

Multimomics characterization of dose- and time-dependent effects of ionizing radiation on human skin keratinocytes

Won-Suk Song^{*,‡}, Jae-Seung Lee^{*,‡}, Jun Woo Lim^{*,‡}, JiEung Kim^{**}, Sung-Hyun Jo^{*}, Ji-Eun Kwon^{*}, Ji-Hyeon Park^{*}, Sang Hyoun Choi^{***}, Dongchan Jang^{**}, Il Won Kim^{*}, Jae Hyun Jeong^{*}, and Yun-Gon Kim^{*,†}

^{*}Department of Chemical Engineering, Soongsil University, Seoul 06978, Korea

^{**}Department of Nuclear and Quantum Engineering, Korea Advanced Institute of Science and Technology, Daejeon 34141, Korea

^{***}Research Team of Radiological Physics and Engineering, Korea Institute of Radiological and Medical Sciences, Seoul 01812, Korea

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Abstract—Ionizing radiation is used for various purposes, such as cancer treatment and medical diagnosis. As skin keratinocytes are frequently exposed to various radiation doses, the risk of developing skin diseases is also increasing. However, knowledge of the biological response of human keratinocytes to radiation doses and time-points is still limited despite its importance. Here, we characterized the proteomic and metabolomic changes in HEK cells on day 0 and 2 after irradiation with control, 0.1, 0.5, and 2 Gy to identify biological effects depending on IR dose and time. First, we found that the expression levels of proteins and metabolites involved in energy metabolism, DNA repair system, and epidermal cornification were changed following irradiation. In particular, fumarate and fumarate hydratase, which promote DNA repair, were significantly increased in response to irradiation with 2 Gy on day 2. Furthermore, all doses of IR-induced proteomic changes correlated with epidermal cornification and inhibition of cell death on day 2 after irradiation. Using a human skin 3D full-thickness model, we observed dose-dependent increases in the cornified layer and the expression of involucrin. The multimomics signatures of cellular responses depending on IR dose and time may constitute a high-value resource, providing biological effects on IR applications.

Keywords: Skin Keratinocytes, Ionizing Radiation, LC-MS/MS, Proteomics, Metabolomics

INTRODUCTION

In our modern society, ionizing radiation (IR) is predominantly employed in the human body for medical applications [1]. Low doses of IR (0.1–0.5 Gy) are used for the diagnosis of diseases, such as cross-section scanning of the human body and three-dimensional (3D) scanning from computed tomography (CT). High doses of IR (approximately 2 Gy) are used for radiation therapy to treat tumors by selectively killing cancer cells [2,3]. IR-mediated medical application is a widely useful tool for medical engineering techniques; however, IR can induce significant problems with excess radiation exposure, such as functional damage to normal human tissues, oxidative stress, proinflammatory responses, and cancer development [4–6]. Therefore, understanding the biological changes in human cells caused by dose-dependent radiation is necessary to use IR and prevent IR-induced body injury properly.

The skin is an organ in the human body that plays a role in the physiological barrier against external stimuli such as IR [7]. In particular, the skin epidermis, the outermost layer of skin, is sensitively affected by these stresses. In this respect, there have been some stud-

ies on the pathological changes in the epidermis to dose-dependent IR to determine the responses of a human body in medical applications [8]. Revenco et al. reported that low-dose IR caused apoptosis in sebaceous glands in the epidermis and stem cells [9]. Erythema predominantly occurs with high-dose IR radiation therapy [10]. Additionally, continuous exposure to radiation doses causes an increase in the thickness of the epidermis [11]. At its severe stage, IR induces skin ulceration through inflammation with a decrease in regulatory T cells, and DNA mutation is caused by irreversible DNA breaks or intracellular free radicals [11]. Since the effects of irradiation on the host vary in a dose-dependent manner, further research is required to understand the changes in physiological metabolism following low- and high-dose irradiation.

Previous studies investigated the molecular changes in skin cells to understand the effects of irradiation on the skin [12–14]. Hu and coworkers revealed that different doses of IR treatment showed dose-dependent changes in the production of fatty acids [12]. These results indicated that IR exposure led to the downregulation of energy metabolism and the activation of the DNA repair process. Sekihara et al. suggested that proteins associated with cell growth arrest in keratinocytes were downregulated following irradiation with low-dose IR [13]. In addition, Lamartine et al. showed that energy metabolism was overexpressed by a high-dose IR of 2 Gy [14]. Although these findings provide background information for predicting biological changes in irradiated skin cells, a comprehensive analysis of

[†]To whom correspondence should be addressed.
E-mail: ygkim@ssu.ac.kr

[‡]These authors contributed equally to this work.

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human skin cells in response to various doses of IR is still needed.

To understand the biological effects on human skin keratinocytes in response to low- and high-dose IR, this study investigated proteomic and metabolomic changes in HEK cells after no irradiation or irradiation with 0.1, 0.5, and 2 Gy on day 0 and day 2. First, we observed different metabolic responses depending on IR doses in HEK cells. In addition, we focused on the changes in energy metabolism, the DNA repair process, and cornification that were regulated by IR exposure and tried to explore dose-dependent biomarkers. Moreover, we showed the development of the cornification process in a dose-dependent manner at the tissue level using a 3D full-thickness skin model. Taken together, this study investigated the biological changes in irradiated skin cells by multiomics approaches. These results will be necessary for medical applications related to IR exposure.

MATERIALS AND METHODS

1. Human Epidermal Keratinocyte neonatal (HEK) Cell Culture and Irradiation

Neonatal human epidermal keratinocyte cells (HEK cells in passages 1 to 3, Gibco, NY, USA) were cultured in a growth medium consisting of EpiLife (Gibco, NY, USA), high-serum growth supplement (HSGS, Gibco, NY, USA), and 1% penicillin-streptomycin (P/S, 100x, Biowest, MA, USA) in a 25-cm² cell culture flask. The cells were maintained at 37 °C in a 5% CO₂ environment. The medium was changed to fresh medium every 2-3 days. After culture for five days to allow more than 90% confluence, the cell culture flasks were irradiated with different doses of 0.1 Gy, 0.5 Gy, and 2 Gy. Cells were exposed to ionizing radiation (IR) at room temperature using a Clinac iX linear accelerator (Varian, UK). HEK cells were irradiated with a 6 MV high-energy photon beam placed on the beam axis at a source-to-axis distance of 100 cm. The field size was 20 cm×20 cm. The monitor units (MUs) needed to deliver a treatment plan were calculated to irradiate HEK cells by treatment planning systems (TPSs).

2. Intracellular Proteome and Metabolome Extraction in HEK Cells

We obtained the proteins and metabolites for multiomics analysis based on a previous study [15]. Briefly, HEK cells were trypsinized after washing out with sterile phosphate-buffered saline (PBS). The cells were collected and added to 1 mL of cold methanol. The cell suspensions were quenched using liquid nitrogen for 1 min. The cells were lysed for 10 min using a probe sonicator (Sonics & Materials Inc, CT, USA). Then, 3.3 mL of cold methyl-tert-butyl-ether was added, and the mixture was incubated for 1 hour at 4 °C under gentle agitation. A total of 840 µL of distilled water with 0.1% ammonium acetate was added to the mixture for phase separation. The mixture was centrifuged at 4,000 rpm for 15 min, and the organic layer was removed. We added 2.4 mL of cold methanol to the extract to precipitate proteins. The extract was centrifuged at 4,000 rpm for 20 min, and we obtained the upper phase and precipitated proteins. The upper phase was concentrated using a centrifugal vacuum evaporator (Hanil Science Industrial, Korea).

3. Metabolomic Analysis of HEK Cells

The concentrated extracts were dissolved in 50% MeOH con-

taining 10 µg/mL L-phenylalanine-¹³C₉, ¹⁵N (Sigma, MO, USA) as an internal standard (IS). The samples were filtered with PVDF syringe filters. Ten microliters of the samples was injected into a 1260 Infinity Binary HPLC system (Agilent, CA, USA) combined with a 6420 Triple Quadrupole LC-MS system (Agilent, CA, USA) for metabolomic analysis. Buffer A was water/acetonitrile (95:5 v/v) with 20 mM ammonium acetate and 20 mM ammonium hydroxide, and buffer B was 100% acetonitrile. Chromatographic separation was performed using a Luna NH₂ column (250×2 mm, 5-µm particle size, Phenomenex, NJ, USA) operating at a flow rate of 500 µL/min and eluted with a gradient. The gradient conditions were as follows: solution B was set from 85% to 0% for 28 minutes and from 0% to 85% for the next 2 minutes, followed by maintenance for 10 minutes. The electrospray voltage was 4 kV, and the multiple reaction monitoring (MRM) mode was used to detect the metabolites of interest as previously described [16]. The peak areas were annotated using Agilent Mass Hunter Qualitative Analysis (version B.07.00), and the annotated peak areas were normalized to the peak area of IS.

4. Preparation and Analysis of Intracellular Proteins of HEK Cells

The precipitated proteins were resuspended in 0.5 mL of 8 M urea solution. The protein concentration was measured with a bicinchoninic acid assay (BCA assay; Thermo Scientific, MA, USA) according to the instructions provided by the manufacturer. One hundred micrograms of soluble protein was transferred to a new microcentrifuge tube. Proteins were reduced using dithiothreitol and incubated for 30 min at 55 °C. Proteins were alkylated by iodoacetamide treatment. Then, water containing 25 mM ammonium bicarbonate was added to the alkylated protein solution. The prepared proteins were trypsinized for 18 hours at 37 °C. Peptide samples were purified using a Sep-pak C18 cartridge (Waters, MA, USA) and dried with a centrifugal vacuum concentrator (Vision Scientific, Seoul, Korea).

The dried peptides were dissolved in water containing 0.1% v/v formic acid. Proteomic analysis was performed using a Q Exactive Hybrid Quadrupole-Orbitrap (Thermo Scientific, MA, USA) equipped with a nanoelectrospray ionization source coupled to an Ultimate 3000 RSLCnano LC system (Thermo Scientific, MA, USA). The injected samples were trapped in an Acclaim PepMap 100 trap column (100 mm×2 cm, nanoViper C18, 5 mm, 100 Å, Thermo Scientific, MA, USA). Water containing 0.1% v/v formic acid was used for buffer C, and acetonitrile containing 0.1% v/v formic acid was used for buffer D. First, the column was washed with buffer C at a flow rate of 4 mL/min for 6 min. Then, the samples were separated at a flow rate of 350 nL/min. LC separation was performed using an Acclaim PepMap 100 capillary column (75 mm×15 cm, nanoViper C18, 3 mm, 100 Å, Thermo Scientific, MA, USA). Gradient conditions were as follows: 0 min, 2% D; 30 min, 35% D; 40 min 90% D, 45 min, 90% D; and 60 min, 5% D. The ion spray voltage was set at 2,100 eV. MS data were obtained by Xcaliber software (Thermo Scientific, MA, USA). The MS analyzer scanned precursor ions with a mass range of 350-1,800 m/z and a resolution of 70,000. The top 15 abundant precursor ions were selected for collision-induced dissociation (CID). The normalized collision energy was set at 32. Protein identification and quantification were per-

formed using MaxQuant software. Proteomic quantification and data analysis were processed using Perseus software [17,18]. Gene ontology enrichment analyses were performed using the PANTHER classification system (www.pantherdb.org) [19]. Briefly, the UniProt accessions of the proteins that were identified in each dose of IR were applied in the Gene List Analysis system. The significant gene ontology pathways were calculated by the false discovery rate (FDR) correction. And p-values for each pathway in the IR doses were compared for the gene ontology-based enrichment analysis.

