	-0.19
GNB1L	19808120	19808246	chr22	0.023	0.33	-0.33
GOLT1B	21661316	21661495	chr12	0.000	0.29	-0.11
GON4L	155722994	155723205	chr1	0.000	0.42	-0.18
GOSR1	28837897	28837927	chr17	0.017	0.11	-0.12
GSE1	85698620	85698734	chr16	0.017	0.13	-0.13
HACL1	15616483	15616589	chr3	0.043	0.22	-0.11
HECA	139487420	139488461	chr6	0.034	0.17	-0.17
HERC4	69749967	69750157	chr10	0.000	0.10	-0.10
HNRNPA1L2	53206556	53206629	chr13	0.005	0.29	-0.25
HSCB	29139869	29139966	chr22	0.000	0.32	-0.13
HSF2	122749047	122749101	chr6	0.027	0.25	-0.17
HSPA14	14890788	14890894	chr10	0.034	0.24	-0.24
HSPA14	14893217	14893322	chr10	0.013	0.13	-0.13
IDE	94239033	94239178	chr10	0.005	0.12	-0.13
IFI44	79126238	79126339	chr1	0.010	0.44	-0.23
IGF2BP3	23383336	23383472	chr7	0.002	0.23	-0.31
ILF3	10798021	10798384	chr19	0.030	0.25	-0.15
IMMP1L	31477806	31477933	chr11	0.000	0.29	-0.17
IMMP1L	31484718	31484852	chr11	0.006	0.16	-0.10
INPP4B	143114239	143114348	chr4	0.000	0.13	-0.13
INPP5B	38334172	38334286	chr1	0.003	0.13	-0.13
JMY	78608225	78608321	chr5	0.001	0.58	-0.59
KIAA0430	15718625	15718784	chr16	0.000	0.20	-0.20
KIAA0753	6515238	6515468	chr17	0.005	0.13	-0.14
KIAA1432	5753199	5753238	chr9	0.002	0.35	-0.35
KLHDC4	87764157	87764250	chr16	0.009	0.12	-0.11
LARS2	45565488	45565600	chr3	0.030	0.18	-0.18
LDLR	11215895	11216276	chr19	0.005	0.15	-0.13
LEF1	109002741	109002825	chr4	0.003	0.55	-0.53
LOC100506054	3606993	3607319	chr2	0.020	0.25	-0.27
LOC100506054	3607037	3607319	chr2	0.004	0.31	-0.17
LPIN2	2928588	2928658	chr18	0.003	0.11	-0.12
LRRC23	7019053	7019190	chr12	0.042	0.35	-0.55
LRRC23	7016478	7016609	chr12	0.003	0.11	-0.13

Gene ID	exon Start (0 base)	exon End	chr.(x)	no UV vs UV p Value	no UV vs UV Inc.Level Dif.	UV vs ATMi+UV Inc.Level Dif.
LSM1	38027319	38027435	chr8	0.000	0.44	-0.23
MADD	47310518	47310578	chr11	0.024	0.27	-0.18
MAP2K4	11984672	11984847	chr17	0.030	0.14	-0.17
MAP4K3	39494329	39494388	chr2	0.001	0.27	-0.27
MBD1	47797838	47797910	chr18	0.000	0.41	-0.17
MBNL1	152150505	152150709	chr3	0.007	0.13	-0.14
MED13	60033040	60033199	chr17	0.000	0.41	-0.44
MELK	36583623	36583709	chr9	0.007	0.33	-0.19
METTL16	2371054	2371170	chr17	0.014	0.33	-0.33
METTL16	2405497	2405625	chr17	0.023	0.22	-0.25
MINA	97686005	97686476	chr3	0.035	0.16	-0.16
MITF	69988248	69988332	chr3	0.026	0.50	-0.50
MLX	40720487	40720577	chr17	0.000	0.36	-0.27
MLXIP	122616838	122616930	chr12	0.010	0.12	-0.14
MPPE1	11884877	11885042	chr18	0.002	0.25	-0.32
MRPL22	154330380	154330498	chr5	0.004	0.40	-0.26
MRTO4	19583947	19584015	chr1	0.000	0.10	-0.10
MTERFD1	97256146	97256308	chr8	0.003	0.13	-0.13
MTMR12	32271938	32272011	chr5	0.007	0.29	-0.30
MTMR6	25825786	25825913	chr13	0.001	0.13	-0.11
MTOR	11276204	11276291	chr1	0.011	0.12	-0.12
MTR	236995265	236995378	chr1	0.001	0.19	-0.14
MYO10	16762153	16762222	chr5	0.000	0.20	-0.17
MZF1	59081710	59081894	chr19	0.017	0.20	-0.19
N4BP1	48585296	48585393	chr16	0.002	0.19	-0.20
NAPB	23377708	23377825	chr20	0.041	0.67	-0.81
NCAPD3	134079038	134079100	chr11	0.002	0.20	-0.14
NFYA	41046767	41046903	chr6	0.018	0.11	-0.11
NHLRC3	39616241	39616442	chr13	0.018	0.30	-0.17
NOX4	89135493	89135710	chr11	0.001	0.14	-0.14
NUFIP1	45533515	45533709	chr13	0.019	0.11	-0.11
NUP98	3723692	3724122	chr11	0.010	0.11	-0.11
ORC4	148733470	148733544	chr2	0.028	0.11	-0.13
OSBPL11	125271024	125271523	chr3	0.010	0.29	-0.29
OSBPL2	60835072	60835181	chr20	0.028	0.24	-0.24
OSBPL2	60835036	60835181	chr20	0.007	0.12	-0.12
OSBPL5	3124468	3124550	chr11	0.031	0.11	-0.11
PAPD4	78952780	78952824	chr5	0.007	0.11	-0.12
PAPD4	78944884	78945013	chr5	0.040	0.11	-0.11
PAQR6	156214932	156215029	chr1	0.019	0.20	-0.25
PATL1	59423428	59423518	chr11	0.013	0.17	-0.18
PCGF6	105093681	105093709	chr10	0.005	0.16	-0.16
PCNX	71455283	71455416	chr14	0.008	0.16	-0.12
PDE8A	85634274	85634412	chr15	0.003	0.25	-0.20
PDHX	34952950	34953031	chr11	0.001	0.11	-0.11
PEX14	10596269	10596354	chr1	0.014	0.26	-0.26
PEX3	143780221	143780353	chr6	0.014	0.14	-0.14
PEX5	7354836	7354947	chr12	0.000	0.32	-0.18

