

**Table S1. Proteomic data and identifications of differential spots in Dsup-/+ HEK293T cells at basal condition**

Table reports the spot number corresponding to that in Figure S3, protein name when the protein was identified by MALDI-ToF MS, UniProt Entry name and accession number (AC), the ANOVA Test and the mean of the %V of the specific spot in Dsup- and Dsup+ cells, the fold change of the %V means of Dsup- vs Dsup+ and viceversa, pI and MW. Last part of the table is dedicated to Mascot Search Results such as Score and Expect, Matched Peptides and sequence Coverage (%).

Spot n°	Protein name	Entry name	AC	Anova test			Ratio		pI - MW	Mascot Search Results			
				Anova (p)	(Basal) Dsup-	(Basal) Dsup+	(Basal) Dsup-/+	(Basal) Dsup+/-		Score Expect	Matched peptides	Coverage (%)	
1				0.003	0.043355	0.016045	2.702161872	0.370074054					
2				0.011	0.019463	0.007949	2.448426838	0.408425518					
3	Prostaglandin E synthase 3	TEBP_HUMAN	Q15185	0.040	0.025233	0.050755	0.497158563	2.011430708	4.35 - 18971	128 3.2E <sup>-09</sup>		8/12	45
4	Heat shock 70 kDa protein 1A <u>N-term</u> fragment	HS71A_HUMAN	P0DMV8	0.009	0.074455	0.165706	0.449321792	2.225576452	5.48 - 70294	224	169 2.6E <sup>-13</sup>	17/30	26
	Heat shock cognate 71 kDa protein <u>N-term</u> fragment	HSP7C_HUMAN	P11142						5.37 - 71082		89 2.3E <sup>-05</sup>	12/30	21
5	Peroxiredoxin-1	PRDX1_HUMAN	Q06830	0.018	0.161855	0.040361	4.010171485	0.249365895	8.27 - 22324	230 2E <sup>-19</sup>		13/15	62
6	Heat shock 70 kDa protein 1A <u>C-term</u> fragment	HS71A_HUMAN	P0DMV8	0.007	0.006086	0.038048	0.159949258	6.251982753	5.48 - 70294	111 1.6E <sup>-07</sup>		10/14	16
7	Pyruvate kinase PKM <u>N-term</u> fragment	KPYM_HUMAN	P14618	0.010	0.002012	0.0199	0.101115909	9.889640595	7.96 - 58470	152 1.3E <sup>-11</sup>		12/20	26
8	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	0.036	0.07028	0.030466	2.306830143	0.433495289	8-97 - 37464	173 1E <sup>-13</sup>		12/15	42
9	Pyruvate kinase PKM <u>N-term</u> fragment	KPYM_HUMAN	P14618	0.046	0.004739	0.030441	0.155674606	6.423655244	7.96 - 58470	181 1.6E <sup>-14</sup>		14/17	27

10	Alpha-enolase	ENOA_HUMAN	P06733	0.037	0.018212	0.008153	2.23389549	0.447648516	7.01 - 47481	122 1.3E <sup>-08</sup>	8/10	16	
11	Actin. cytoplasmic 1 / Actin. cytoplasmic 2	ACTB_HUMAN / ACTG_HUMAN	P60709 / P63261	0.037	0.046185	0.10382	0.444861478	2.247890748	5.29 - 42052 5.31 - 42108	197 4.1E <sup>-16</sup>	18/30	45	
12	Eukaryotic initiation factor 4A-II	IF4A2_HUMAN	Q14240	0.012	0.043265	0.132976	0.325356519	3.073551449	5.33 - 46601	93 9.3E <sup>-06</sup>	10/28	26	
13	Eukaryotic initiation factor 4A-II	IF4A2_HUMAN	Q14240	0.005	0.020374	0.046276	0.440278618	2.27128904	5.33 - 46601	75 6.4E <sup>-04</sup>	9/32	25	
14				0.004	0.051314	0.025473	2.014449267	0.496413594					
15	Asparagine synthetase [glutamine-hydrolyzing]	ASNS_HUMAN	P08243	0.030	0.058045	0.027783	2.089232774	0.478644607	6.39 - 64899	139 2.6E <sup>-10</sup>	9/10	14	
16				0.020	0.005422	0.002635	2.057749068	0.485967903					
17				0.049	0.055061	0.02651	2.076969696	0.481470674					
18	Striatin-4	STRN4_HUMAN	Q9NRL3	0.047	0.008072	0.020211	0.399375914	2.503906631	5.21 - 81287	103 1E <sup>-06</sup>	8/11	13	
19	Heat shock protein HSP 90-beta	HS90B_HUMAN	P08238	0.020	0.013532	0.038488	0.351600345	2.844138278	4.97 - 83554	168	106 5.1E <sup>-07</sup>	14/36	21
	Cleavage and polyadenylation specificity factor subunit 2	CPSF2_HUMAN	Q9P2I0						4.98 - 89286		84 7.7E <sup>-05</sup>	15/36	16
20	DNA replication licensing factor MCM6	MCM6_HUMAN	Q14566	0.049	0.014905	0.033412	0.446097602	2.241661905	5.29 - 93801	163 1E <sup>-12</sup>	16/25	19	
21	DNA replication licensing factor MCM6	MCM6_HUMAN	Q14566	0.043	0.020144	0.041181	0.489161616	2.044314124	5.29 - 93801	146 5.1E <sup>-11</sup>	13/17	15	
22				0.027	0.006606	0.020521	0.321895365	3.106599559					
23				0.013	0.000986	0.002336	0.421981066	2.369774571					
24				0.012	0.001525	0.004027	0.378789183	2.639990909					
25				0.045	0.002205	0.004461	0.494212097	2.023422748					