5. Development of 3D Human Reconstructed Full-thickness Skin (FT-skin)

3D human reconstructed full-thickness skin (FT-skin) was fabricated to evaluate changes in skin tissue induced by irradiation. First, the dermal layers were fabricated with collagen compound and human dermal neonatal fibroblasts (HDFn, Gibco, NY, USA) at 1×10^5 cells/mL (Fig. S1(a)). The dermal layers were cultured for seven days at 37°C and 5% CO₂ with fibroblast growth medium consisting of medium 106 (M106, Thermo Fisher Scientific, MA, USA), low-serum growth supplement (LSGS, Gibco, NY, USA), and 1% P/S. The culture medium was changed three times a week. Then, the epidermal layer was seeded by 1×10^5 HEK cells on the dermal layer and submerged in a keratinocyte culture medium for seven days to form a monolayered epidermis (Fig. S1(b)). Finally, 3D human reconstructed full-thickness skin (FT-skin) was cultured with air-liquid interface conditions for epidermal differentiation (Fig. S1(a)) [20,21]. After culture for seven days, the FT-skins were irradiated with different irradiation doses at 0.1 Gy, 0.5 Gy, and 2 Gy, respectively.

6. Histological Analysis and Immunofluorescence

After incubation for one, nine, and 14 days, the FT-skin was fixed with 10% neutral buffered formalin to image the morphological structure in tissues. The fixed skin was also embedded in paraffin, and tissue sections were stained with hematoxylin and eosin (H&E), and involucrin. Sections (4 µm) were deparaffinized in xylene and rehydrated in alcohol gradients before H&E staining or immunofluorescence analysis. For immunofluorescence buffer, tissues were blocked in 2.5% normal horse serum for 30 mins and then incubated with involucrin antibody (Abcam, UK) for two hours at room temperature. Slides were then incubated with a secondary fluores-

cent antibody (Abcam, UK) for 1 hour at room temperature in the dark. The chamber slides were coverslipped using Fluoroshield mounting medium with DAPI fluorescence (ImmunoBioScience Corp., WA, USA). Fluorescence images were acquired using an Eclipse TS100 fluorescence microscope (Nikon, Japan).

7. Statistical Analysis

Student's t-test and one-way analysis of variance (ANOVA) followed by Tukey's honestly significant difference (Tukey's HSD) test were conducted using the R statistical programming environment. Bar graphs with error bars indicate the mean and standard deviation.

RESULTS AND DISCUSSION

1. Proteomic and Metabolomic Changes in HEK Cells Following Irradiation

To investigate the biological responses to dose- and time-dependent IR in human keratinocytes, we irradiated HEK cells at different doses (0, 0.1, 0.5, and 2 Gy) and observed proteomic and metabolic changes by multiomics technologies on day 0 and day 2 (Fig. 1, Supplementary Table S1, S2). First, principal component analysis (PCA) showed that proteome expression was marginally changed at irradiation doses of 0, 0.1, and 0.5 Gy (Fig. 2(a)). In contrast, the irradiation dose of 2 Gy marked drastic proteome expression changes, which were maintained after two days. In addition, irradiation with 2 Gy also changed the metabolic profiles of HEK cells on both day 0 and day 2 (Fig. 2(b), Supplementary Table S3, S4). The ranges for low doses of IR are still unclear, and the biological effects of low doses of IR on the epidermis are not as well understood [13,22]. Irradiation with 0.1 or 0.5 Gy showed similar proteomic profiles to the control; therefore, our proteomic results suggest that these two doses are involved in low-dose levels of IR, contrary to 2 Gy in terms of biological responses. Moreover, proteomic profiles among all doses on day 2 improved PCA similarity compared to those on day 0, revealing the normalization in cellular physiologies after irradiation. Accordingly, we focused on the specific biological responses in HEK cells after irradiation with low and high doses.

First, we observed the changes in biological pathways after irradiation based on gene ontology (GO) statistical analysis. On day 0, irradiation at low doses inhibited the expression levels of func-

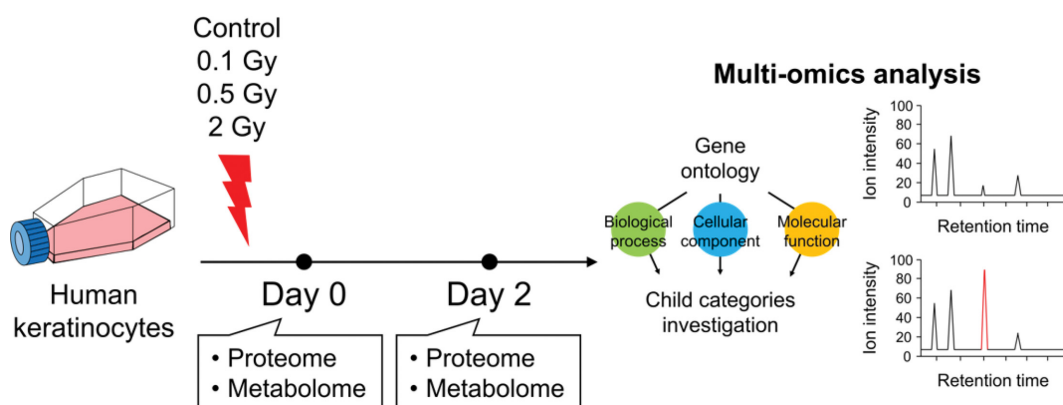


Fig. 1. Overall scheme of the processes for proteome and metabolome extraction and multiomics analysis.

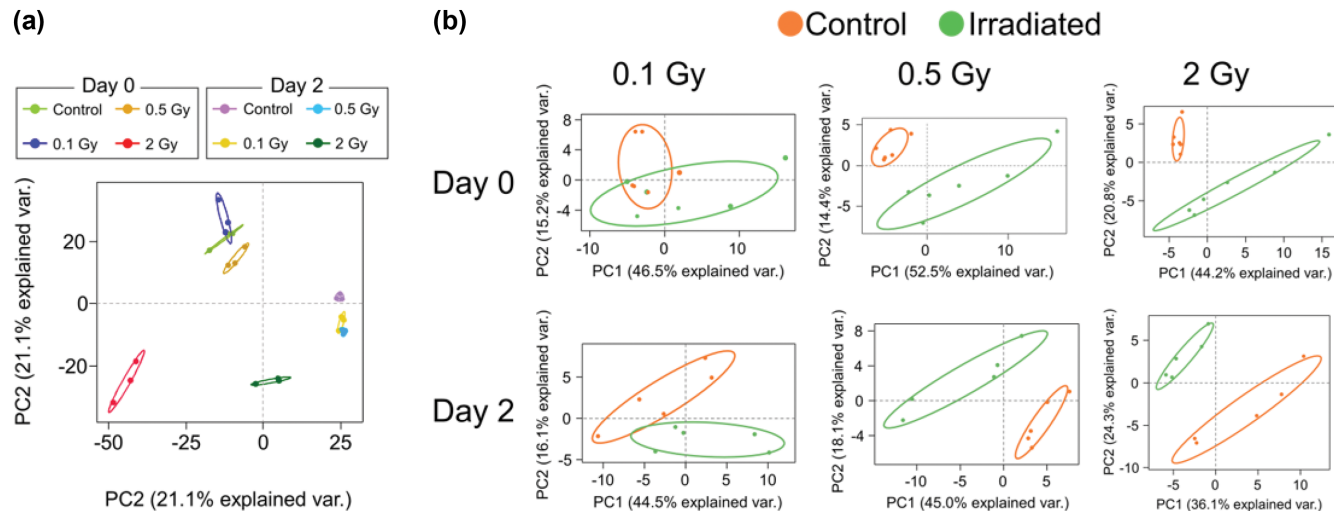


Fig. 2. Multiomics analysis provided the changes of proteomic and metabolomic overview. (a) Principal component analysis (PCA) of intracellular proteome at different doses and post-irradiation time. (b) Principal component analysis (PCA) of intracellular metabolome at IR dose- and time-dependent manner. Proteomics and metabolomics were performed by LC-MS/MS. Proteomic analysis was performed with $n=3$, and metabolomic analysis was performed with $n=5$.

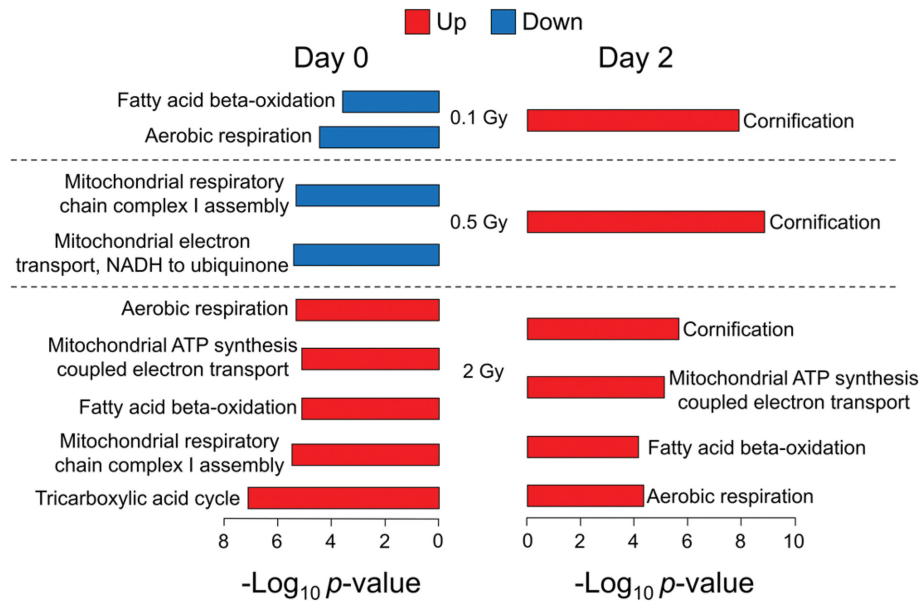


Fig. 3. Significantly changed biological processes regulated by IR treatment in HEKn at day 0 or day 2. Proteomics was performed by LC-MS/MS with the different three samples ($n=3$).

tional proteins related to energy metabolisms, such as aerobic respiration, mitochondrial electron transport, fatty acid beta-oxidation, and mitochondrial respiratory chain complex I assembly (Fig. 3). Conversely, irradiation with 2 Gy increased the proteomic expression of energy metabolism on both days 0 and 2. In addition, proteins related to epidermal cornification were significantly upregulated at all IR doses on day 2. Exposure to IR rewires an intricate network of metabolic circuits related to fatty acid oxidation [23]. And the abnormal fatty acid metabolism affects synthesizing biological membranes and delivering molecular signals to induce apoptotic cell death. In addition, exposure to high-dose IR induced a few genes involved in energy metabolism, but low doses of IR caused

energy depletion in the skin [12,14]. Furthermore, the development of epidermal cornification in the skin is characterized by long-term exposure to IR [24,25]. In this sense, we tried to investigate the discovery of molecular markers and mechanistic changes in energy metabolism and epidermal cornification based on multiomics signatures.

