Supplementary Table SII. The list of 131 quantificated candidates in ASC-pulled down complexes after treatments

Gene symbol	Accession No.	Protein name	Protein probability	No. of identified peptides	Percent coverage %	iTRAQ ratio						Spectrum No. for quantification
						H_2O_2/UN (116/114)	SD	dAdT/UN (117/114)	SD	EBER/UN (115/114)	SD	
A2M	P01023	Alpha-2-macroglobulin	1.00	5	4.2	1.06	0.19	0.97	0.15	0.98	0.20	17
ACTA2	P62736	Actin, aortic smooth muscle	1.00	10	31.9	1.02	0.24	1.15	0.26	0.91	0.39	51
AGAP3	Q96P47	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	1.00	3	5.4	1.00	0.11	0.95	0.14	1.00	0.14	9
ALB	P02768	Serum albumin	1.00	8	11.7	1.21	0.40	1.06	0.27	1.04	0.41	29
ALDH1A3	P47895	Aldehyde dehydrogenase family 1 member A3	1.00	4	12.9	0.88	0.21	0.99	0.22	0.89	0.25	11
ALS2CR4	Q96Q45	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 4 protein	1.00	4	15.3	1.31	0.23	1.06	0.23	1.11	0.24	11
ARF1	P84077	ADP-ribosylation factor 1	1.00	2	19.3	0.92	0.32	1.11	0.27	0.88	0.26	5
C22orf28	Q9Y3I0	UPF0027 protein C22orf28	1.00	2	4.4	0.82	0.13	0.94	0.17	1.13	0.51	6
C3	P01024	Complement C3	1.00	3	1.7	0.97	0.10	0.98	0.09	0.89	0.13	6
CAD	P27708	CAD protein	1.00	6	3.3	0.81	0.16	0.94	0.11	1.06	0.26	11
CARM1	Q86X55	Histone-arginine methyltransferase CARM1	1.00	7	8.0	1.07	0.30	1.02	0.23	1.09	0.37	19
CAV1	Q03135	Caveolin-1	1.00	2	9.6	0.73	0.15	0.84	0.08	0.80	0.10	7
CCT3	P49368	T-complex protein 1 subunit gamma	1.00	3	6.2	0.88	0.15	0.95	0.14	0.76	0.11	6
CCT6A	P40227	T-complex protein 1 subunit zeta	1.00	5	18.5	0.98	0.16	1.33	0.15	0.95	0.21	5
CPSF7	Q8N684	Cleavage and polyadenylation specificity factor subunit 7	1.00	9	24.6	0.95	0.12	1.03	0.15	0.97	0.16	21
DDX3X	O00571	ATP-dependent RNA helicase DDX3X	1.00	2	3.2	0.88	0.12	1.12	0.07	1.07	0.12	3
DERA	Q9Y315	Putative deoxyribose-phosphate aldolase	1.00	2	6.9	1.10	0.19	0.98	0.19	1.24	0.18	7
DHX9	Q08211	ATP-dependent RNA helicase A	1.00	3	2.0	1.07	0.09	0.93	0.06	1.43	0.20	7
DLAT	P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	1.00	9	25.3	0.94	0.12	0.89	0.10	0.93	0.16	13
DLST	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	1.00	2	4.6	1.66	0.70	2.42	1.46	2.19	1.19	3
DSP	P15924	Desmoplakin	1.00	13	5.9	1.14	0.31	0.96	0.27	1.07	0.33	14
DYNC1H1	Q14204	Cytoplasmic dynein 1 heavy chain 1	1.00	3	0.9	0.92	0.11	0.94	0.16	0.79	0.13	5
