

SUPPLEMENTAL MATERIAL

Table S1. Antibodies used in this study.

Antibody	Catalog Number	Species	Source
P21 (Waf1/Cip1)	sc-6246	Mouse monoclonal	Santa Cruz
MAP L3CB	sc-376404	Mouse monoclonal	Santa Cruz
PAI-1	sc-8979	Rabbit polyclonal	Santa Cruz
ICAM-1	sc-1511R	Rabbit polyclonal	Santa Cruz
TLR2	sc-10739	Rabbit polyclonal	Santa Cruz
NEST	sc-20978	Rabbit polyclonal	Santa Cruz
NEO1	sc-15337	Rabbit polyclonal	Santa Cruz
P16 (CDKN2A)	PAI-46620	Rabbit polyclonal	ThermoFisher
α -Tubulin	ab6046	Rabbit polyclonal	Abcam
Caveolin1	ab2910	Rabbit polyclonal	Abcam
Ki67	ab16667	Rabbit monoclonal	Abcam
P62	ab56416	Mouse monoclonal	Abcam
DDX58	ab45428	Rabbit polyclonal	Abcam
ADAM10	ab2124695	Rabbit monoclonal	Abcam
LICAM	ab24345	Mouse monoclonal	Abcam
GAPDH	ab181602	Rabbit monoclonal	Abcam
Wheat germ agglutinin – AF488	W11261	-	Life Technologies

Table S2. Proteins increased at cell surface (≥ 1.5 -fold).

Protein	Fold Change ^a	P value ^b	Protein Name
P22777 PAI1	9.5	0.00	Plasminogen activator inhibitor 1
P97798 NEO1	9.3	0.03	Neogenin
Q9QUN7 TLR2	5.2	0.07	Toll-like receptor 2
P23927 CRYAB	6.8	0.00	Alpha-crystallin B chain
Q9D0J4 ARL2	3.3	0.10	ADP-ribosylation factor-like protein 2
Q6Q899 DDX58	2.9	0.04	Probable ATP-dependent RNA helicase DDX58, retinoic acid inducible gene 1 protein (RIG-1)
P49945 FRIL2	2.8	0.04	Ferritin light chain 2
P07724 ALBU	2.8	0.35	Serum albumin
Q8BHN3 GANAB	2.8	0.10	Neutral alpha-glucosidase AB
Q9DC70 NDUS7	2.8	0.50	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial
Q8K1N2 PHLB2	2.5	0.11	Pleckstrin homology-like domain family B member 2
O08638 MYH11	2.5	0.05	Myosin-11
Q6PHZ2 KCC2D	2.3	0.43	Calcium/calmodulin-dependent protein kinase type II subunit delta
P11276 FINC	2.3	0.01	Anastellin
Q08879 FBLN1	2.3	0.22	Fibulin-1
Q8BMF4 ODP2	2.2	0.01	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (PDC-E2), mitochondrial
Q9QZQ1 AFAD	2.1	0.43	Afadin
Q9Z0R6 ITSN2	2.1	0.09	Intersectin-2
Q60680 IKKA	2.0	0.15	Inhibitor of nuclear factor kappa-B kinase subunit alpha
P99029 PRDX5	2.0	0.21	Peroxisiredoxin-5, mitochondrial
Q64133 AOFA	1.9	0.00	Amine oxidase [flavin-containing] A
P97770 THUM3	1.9	0.47	THUMP domain-containing protein 3
Q6P5H2 NEST	1.9	0.02	Nestin