2. Irradiation-mediated Changes in Energy Metabolism

To understand the changes in energy metabolism on the effects of IR, we observed the proteomic expression involved in the tricarboxylic acid (TCA) cycle. Mitochondrial aconitase (ACO2) was downregulated by 0.79- and 0.83-fold after irradiation with 0.1 and 0.5 Gy on day 0, respectively (Table 1). In addition, the expres-

Table 1. TCA cycle proteins changed by IR irradiation at day 0 or day 2. * $p < 0.05$, ** $p < 0.005$, * $p < 0.0005$ according to one-way ANOVA followed by Tukey's HSD test**

Uniprot accession	Protein names	Gene names	Day 0			Day 2		
			0.1 Gy	0.5 Gy	2 Gy	0.1 Gy	0.5 Gy	2 Gy
			Fold change	Fold change	Fold change	Fold change	Fold change	Fold change
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	<i>Sdha</i>	0.89	0.93	1.30***	1.07	1.25	1.35
P53396	ATP-citrate synthase	<i>Acly</i>	1.03	0.95	0.79***	0.85**	0.79***	0.69***
P10515	Dihydrolipoyllysine-residue acetyltransferase Component of pyruvate dehydrogenase complex, mitochondrial	<i>Dlat</i>	0.86	1.10	1.66**	1.03	0.98	0.99
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	<i>Idh1</i>	1.04	1.07	0.78**	0.96	0.88	0.77**
P40926	Malate dehydrogenase, mitochondrial	<i>Mdh2</i>	0.87*	0.92	1.38***	1.01	1.00	1.20*
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	<i>Dlst</i>	0.85	0.88	1.29*	0.94	0.93	1.19*
P09622	Dihydrolipoyl dehydrogenase, mitochondrial	<i>Dld</i>	0.91	1.00	1.29**	0.97	0.95	1.19*
O75390	Citrate synthase, mitochondrial	<i>Cs</i>	0.89	0.92	1.27**	1.11	1.06	1.24*
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	<i>Pdha1</i>	0.84	0.89	1.31*	0.97	0.98	1.07
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	<i>Sdhb</i>	1.04	0.98	1.51**	1.06	1.10	1.25*
O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	<i>Idh3b</i>	1.03	0.98	1.31*	1.02	1.07	1.19
Q99798	Aconitate hydratase, mitochondrial	<i>Aco2</i>	0.79*	0.83	1.31**	1.19	1.22	1.37*
Q99643	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	<i>Sdhc</i>	1.59	1.39	2.40	-	-	-
P07954	Fumarate hydratase, mitochondrial	<i>Fh</i>	0.87	0.95	1.23*	1.04	1.05	1.26***
Q9P2R7	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	<i>Sucl2</i>	0.82	0.85	1.34	1.18	1.21	1.49
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	<i>Pdhb</i>	0.85	0.83*	1.24*	1.11	1.02	1.13
P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	<i>Suclg1</i>	1.00	1.08	1.43*	0.79	0.85	1.00
Q02218	2-oxoglutarate dehydrogenase, mitochondrial	<i>Ogdh</i>	0.88	0.85	1.26*	0.99	0.91	1.15
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	<i>Idh3a</i>	0.85	1.07	1.46**	1.14	1.23	1.27
P00367	Glutamate dehydrogenase 1, mitochondrial	<i>Glud1</i>	0.84	1.00	1.43***	1.14	1.12	1.30**
P51553	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	<i>Idh3g</i>	0.89	0.94	1.41	0.08**	0.11***	1.17*
P53007	Tricarboxylate transport protein, mitochondrial	<i>Slc25a1</i>	0.84	1.08	1.50*	1.20	1.23	1.23
Q96HY7	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	<i>Dhtkd1</i>	1.01	1.23	1.45*	-	-	-
P40925	Malate dehydrogenase, cytoplasmic	<i>Mdh1</i>	0.98	0.94	0.76**	1.05	1.07	0.92
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	<i>Idh2</i>	0.81	0.98	1.54***	1.06	1.17	1.38*
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	<i>Suclg2</i>	0.84	1.01	1.48*	1.10	1.25	1.46**
Q13423	NAD(P) transhydrogenase, mitochondrial	<i>Nnt</i>	-	-	-	1.02	1.28	1.04
P21399	Cytoplasmic aconitate hydratase	<i>Aco1</i>	-	-	-	0.83	0.90	0.93

sion levels of fumarate hydratase (FH) and the flavoprotein subunit of succinate dehydrogenase (SDHA) were also inhibited after irradiation at low doses. However, more interestingly, the expres-

sion levels of ACO2, FH, and SDHA were upregulated compared to the control on day 2. Exposure to external stimuli such as IR reduces cellular adenosine triphosphate (ATP) levels and activates

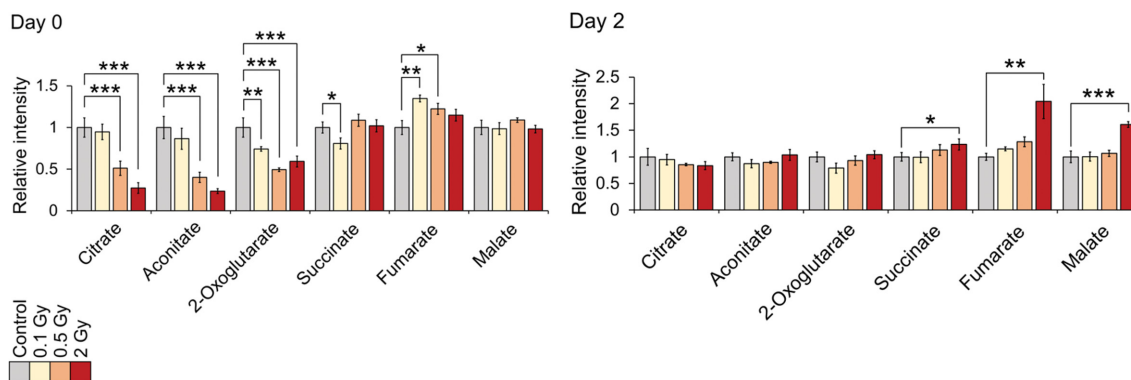


Fig. 4. The alteration of the expression levels of metabolites associated with the TCA cycle induced by IR exposure in HEK cells at day 0 or day 2. Metabolomic analysis was performed with $n=5$. Data are presented as means $\pm$ S.D. * $p<0.05$, ** $p<0.005$, *** $p<0.0005$ according to one-way ANOVA followed by Tukey's HSD test.

ATP-producing processes [23]. These responses help to restore cytotoxic stresses [26]. Moreover, ACO2, FH, and SDHA play essential roles in ATP production and activation of the TCA cycle [27–29]. Our results showed that irradiation with low doses of IR downregulated the proteins related to TCA cycles on day 0. Still, the expression levels of those proteins were increased or similar compared to the control on day 2. We suggested that these changes reveal the restoration of energy metabolism damage in skin keratinocytes in response to all doses of IR.

We further investigated the changes in TCA cycle intermediates of HEK cells in response to IR. First, all doses of IR inhibited the production of citrate, aconitate, and 2-oxoglutarate on day 0 (Fig. 4). Conversely, almost all TCA cycle intermediates were increased compared to the control on day 2. In particular, fumarate was increased by 1.15-, 1.28-, and 2.04-fold two days after irradiation with 0.1, 0.5, and 2 Gy, respectively. ATP levels were decreased on days 0 and 2 after irradiation with 2 Gy (Fig. S2). Irradiation inhibits TCA cycle metabolism and reduces ATP levels, postponing the DNA repair process [12,30]. We also observed these responses on day 0 when HEK cells were irradiated, and the production of TCA cycle intermediates was normalized two days after irradiation with low doses of IR. Interestingly, several kinds of TCA cycle intermediates, especially fumarate, were overproduced on day 2 after irradiation with 2 Gy. A previous study reported that fumarate accumulates in cells and localizes to the nucleus in response to irradiation, followed by utilization in DNA repair [31,32]. Local-

ized synthesis of fumarate can dramatically affect chromatin structure, resulting in epigenetic changes and consequently regulation of cellular processes such as gene DNA repair [33]. These results demonstrate the possibility that fumarate could be used as a metabolic marker for irradiation exposure in the human epidermis. Although irradiation enhanced TCA cycle metabolism, ATP levels remained reduced for two days. ATP is involved in DNA replication processes during DNA repair; therefore, HEK cells still do not recover from DNA damage [34]. ATP depletion in the epidermis is positively correlated with various pathologies, such as skin cancer [35]. Consequently, these results suggest that improving ATP levels would be needed after irradiation exposure at high doses.

3. Increase in the Activation of the DNA Repair System Following IR Exposure

IR induces cellular senescence with DNA damage; therefore, we observed expression changes in proteins of irradiated HEK cells related to the DNA repair process [7]. Our proteomic analysis showed that serine-protein kinase ATM (ATM) and DNA-dependent protein kinase catalytic subunit (PRKDC) were upregulated by 1.35- and 1.5-fold in response to irradiation with 2 Gy, respectively (Table 2). In addition, an IR dose of 2 Gy also increased the expression levels of X-ray repair cross-complementing protein 5 (XRCC5) and X-ray repair cross-complementing protein 6 (XRCC6). IR exposure causes the DNA damage response (DDR), and the activation of ATM is triggered as a primary mediator [36]. After activation of ATM, XRCC6 and XRCC5 form a DNA-dependent protein kinase

Table 2. The changes of the expression level in proteins associated with the DNA repair system. * $p<0.05$, ** $p<0.005$, *** $p<0.0005$ according to one-way ANOVA followed by Tukey's HSD test

Uniprot accession	Protein names	Gene names	Day 0			Day 2		
			0.1 Gy	0.5 Gy	2 Gy	0.1 Gy	0.5 Gy	2 Gy
			Fold change	Fold change	Fold change	Fold change	Fold change	Fold change
P12956	X-ray repair cross-complementing protein 6	<i>Xrcc6</i>	1.03	1.03	1.27***	0.97	0.93	1.04
P78527	DNA-dependent protein kinase catalytic subunit	<i>Prkdc</i>	1.02	1.15	1.50***	1.10*	1.07	1.18**
P13010	X-ray repair cross-complementing protein 5	<i>Xrcc5</i>	0.99	1.06	1.20***	1.12*	1.08	1.22**
Q13315	Serine-protein kinase ATM	<i>Atm</i>	0.95	0.98	1.35*	1.07	1.03	1.42

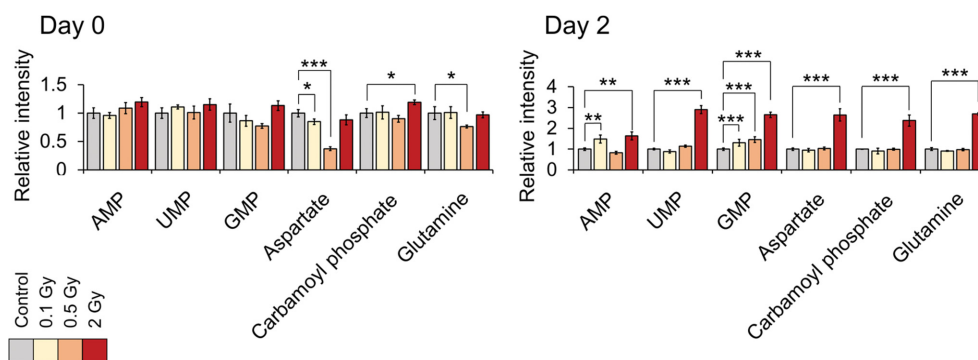


Fig. 5. Metabolites associated with nucleotide biosynthesis were changed the production following IR irradiation at indicated time points. Metabolomic analysis was performed with $n=5$. Data are presented as means $\pm$ S.D. * $p<0.05$, *** $p<0.0005$ according to one-way ANOVA followed by Tukey's HSD test.