EEF1A1	P68104	Elongation factor 1-alpha 1	1.00	12	28.1	0.92	0.17	1.04	0.16	0.92	0.14	40

EEF2	P13639	Elongation factor 2	1.00	3	7.2	0.92	0.35	0.92	0.35	1.11	0.22	3
EIF4A1	P60842	Eukaryotic initiation factor 4A-I	1.00	5	17.6	1.03	0.28	1.05	0.18	1.02	0.33	24
EPRS	P07814	Bifunctional aminoacyl-tRNA synthetase	1.00	5	5.4	1.14	0.22	1.11	0.14	1.12	0.20	7
FAM136A	Q96C01	Protein FAM136A	1.00	10	68.1	1.14	0.34	1.02	0.24	1.04	0.29	56
FAM83H	Q6ZRV2	Protein FAM83H	1.00	3	2.5	0.91	0.17	0.93	0.31	1.05	0.22	5
FASN	P49327	Fatty acid synthase	1.00	9	5.7	0.74	0.19	0.97	0.15	0.95	0.17	10
FLNA	P21333	Filamin-A	1.00	4	2.0	1.07	0.14	1.03	0.20	0.93	0.23	10
FN1	P02751	Fibronectin	1.00	2	0.8	1.21	0.19	1.06	0.16	1.49	0.58	8
FUS	P35637	RNA-binding protein FUS	1.00	6	18.7	0.93	0.20	0.94	0.22	1.20	0.32	22
GPHN	Q9NQX3	Gephyrin	1.00	9	14.9	1.00	0.29	0.98	0.27	1.31	0.48	13
GRN	P28799	Granulins	1.00	7	16.5	1.05	0.48	0.90	0.29	0.74	0.55	27
H1FX	Q92522	Histone H1x	1.00	2	14.6	1.07	0.15	0.67	0.33	0.74	0.05	5
HIST1H1C	P16403	Histone H1.2	1.00	3	10.3	1.14	0.29	0.88	0.33	1.13	0.25	7
HIST1H2AB	P04908	Histone H2A type 1-B/E	1.00	2	21.7	1.07	0.13	1.26	0.18	1.54	0.29	4
HNRNPA1	P09651	Heterogeneous nuclear ribonucleoprotein A1	1.00	6	30.9	1.00	0.12	1.01	0.16	1.82	0.17	11
HNRNPA2B1	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	1.00	8	25.5	1.07	0.21	0.98	0.12	1.84	0.33	25
HNRNPA3	P51991	Heterogeneous nuclear ribonucleoprotein A3	1.00	3	16.7	0.94	0.20	0.96	0.10	1.47	0.38	6
HNRNPD	Q14103	Heterogeneous nuclear ribonucleoprotein D0	1.00	3	12.5	1.07	0.44	1.03	0.23	1.84	1.23	11
HNRNPH1	P31943	Heterogeneous nuclear ribonucleoprotein H	1.00	3	6.2	0.96	0.17	0.88	0.07	1.67	0.14	4
HNRNPU	Q00839	Heterogeneous nuclear ribonucleoprotein U	1.00	5	7.5	1.04	0.12	1.44	0.35	1.54	0.28	4
HRG	P04196	Histidine-rich glycoprotein	1.00	2	4.0	0.98	0.11	1.02	0.18	0.98	0.13	8
HSPA8	P11142	Heat shock cognate 71 kDa protein	1.00	12	22.0	0.87	0.24	0.97	0.23	0.99	0.22	19
HSPA9	P38646	Stress-70 protein, mitochondrial	1.00	26	39.6	0.98	0.18	0.84	0.16	1.13	0.19	81
HTRA2	O43464	Serine protease HTRA2, mitochondrial	1.00	6	21.8	1.21	0.30	0.98	0.22	1.11	0.30	10
IFFO2	Q5TF58	Intermediate filament family orphan 2	1.00	3	17.1	0.83	0.09	1.99	0.37	2.05	0.29	10
KARS	Q15046	Lysyl-tRNA synthetase	1.00	2	2.5	0.78	0.07	0.94	0.05	0.83	0.07	10