Gene ID	exon Start (0 base)	exon End	chr.(x)	no UV vs UV p Value	no UV vs UV Inc.Level Dif.	UV vs ATMi+UV Inc.Level Dif.
PHACTR4	28817462	28817524	chr1	0.006	0.21	-0.21
PHF20L1	133826881	133827134	chr8	0.019	0.26	-0.26
PHF20L1	133851631	133851827	chr8	0.030	0.13	-0.13
PHF7	52456237	52456354	chr3	0.046	0.50	-0.17
PHF8	54020033	54020336	chrX	0.032	0.42	-0.31
PHKA1	71840574	71840751	chrX	0.041	0.19	-0.11
PKN2	89270073	89270217	chr1	0.010	0.16	-0.16
PLAGL1	144269121	144269597	chr6	0.001	0.32	-0.17
POLB	42196529	42196587	chr8	0.000	0.47	-0.30
POLM	44113996	44114129	chr7	0.032	0.25	-0.25
POLR2D	128610498	128610679	chr2	0.000	0.18	-0.12
POLR3E	22343443	22343506	chr16	0.001	0.14	-0.12
POLR3E	22343380	22343506	chr16	0.001	0.14	-0.11
POLR3F	18449587	18449705	chr20	0.006	0.25	-0.25
PPHLN1	42745686	42745851	chr12	0.009	0.15	-0.17
PPOX	161139695	161139814	chr1	0.013	0.17	-0.17
PPP6R3	68337215	68337365	chr11	0.003	0.12	-0.12
PRKCA	64492318	64492401	chr17	0.031	0.14	-0.14
PROSER1	39608267	39608333	chr13	0.007	0.33	-0.12
PTCD2	71617998	71618091	chr5	0.016	0.17	-0.18
PTPN13	87690921	87691136	chr4	0.006	0.13	-0.13
PUM1	31452908	31453010	chr1	0.006	0.24	-0.25
PUM1	31418192	31418330	chr1	0.000	0.20	-0.20
RAB8B	63541843	63541904	chr15	0.024	0.22	-0.22
RABEPK	127982817	127982979	chr9	0.001	0.20	-0.11
RBM27	145638011	145638156	chr5	0.011	0.20	-0.20
RBM28	127965870	127965944	chr7	0.034	0.11	-0.11
RBM5	50129475	50129641	chr3	0.000	0.13	-0.11
RBMS2	56982715	56982802	chr12	0.029	0.13	-0.16
RECQL4	145741147	145741274	chr8	0.047	0.28	-0.22
REV1	100065797	100065966	chr2	0.028	0.20	-0.22
RFWD3	74685817	74686020	chr16	0.012	0.19	-0.22
RGS20	54852135	54852284	chr8	0.000	0.37	-0.33
RHPN1	144458694	144458823	chr8	0.020	0.31	-0.27
RIC8B	107245227	107245372	chr12	0.044	0.13	-0.13
RNF115	145683574	145683647	chr1	0.012	0.15	-0.15
ROCK2	11362208	11362300	chr2	0.002	0.14	-0.14
RPAIN	5331390	5331531	chr17	0.000	0.41	-0.14
RPP14	58296035	58296133	chr3	0.000	0.47	-0.78
RPP14	58296035	58296133	chr3	0.000	0.33	-0.20
RPRD2	150390071	150390201	chr1	0.001	0.29	-0.29
RPS6KB1	57991995	57992064	chr17	0.004	0.15	-0.15
RXRB	33166945	33167193	chr6	0.000	0.21	-0.15
SAMD4A	55215532	55215642	chr14	0.039	0.19	-0.19
SARS	109774252	109774408	chr1	0.000	0.17	-0.15
SBDSP1	72301271	72301393	chr7	0.000	0.24	-0.17
SBNO1	123832575	123832680	chr12	0.004	0.39	-0.42
SBNO1	123832575	123832680	chr12	0.003	0.24	-0.25