(DNA-PK) complex, which contributes to IR-induced DNA repair. Consequently, the DNA-PK complex improves the expression of FH, followed by an overproduction of fumarate for DNA repair [31]. Additionally, we observed that low doses of IR did not change the expression of the DNA repair process, and it is supposed that low doses could not cause severe DNA damage to human keratinocytes [6]. Taken together, high doses of IR induced the process of DNA repair to overcome DDR, in contrast to low doses. Furthermore, we found that fumarate is a sensitive metabolic marker induced by a high dose of IR.

We also investigated the changes in nucleotide metabolism that are associated with DNA repair after irradiation. On day 0, irradiation at all doses rarely changed the production of AMP, UMP, and GMP in HEK cells (Fig. 5). However, irradiation with 2 Gy overproduced AMP, UMP, and GMP on day 2 by 2.91-, 1.64-, and 2.65-fold, respectively. In addition, glutamine, aspartate, and carbamoyl phosphate, which are precursors to produce nucleotides, were also significantly increased after irradiation with 2 Gy on day 2. One of the primary mechanisms for regulating DNA repair or DNA damage is the regulation of the pool of nucleotides used for DNA replication and repair [37]. Glutamine synthetic activity facilitates nucleotide metabolism and subsequent DNA damage repair [38]. We found that nucleotide metabolites with their precursors were overproduced two days after high-dose irradiation. Therefore, we suggest that the dose of 2 Gy of IR promotes radiation resistance

in human keratinocytes by facilitating nucleotide metabolism, and it is unlikely to occur immediately after irradiation.

4. Development of Keratinocyte Differentiation and Thickness of the Cornified Layer

GO-based statistical enrichment analysis of the proteome results revealed changes in epidermal cornification on day 2 after irradiation at all doses (Fig. 2). Epidermal cornification is an event leading to the formation of keratin filaments, and the generation of keratin is only one of many molecular events associated with epidermal terminal differentiation [39]. Many studies have shown that irradiation of skin tissues facilitates the overexpression of epidermal cornification with pathological development [24,40,41]. Therefore, we also focused on the changes in proteins involved in epidermal cornification depending on the doses and time after irradiation. On day 2, desmoglein-1 (DSG1) was upregulated by 1.18-, 1.41-, and 1.82-fold after irradiation with 0.1, 0.5, and 2 Gy, respectively (Table 3). In addition, cathepsin D (CTSD), protein S100-A10 (S100A10), plakoglobin (JUP), and desmoplakin (DSP), which play vital roles in epidermal cornification, were also increased after irradiation at all doses on day 2. Interestingly, transglutaminase 1 (TGM1), which formed the cornified layer, was significantly upregulated following irradiation with low doses compared to 2 Gy. DSG1, CTSD, S100A10, JUP, and DSP, which are constituents of the cornified layer, were induced after irradiation with X-ray and linked with an increase in thickness in the cornified layer as well as epidermal

Table 3. The changes of the expression level in proteins associated with cornification on day 2. * $p<0.05$, ** $p<0.005$, *** $p<0.0005$ according to one-way ANOVA followed by Tukey's HSD test

Uniprot accession	Protein names	Gene names	0.1 Gy	0.5 Gy	2 Gy
			Fold change	Fold change	Fold change
P14923	Junction plakoglobin	<i>Jup</i>	1.39*	1.58**	1.62**
P15924	Desmoplakin	<i>Dsp</i>	1.35**	1.53***	1.44***
P22735	Protein-glutamine gamma-glutamyltransferase K	<i>Tgm1</i>	1.58*	1.69**	1.32
Q02413	Desmoglein-1	<i>Dsg1</i>	1.18	1.41	1.82*
P07339	Cathepsin D	<i>Ctsd</i>	1.08	1.13	1.43**
P60903	Protein S100-A10	<i>S100a10</i>	1.09	1.11	1.50
P04632	Calpain small subunit 1	<i>Capns1</i>	0.98	1.01	0.86*
P07384	Calpain-1 catalytic subunit	<i>Capn1</i>	1.13	1.11	0.89

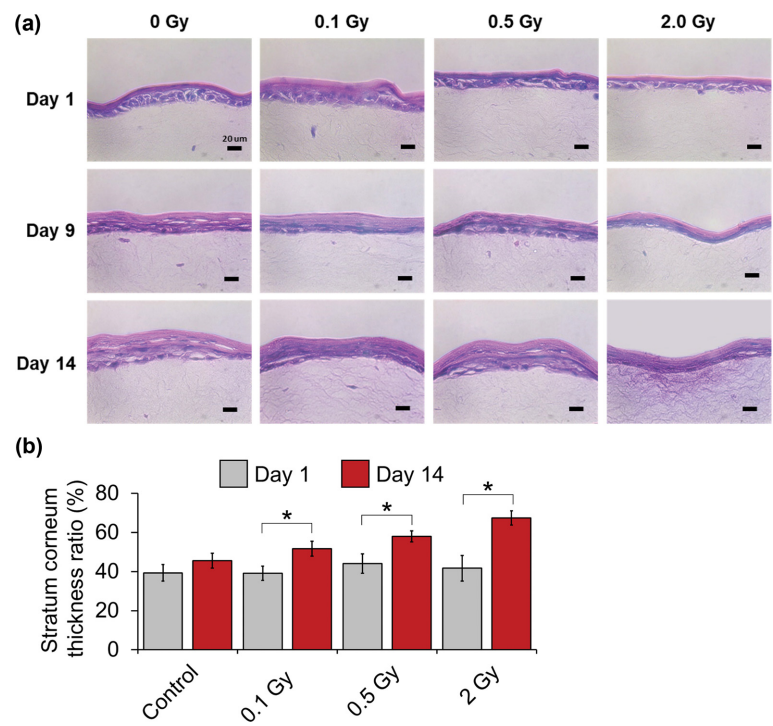


Fig. 6. The changes of the outermost layer thickness in 3D skin full thickness model induced by IR irradiation. (a) The histological images of reconstructed skins irradiated radioactive rays at 0, 0.1, 0.5, 2 Gy. The epidermal thickness and cornified layer thickness were measured in HE-stained sections. (b) The ratio of the cornified layer thickness and the epidermal thickness with different radiation dosage at day 1 and 14. The error bars represent the standard deviation of triplicate samples. ** $p < 0.005$ according to one-way ANOVA followed by Tukey's HSD test.

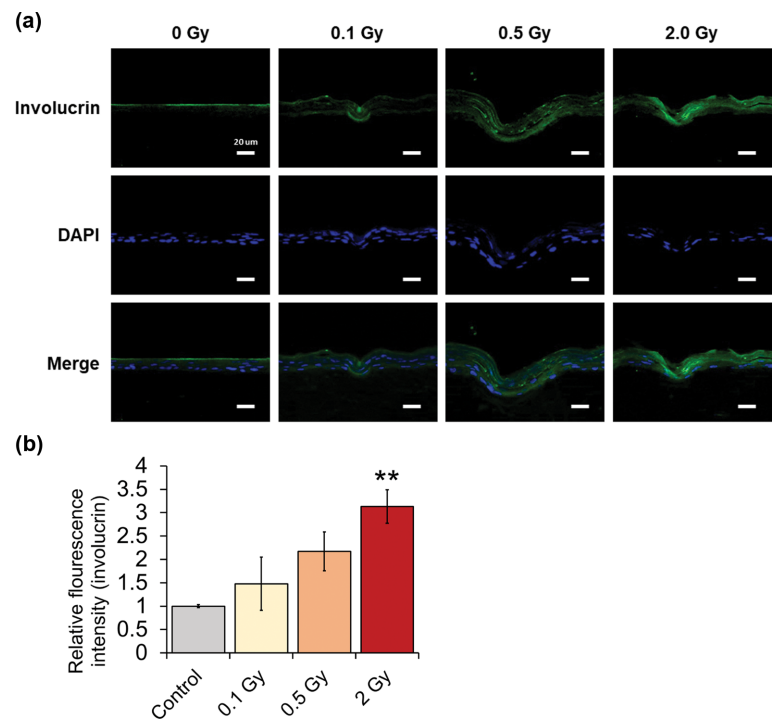


Fig. 7. The increase in the expression level of a constituent in the cornified layer following IR treatment at day 14. (a) The immunofluorescence staining images of 3D skin full thickness model stained with antibody to keratinocyte differentiation marker, involucrin (green) and counterstained with DAPI (blue). (b) The effect of low- and high-dose on differentiation of keratinocytes in 3D skin full thickness models. The irradiated group was compared to control. The error bars represent the standard deviation of triplicate samples. * $p < 0.05$ according to Student's t-test.

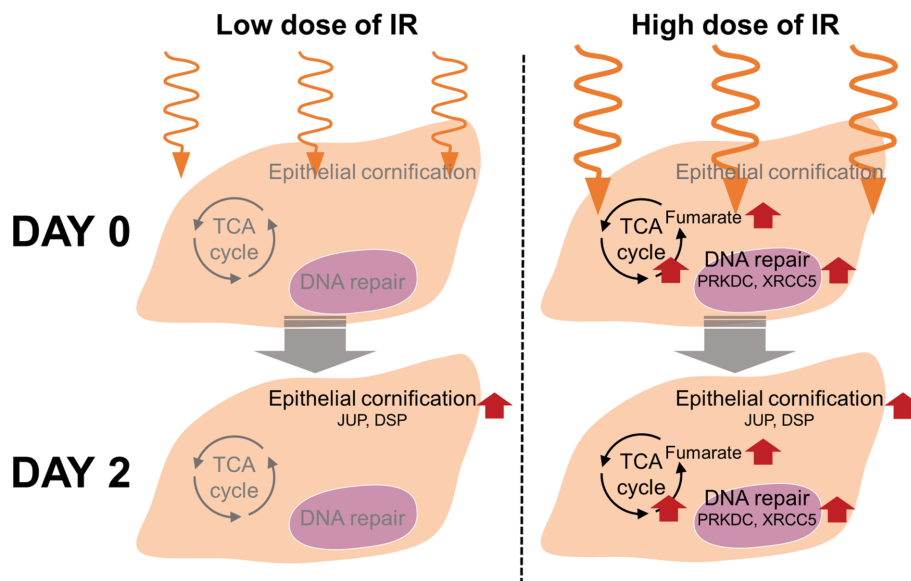


Fig. 8. Schematic diagram showing the molecular changes in human keratinocytes after low or high doses of IR exposure.

inflammation [39,42,43]. Interestingly, epidermal cornification was activated on day 2 compared to immediately after IR exposure. These results indicate that an optimal response at the initial time is important for blocking the development of epidermal cornification, which will lead to the development of various skin diseases.

To examine phenotypic changes in the epidermis of human skin involved in epidermal cornification after irradiation, we performed a morphological analysis of the epidermis of a 3D full-thickness skin model (FT-skin) following IR doses (control, 0.1, 0.5, and 2 Gy) and time (days 1, 9, and 14) (Fig. 6(a)). The FT skin model is ideally used to study the interactions between the epidermis and dermis during exogenous treatment [44]. Using this skin model, we found that the higher the IR dose was exposed to FT-skin, the higher the thickness ratio of the stratum corneum on day 14 (Fig. 6(b)). UV irradiation led to the accumulation of epidermal keratinocytes and increased epidermal thickness [45]. However, studies have been limited to changes in the thickness of the epidermis after irradiation with IR. We observed that irradiation with low doses of IR showed a similar tendency to increase the thickness of the epidermis and protein expression related to epidermal cornification as well as 2 Gy of IR.