KCTD3	Q9Y597	BTB/POZ domain-containing protein KCTD3	1.00	4	8.3	0.93	0.11	0.78	0.11	0.77	0.15	8
LIMD1	Q9UGP4	LIM domain-containing protein 1	1.00	8	18.6	0.95	0.18	1.11	0.40	1.24	0.37	9
LMNA	P02545	Lamin-A/C	1.00	2	3.9	0.81	0.32	0.75	0.23	0.72	0.26	3
LPP	Q93052	Lipoma-preferred partner	1.00	3	7.4	0.87	0.33	1.13	0.19	1.15	0.18	4
LTF	P02788	Lactotransferrin	1.00	2	2.2	1.00	0.21	0.95	0.16	0.94	0.19	8
LUZP1	Q86V48	Leucine zipper protein 1	1.00	2	2.0	0.93	0.14	1.06	0.20	1.10	0.46	5
LZTFL1	Q9NQ48	Leucine zipper transcription factor-like protein 1	1.00	8	26.1	1.07	0.20	1.04	0.17	1.00	0.19	27
MAP4	P27816	Microtubule-associated protein 4	1.00	2	3.6	0.90	0.09	1.06	0.07	1.10	0.09	9
MAPRE1	Q15691	End binding protein 1	1.00	4	17.5	1.70	0.29	1.47	0.20	1.49	0.27	32
MCM5	P33992	DNA replication licensing factor MCM5	1.00	2	3.7	0.79	0.17	1.00	0.20	1.09	0.17	3
MCM7	P33993	DNA replication licensing factor MCM7	1.00	3	4.2	0.89	0.08	0.84	0.17	0.92	0.11	3

MTHFD1	P11586	C-1-tetrahydrofolate synthase, cytoplasmic	1.00	2	3.7	0.80	0.09	0.79	0.13	0.64	0.18	7
MTHFD1L	Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	1.00	3	5.2	1.09	0.20	1.05	0.10	0.96	0.09	7
MVP	Q14764	Major vault protein	1.00	11	21.2	0.86	0.24	0.72	0.24	1.56	0.68	18
MYH9	P35579	Myosin-9	1.00	3	2.6	1.42	0.27	1.00	0.17	1.53	0.56	3
MYO1B	O43795	Myosin-Ib	1.00	3	3.3	0.78	0.13	0.84	0.11	0.70	0.22	11
NCL	P19338	Nucleolin	1.00	7	8.6	0.83	0.13	1.05	0.21	1.35	0.22	10
NIF3L1	Q9GZT8	NIF3-like protein 1	1.00	2	4.8	1.21	0.16	1.02	0.07	1.02	0.10	7
NOLC1	Q14978	Nucleolar and coiled-body phosphoprotein 1	1.00	3	6.3	0.84	0.09	1.27	0.13	1.35	0.21	3
NPM1	P06748	Nucleophosmin	1.00	3	16.1	1.04	0.20	1.25	0.17	1.88	0.29	8
NUDT21	O43809	Cleavage and polyadenylation specificity factor subunit 5	1.00	8	41.4	1.00	0.17	1.01	0.16	1.02	0.15	35
PCNA	P12004	Proliferating cell nuclear antigen	1.00	3	12.3	1.04	0.30	0.93	0.07	0.84	0.44	3
PHB	P35232	Prohibitin	1.00	2	7.0	1.05	0.08	0.97	0.11	0.87	0.11	3
PHB2	Q99623	Prohibitin-2	1.00	7	26.8	1.01	0.22	0.91	0.20	0.83	0.17	18
PKM2	P14618	Pyruvate kinase isozymes M1/M2	1.00	13	41.1	0.77	0.17	0.84	0.18	0.61	0.21	29
PPP2R3A	Q06190	Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha	1.00	6	7.4	1.00	0.22	1.08	0.17	1.24	0.35	13
PRKDC	P78527	DNA-dependent protein kinase catalytic subunit	1.00	7	3.1	0.92	0.29	0.95	0.14	0.85	0.25	13