Gene ID	**exon Start (0 base)**	**exon End**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
SCFD1	31097414	31097485	chr14	0.006	0.24	-0.11
SETDB1	150922933	150923566	chr1	0.020	0.21	-0.22
SETDB1	150935449	150935615	chr1	0.002	0.15	-0.16
SHROOM3	77651956	77652088	chr4	0.028	0.19	-0.20
SIN3A	75681992	75682162	chr15	0.000	0.11	-0.11
SIPA1L3	38633212	38633350	chr19	0.000	0.16	-0.11
SIRT3	233342	233534	chr11	0.001	0.20	-0.24
SLC12A6	34549842	34549989	chr15	0.007	0.25	-0.25
SLC18B1	133093270	133093345	chr6	0.048	0.17	-0.17
SLC25A12	172644080	172644171	chr2	0.001	0.31	-0.31
SLC25A43	118544152	118544325	chrX	0.030	0.22	-0.22
SLC33A1	155560220	155560408	chr3	0.026	0.14	-0.14
SLC33A1	155551645	155551830	chr3	0.013	0.21	-0.12
SLC33A1	155551645	155551830	chr3	0.007	0.10	-0.10
SLC38A2	46764294	46764410	chr12	0.000	0.50	-0.14
SLC7A6	68324298	68324443	chr16	0.001	0.43	-0.28
SLTM	59182479	59182660	chr15	0.018	0.11	-0.14
SNX17	27595906	27595980	chr2	0.025	0.33	-0.11
SPAG9	49053223	49053262	chr17	0.018	0.11	-0.24
SPECC1	20107645	20109225	chr17	0.000	0.33	-0.15
SPEN	16245898	16246012	chr1	0.020	0.20	-0.20
SPOP	47685235	47685291	chr17	0.001	0.11	-0.11
ST5	8772167	8772272	chr11	0.021	0.40	-0.40
STK19	31947190	31947330	chr6	0.012	0.14	-0.14
STX18	4426890	4426949	chr4	0.002	0.21	-0.21
STX3	59564755	59564869	chr11	0.000	0.67	-0.58
STYXL1	75651168	75651310	chr7	0.002	0.19	-0.16
STYXL1	75643059	75643205	chr7	0.001	0.17	-0.16
SYNRG	35930735	35930984	chr17	0.014	0.19	-0.20
SYNRG	35896080	35896229	chr17	0.005	0.12	-0.13
SYNRG	35928892	35929026	chr17	0.006	0.10	-0.10
TAB3	30861082	30861166	chrX	0.044	0.13	-0.13
TAOK3	118639100	118639268	chr12	0.041	0.11	-0.11
TATDN1	125534391	125534441	chr8	0.011	0.13	-0.10
TATDN3	212985568	212985670	chr1	0.041	0.19	-0.22
TATDN3	212985589	212985670	chr1	0.043	0.12	-0.15
TBC1D15	72274248	72274387	chr12	0.010	0.10	-0.11
TENM4	78859754	78859851	chr11	0.023	0.25	-0.19
TEP1	20849711	20849845	chr14	0.004	0.46	-0.66
TFPT	54617821	54618080	chr19	0.024	0.14	-0.14
THAP5	108206273	108206466	chr7	0.043	0.16	-0.18
THAP9-AS1	83819141	83819215	chr4	0.000	0.45	-0.29
THUMPD2	39982434	39982549	chr2	0.036	0.20	-0.22
TJP1	30012561	30012912	chr15	0.001	0.12	-0.12
TLK1	171974248	171974367	chr2	0.006	0.13	-0.13
TMEM131	98460607	98460724	chr2	0.017	0.15	-0.17
TMEM25	118404134	118404266	chr11	0.021	0.30	-0.19
TMEM53	45125845	45125967	chr1	0.013	0.32	-0.35