In addition, we observed changes in the expression of involucrin, which is a protein in the terminal differentiation pathway [46]. IR exposure caused the breakdown of the stratum corneum structure and increased the expression of involucrin (Fig. 7(a)). In particular, irradiation with 2 Gy overexpressed involucrin by 3.1-fold compared to the control at day 14 (Fig. 7(b)). Over differentiation in the stratum corneum related to epidermal cornification activation can result in pathologies such as keratosis follicularis and psoriasis [47]. Irradiation with ionizing radiation was linked to these pathologies, such as skin psoriasis [48]. Therefore, there is likely a connection between the over-differentiation of the epidermis and the overexpression of DSG1 and CTSD related to the differentiation of keratinocytes after IR irradiation [49,50]. These results suggest that it would be necessary to study those proteins that were

overexpressed related to cornification in this study and treat them in an initial phase after IR exposure to hamper the development of skin pathologies related to epidermal cornification. Taken together, this study proposes molecular changes in human keratinocytes after the exposure with ionizing radiation according to dose and time-dependent manners (Fig. 8).

CONCLUSIONS

Modern society uses a variety of doses of IR for cancer therapy, medical diagnostics, and industry. However, the biological effects generated by IR exposure on normal skin tissue have generally been ignored. This study explored the dose- and time-dependent changes in human keratinocytes after IR exposure by LC-MS/MS-based multiomics technologies. Our results revealed that IR exposure provided noticeable changes in energy metabolism, DNA repair, and epidermal cornification. In particular, we showed that a high dose of IR activated TCA cycle metabolism to restore low levels of ATP, and fumarate was overproduced in the process. In addition, metabolites involved in the DNA repair process were overproduced after irradiation. Proteins related to the epidermal cornification process were overexpressed after two days rather than immediately after IR exposure, and then we also verified the phenotypes using the 3D human skin tissue model. These results provide comprehensive insight to understand interactions and predict the effects on the human epidermis following IR exposure.

ACKNOWLEDGEMENTS

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SUPPORTING INFORMATION

Additional information as noted in the text. This information is available via the Internet at <http://www.springer.com/chemistry/journal/11814>.

REFERENCES

1. C. E. Redon, J. S. Dickey, W. M. Bonner and O. A. Sedelnikova, *Adv. Space Res.*, **43**, 1171 (2009).
2. U. Veronesi, M. D. Vecchio, M. Greco, V. Galimberti, M. Merson, F. Rilke, V. Sacchini, R. Saccozzi, T. Savio, R. Zucali, S. Zurrida and B. Salvadori, *N. Engl. J. Med.*, **328**, 1587 (1993).
3. M. B. M. M. Rehani, *Br. Med. J.*, **320**, 593 (2000).
4. W. Kim, S. Lee, D. Seo, D. Kim, K. Kim, E. Kim, J. Kang, K. M. Seong, H. Youn and B. Youn, *Cells*, **8**, 1105 (2019).
5. H. P. Rodemann and M. A. Blaese, *Semin. Radiat. Oncol.*, **17**, 81 (2007).
6. K. Lumniczky, N. Impens, G. Armengol, S. Candeias, A. G. Georgakilas, S. Hornhardt, O. A. Martin, F. Rodel and D. Schaeue, *Environ. Int.*, **149**, 106212 (2021).
7. T. Miyake, M. Shimada, Y. Matsumoto and A. Okino, *Int. J. Radiat. Oncol. Biol. Phys.*, **105**, 193 (2019).
8. F. A. Mendelsohn, C. M. Divino, E. D. Reis and M. D. Kerstein, *Adv. Skin Wound Care*, **15**, 216 (2002).
9. T. Revenco, G. Lapouge, V. Moers, S. Brohee and P. A. Sotiropoulou, *Stem Cells*, **35**, 1355 (2017).
10. K. R. Brown and E. Rzucidlo, *J. Vasc. Surg.*, **53**, 15S (2011).
11. A. B. Wolbarst, A. L. Wiley, J. B. Nemhauser, D. M. Christensen and W. R. Hendee, *Radiology*, **254**, 660 (2010).
12. Z. P. Hu, Y. M. Kim, M. B. Sowa, R. J. Robinson, X. Gao, T. O. Metz, W. F. Morgan and Q. Zhang, *Mol. Biosyst.*, **8**, 1979 (2012).
13. K. Sekihara, K. Saitoh, H. Yang, H. Kawashima, S. Kazuno, M. Kikawa, H. Arai, T. Miida, N. Hayashi, F. Niyonsaba, K. Sasai and Y. Tabe, *PLoS One*, **13**, e0199117 (2018).
14. J. Lamartine, N. Franco, P. Le Minter, P. Soularue, O. Alibert, J. J. Leplat, X. Gidrol, G. Waksman and M. T. Martin, *J. Cell. Biochem.*, **95**, 620 (2005).
15. C. Coman, F. A. Solari, A. Hentschel, A. Sickmann, R. P. Zahedi and R. Ahrends, *Mol. Cell. Proteom.*, **15**, 1453 (2016).
16. W.-S. Song, S. G. Shin, S.-H. Jo, J.-S. Lee, H.-J. Jeon, J.-E. Kwon, J.-H. Park, S. Cho, J. H. Jeong, B.-G. Kim and Y.-G. Kim, *Biotechnol. Bioeng.*, **118**, 1612 (2021).
17. S. Tyanova, T. Temu, P. Sinitcyn, A. Carlson, M. Y. Hein, T. Geiger, M. Mann and J. Cox, *Nat. Methods*, **13**, 731 (2016).
18. J.-S. Lee, W.-S. Song, J. W. Lim, T.-R. Choi, S.-H. Jo, H.-J. Jeon, J.-E. Kwon, J.-H. Park, Y.-R. Kim, Y.-H. Yang, J. H. Jeong and Y.-G. Kim, *Biotechnol. J.*, **17**, e2100397 (2022).
19. H. Mi, A. Muruganujan, X. Huang, D. Ebert, C. Mills, X. Guo and P. D. Thomas, *Nat. Protoc.*, **14**, 703 (2019).
20. P. Gangatirkar, S. Paquet-Fifield, A. Li, R. Rossi and P. Kaur, *Nat. Protoc.*, **2**, 178 (2007).
21. H.-J. Kim, D. J. Min, S. H. Lee, J. W. Lim, N. Jung, H. W. Ryu, J. H. Jeong, *Mater. Lett.*, **253**, 298 (2019).
22. E. Shin, S. Lee, H. Kang, J. Kim, K. Kim, H. Youn, Y. W. Jin, S. Seo and B. Youn, *Front. Genet.*, **11**, 566244 (2020).
23. O. Chatzidoukaki, E. Goulielmaki, B. Schumacher and G. A. Garinis, *Trends Genet.*, **36**, 777 (2020).
24. W. Wang, J. Luo, W. Sheng, J. Xue, M. Li, J. Ji, P. Liu, X. Zhang, J. Cao and S. Zhang, *Int. J. Radiat. Oncol. Biol. Phys.*, **95**, 751 (2016).
25. H. B. Forrester, D. M. de Kretser, T. Leong, J. Hagekyriakou and C. N. Sprung, *PLoS One*, **12**, e0173788 (2017).
26. D. Bungard, B. J. Fuerth, P. Zeng, B. Faubert, N. L. Maas, B. Viollet, D. Carling, C. B. Thompson, R. G. Jones and S. L. Berger, *Science*, **329**, 1201 (2010).
27. N. Dhami, D. K. Trivedi, R. Goodacre, D. Mainwaring and D. P. Humphreys, *Metabolomics*, **14**, 136 (2018).
28. Y. Yang, A. N. Lane, C. J. Ricketts, C. Sourbier, M. H. Wei, B. Shuch, L. Pike, M. Wu, T. A. Rouault, L. G. Boros, T. W. Fan and W. M. Linehan, *PLoS One*, **8**, e72179 (2013).
29. I. Martinez-Reyes and N. S. Chandel, *Nat. Commun.*, **11**, 102 (2020).
30. T. W. Miller, D. R. Soto-Pantoja, A. L. Schwartz, J. M. Sipes, W. G. DeGraff, L. A. Ridnour, D. A. Wink and D. D. Roberts, *J. Biol. Chem.*, **290**, 24858 (2015).
31. M. Leshets, Y. B. H. Silas, N. Lehming and O. Pines, *Front. Mol. Biosci.*, **5**, 68 (2018).
32. O. Yogev, O. Yogev, E. Singer, E. Shaulian, M. Goldberg, T. D. Fox and O. Pines, *PLoS Biol.*, **8**, e1000328 (2010).
33. S. P. Lees-Miller, *Nat. Cell Biol.*, **17**, 1096 (2015).
34. H. Maruta, N. Okita, R. Takasawa, F. Uchiumi, T. Hatano and S. Tanuma, *Biol. Pharm. Bull.*, **30**, 447 (2007).
35. A. Sreedhar, L. Aguilera-Aguirre and K. K. Singh, *Cell Death Dis.*, **11**, 444 (2020).
36. W. L. Santivasi and F. Xia, *Antioxid. Redox Signal.*, **21**, 251 (2014).
37. M.-O. Turgeon, N. J. S. Perry and G. Poulogiannis, *Front. Oncol.*, **8**, 15 (2018).
38. H. C. Yoo, Y. C. Yu, Y. Sung and J. M. Han, *Exp. Mol. Med.*, **52**, 1496 (2020).
39. P. Simonello, J. Wiedemann, J. Zink, E. Thoenes, M. Stange, P. G. Layer, M. Kovacs, M. Podda, M. Durante and C. Fournier, *Front. Oncol.*, **5**, 294 (2015).
40. H. Jang, H. Myung, J. Lee, J. K. Myung, W. S. Jang, S. J. Lee, C. H. Bae, H. Kim, S. Park and S. Shim, *Int. J. Mol. Sci.*, **19**, 892 (2018).
41. K. Kinoshita, H. Ishimine, K. Shiraishi, H. Kato, K. Doi, S. Kuno, K. Kanayama, K. Mineda, T. Mashiko, J. Feng, K. Nakagawa, A. Kuriaki, S. Itami and K. Yoshimura, *Cells Tissues Organs*, **200**, 240 (2014).
42. N. A. Robinson, S. Lapic, J. F. Welter and R. L. Eckert, *J. Biol. Chem.*, **272**, 12035 (1997).
43. E. Candi, R. Schmidt and G. Melino, *Nat. Rev. Mol. Cell. Biol.*, **6**, 328 (2005).
44. K. Ackermann, S. L. Borgia, H. C. Korting, K. R. Mewes and M. Schäfer-Korting, *Skin Pharmacol. Physiol.*, **23**, 105 (2010).
45. J. D'Orazio, S. Jarrett, A. Amaro-Ortiz and T. Scott, *Int. J. Mol. Sci.*, **14**, 12222 (2013).
46. F. M. Watt, *J. Invest. Dermatol.*, **81**, 100s (1983).
47. P. M. Elias, M. L. Williams, M. E. Maloney, J. A. Bonifas, B. E. Brown, S. Grayson and E. H. Epstein, Jr., *J. Clin. Invest.*, **74**, 1414 (1984).
48. F. N. Bray, B. J. Simmons, A. H. Wolfson and K. Nouri, *Dermatol. Ther.*, **6**, 185 (2016).
49. C. M. Hammers and J. R. Stanley, *J. Clin. Invest.*, **123**, 1419 (2013).
50. A. C. Thomas, D. Tattersall, E. E. Norgett, E. A. O'Toole and D. P. Kelsell, *Ame. J. Pathol.*, **174**, 970 (2009).