P13597 ICAM1	1.9	0.21	Intercellular adhesion molecule 1
P07356 ANXA2	1.8	0.00	Annexin A2
P02089 HBB2	1.8	0.06	Hemoglobin subunit beta-2
Q0KL02 TRIO	1.8	0.00	Triple functional domain protein
Q9WTR1 TRPV2	1.8	0.03	Transient receptor potential cation channel subfamily V member 2
Q9QUM9 PSA6	1.8	0.15	Proteasome subunit alpha type-6
Q64727 VINC	1.8	0.07	Vinculin
P40124 CAP1	1.8	0.00	Adenylyl cyclase-associated protein 1
P85094 ISC2A	1.7	0.02	Isochorismatase domain-containing protein 2A, mitochondrial
Q03963 E2AK2	1.7	0.03	Interferon-induced, double-stranded RNA-activated protein kinase
Q5U430 UBR3	1.7	0.23	E3 ubiquitin-protein ligase UBR3
Q80X90 FLNB	1.7	0.00	Filamin-B
P54116 STOM	1.7	0.01	Erythrocyte band 7 integral membrane protein
Q9CZ30 OLA1	1.7	0.10	Obg-like ATPase 1
Q9Z331 K2C6B	1.7	0.04	Keratin, type II cytoskeletal 6B
O09172 GSH0	1.6	0.28	Glutamate--cysteine ligase regulatory subunit
Q02053 UBA1	1.6	0.05	Ubiquitin-like modifier-activating enzyme 1
P00493 HPRT	1.6	0.01	Hypoxanthine-guanine phosphoribosyltransferase
Q61171 PRDX2	1.6	0.01	Peroxiredoxin-2
Q7TPR4 ACTN1	1.6	0.01	Alpha-actinin-1
P03995 GFAP	1.6	0.14	Glial fibrillary acidic protein
P97434 MPRIIP	1.6	0.10	Myosin phosphatase Rho-interacting protein
P26041 MOES	1.6	0.00	Moesin
Q9D6K9 CERS5	1.6	0.21	Ceramide synthase 5
P48678 LMNA	1.6	0.09	Lamin-A/C
Q8BHY3 ANO1	1.6	0.17	Anoctamin-1
Q8C522 ENDD1	1.5	0.16	Endonuclease domain-containing 1 protein
P10107 ANXA1	1.5	0.00	Annexin A1
A6X935 ITIH4	1.5	0.16	Inter alpha-trypsin inhibitor, heavy chain 4
P11627 L1CAM	1.5	0.19	Neural cell adhesion molecule L1
Q9WVL2 STAT2	1.5	0.19	Signal transducer and activator of transcription 2
Q8VED5 K2C79	1.5	0.09	Keratin, type II cytoskeletal 79
P21279 GNAQ	1.5	0.21	Guanine nucleotide-binding protein G(q) subunit alpha
Q80X95 RRAGA	1.5	0.30	Ras-related GTP-binding protein A
Q64261 CDK6	1.5	0.02	Cyclin-dependent kinase 6
Q8CGE9 RGS12	1.5	0.89	Regulator of G-protein signaling 12
P26039 TLN1	1.5	0.25	Talin-1
Q9R112 SQRD	1.5	0.00	Sulfide:quinone oxidoreductase, mitochondrial
Q99PT1 GDIR1	1.5	0.17	Rho GDP-dissociation inhibitor 1
P34884 MIF	1.5	0.01	Macrophage migration inhibitory factor
Q8R2Q8 BST2	1.5	0.20	Bone marrow stromal antigen 2
Q9WUP4 PORED	1.5	0.04	Polyprenol reductase
Q61595 KTN1	1.5	0.05	Kinectin
Q61584 FXR1	1.5	0.35	Fragile X mental retardation syndrome-related protein 1
A2A699 F1712	1.5	0.32	Protein FAM171A2
Q9WTI7 MYO1C	1.5	0.05	Unconventional myosin-Ic
A6H6E2 MMRN2	1.5	0.04	Multimerin-2
Q9EPL8 IPO7	1.5	0.10	Importin-7
P70275 SEM3E	1.5	0.37	Semaphorin-3E
P48036 ANXA5	1.5	0.10	Annexin A5

^a Fold change (Ratio irradiated/controls; mean of 3 independent experiments). ^b P value (Student's t-test).

Table S3. Proteins decreased at the cell surface (≤ 1.5 -fold).