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TOX2	42693416	42693497	chr20	0.009	0.44	-0.29
TRAPPC8	29419274	29419420	chr18	0.001	0.18	-0.20
TRIM16	15535822	15535988	chr17	0.005	0.13	-0.13
TRIM56	100730286	100730449	chr7	0.003	0.12	-0.12
TRPT1	63993257	63993341	chr11	0.000	0.31	-0.14
TSTD2	100367008	100367147	chr9	0.022	0.10	-0.10
TTBK2	43102811	43102937	chr15	0.018	0.22	-0.15
TTC27	32961760	32961883	chr2	0.043	0.13	-0.13
UBAP1	34234213	34234338	chr9	0.009	0.15	-0.19
UBAP1	34220905	34220946	chr9	0.007	0.17	-0.10
UBE3B	109961782	109961920	chr12	0.012	0.11	-0.11
UBE4B	10190557	10190674	chr1	0.002	0.13	-0.13
UBN1	4902879	4903167	chr16	0.004	0.13	-0.11
UFSP2	186343638	186343717	chr4	0.016	0.16	-0.13
USP42	6185778	6185879	chr7	0.042	0.33	-0.33
USP54	75279554	75279750	chr10	0.004	0.17	-0.17
UVSSA	1345502	1345623	chr4	0.019	0.13	-0.13
VPS33B	91549601	91549675	chr15	0.041	0.23	-0.23
VPS4B	61066474	61066556	chr18	0.001	0.14	-0.14
VPS53	613772	613853	chr17	0.019	0.29	-0.29
VPS54	64208779	64209021	chr2	0.042	0.38	-0.41
WDR20	102661274	102661457	chr14	0.001	0.21	-0.25
WDR37	1123846	1123943	chr10	0.022	0.34	-0.40
WHSC1L1	38156961	38157108	chr8	0.016	0.44	-0.23
XPO4	21381595	21381773	chr13	0.018	0.36	-0.26
YIPF1	54354579	54354659	chr1	0.004	0.13	-0.15
ZC3H3	144620172	144621490	chr8	0.018	0.12	-0.12
ZC3H4	47572348	47572600	chr19	0.006	0.16	-0.18
ZCCHC8	122975008	122975114	chr12	0.015	0.22	-0.22
ZFAND1	82629483	82629523	chr8	0.014	0.26	-0.20
ZFAND6	80390757	80390920	chr15	0.004	0.14	-0.12
ZFYVE19	41104896	41105100	chr15	0.036	0.15	-0.14
ZMYM5	20425494	20425588	chr13	0.030	0.40	-0.36
ZNF263	3338453	3338570	chr16	0.000	0.51	-0.11
ZNF271	32870973	32871196	chr18	0.035	0.12	-0.14
ZNF410	74358729	74358911	chr14	0.000	0.26	-0.23
ZZEF1	3928212	3928412	chr17	0.026	0.13	-0.14

INCLUDED EXONS

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ABI1	27060003	27060018	chr10	0.032	0.23	-0.28
ACIN1	23559190	23559310	chr14	0.027	0.14	-0.13
AFMID	76201520	76201599	chr17	0.047	0.65	-0.38
ALAS1	52232687	52232864	chr3	0.000	0.13	-0.11
ANKRD11	89358088	89358185	chr16	0.000	0.41	-0.12
APTX	32988080	32988127	chr9	0.026	0.14	-0.16