26				0.035	0.002161	0.00501	0.431435301	2.31784464				
27	Tyrosine--tRNA ligase. cytoplasmic	SYYC_HUMAN	P54577	0.027	0.097784	0.036367	2.688779653	0.371915935	6.61 - 59448	118 3.2E <sup>-08</sup>	9/13	25
28	Tyrosine--tRNA ligase. cytoplasmic	SYYC_HUMAN	P54577	0.027	0.183837	0.081087	2.267169064	0.441078707	6.61 - 59448	119 2.6E <sup>-08</sup>	10/15	21
29	T-complex protein 1 subunit delta	TCPD_HUMAN	P50991	0.013	0.174077	0.066644	2.612048545	0.382841277	7.96 - 58401	161 1.6E <sup>-12</sup>	13/16	27

**Table S2: Proteomic data and identifications of differential spots in Dsup-/+ HEK293T cells at 24h recovery after 15 seconds of UV-C radiation**

Table reports the spot number corresponding to that in Figure S4, protein name when the protein was identified by MALDI-ToF MS, UniProt Entry name and accession number (AC), the ANOVA Test and the mean of the %V of the specific spot in Dsup- and Dsup+ cells, the fold change of the %V means of Dsup- vs Dsup+ and viceversa, pI and MW. Last part of the table is dedicated to Mascot Search Results such as Score and Expect, Matched Peptides and sequence Coverage (%).

Spot n°	Protein name	Entry name	AC	Anova test			Ratio		pI - MW	Mascot Search Results			
				Anova (p)	(UV) Dsup–	(UV) Dsup+	(UV) Dsup –/+	(UV) Dsup +/-		Score Expect	Matched peptides	Covera ge (%)	
1				0.030	0.021045	0.0093442	2.252196461	0.444010999					
2	Regulator complex protein LAMTOR2	LTOR2_HUMAN	Q9Y2Q5	0.026	0.0190797	0.0040741	4.683227283	0.213527967	5.30 - 13613	103	78 2.9E <sup>-04</sup>	5/14	38
	Replication protein A 14 kDa subunit	RFA3_HUMAN	P35244						4.96 - 13674		63 9.5E <sup>-03</sup>	4/14	54
3	Thioredoxin	THIO_HUMAN	P10599	0.013	0.0270251	0.0090355	2.99097785	0.334338818	4.82 - 12015	69 2.8E <sup>-03</sup>	5/7	32	
4				0.050	0.0481777	0.011223	4.292765278	0.232950077					
5				0.005	0.0467749	0.0196331	2.382453412	0.419735385					
6				0.028	0.0379288	0.0156038	2.430736037	0.411398023					
7	Peptidyl-prolyl cis-trans isomerase A	PPIA_HUMAN	P62937	0.015	0.0833672	0.0167316	4.982629633	0.200697237	7.68-18229	182 1.3E <sup>-14</sup>	13/26	58	
8	Actin-related protein 2/3 complex subunit 5	ARPC5_HUMAN	O15511	0.030	0.0273185	0.0094444	2.892558075	0.345714753	5.47-16367	146 5.1E <sup>-11</sup>	11/17	52	
9	Peroxiredoxin- 1	PRDX1_HUMAN	Q06830	0.022	0.0184992	0.0615035	0.300783424	3.324651292	8.27- 22324	100 2E <sup>-06</sup>	7/16	35	
10				0.042	0.0711136	0.0263909	2.694627939	0.371108748					
11	S-	ESTD_HUMAN	P10768	0.037	0.0474349	0.0213141	2.225519297	0.449333331	6.54-31956	158	11/17	50	