Supporting Information

Multimomics characterization of dose- and time-dependent effects of ionizing radiation on human skin keratinocytes

Won-Suk Song^{*,‡}, Jae-Seung Lee^{*,‡}, Jun Woo Lim^{*,‡}, JiEung Kim^{**}, Sung-Hyun Jo^{*}, Ji-Eun Kwon^{*}, Ji-Hyeon Park^{*}, Sang Hyoun Choi^{***}, Dongchan Jang^{**}, Il Won Kim^{*}, Jae Hyun Jeong^{*}, and Yun-Gon Kim^{*,†}

^{*}Department of Chemical Engineering, Soongsil University, Seoul 06978, Korea

^{**}Department of Nuclear and Quantum Engineering, Korea Advanced Institute of Science and Technology, Daejeon 34141, Korea

^{***}Research Team of Radiological Physics and Engineering, Korea Institute of Radiological and Medical Sciences, Seoul 01812, Korea

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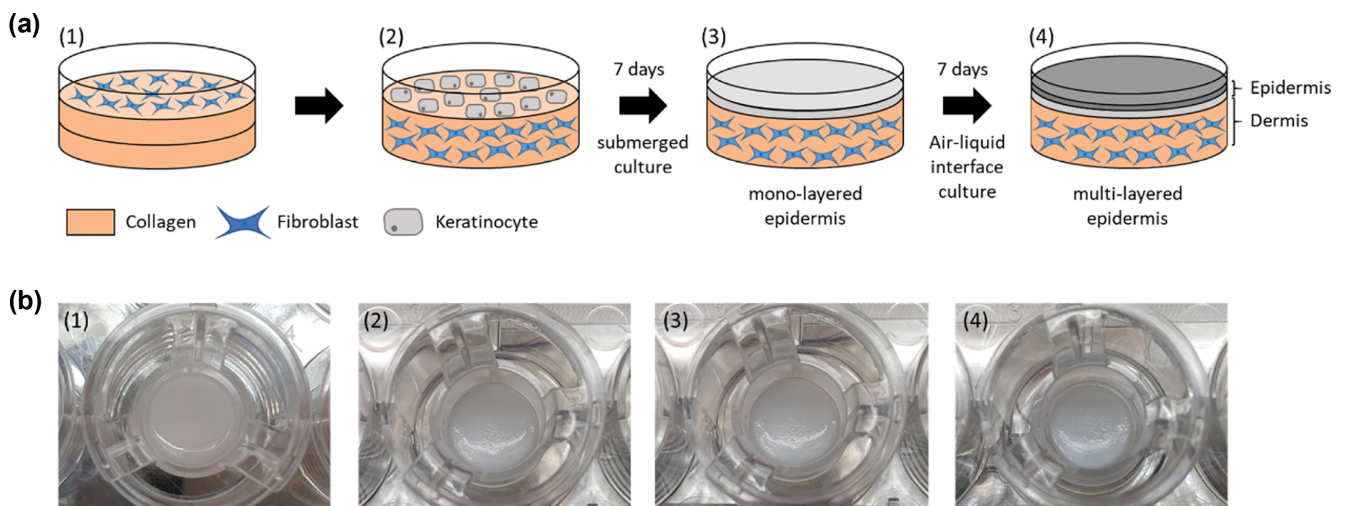


Fig. S1. 3D skin full-thickness model was developed to assess the morphological effects of skin epidermis regulated by IR. The schematic (a) and bright-field images (b) of the 3D skin full-thickness preparation procedure.

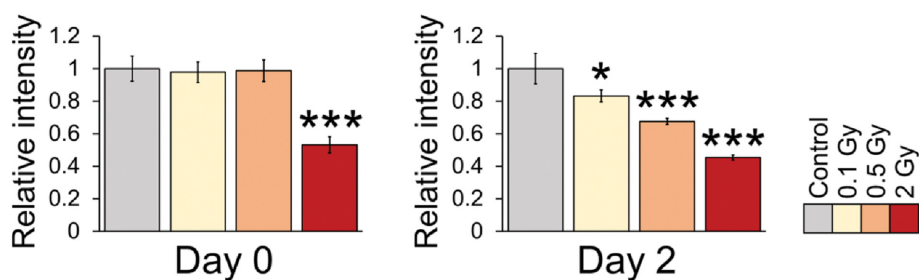


Fig. S2. Significantly time-dependent decrease in the expression level of ATP. Metabolomic analysis was performed with $n=5$. Data are presented as means $\pm$ S.D. * $p < 0.05$, *** $p < 0.0005$ according to one-way ANOVA followed by Tukey's HSD test.

Table S1. Proteomic changes on day 0 after irradiation

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Mitochondrial ribonuclease P protein 1	TRMT10C	C9JVB6	0.58	5.23	8.47
Tropomyosin alpha-4 chain	TPM4	P67936-2	7.04	7.80	5.09
Cystatin-C	CST3	A0A0K0K1J1	0.95	1.42	4.68
DCN1-like protein	DCUN1D1	B4DM76	3.03	3.63	4.22
Carboxypeptidase D	CPD	B7Z843	1.49	1.12	3.71
Pleiotropic regulator 1	PLRG1	H0YA24	1.13	2.51	3.53
39S ribosomal protein L19, mitochondrial	MRPL19	A8K5D5	1.13	0.56	3.53
Protein-glutamine gamma-glutamyltransferase K	TGM1	B4DRV1	0.34	2.21	3.50
Protein DEK	DEK	A0A494C198	2.74	2.73	3.41
High mobility group protein HMG-I/HMG-Y	HMGA1	P17096	1.23	1.41	3.41
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	A0A024R5X7	1.18	0.24	3.28
Cellular retinoic acid-binding protein 2	CRABP2	P29373	0.85	4.40	3.24
28S ribosomal protein S29, mitochondrial	DAP3	P51398-2	1.33	1.75	3.24
KN motif and ankyrin repeat domain-containing protein 1	KANK1	Q6PIB3	1.50	3.53	3.23
Gap junction protein	GJB2	A8DU55	1.03	3.19	3.21
Mitochondrial import receptor subunit TOM6 homolog	TOMM6	Q96B49	1.02	1.41	3.17
F-box/LRR-repeat protein 18	FBXL18	B3KTC9	4.05	5.79	3.03
CCAAT/enhancer-binding protein zeta	CEBPZ	B2R5U7	0.97	5.55	3.00
Membrane-associated progesterone receptor component 2	PGRMC2	O15173	1.60	2.41	2.99
Ragulator complex protein LAMTOR2	LAMTOR2	Q9Y2Q5	0.65	0.76	2.98
Glucosylceramidase	GBA	A0A0G2JNZ5	2.35	31.62	2.93
Cadherin-1	CDH1	D3XNU5	0.59	1.78	2.88
Desmoglein-3	DSG3	A0A024RC30	1.63	2.14	2.83
THO complex subunit 2	THOC2	Q8NI27	1.19	2.29	2.59
Prenylcysteine oxidase 1	PCYOX1	Q53ST0	0.75	1.67	2.56
AT-rich interactive domain-containing protein 1A	ARID1A	Q96T01	2.36	2.71	2.51
ATP synthase-coupling factor 6, mitochondrial	ATP5J	Q6IB54	1.04	1.53	2.46
Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	A6NHR9-2	1.34	1.44	2.45
Radical S-adenosyl methionine domain-containing protein 2	RSAD2	B2R6Q5	2.70	1.49	2.44
Mitochondrial import inner membrane translocase subunit Tim9	TIMM9	A0A024R648	1.14	1.21	2.42
Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	SDHC	D3DVH1	1.59	1.39	2.40
Galectin-7	LGALS7	P47929	0.61	2.73	2.37
Polypeptide N-acetylgalactosaminyltransferase	GALNT2	G3V1S6	0.83	1.47	2.36
Envoplakin	EVPL	A0A024R8L8	1.68	2.36	2.35
Cytochrome c oxidase assembly factor 4 homolog, mitochondrial	CHCHD8	A0A024R5J6	2.13	1.92	2.32

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Fanconi anemia group M protein	FANCM	Q8IYD8-2	1.03	2.29	2.28
Transcriptional enhancer factor TEF-1	TEAD1	P28347-2	2.35	2.08	2.27
Histone deacetylase	HDAC1	Q6IT96	1.45	1.56	2.26
WD repeat-containing protein 18	WDR18	U3KQC1	1.18	1.62	2.24
Carboxymethylenebutenolidase homolog	CMBL	B2RD36	1.82	2.94	2.20
Prosaposin	PSAP	B4DEK5	0.96	1.96	2.17
Double-stranded RNA-specific adenosine deaminase	ADAR	A0A024DAK3	1.21	1.43	2.14
Mitochondrial chaperone BCS1	BCS1L	H7C492	1.18	2.19	2.13
RNA-binding protein 28	RBM28	A0A0S2Z5E5	1.25	1.19	2.13
Catalase	CAT	A0A384P5Q0	1.02	1.28	2.10
Serine/threonine-protein kinase MARK2	MARK2	Q7KZI7-12	1.44	1.01	2.08
Transformer-2 protein homolog alpha	HSU53209	Q549U1	0.99	1.19	2.08
Protein Mpv17	MPV17	A0A0S2Z469	1.09	1.38	2.07
Cirhin	CIRH1A	H3BSH7	1.10	0.80	2.06
Ancient ubiquitous protein 1	DKFZp686P12272	Q68CX8	0.83	1.56	2.05
Anion exchange protein	SLC4A7	C9JRP1	0.70	1.25	2.04
DNA helicase	HCC5	Q8NHX6	1.70	1.57	2.02
Brain acid soluble protein 1	BASP1	P80723	1.14	1.37	2.01
Pescadillo homolog	PES1	B3KXD6	1.74	1.66	2.01
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	B3KN45	1.37	1.53	2.01
SWI/SNF complex subunit SMARCC2	SMARCC2	Q59G16	1.55	2.07	2.00
POU domain protein	POU5F1P4	E9LRT1	1.56	1.81	1.99
U4/U6.U5 tri-snRNP-associated protein 2	USP39	A0A087X1B2	1.06	1.73	1.98
Remodeling and spacing factor 1	RSF1	Q05DG0	1.15	1.04	1.98
Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	B3KVN0	1.00	1.54	1.98
Cartilage-associated protein	CRTAP	B3KS71	1.05	1.40	1.98
28 kDa heat- and acid-stable phosphoprotein	PDAP1	Q13442	1.62	2.12	1.97
Nucleolar pre-ribosomal-associated protein 1	URB1	O60287	0.84	1.32	1.96
Glycine cleavage system H protein, mitochondrial	GCSH	A0A1W2PQV2	1.26	1.08	1.94
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	A0A024R5K6	0.96	0.81	1.93
ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	Q16740	1.06	1.79	1.93
Lysine-rich nucleolar protein 1	KNOP1	H3BPL4	2.25	2.35	1.92
Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	E9PAM4	1.42	1.46	1.91
Metastasis-associated protein MTA2	MTA2	A0A024R534	2.30	2.22	1.90
Protein scribble homolog	SCRIB	A0A0G2JNZ2	1.18	1.62	1.90
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	P08754	1.33	1.28	1.89
39S ribosomal protein L45, mitochondrial	MRPL45	A0A0G2JMS5	0.92	0.81	1.89
DNA topoisomerase 2	TOP2B	E9PCY5	1.16	0.75	1.89