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ASNS	97501030	97501308	chr7	0.000	0.31	-0.19
ATP5SL	41939176	41939339	chr19	0.004	0.15	-0.17
ATRIP	48491898	48491981	chr3	0.017	0.25	-0.24
AURKB	8113494	8113567	chr17	0.004	0.36	-0.19
BRD8	137495243	137495288	chr5	0.000	0.25	-0.16
BTN3A2	26368410	26368495	chr6	0.007	0.30	-0.16
BTN3A2	26368405	26368495	chr6	0.002	0.26	-0.11
C12orf23	107350859	107350927	chr12	0.000	0.48	-0.29
C17orf80	71238382	71238490	chr17	0.000	0.44	-0.15
C7orf10	40314111	40314255	chr7	0.043	0.28	-0.17
CACFD1	136333461	136333586	chr9	0.032	0.14	-0.17
CCSER2	86259630	86259715	chr10	0.022	0.42	-0.47
CCT6P1	65219513	65219648	chr7	0.013	0.37	-0.17
CD44	35226058	35226187	chr11	0.004	0.22	-0.12
CDCA7	174223982	174224219	chr2	0.042	0.31	-0.22
CDK10	89755659	89755732	chr16	0.046	0.13	-0.30
CREB1	208425842	208425884	chr2	0.006	0.35	-0.18
CREBZF	85372680	85372793	chr11	0.001	0.58	-0.29
CSNK1G3	122930732	122930828	chr5	0.010	0.34	-0.34
CYLD	50778640	50778777	chr16	0.017	0.19	-0.21
DMD	31144758	31144790	chrX	0.023	0.23	-0.17
DTYMK	242619643	242619734	chr2	0.000	0.16	-0.16
ECT2	172469939	172470262	chr3	0.006	0.38	-0.56
EIF4G1	184033550	184033644	chr3	0.002	0.54	-0.20
EPN2	19188932	19189103	chr17	0.044	0.13	-0.17
ERP29	112457559	112457698	chr12	0.000	0.22	-0.21
EXOSC9	122737298	122737349	chr4	0.000	0.70	-0.21
FAM86B1	12043860	12044126	chr8	0.025	0.27	-0.39
FAM86DP	75476925	75477059	chr3	0.000	0.41	-0.46
FDPS	155279579	155279756	chr1	0.003	0.13	-0.11
FGFR1OP2	27113447	27113561	chr12	0.000	0.17	-0.18
FHL2	106013103	106013154	chr2	0.000	0.19	-0.17
FLNB	58127584	58127623	chr3	0.048	0.11	-0.11
G3BP2	76579166	76579265	chr4	0.000	0.21	-0.12
GALNS	88909113	88909237	chr16	0.005	0.17	-0.14
GEMIN7	45583164	45583287	chr19	0.000	0.31	-0.23
GGA3	73244920	73245089	chr17	0.025	0.37	-0.14
GPR56	57675498	57675620	chr16	0.000	0.28	-0.23
GPR56	57675502	57675620	chr16	0.001	0.24	-0.16
GTF3C2	27573180	27573256	chr2	0.011	0.35	-0.49
HAUS7	152720334	152720511	chrX	0.011	0.25	-0.11
HDAC7	48189688	48189799	chr12	0.003	0.22	-0.23
HERC4	69718869	69718893	chr10	0.001	0.30	-0.23
HINFP	118994277	118994394	chr11	0.024	0.36	-0.34
HIRIP3	30005226	30006164	chr16	0.046	0.12	-0.13
HNRPDL	83346715	83346820	chr4	0.000	0.33	-0.21
IKBIP	99028073	99028191	chr12	0.002	0.17	-0.10
IL1RAP	190273918	190274005	chr3	0.045	0.30	-0.12

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KIAA0391	35595940	35595988	chr14	0.039	0.20	-0.23
KXD1	18671229	18671360	chr19	0.000	0.13	-0.12
LARP4	50806187	50806236	chr12	0.032	0.20	-0.23
LETMD1	51449926	51450028	chr12	0.008	0.13	-0.16
LGMN	93207406	93207524	chr14	0.009	0.15	-0.12
LINC00674	66102562	66102694	chr17	0.000	0.34	-0.11
LOC388796	37054582	37054700	chr20	0.000	0.84	-0.43
LOC388796	37054582	37054700	chr20	0.000	0.27	-0.23
LOC401074	75725118	75725279	chr3	0.000	0.53	-0.23
LOXL3	74763835	74764055	chr2	0.019	0.61	-0.42
LRR1	50070269	50070336	chr14	0.000	0.63	-0.29
LRRC42	54413460	54413494	chr1	0.020	0.27	-0.34
LRRCC1	86021829	86022035	chr8	0.041	0.49	-0.19
LYRM1	20913807	20914039	chr16	0.001	0.29	-0.28
MAP4K4	102487955	102488147	chr2	0.045	0.12	-0.18
MAST4	66445216	66445417	chr5	0.013	0.60	-0.67
MBD1	47799703	47799841	chr18	0.007	0.11	-0.11
MECOM	168825713	168825740	chr3	0.008	0.71	-0.85
METTL15	28349641	28349712	chr11	0.010	0.45	-0.27
MFF	228207460	228207535	chr2	0.000	0.26	-0.18
MORF4L2	102939608	102939657	chrX	0.000	0.35	-0.22
MPDZ	13143464	13143563	chr9	0.001	0.46	-0.36
MRPL10	45906504	45906602	chr17	0.000	0.16	-0.14
MTO1	74190015	74190090	chr6	0.008	0.26	-0.11
MUM1	1358586	1358699	chr19	0.005	0.21	-0.16
MYO1B	192267357	192267444	chr2	0.021	0.22	-0.17
NABP1	192547217	192547321	chr2	0.009	0.51	-0.15
NF2	30079008	30079068	chr22	0.029	0.29	-0.28
NF2	30079008	30079053	chr22	0.001	0.29	-0.26
NFAT5	69602397	69602451	chr16	0.030	0.29	-0.27
NIPA2	23026021	23026119	chr15	0.038	0.12	-0.13
NMRK1	77693241	77693498	chr9	0.016	0.32	-0.33
NOSIP	50080015	50080134	chr19	0.000	0.27	-0.21
NT5C2	104940987	104941085	chr10	0.000	0.22	-0.16
NUBP2	1836757	1836956	chr16	0.000	0.17	-0.14
PAX8	113992970	113993080	chr2	0.033	0.23	-0.19
PAX8	113992970	113993159	chr2	0.039	0.17	-0.13
PHACTR2	144081537	144081777	chr6	0.000	0.69	-0.25
PI4KB	151298647	151298849	chr1	0.001	0.28	-0.12
PIP5K1C	3633434	3633518	chr19	0.014	0.57	-0.51
PLEKHA5	19423121	19423139	chr12	0.024	0.20	-0.20
PLXNB2	50733147	50733207	chr22	0.028	0.16	-0.19
PPP1R9A	94832976	94833042	chr7	0.023	0.59	-0.21
PPP3CC	22396981	22397011	chr8	0.018	0.28	-0.34
PQLC1	77679183	77679400	chr18	0.049	0.19	-0.14
PRMT7	68355328	68355365	chr16	0.003	0.18	-0.28
PRR16	119816863	119816988	chr5	0.000	0.29	-0.20
PSMG4	3264442	3264559	chr6	0.016	0.18	-0.17