	formylglutathione hydrolase									3.2E <sup>-12</sup>		
12	Phosphatidylinositol transfer protein beta isoform	PIPNB_HUMAN	P48739	0.010	0.0342307	0.0064848	5.278594214	0.189444378	6.41-31805	356 5.1E <sup>-32</sup>	23/26	67
13	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	0.010	0.0270482	0.0973908	0.277728245	3.600642064	8.97-37464	143 1E <sup>-10</sup>	10/15	38
14				0.049	0.0118442	0.0021141	5.602421492	0.178494246				
15	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	0.001	0.0135462	0.0539949	0.250879095	3.985983769	8.97-37464	213 1E <sup>-17</sup>	14/17	42
16	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	0.008	0.0281454	0.0620498	0.453592945	2.204619825	8.97-37464	114 8.1E <sup>-08</sup>	8/13	35
17	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	0.042	0.0395889	0.1261191	0.313901255	3.1857152	8.97-37464	186 5.1E <sup>-15</sup>	13/18	42
18	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	<0.0001	0.0243909	0.064495	0.378182093	2.644228851	8.97-37464	344 8.1E <sup>-31</sup>	23/25	53
19	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	P22626	<0.0001	0.0170888	0.0497053	0.343801701	2.908653443	8.97-37464	167 4.1E <sup>-13</sup>	11/14	42
20	Poly(rC)-binding protein 1	PCBP1_HUMAN	Q15365	0.035	0.0688577	0.0337199	2.042048324	0.489704376	6.66-37987	137 4.1E <sup>-10</sup>	10/15	41
21				0.016	0.0061338	0.0013465	4.555468387	0.219516395				
22	Mitogen-activated protein kinase	MK01_HUMAN	P28482	0.019	0.0164557	0.0342318	0.480713334	2.080241862	6.50 - 41762	175 5.1e <sup>-09</sup>	10/20	24

	1											
	Sialic acid synthase	SIAS_HUMAN	Q9NR45									
23	Translation initiation factor eIF-2B subunit beta	EI2BB_HUMAN	P49770	0.047	0.0113539	0.0031515	3.602685479	0.277570719	5.77-39193	216 5.1E <sup>-18</sup>	17/24	45
24	D-3-phosphoglycerate dehydrogenase	SERA_HUMAN	O43175	0.003	0.022067	0.07731	0.285434953	3.50342518	6.29-57356	160 2E <sup>-12</sup>	14/24	31
25	Heat shock 70 kDa protein 1A	HS71A_HUMAN	P0DMV8	0.037	0.03986	0.0879722	0.453097683	2.207029604	5.48- 70294	275 6.4E <sup>-24</sup>	21/29	43
	Heat shock 70 kDa protein 1B	HS71B_HUMAN	P0DMV9						5.48- 70294	275 6.4E <sup>-24</sup>	21/29	43
26	Heat shock 70 kDa protein 1A	HS71A_HUMAN	P0DMV8	0.047	0.0059819	0.0130175	0.459529213	2.176140214	5.48- 70294	161 1.6E <sup>-12</sup>	12/15	23
	Heat shock 70 kDa protein 1B	HS71B_HUMAN	P0DMV9						5.48- 70294	161 1.6E <sup>-12</sup>	12/15	23
27	Heat shock protein HSP 90-beta	HS90B_HUMAN	P08238	0.017	0.0833278	0.1669537	0.499107138	2.003577839	4.97-83554	169 2.6E <sup>-13</sup>	20/35	29
28	Heat shock protein HSP 90-beta	HS90B_HUMAN	P08238	0.032	0.040419	0.0918989	0.439820484	2.273654904	4.97-83554	169 2.6E <sup>-13</sup>	20/35	29
29	Cold shock domain-containing protein E1	CSDE1_HUMAN	O75534	0.048	0.003588	0.0085877	0.417811	2.393426693	5.88-89684	117 4.1E <sup>-08</sup>	11/17	17
30	Cold shock domain-containing protein E1	CSDE1_HUMAN	O75534	0.003	0.0022853	0.0064755	0.352919859	2.833504472	5.88-89684	236 5.1E <sup>-20</sup>	21/28	28
31	Cold shock domain-	CSDE1_HUMAN	O75534	0.047	0.0035469	0.0075604	0.469145453	2.131535099	5.88-89684	101 1.6E <sup>-06</sup>	9/13	13