Protein	Fold Change^a	P value^b	Protein Name
O88342 WDR1	0.2	0.10	WD repeat-containing protein 1
P97310 MCM2	0.2	0.00	DNA replication licensing factor MCM2
P14869 RLA0	0.2	0.02	60S acidic ribosomal protein P0
Q8CGP2 H2B1P	0.3	0.08	Histone H2B type 1-P
P09242 PPBT	0.3	0.00	Alkaline phosphatase, tissue-nonspecific isozyme
P35969 VGFR1	0.3	0.03	Vascular endothelial growth factor receptor 1
P62880 GBB2	0.3	0.01	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2
P16382 IL4RA	0.3	0.02	Interleukin-4 receptor subunit alpha
P08113 ENPL	0.3	0.07	Endoplasmic
Q9D662 SC23B	0.3	0.03	Protein transport protein Sec23B
Q9D7S7 RL22L	0.4	0.02	60S ribosomal protein L22-like 1
Q9CZJ2 HS12B	0.4	0.00	Heat shock 70 kDa protein 12B
P97311 MCM6	0.4	0.06	DNA replication licensing factor MCM6
Q6P4T2 U520	0.4	0.14	U5 small nuclear ribonucleoprotein 200 kDa helicase
Q99JW4 LIMS1	0.4	0.08	LIM and senescent cell antigen-like-containing domain protein 1
Q7TPV4 MBB1A	0.4	0.09	Myb-binding protein 1A
P49718 MCM5	0.4	0.00	DNA replication licensing factor MCM5
Q9JJI8 RL38	0.4	0.01	60S ribosomal protein L38
O35598 ADA10	0.4	0.05	Disintegrin and metalloproteinase domain-containing protein 10
Q9Z2X1 HNRPF	0.4	0.00	Heterogeneous nuclear ribonucleoprotein F, N-terminally processed
P19253 RL13A	0.4	0.01	60S ribosomal protein L13a
Q99J27 ACATN	0.4	0.07	Acetyl-coenzyme A transporter 1
Q62465 VAT1	0.4	0.14	Synaptic vesicle membrane protein VAT-1 homolog
P49717 MCM4	0.4	0.05	DNA replication licensing factor MCM4
Q9QYJ0 DNJA2	0.4	0.04	DnaJ homolog subfamily A member 2
P97857 ATS1	0.4	0.03	A disintegrin and metalloproteinase with thrombospondin motifs 1
Q3TDQ1 STT3B	0.4	0.04	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit
Q91WF3 ADCY4	0.4	0.01	Adenylate cyclase type 4
P13864 DNMT1	0.5	0.02	DNA (cytosine-5)-methyltransferase 1
Q8BK67 RCC2	0.5	0.20	Protein RCC2
P61164 ACTZ	0.5	0.29	Alpha-centractin
P61211 ARL1	0.5	0.10	ADP-ribosylation factor-like protein 1
P62245 RS15A	0.5	0.02	40S ribosomal protein S15a
Q64337 SQSTM	0.5	0.01	Sequestosome-1
P02468 LAMC1	0.5	0.17	Laminin subunit gamma-1
P62918 RL8	0.5	0.67	60S ribosomal protein L8
P15116 CADH2	0.5	0.23	Cadherin-2
Q8R422 CD109	0.5	0.04	CD109 antigen
Q80TN5 ZDH17	0.5	0.02	Palmitoyltransferase ZDHHC17
Q9ES46 PARVB	0.5	0.15	Beta-parvin
Q9CXW4 RL11	0.5	0.02	60S ribosomal protein L11
P62270 RS18	0.5	0.23	40S ribosomal protein S18
Q03145 EPHA2	0.5	0.09	Ephrin type-A receptor 2
P62301 RS13	0.5	0.01	40S ribosomal protein S13
Q6P5D8 SMHD1	0.5	0.27	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
P25206 MCM3	0.5	0.02	DNA replication licensing factor MCM3
P16330 CN37	0.5	0.07	2',3'-cyclic-nucleotide 3'-phosphodiesterase
P97351 RS3A	0.5	0.00	40S ribosomal protein S3a
P11688 ITA5	0.5	0.08	Integrin alpha-5 light chain
O08573 LEG9	0.5	0.05	Galectin-9
Q9JHJ0 TMOD3	0.5	0.00	Tropomodulin-3