Gene ID	**exon Start (0 base)**	**exon End**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
PTPN2	12819212	12819281	chr18	0.006	0.18	-0.11
PTPRA	2955860	2955887	chr20	0.015	0.14	-0.19
R3HCC1L	99971063	99971105	chr10	0.010	0.17	-0.17
R3HDM1	136373721	136373763	chr2	0.041	0.32	-0.13
RCC1	28857034	28857127	chr1	0.009	0.21	-0.14
REPIN1	150067848	150067973	chr7	0.003	0.47	-0.13
RHOT1	30538134	30538257	chr17	0.031	0.31	-0.11
RPAIN	5329555	5329619	chr17	0.002	0.16	-0.12
RTCA	100733055	100733094	chr1	0.014	0.20	-0.16
RTN2	45996417	45996636	chr19	0.010	0.17	-0.23
RWDD1	116895220	116895334	chr6	0.000	0.18	-0.12
SDHAP1	195711362	195711608	chr3	0.002	0.38	-0.37
SLC35E2	1675689	1676107	chr1	0.040	0.38	-0.20
SMTN	31489769	31489862	chr22	0.000	0.12	-0.10
SNHG16	74555026	74555125	chr17	0.000	0.26	-0.18
SOCS4	55498580	55498709	chr14	0.000	0.42	-0.13
SPECC1L	24672667	24672771	chr22	0.002	0.29	-0.31
SPIRE1	12485957	12485999	chr18	0.002	0.15	-0.13
SRSF3	36567597	36568053	chr6	0.000	0.56	-0.13
ST6GALNAC4	130678686	130678773	chr9	0.004	0.23	-0.18
STK40	36833448	36833685	chr1	0.003	0.29	-0.35
TACC2	123903086	123903221	chr10	0.023	0.57	-0.71
TCF7L2	114849158	114849299	chr10	0.011	0.15	-0.20
TGFB2	218536675	218536759	chr1	0.002	0.12	-0.14
TGFBR2	30664690	30664765	chr3	0.040	0.17	-0.10
TPM1	63356262	63356341	chr15	0.011	0.10	-0.12
TRIM33	114940561	114940612	chr1	0.000	0.32	-0.15
UBP1	33450181	33450289	chr3	0.000	0.36	-0.13
UPP1	48142893	48143008	chr7	0.012	0.14	-0.26
USP10	84738345	84738466	chr16	0.001	0.33	-0.34
USP3	63821212	63821365	chr15	0.002	0.62	-0.17
USP33	78211105	78211284	chr1	0.001	0.24	-0.34
WASF1	110499800	110499945	chr6	0.015	0.57	-0.18
ZFAND5	74978385	74978522	chr9	0.000	0.34	-0.17
ZNF195	3381949	3382018	chr11	0.021	0.38	-0.38
ZNF23	71489974	71490024	chr16	0.030	0.64	-1.00
ZNF260	37008931	37009045	chr19	0.001	0.29	-0.24
ZNF419	58003480	58003579	chr19	0.000	0.23	-0.13
ZNF419	58001514	58001553	chr19	0.001	0.22	-0.12
ZNF706	102214560	102214675	chr8	0.000	0.22	-0.11
ZNF83	53119970	53120068	chr19	0.002	0.19	-0.15
ZNF83	53119970	53120094	chr19	0.002	0.19	-0.15