PSMC1	P62191	26S protease regulatory subunit 4	1.00	2	7.3	0.93	0.11	0.86	0.06	0.73	0.13	4
PYCARD	Q9ULZ3	Apoptosis-associated speck-like protein containing a CARD	1.00	16	61.5	1.07	0.30	1.02	0.25	0.89	0.27	236
RAN	P62826	GTP-binding nuclear protein Ran	1.00	4	25.5	0.90	0.15	0.62	0.06	0.64	0.14	9
RPL10	P27635	60S ribosomal protein L10	1.00	3	18.7	0.86	0.06	1.28	0.13	0.94	0.05	7
RPL13	P26373	60S ribosomal protein L13	1.00	3	14.2	1.14	0.08	1.29	0.17	1.28	0.24	7
RPL13A	P40429	60S ribosomal protein L13a	1.00	3	9.9	1.14	0.29	1.11	0.15	1.26	0.31	3
RPL15	P61313	60S ribosomal protein L15	1.00	2	19.6	1.12	0.28	1.12	0.31	1.04	0.18	6
RPL17	P18621	60S ribosomal protein L17	1.00	3	13.6	0.72	0.11	1.15	0.25	0.97	0.16	5
RPL18	Q07020	60S ribosomal protein L18	1.00	3	25.5	0.82	0.15	0.78	0.23	1.00	0.23	9
RPL18A	Q02543	60S ribosomal protein L18a	1.00	2	16.5	0.96	0.07	1.04	0.05	1.10	0.19	5
RPL23	P62829	60S ribosomal protein L23	1.00	2	11.4	0.94	0.18	1.04	0.15	0.94	0.16	8
RPL24	P83731	60S ribosomal protein L24	1.00	4	24.2	1.05	0.52	1.19	0.46	1.13	0.42	3
RPL26	P61254	60S ribosomal protein L26	1.00	5	29.0	0.86	0.22	0.93	0.25	1.00	0.17	9
RPL27	P61353	60S ribosomal protein L27	1.00	3	19.9	1.00	0.16	1.08	0.14	1.13	0.12	5
RPL28	P46779	60S ribosomal protein L28	1.00	3	17.5	1.11	0.21	1.14	0.27	1.12	0.27	7
RPL3	P39023	60S ribosomal protein L3	1.00	3	5.2	1.14	0.20	1.11	0.21	1.24	0.14	7
RPL30	P62888	60S ribosomal protein L30	1.00	2	15.7	0.83	0.04	0.88	0.11	1.00	0.03	6

RPL34	P49207	60S ribosomal protein L34	1.00	2	13.7	1.22	0.26	1.29	0.26	1.58	0.36	6
RPL35A	P18077	60S ribosomal protein L35a	1.00	4	20.0	0.92	0.14	0.95	0.14	1.07	0.17	12
RPL4	P36578	60S ribosomal protein L4	1.00	5	13.8	1.05	0.29	1.01	0.29	1.16	0.34	12
RPL5	P46777	60S ribosomal protein L5	1.00	4	10.8	0.95	0.07	1.03	0.22	1.29	0.17	6
RPL6	Q02878	60S ribosomal protein L6	1.00	3	10.8	1.05	0.14	1.07	0.09	1.09	0.09	6
RPL7	P18124	60S ribosomal protein L7	1.00	2	12.1	1.07	0.20	1.15	0.13	1.04	0.13	5
RPL7A	P62424	60S ribosomal protein L7a	1.00	4	16.5	0.97	0.13	1.09	0.14	1.11	0.13	8
RPL8	P62917	60S ribosomal protein L8	1.00	3	9.7	1.04	0.11	1.18	0.14	1.21	0.17	12
RPS11	P62280	40S ribosomal protein S11	1.00	5	37.3	0.90	0.13	1.01	0.13	0.82	0.12	10
RPS14	P62263	40S ribosomal protein S14	1.00	3	15.4	1.00	0.19	1.01	0.20	0.96	0.13	9
RPS15A	P62244	40S ribosomal protein S15a	1.00	3	18.5	1.01	0.23	0.95	0.17	0.95	0.36	19