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Prelamin-A/C	LMNA	A0A384MQX1	1.35	1.88	1.88
Carnitine O-palmitoyltransferase 2, mitochondrial	CPT2	A0A1B0GTB8	0.90	1.22	1.88
Splicing factor 3B subunit 4	SF3B4	Q53FG6	1.01	1.30	1.87
Serum paraoxonase/arylesterase 2	PON2	B4DKM6	0.96	1.04	1.86
Early endosome antigen 1	EEA1	A8K7J3	1.90	1.52	1.84
Desmoglein-1	DSG1	Q02413	1.15	2.35	1.84
ATP-dependent RNA helicase DDX50	DDX50	B4DED6	1.17	1.22	1.83
Ribosome biogenesis protein NSA2 homolog	CDK105	Q5J7U2	1.35	0.19	1.83
Nesprin-1	SYNE1	E7ENN3	1.18	0.79	1.83
Condensin-2 complex subunit D3	NCAPD3	E9PKK4	2.81	1.00	1.83
Metaxin-2	MTX2	C9JAZ1	0.91	1.18	1.83
Cytochrome c oxidase assembly factor 6 homolog	COA6	B4DM08	1.31	1.52	1.82
Cytochrome b-c1 complex subunit 6, mitochondrial	UQCRH	Q567R0	1.27	1.16	1.82
39S ribosomal protein L38, mitochondrial	MRPL38	B2R894	1.11	1.01	1.82
Myosin light chain kinase, smooth muscle	MYLK	Q15746-9	1.24	1.94	1.82
Mitochondrial ribonuclease P protein 3	KIAA0391	O15091-4	0.94	1.21	1.82
Mitochondrial intermediate peptidase	MIPEP	Q99797	1.38	1.06	1.82
rRNA/tRNA 2-O-methyltransferase fibrillarin-like protein 1	FBLL1	A6NHQ2	1.10	1.36	1.81
5-3 exoribonuclease 2	XRN2	B4E0B9	1.21	1.11	1.80
Periplakin	PPL	K7EQ71	1.12	2.05	1.80
ER lumen protein-retaining receptor	KDELRL2	A0A024QZT7	0.95	1.49	1.80
Transmembrane emp24 domain-containing protein 2	TMED2	F5GX39	0.96	1.57	1.79
CDKN2AIP N-terminal-like protein	CDKN2AIPNL	Q96HQ2-2	0.59	1.00	1.79
Microsomal glutathione S-transferase 2	MGST2	Q99735-2	0.89	0.14	1.79
Plakophilin-1	PKP1	A0A024R952	0.90	1.88	1.78
Elongation factor Ts, mitochondrial	TSFM	B4DHY8	0.67	1.02	1.78
Junctional adhesion molecule A	F11R	Q9Y5B2	0.91	1.27	1.78
Protein FAM210A	FAM210A	K7EK00	0.96	1.37	1.77
Dipeptidyl peptidase 2	DPP7	R4GN05	1.08	1.15	1.76
Heterogeneous nuclear ribonucleoprotein A3	HNRPA3	B4DDB6	0.84	1.26	1.76
ADP-ribosylation factor-like protein 8B	ARL8B	B4DQT8	1.13	1.80	1.76
Syntaxin-4	STX4	C9JFM5	1.43	1.53	1.76
Cat eye syndrome critical region protein 5	CECR5	A8MYZ9	0.91	1.14	1.76
RNA polymerase-associated protein CTR9 homolog	CTR9	H0YCE8	1.22	0.93	1.76
Protein NipSnap homolog 3A	NIPSNAP3A	B4DW81	1.50	1.46	1.75
Chorionic somatomammotropin hormone 2	CSH1	A0A087WUG6	1.69	1.30	1.75
Cell division cycle 5-like protein	CDC5L	B4DSH1	0.99	2.03	1.75
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	R4GN43	0.93	0.91	1.74
Something about silencing protein 10	UTP3	Q9NQZ2	1.06	1.44	1.74

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Fermitin family homolog 2	FERMT2	A8K6S3	1.33	1.34	1.74
H/ACA ribonucleoprotein complex subunit 1	GAR1	Q9NY12-2	1.03	1.15	1.74
Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	Q6FHM4	1.32	1.33	1.74
FAST kinase domain-containing protein 5	FASTKD5	B4DWZ8	2.04	1.52	1.74
V-type proton ATPase 16 kDa proteolipid subunit	ATP6V0C	P27449	1.56	1.21	1.73
39S ribosomal protein L48, mitochondrial	MRPL48	F5H702	2.04	1.88	1.72
Retinoid-inducible serine carboxypeptidase	SCPEP1	I3L4Z3	0.77	0.99	1.72
Ras-related protein Rab-4A	RAB4A	A0A023HJ61	1.06	1.03	1.71
S1 RNA-binding domain-containing protein 1	SRBD1	B3KPM8	0.96	0.90	1.70
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	A0A087WVZ9	0.37	1.08	1.70
Mannose-P-dolichol utilization defect 1 protein	MPDU1	J3KSI4	0.91	1.20	1.70
Nucleoprotein TPR	TPR	P12270	1.26	1.34	1.70
Flotillin-1	FLOT1	A0A140T9W4	0.79	1.51	1.69
Up-regulated during skeletal muscle growth protein 5	USMG5	Q96IX5	0.87	0.93	1.69
DNA repair protein complementing XP-C cells	XPC	D2CPJ9	1.09	1.11	1.68
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	Q9Y6G9	2.44	2.32	1.68
28S ribosomal protein S22, mitochondrial	MRPS22	Q59GX8	0.72	0.97	1.68
Nicalin	NCLN	K7EMW4	1.25	1.04	1.68
Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	B3KMV8	0.97	0.94	1.67
Volume-regulated anion channel subunit LRRC8D	LRRC8D	E9PJ89	0.74	0.68	1.67
Fibronectin type III domain-containing protein 3B	FNDC3B	Q53EP0	0.96	1.03	1.67
Actin-like protein 6A	BAF53A	Q6FI97	1.21	1.32	1.67
Saccharopine dehydrogenase-like oxidoreductase	SCCPDH	A0A384NPM7	0.98	1.12	1.67
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	B4E043	1.25	1.27	1.67
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	A0A0S2Z3L0	0.85	1.10	1.66
Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	B4DS43	0.86	1.10	1.66
Small subunit processome component 20 homolog	UTP20	O75691	1.20	1.07	1.65
Golgi SNAP receptor complex member 1	GOSR1	B4DQA8	1.34	1.27	1.65
Transmembrane protein 258	TMEM258	P61165	1.87	2.41	1.65
Ribosomal RNA small subunit methyltransferase NEP1	EMG1	Q92979	1.17	0.99	1.65
Serine/arginine-rich splicing factor 1	SRSF1	J3KTL2	1.14	1.27	1.65
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUFA11	K7EQ77	1.07	0.99	1.65
Paraspeckle component 1	PSPC1	A0A024RDP4	1.03	1.09	1.64
Protein IWS1 homolog	IWS1	B4DGM5	1.50	1.49	1.64
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	A0A024RAC7	0.98	1.20	1.63

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	M0R0C3	0.63	1.08	1.63
Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	Q9NQG5	1.04	1.10	1.63
Splicing factor 3A subunit 2	SF3A2	Q05DF2	1.10	1.08	1.62
Kinesin-like protein KIF15	KIF15	H7BZT2	0.79	0.94	1.62
Integrator complex subunit 1	DKFZP586J0619	A4D212	1.00	1.16	1.62
Transducin beta-like protein 3	TBL3	Q12788	1.30	1.23	1.62
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	Q6YN16	0.96	1.17	1.62
Probable RNA-binding protein 19	RBM19	A0A024RBL4	0.99	1.12	1.62
Syntaxin-12	STX12	B1AJQ6	1.35	1.63	1.62
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	A0A384MR44	0.85	1.08	1.62
GlutaminyI-peptide cyclotransferase-like protein	QPCTL	Q9NXS2	1.00	0.70	1.61
Periodic tryptophan protein 2 homolog	PWP2	A0A0B4J2E5	1.11	1.06	1.61
Nucleolar protein 56	NOP56	O00567	1.13	1.13	1.61
E3 ubiquitin-protein ligase UBR5	UBR5	E7EMW7	0.89	1.12	1.61
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	Q6IB91	0.82	1.02	1.61
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	O14979-3	1.08	1.12	1.60
28S ribosomal protein S12, mitochondrial	MRPS12	A0A024R0H2	1.04	1.00	1.60
Tyrosine--tRNA ligase, mitochondrial	YARS2	Q9Y2Z4	1.07	1.16	1.60
Exosome complex component RRP41	EXOSC4	E9PPI9	1.06	1.05	1.60
Lysosomal Pro-X carboxypeptidase	PRCP	E9PLY4	0.91	0.95	1.60
Regulator of chromosome condensation	RCC1	Q5T081	1.00	1.14	1.60
Pyrroline-5-carboxylate reductase	PYCR1	E2QRB3	0.92	0.91	1.60
rRNA 2-O-methyltransferase fibrillarin	FBL	Q96BS4	1.19	1.20	1.60
U2 small nuclear ribonucleoprotein A	SNRPA1	H0YKK0	1.14	1.11	1.59
28S ribosomal protein S17, mitochondrial	MRPS17	E9PE17	0.92	0.89	1.59
Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	P46087-2	1.11	1.15	1.59
Protein FAM162A	FAM162A	F8W7Q4	1.13	1.38	1.58
Myb-binding protein 1A	MYBBP1A	Q9BQG0	0.98	1.14	1.58
Syntaxin-binding protein 3	STXBP3	O00186	1.19	1.40	1.58
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	F8W6I7	1.16	1.19	1.58
Unconventional myosin-VI	MYO6	A0A590UK71	3.06	0.76	1.58
Splicing factor 3B subunit 5	SF3B5	Q9BWJ5	1.14	1.30	1.58
CD59 glycoprotein	CD59	A0A3Q8TLE1	0.92	1.33	1.58
Mitochondrial import inner membrane translocase subunit TIM44	hTIM44	Q9UPE4	1.71	1.24	1.58
WD repeat-containing protein 43	WDR43	Q15061	0.68	1.02	1.58
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	Q9P0J0	0.93	0.96	1.58

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Polymerase delta-interacting protein 3	POLDIP3	Q96DI9	0.84	1.07	1.57
Nucleolar protein 58	NOP58	Q9Y2X3	1.01	1.07	1.57
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	D6R9P3	1.06	1.13	1.57
Nuclear pore complex protein Nup160	NUP160	G3V198	0.91	1.20	1.57
E3 ubiquitin-protein ligase TRIP12	TRIP12	Q14669-4	0.97	1.12	1.57
Aspartate--tRNA ligase, mitochondrial	DARS2	A0A3B3ITS3	0.80	1.01	1.57
GPI transamidase component PIG-S	PIGS	Q8NBL9	0.91	1.41	1.57
Reticulon	RTN3	A0A024R5C4	1.03	1.03	1.56
Acyl-CoA synthetase family member 3, mitochondrial	ACSF3	F5H5A1	1.04	1.38	1.56
Ribonuclease P protein subunit p30	RPP30	B4DJR3	1.28	1.27	1.56
U3 small nucleolar RNA-associated protein 18 homolog	UTP18	B2RAX6	1.03	0.95	1.56
Testis-expressed sequence 10 protein	TEX10	B4DQR0	1.03	1.05	1.56
39S ribosomal protein L21, mitochondrial	MRPL21	A0A024R5G7	0.99	1.10	1.56
Protein mago nashi homolog	FLJ10292	A0A023T6R1	1.45	1.40	1.56
Ras-related protein Rab-11B	RAB11B	Q15907	1.10	1.08	1.56
Coiled-coil domain-containing protein 58	CCDC58	Q4VC31	0.99	0.83	1.56
Ribosome biogenesis protein WDR12	WDR12	Q53T99	0.87	1.10	1.56
Heterochromatin protein 1-binding protein 3	HP1BP3	B0QZK4	0.98	1.04	1.56
Structural maintenance of chromosomes protein	SMC1A	Q7Z4C6	1.18	1.41	1.56
Alanine--tRNA ligase, mitochondrial	AARS2	Q5J TZ9	0.91	1.02	1.56
39S ribosomal protein L11, mitochondrial	MRPL11	Q53G19	1.46	1.74	1.55
Syntaxin-5	STX5A	B4DKR0	1.31	1.96	1.55
H/ACA ribonucleoprotein complex subunit 4	DKC1	H7C0M1	1.76	1.52	1.55
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	B4DSM4	1.10	1.09	1.55
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	B4DM30	1.19	1.08	1.55
Splicing factor 3B subunit 1	SF3B1	O75533	1.01	1.07	1.55
Tumor-associated calcium signal transducer 2	TACSTD2	P09758	0.73	1.33	1.54
Enoyl-CoA delta isomerase 2, mitochondrial	ECI2	Q53HG3	1.04	1.14	1.54
Probable ATP-dependent RNA helicase DDX47	E4-DBP	B4DYP6	0.90	1.10	1.54
Adenylate kinase 4, mitochondrial	AK4	A0A384N647	0.92	0.96	1.54
3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	A0A024R2M6	1.06	1.10	1.54
Ribosomal L1 domain-containing protein 1	RSL1D1	Q32Q62	1.16	1.15	1.54
Cytochrome c1, heme protein, mitochondrial	CYC1	Q8TBT6	1.00	1.04	1.54
Nucleolar RNA helicase 2	DDX21	Q9NR30	1.22	1.14	1.54
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2-BSCL2	H3BQZ7	1.11	1.13	1.54
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	Q53GL5	0.81	0.98	1.54
L-xylulose reductase	DCXR	A0A384NY14	0.99	1.30	1.53
Alpha-mannosidase	MAN2B1	B4E0K9	0.94	1.14	1.53
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	D6RD67	0.81	0.94	1.53