MUTUALLY EXCLUSIVE EXONS

Gene ID	1st ExonStart (0 base)	1st ExonEnd	2nd ExonStart (0 base)	2nd ExonEnd	chr.(x)	no UV vs UV p Value	no UV vs UV Inc.Level Dif.	UV vs ATMi+UV Inc.Level Dif.
CAMLG	134076752	134077213	134079676	134079742	chr5	0.000	0.21	-0.11
CREM	35477127	35477316	35490378	35490414	chr10	0.016	0.61	-0.12
FAM86DP	75476925	75477059	75478286	75478388	chr3	0.000	0.36	-0.52
FUT8	65922338	65922436	66028054	66028484	chr14	0.045	0.13	-0.13
LETMD1	51442816	51442968	51449926	51450028	chr12	0.003	0.11	-0.14
MARK3	103964838	103964865	103966492	103966537	chr14	0.003	0.24	-0.15
MICAL2	12270730	12270793	12277189	12277297	chr11	0.018	0.30	-0.18
MYO10	16783443	16783578	16794754	16794942	chr5	0.023	0.18	-0.24
POLB	42206533	42206608	42207524	42207583	chr8	0.009	0.22	-0.35
PPOX	161139695	161139814	161140198	161140309	chr1	0.015	0.19	-0.13
RAB34	27043920	27044012	27044230	27044443	chr17	0.000	0.31	-0.17
RAB34	27043920	27044012	27044230	27044309	chr17	0.003	0.14	-0.17
RAP1GDS1	99325627	99325753	99337895	99338039	chr4	0.034	0.11	-0.14
TOM1L1	53016284	53016381	53024621	53024673	chr17	0.026	0.13	-0.10
USP20	132625464	132625578	132627581	132627660	chr9	0.002	0.24	-0.12

RETAINED INTRONS (RI)

Gene ID	RI-Start (0 base)	RI-End	chr.(x)	no UV vs UV p Value	no UV vs UV Inc.Level Dif.	UV vs ATMi+UV Inc.Level Dif.
ARMCX6	100870750	100871661	chrX	0.000	0.30	-0.14
ATPIF1	28562963	28564271	chr1	0.000	0.32	-0.15
C1QTNF6	37576907	37578191	chr22	0.000	0.60	-0.29
CMTM4	66651261	66655964	chr16	0.008	0.13	-0.11
DHRS4-AS1	24423242	24423333	chr14	0.043	0.47	-0.40
GLYCTK	52326585	52327061	chr3	0.033	0.26	-0.12
HES4	935167	935245	chr1	0.000	0.21	-0.17
KDM2B	121867966	121868144	chr12	0.002	0.22	-0.16
NFATC4	24845760	24846843	chr14	0.003	0.14	-0.13
NGRN	90809108	90809519	chr15	0.000	0.10	-0.16
PIGO	35091288	35092539	chr9	0.009	0.23	-0.24
QKI	163984751	163985698	chr6	0.000	0.41	-0.54
RAB43	128840335	128840586	chr3	0.038	0.20	-0.23
ARMCX6	100870750	100871661	chrX	0.000	0.30	-0.14
RASSF7	563317	563557	chr11	0.042	0.28	-0.11
SEC14L1	75210101	75212630	chr17	0.002	0.24	-0.10
SLC11A2	51373841	51375421	chr12	0.000	0.43	-0.19
SMOX	4162970	4163129	chr20	0.042	0.13	-0.13
TMEM138	61131787	61131904	chr11	0.000	0.32	-0.21
TULP3	3048590	3049695	chr12	0.000	0.28	-0.21
ZDHHC4	6617129	6617220	chr7	0.002	0.37	-0.13
ZNF248	38120240	38121952	chr10	0.033	0.52	-0.48

ALTERNATIVE 5' SPLICE SITE

Gene ID	**LongExonStart (0 base)**	**LongExonEnd**	**ShortExonStart**	**ShortExonEnd**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
AMN1	31881904	31882108	31881924	31882108	chr12	0.030	0.27	-0.46
APEX1	20923289	20923497	20923289	20923487	chr14	0.000	0.27	-0.13
C14orf159	91580356	91580872	91580356	91580627	chr14	0.028	0.22	-0.59
C17orf58	65989016	65989351	65989159	65989351	chr17	0.017	0.17	-0.16
C1D	68290076	68290159	68290089	68290159	chr2	0.034	0.17	-0.12
ERC1	1100403	1100653	1100403	1100488	chr12	0.043	0.36	-0.55
LOC81691	20817766	20818139	20817766	20818027	chr16	0.038	0.24	-0.20
MCM8	5931297	5931723	5931297	5931669	chr20	0.020	0.34	-0.68
MSTO1	155583447	155583557	155583447	155583524	chr1	0.031	0.55	-0.36
NFATC4	24845499	24846084	24845499	24845760	chr14	0.001	0.21	-0.13
OCIAD1	48853822	48854037	48853822	48853992	chr4	0.014	0.13	-0.12
PGAP2	3845499	3845685	3845499	3845594	chr11	0.000	0.40	-0.13
PGAP2	3845499	3845606	3845499	3845594	chr11	0.017	0.23	-0.13
PGAP2	3845499	3845685	3845499	3845606	chr11	0.007	0.22	-0.10
PPFIA1	70184479	70184559	70184479	70184540	chr11	0.016	0.32	-0.11
PRDM10	129781979	129782120	129782018	129782120	chr11	0.018	0.46	-0.40
STX16	57226308	57227194	57226308	57227143	chr20	0.000	0.24	-0.10
TRIB2	12856997	12858703	12856997	12857136	chr2	0.026	0.16	-0.20
ZC3H14	89069171	89069404	89069171	89069389	chr14	0.035	0.10	-0.15
ZDHHC4	6617064	6617351	6617064	6617129	chr7	0.048	0.12	-0.11