Q9D819 IPYR	0.5	0.21	Inorganic pyrophosphatase
Q8BWX3 ERF1	0.5	0.19	Eukaryotic peptide chain release factor subunit 1
Q7TNC4 LC7L2	0.5	0.12	Putative RNA-binding protein Luc7-like 2
Q5SWU9 ACACA	0.5	0.00	Biotin carboxylase
P54761 EPHB4	0.5	0.07	Ephrin type-B receptor 4
P62830 RL23	0.5	0.09	60S ribosomal protein L23
P20029 GRP78	0.5	0.02	78 kDa glucose-regulated protein
P20444 KPCA	0.6	0.11	Protein kinase C alpha type
Q8VDW0 DX39A	0.6	0.04	ATP-dependent RNA helicase DDX39A
Q64151 SEM4C	0.6	0.34	Semaphorin-4C
P02463 CO4A1	0.6	0.79	Arresten
Q9D5V5 CUL5	0.6	0.25	Cullin-5
Q8R1F1 NIBL1	0.6	0.34	Niban-like protein 1
Q01705 NOTC1	0.6	0.30	Neurogenic locus notch homolog protein 1
Q9D8N0 EF1G	0.6	0.10	Elongation factor 1-gamma
P62242 RS8	0.6	0.05	40S ribosomal protein S8
P61620 S61A1	0.6	0.00	Protein transport protein Sec61 subunit alpha isoform 1
Q8BX57 PXK	0.6	0.23	PX domain-containing protein kinase-like protein
Q7M759 AB17B	0.6	0.03	Alpha/beta hydrolase domain-containing protein 17B
P35979 RL12	0.6	0.01	60S ribosomal protein L12
P08775 RPB1	0.6	0.59	DNA-directed RNA polymerase II subunit RPB1
Q9JLV5 CUL3	0.6	0.22	Cullin-3
Q9QUR6 PPCE	0.6	1.00	Prolyl endopeptidase
Q9CU62 SMC1A	0.6	0.89	Structural maintenance of chromosomes protein 1A
Q8R1M2 H2AJ	0.6	0.26	Histone H2A.J
Q60605 MYL6	0.6	0.16	Myosin light polypeptide 6
P11440 CDK1	0.6	0.84	Cyclin-dependent kinase 1
P62908 RS3	0.6	0.01	40S ribosomal protein S3
O55222 ILK	0.6	0.07	Integrin-linked protein kinase
P13439 UMPS	0.6	0.13	Orotidine 5'-phosphate decarboxylase
Q9Z0L0 TPBG	0.6	0.15	Trophoblast glycoprotein
Q05793 PGBM	0.6	1.00	Basement membrane-specific heparan sulfate proteoglycan core protein
P51410 RL9	0.6	0.02	60S ribosomal protein L9
B2RU80 PTPRB	0.6	0.03	Receptor-type tyrosine-protein phosphatase beta
Q80U95 UBE3C	0.6	0.20	Ubiquitin-protein ligase E3C
Q61739 ITA6	0.6	0.09	Integrin alpha-6 light chain
Q9D1R9 RL34	0.6	0.58	60S ribosomal protein L34
O70475 UGDH	0.6	0.99	UDP-glucose 6-dehydrogenase
P14131 RS16	0.6	0.00	40S ribosomal protein S16
Q9JIK5 DDX21	0.6	0.07	Nucleolar RNA helicase 2
P97333 NRP1	0.6	0.11	Neuropilin-1
Q9D0E1 HNRPM	0.6	0.00	Heterogeneous nuclear ribonucleoprotein M
Q8BP67 RL24	0.6	0.01	60S ribosomal protein L24
Q9D198 SYF2	0.6	0.89	Functional Spliceosome-Associated Protein 29
P17225 PTBP1	0.6	0.26	Polypyrimidine tract-binding protein 1
Q9JJ28 FLII	0.6	0.12	Protein flightless-1 homolog
O35286 DHX15	0.6	0.31	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase
P70168 IMB1	0.6	0.09	Importin subunit beta-1
O35218 CPSF2	0.6	0.25	Cleavage and polyadenylation specificity factor subunit 2
Q9D8Z1 ASCC1	0.6	0.99	Activating signal cointegrator 1 complex subunit 1
Q9QZM4 TR10B	0.6	0.03	Tumor necrosis factor receptor superfamily member 10B
Q8BIJ6 SYIM	0.6	0.32	Isoleucine--tRNA ligase, mitochondrial
P16056 MET	0.6	0.06	Hepatocyte growth factor receptor
P97363 SPTC2	0.6	0.34	Serine palmitoyltransferase 2
Q62167 DDX3X	0.6	0.23	ATP-dependent RNA helicase DDX3X