RPS18	P62269	40S ribosomal protein S18	1.00	2	19.1	0.92	0.10	0.93	0.10	1.05	0.11	6
RPS2	P15880	40S ribosomal protein S2	1.00	4	23.3	0.92	0.27	1.10	0.12	0.93	0.18	10
RPS23	P62266	40S ribosomal protein S23	1.00	2	16.1	1.17	0.19	1.26	0.14	1.22	0.19	5
RPS27A	P62988	Ubiquitin	1.00	2	15.8	0.86	0.04	0.88	0.16	0.78	0.07	5
RPS3	P23396	40S ribosomal protein S3	1.00	3	11.5	0.97	0.23	1.01	0.25	1.01	0.27	7
RPS3A	P61247	40S ribosomal protein S3a	1.00	3	12.7	1.02	0.13	1.04	0.14	1.02	0.25	7
RPS4X	P62701	40S ribosomal protein S4, X isoform	1.00	3	8.0	1.12	0.17	1.62	0.22	1.82	0.26	7
RPS7	P62081	40S ribosomal protein S7	1.00	3	19.6	0.77	0.30	0.98	0.39	0.90	0.17	3
RPS9	P46781	40S ribosomal protein S9	1.00	6	25.4	0.93	0.14	1.03	0.15	0.82	0.12	8
SERBP1	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	1.00	2	6.6	1.02	0.52	1.17	0.21	1.24	0.48	3
SFPQ	P23246	Splicing factor, proline- and glutamine-rich	1.00	6	11.2	1.00	0.15	1.10	0.14	1.32	0.25	14
SLC25A3	Q00325	Phosphate carrier protein, mitochondrial	1.00	2	5.3	1.10	0.21	1.02	0.32	0.84	0.24	5
SLC25A5	P05141	ADP/ATP translocase 2	1.00	6	18.8	0.94	0.32	0.99	0.25	0.84	0.37	14
SMC3	Q9UQE7	Structural maintenance of chromosomes protein 3	1.00	2	4.6	0.74	0.15	0.83	0.11	0.83	0.03	4
TCOF1	Q13428	Treacle protein	1.00	2	2.1	0.99	0.06	1.19	0.17	0.86	0.08	3
TCP1	P17987	T-complex protein 1 subunit alpha	1.00	3	5.8	1.03	0.05	0.93	0.17	0.78	0.17	5
TECR	Q9NZ01	Trans-2,3-enoyl-CoA reductase	1.00	2	5.5	0.92	0.08	0.88	0.18	0.70	0.08	3
THBS1	P07996	Thrombospondin-1	1.00	2	2.2	0.71	0.21	0.69	0.13	0.70	0.21	3
TMF1	P82094	TATA element modulatory factor	1.00	3	5.3	1.13	0.12	1.14	0.13	1.05	0.14	8
TRIM21	P19474	52 kDa Ro protein	1.00	25	57.5	1.35	0.35	1.02	0.26	1.27	0.59	113
TSC1	Q92574	Hamartin	1.00	3	2.9	1.02	0.21	1.02	0.36	0.62	0.14	3
TTN	Q8WZ42	Titin	1.00	4	0.2	0.62	0.06	0.82	0.09	0.61	0.06	180
TUBB	P07437	Tubulin beta chain	1.00	15	45.3	0.95	0.29	0.97	0.29	0.82	0.22	42
TUFM	P49411	Elongation factor Tu, mitochondrial	1.00	2	3.8	0.86	0.14	0.92	0.11	0.85	0.18	4
UQCRC2	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	1.00	3	9.1	0.92	0.34	0.81	0.24	0.88	0.53	6
XIAP	P98170	Baculoviral IAP repeat-containing protein 4	1.00	13	30.6	1.03	0.17	0.97	0.16	0.90	0.19	29

ZFYVE19	Q96K21	Zinc finger FYVE domain-containing protein 19	1.00	2	3.1	0.99	0.16	1.02	0.09	1.05	0.21	4