ALTERNATIVE 3' SPLICE SITE

Gene ID	**longExonStart (0 base)**	**longExonEnd**	**ShortExonStart**	**ShortExonEnd**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
ALKBH2	109530311	109530742	109530311	109530592	chr12	0.002	0.19	-0.24
ARFIP2	6501552	6501693	6501552	6501653	chr11	0.003	0.12	-0.11
BRD9	886706	886882	886706	886822	chr5	0.000	0.28	-0.14
C19orf60	18700222	18700493	18700288	18700493	chr19	0.039	0.21	-0.26
CAPRIN2	30867892	30868078	30867892	30868015	chr12	0.000	0.19	-0.10
CLINT1	157216370	157216575	157216370	157216521	chr5	0.001	0.21	-0.13
DYRK1B	40317311	40317627	40317311	40317507	chr19	0.023	0.16	-0.24
FAM213A	82180221	82180401	82180238	82180401	chr10	0.010	0.33	-0.17
IFFO1	6657833	6658015	6657833	6657991	chr12	0.046	0.26	-0.31
KANSL3	97297048	97297280	97297048	97297219	chr2	0.014	0.18	-0.12
MLLT10	22028958	22029165	22029082	22029165	chr10	0.045	0.23	-0.34
MLST8	2256031	2256215	2256061	2256215	chr16	0.025	0.33	-0.47
MOK	102698871	102699045	102698871	102699008	chr14	0.000	0.24	-0.20
MORF4L2	102933426	102933579	102933426	102933548	chrX	0.005	0.15	-0.12
MPPE1	11886711	11886780	11886711	11886777	chr18	0.021	0.27	-0.13
MRPS31P5	52744121	52744234	52744121	52744191	chr13	0.037	0.34	-0.16
MTERFD3	107378892	107379003	107378892	107378993	chr12	0.013	0.53	-0.92
NFYC	41236380	41237275	41236383	41237275	chr1	0.002	0.26	-0.26
PKMYT1	3023138	3023254	3023138	3023216	chr16	0.000	0.45	-0.14
PMS2	6045522	6045662	6045522	6045657	chr7	0.004	0.28	-0.13
YY1AP1	155638417	155638568	155638417	155638508	chr1	0.001	0.27	-0.12

Gene ID	**longExonStart (0 base)**	**longExonEnd**	**ShortExonStart**	**ShortExonEnd**	**chr.(x)**	**no UV vs UV p Value**	**no UV vs UV Inc.Level Dif.**	**UV vs ATMi+UV Inc.Level Dif.**
ZFAND5	74975543	74975703	74975543	74975700	chr9	0.000	0.19	-0.15
ZFYVE27	99511132	99511219	99511147	99511219	chr10	0.006	0.15	-0.15
ZNF473	50534148	50534348	50534270	50534348	chr19	0.000	0.39	-0.20

Quiescent RPE cells were mock treated or UV-irradiated with 20 J/m^2 in the presence or absence of an ATM inhibitor. Poly-adenylated RNA was isolated 6 hrs post-irradiation and paired-end RNA-Seq was performed and data analyzed as described in the Methods. Uniquely mapped reads were used for the identification of alternative splicing events using Multivariate Analysis of Transcript Splicing (MATS)[45]. Inclusion Level Difference (Incl.Level.Dif.) is the average (Inclusion Level in sample 1) - average (Inclusion Level in sample 2). Inclusion Levels for each sample were calculated by MATS from normalized counts of expressed sequence tags mapped uniquely to the exon inclusion or skipping exon-exon junctions. Events that were significantly changed by UV irradiation (untreated vs UV-irradiated) ($p \leq 0.05$, *n=2*) and changed in the opposite direction when cells were irradiated in the presence of the ATM inhibitor (UV irradiated vs ATM-treated and UV irradiated) with a difference above 10% (for both comparisons) were considered to be dependent on ATM activity.