	containing protein E1											
32	Cold shock domain-containing protein E1	CSDE1_HUMAN	O75534	0.048	0.0046699	0.0097517	0.478884216	2.088187429	5.88-89684	74 7.9E <sup>-04</sup>	8/18	14
33	Elongation factor 2	EF2_HUMAN	P13639	0.032	0.0081677	0.0196089	0.416530617	2.400783901	6.41-96246	178 3.2E <sup>-14</sup>	16/20	21
34	Neutral alpha-glucosidase AB	GANAB_HUMAN	Q14697	0.028	0.0068976	0.0216881	0.318036493	3.144293254	5.74-107263	316 5.1E <sup>-28</sup>	29/34	32
35	Heat shock 70 kDa protein 4L	HS74L_HUMAN	O95757	0.016	0.0040901	0.0144419	0.283208476	3.530967761	5.63 - 95479	61 1.5E <sup>-02</sup>	5/6	8
36	Heat shock 70 kDa protein 4L	HS74L_HUMAN	O95757	0.028	0.0016363	0.0072614	0.225338917	4.437759864	5.63-95479	124 8.1E <sup>-09</sup>	13/20	16
37	Heat shock 70 kDa protein 4L	HS74L_HUMAN	O95757	0.021	0.0012532	0.0049527	0.253033774	3.952041592	5.63-95479	124 8.1E <sup>-09</sup>	13/20	16
38	Neutral alpha-glucosidase AB	GANAB_HUMAN	Q14697	0.021	0.0079115	0.0167872	0.471280358	2.121879224	5.74-107263	97 2.9E <sup>-06</sup>	10/17	12
39	Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	P22314	0.015	0.0010479	0.0048447	0.216293867	4.623339591	5.49 - 118858	57 3.9E <sup>-02</sup>	4/4	6
40	Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	P22314	0.019	0.0099294	0.0352576	0.281624783	3.550823865	5.49- 118858	307 4.1E <sup>-27</sup>	25/30	35
41	Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	P22314	0.008	0.0075397	0.033307	0.226370933	4.417528287	5.49- 118858	165 6.4E <sup>-13</sup>	17/29	24
42	Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	P22314	0.001	0.0120293	0.0314904	0.381999189	2.617806604	5.49- 118858	303 1E <sup>-26</sup>	25/31	36
43	Transcription intermediary factor 1-beta	TIF1B_HUMAN	Q13263	0.018	0.0103278	0.0218028	0.473691565	2.111078334	5.52-90261	77 3.7E <sup>-04</sup>	7/11	10
44				0.010	0.0121098	0.0732296	0.165366965	6.047157017				

45	Transcription intermediary factor 1-beta	TIF1B_HUMAN	Q13263	0.005	0.0151401	0.0435923	0.347311072	2.879263237	5.52-90261	109 2.6E <sup>-07</sup>	11/22	16
46				0.002	0.0122145	0.0421808	0.289574878	3.453338246				
47				0.027	0.0190551	0.0476007	0.40031134	2.498055639				
48	Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	Q00839	0.004	0.0217492	0.0640288	0.339679092	2.943955113	5.76-91269	60 8.5E <sup>-04</sup>	7/14	10
49	Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	Q00839	0.000	0.0198534	0.0624223	0.318049435	3.144165305	5.76-91269	110 2E <sup>-07</sup>	8/9	13
50	Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	Q00839	0.027	0.0166104	0.043295	0.383655541	2.606504773	5.76-91269	70 1.9E <sup>-03</sup>	5/5	9
51	DNA replication licensing factor MCM2	MCM2_HUMAN	P49736	0.029	0.0012638	0.0041363	0.305540499	3.272888545	5.34-102516	165 6.4E <sup>-13</sup>	17/27	25
52				0.039	0.0012606	0.0041951	0.300503048	3.327753268				
53	Hypoxia up-regulated protein 1	HYOU1_HUMAN	Q9Y4L1	0.029	0.0021725	0.0067587	0.321432887	3.111069342	5.16-111494	101 1.6E <sup>-06</sup>	8/8	10
54				0.039	0.0014627	0.0058263	0.25104775	3.983305971				
55				0.015	0.0065333	0.0216408	0.301897653	3.312380835				
56				0.009	0.0043338	0.0135865	0.318976634	3.135025874				
57				0.001	0.0459592	0.0153109	3.001739505	0.333140167				
58				0.048	0.001202	0.0048902	0.245797664	4.068386919				
59	Eukaryotic translation initiation factor 3 subunit B	EIF3B_HUMAN	P55884	0.026	0.0161619	0.0323538	0.499537406	2.001852089	4.89-92823	153 1E <sup>-11</sup>	14/18	20
60				0.040	0.0165049	0.0848576	0.194500986	5.141362117				
61	Alpha-enolase	ENOA_HUMAN	P06733	0.007	0.0073665	0.0307339	0.23968621	4.172121541	7.01 - 47481	197	15/20	32



										4.1E <sup>-16</sup>		
62	Isocitrate dehydrogenase [NAD] subunit alpha. mitochondrial	IDH3A_HUMAN	P50213	0.004	0.0408057	0.0139044	2.934736121	0.340746138	6.47 - 40022	93 9.8E <sup>-06</sup>	7/12	19
63	Ribose-phosphate pyrophosphokinase 1	PRPS1_HUMAN	P60891	0.001	0.0350293	0.0925712	0.378404227	2.642676614	6.51-35325	152 1.3E <sup>-11</sup>	10/14	35