Q8BTJ4 ENPP4	0.6	0.99	Bis(5'-adenosyl)-triphosphatase enpp4
Q9JL15 LEG8	0.6	0.04	Galectin-8
P61358 RL27	0.6	0.01	60S ribosomal protein L27
Q3UH93 PLXD1	0.6	0.19	Plexin-D1
Q02257 PLAK	0.6	0.05	Junction plakoglobin
O70503 DHB12	0.6	0.35	Very-long-chain 3-oxoacyl-CoA reductase
Q05920 PYC	0.6	0.21	Pyruvate carboxylase, mitochondrial
P62849 RS24	0.6	0.10	40S ribosomal protein S24
P80315 TCPD	0.6	0.00	T-complex protein 1 subunit delta
P12382 K6PL	0.6	0.99	ATP-dependent 6-phosphofructokinase, liver type
P35293 RAB18	0.6	0.32	Ras-related protein Rab-18
Q9D8E6 RL4	0.6	0.01	60S ribosomal protein L4
O89103 C1QR1	0.6	0.06	Complement component C1q receptor
O54890 ITB3	0.6	0.85	Integrin beta-3
P23116 EIF3A	0.6	0.99	Eukaryotic translation initiation factor 3 subunit A
B2RXS4 PLXB2	0.6	0.16	Plexin-B2
O88746 TOM1	0.6	0.34	Target of Myb protein 1
Q61024 ASNS	0.6	0.01	Asparagine synthetase [glutamine-hydrolyzing]
P63037 DNJA1	0.6	0.21	DnaJ homolog subfamily A member 1
Q62351 TFR1	0.7	0.09	Transferrin receptor protein 1
Q60865 CAPR1	0.7	0.13	Caprin-1
Q99LC5 ETFA	0.7	0.34	Electron transfer flavoprotein subunit alpha, mitochondrial
Q06806 TIE1	0.7	0.29	Tyrosine-protein kinase receptor Tie-1
P16110 LEG3	0.7	0.11	Galectin-3
P55284 CADH5	0.7	0.19	Cadherin-5
Q9CZR2 NALD2	0.7	0.49	N-acetylated-alpha-linked acidic dipeptidase 2
Q9DCD0 6PGD	0.7	0.28	6-phosphogluconate dehydrogenase, decarboxylating

^a Fold change (Ratio irradiated/controls; mean of 3 independent experiments). ^b P value (Student's *t*-test).

Table S4. Ingenuity pathway analysis.

TOP CANONICAL PATHWAYS		
Name	p-value	Overlap
EIF2 signalling	2.47E-34	27.6% 51/185
Regulation of eIF4 and p70S6K signalling	1.01E-17	21.2% 31/146
Epithelial adherens junction signalling	6.12E-15	19.2% 28/146
Caveolar-mediated endocytosis signalling	2.56E-13	26.8% 19/71
Germ cell-sertoli cell junction signalling	4.87E-13	16.9% 27/160
TOP NETWORKS		
Name	p-value	# molecules
Cellular movement	1.79E-05 – 4.51E-32	214
Cellular growth and proliferation	8.08E-06 – 5.18E-29	285
Cellular assembly and organization	8.13E-06 – 3.12E-26	211
Cellular function and maintenance	1.79E-05 – 3.12E-26	249
Protein synthesis	1.26E-05 – 2.77E-24	139
TOP TOX LISTS		
Name	p-value	Overlap
Renal necrosis/cell death	3.00E-09	8.5% 42/496
NRF2-mediated oxidative stress response	3.73E-05	8.5% 20/234
PPAR/RXR activation	4.99E-05	9.3% 17/183
Hypoxia-inducible factor signalling	2.74E-04	12.9% 9/70
Mitochondrial dysfunction	3.50E-04	8.5% 15/176
TOP UPSTREAM REGULATORS		
Upstream Regulator	p-value of overlap	Predicted Activation
MYC	1.28E-40	Inhibited
MYCN	1.37E-37	Inhibited
TP53	1.80E-34	-
sirolimus	4.69E-31	Activated
5-fluorouracil	7.19E-28	Activated