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Interleukin enhancer-binding factor 3	ILF3	A0A024R7C7	1.18	1.20	1.53
Protein NipSnap homolog 2	GBAS	O75323-2	0.72	1.14	1.53
Kinectin	KTN1	A0A024R663	1.48	1.70	1.53
ATPase family AAA domain-containing protein 3B	ATAD3B	Q96T67	1.16	1.10	1.53
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8	P51970	0.87	0.98	1.53
WD repeat-containing protein 75	WDR75	A8K330	1.05	1.10	1.53
Nucleolar protein 6	NOL6	B3KPN5	1.04	1.01	1.53
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	A0A384NKJ3	0.84	1.29	1.53
Cornifin-A	SPRR1A	P35321	0.98	1.63	1.52
Dehydrogenase/reductase SDR family member 1	DHRS1	Q96LJ7	1.39	1.63	1.52
Enoyl-CoA hydratase, mitochondrial	ECHS1	A0A384MDW7	0.92	1.05	1.52
U1 small nuclear ribonucleoprotein 70 kDa	SNRP70	A8KAQ5	1.01	1.11	1.52
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	A0A384NL63	1.08	1.07	1.52
Required for meiotic nuclear division protein 1 homolog	RMND1	A0A087WXU0	1.06	0.91	1.52
60S ribosomal protein L7-like 1	RPL7L1	A0A024RD36	0.99	1.08	1.52
ATP-binding cassette sub-family D member 3	ABCD3	B4DZ22	0.85	0.98	1.52
Non-specific lipid-transfer protein	SCP2	B2R761	1.00	1.14	1.52
Serine/arginine-rich splicing factor 3	SFRS3	B2R6F3	1.11	1.09	1.52
Protein RRP5 homolog	PDCD11	A0A3B3IUD7	0.70	1.02	1.52
Protein S100-A14	S100A14	Q9HCY8	0.82	1.10	1.52
NADPH:adenodoxin oxidoreductase, mitochondrial	FDXR	A0A0A0MTN9	0.92	1.01	1.52
Protein transport protein Sec61 subunit gamma	SEC61G	A0A024QYZ0	0.99	0.97	1.51
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	A0A087WWT1	1.04	0.98	1.51
HEAT repeat-containing protein 1	HEATR1	A0A024R3R7	0.94	1.04	1.51
28S ribosomal protein S28, mitochondrial	MRPS28	H0YAT2	0.76	1.02	1.51
Probable ATP-dependent RNA helicase DDX5	DDX5	B4DN41	1.09	1.12	1.51
Splicing factor U2AF 65 kDa subunit	U2AF2	P26368-2	1.02	1.07	1.51
Glutathione S-transferase kappa 1	LOC51064	Q6FII1	0.99	1.15	1.51
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	H0YJW7	0.74	0.97	1.51
NADH-ubiquinone oxidoreductase chain 4	NADH4	A0A342Y607	0.93	0.84	1.51
Ribosome biogenesis protein BRX1 homolog	BRX1	Q8TDN6	1.20	1.20	1.51
Tripeptidyl-peptidase 1	TPP1	B4DSE2	0.97	1.17	1.51
Interferon-induced transmembrane protein 1	IFITM2	H7BYV1	0.96	1.17	1.50
ATP-dependent RNA helicase DDX39A	DDX39A	B4DX78	1.23	0.97	1.50
Interleukin enhancer-binding factor 2	ILF2	F4ZW62	1.03	1.07	1.50
Pre-mRNA-processing-splicing factor 8	PRPF8	Q6P2Q9	1.04	1.12	1.50
Serine/arginine-rich splicing factor 7	SRSF7	A0A0B4J1Z1	1.09	1.06	1.50

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Monocarboxylate transporter 1	SLC16A1	B4E106	1.17	1.31	1.50
DNA-dependent protein kinase catalytic subunit	PRKDC	P78527	1.02	1.15	1.50
Prelamin-A/C	LMNA	A0A384MQX1	1.03	1.24	1.50
Transmembrane protein 14C	TMEM14C	Q53F27	1.00	1.13	1.50
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	G3V576	1.04	1.11	1.50
39S ribosomal protein L17, mitochondrial	MRPL17	E9PKV2	0.98	0.92	1.50
Aladin	AAAS	H3BU82	0.82	0.82	1.50
Tricarboxylate transport protein, mitochondrial	SLC25A1	Q6LAP8	0.84	1.08	1.50
Nucleolar complex protein 4 homolog	NOC4L	Q9BVI4	1.24	0.95	1.50
Protein S100-A8	S100A8	P05109	0.72	1.62	1.50
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	E9KL44	0.86	1.00	1.49
Acylglycerol kinase, mitochondrial	AGK	A0A3B3ITX7	0.76	1.14	1.49
Ras-related protein Ral-A	RALA	P11233	1.09	1.05	1.49
NADH-cytochrome b5 reductase 1	CYB5R1	Q9UHQ9	0.87	1.05	1.49
Mitochondrial carrier homolog 2	MTCH2	Q9Y6C9	0.90	0.92	1.49
Peptidyl-prolyl cis-trans isomerase FKBP9	FKBP9	B7Z230	0.81	1.01	1.49
Junction plakoglobin	JUP	A0A0S2Z487	0.92	1.31	1.49
Splicing factor, proline- and glutamine-rich	SFPQ	Q9BSV4	1.07	1.10	1.49
Probable ATP-dependent RNA helicase DDX17	DDX17	A0A1X7SBZ2	1.19	1.21	1.49
Chromatin target of PRMT1 protein	CHTOP	A0A087X1B7	1.39	1.28	1.48
Ras-related protein Rab-6A	RAB6A	B7Z5Z9	0.93	1.09	1.48
Serine/arginine-rich splicing factor 9	SRSF9	S4R3G0	1.08	1.04	1.48
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	F8VXI1	1.01	0.90	1.48
RNA-binding protein FUS	FUS	Q59H57	1.14	1.22	1.48
H/ACA ribonucleoprotein complex subunit 2	NHP2	D6RC52	1.16	1.17	1.48
Mitochondrial import receptor subunit TOM22 homolog	MST065	Q549C5	0.84	0.91	1.48
Histone H3	HIST2H3PS2	Q5TEC6	0.76	0.90	1.48
Succinyl-CoA ligase subunit beta	SUCLG2	Q3ZCW5	0.84	1.01	1.48
Nuclear pore complex protein Nup155	NUP155	B4DLT2	1.08	1.18	1.48
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	A0A0S2Z2W5	0.76	0.96	1.48
Histone H2A	HIST1H2AB	Q08AJ9	0.94	1.06	1.48
Transmembrane 9 superfamily member 3	TM9SF3	Q5TB53	0.98	0.99	1.47
39S ribosomal protein L37, mitochondrial	MRPL37	S4R369	0.83	0.87	1.47
Pre-mRNA-splicing factor CWC22 homolog	CWC22	B7WP74	0.85	1.18	1.47
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	A0A1W2PPR9	0.75	0.91	1.47
Growth factor receptor-bound protein 2	GRB2	A0A384ME16	1.53	1.97	1.47
N-acetyltransferase 10	NAT10	Q9H0A0	1.00	1.10	1.47
ATP synthase subunit d, mitochondrial	ATP5H	O75947-2	0.87	0.95	1.47
Host cell factor 1	HCFC1	A6NEM2	1.19	1.10	1.47

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Cyclin-dependent kinase 11A	CDC2L2	Q96CA8	1.17	1.03	1.47
Paraplegin	SPG7	A0A2R8Y856	0.81	0.67	1.47
Phospholipase A-2-activating protein	PLAA	Q9Y263	0.39	0.63	1.47
General transcription factor II-I	GTF2I	X5D2J9	1.18	1.32	1.47
Protein dpy-30 homolog	DPY30	Q9C005	1.11	1.52	1.47
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	H0YA96	1.10	1.06	1.47
ORM1-like protein 2	ORMDL2	Q53FV1	0.98	1.08	1.46
Receptor protein-tyrosine kinase	EGFR	E7BSV0	1.10	1.18	1.46
Aminopeptidase N	ANPEP	A0A024RC61	1.15	1.28	1.46
Trifunctional enzyme subunit beta, mitochondrial	HADHB	P55084-2	0.88	0.99	1.46
Sulfurtransferase	TST	Q53EW8	0.98	1.11	1.46
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3A	B4DJB4	0.85	1.07	1.46
Nicastrin	NCSTN	H0Y3Z4	1.06	1.24	1.46
Serine/arginine-rich splicing factor 10	SRSF10	Q5JRI1	0.99	1.06	1.46
Non-specific protein-tyrosine kinase	YES1	B2RA70	0.96	1.25	1.46
Cysteine desulfurase, mitochondrial	NFS1	Q5QP19	1.21	1.11	1.46
39S ribosomal protein L24, mitochondrial	MRPL24	Q96A35	0.92	1.07	1.46
Beta-galactosidase	GLB1	Q53H18	1.16	1.17	1.46
Sideroflexin-1	SFXN1	Q9H9B4	0.89	0.93	1.46
Electron transfer flavoprotein subunit beta	ETFB	P38117	0.77	1.05	1.46
Integrin alpha-3	ITGA3	B4E0H8	0.95	0.94	1.46
ATP-dependent RNA helicase A	DHX9	Q08211	1.11	1.09	1.46
ATP-dependent RNA helicase DDX18	DDX18	Q4ZG72	1.06	1.13	1.46
Nuclear pore complex protein Nup107	NUP107	B3KMK0	0.91	1.10	1.45
Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	DHTKD1	H7C149	1.01	1.23	1.45
Prostaglandin E synthase 2	PTGES2	Q9H7Z7	0.88	0.87	1.45
Cell cycle and apoptosis regulator protein 2	CCAR2	B3KTJ9	1.07	1.02	1.45
2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	B4DI06	0.98	1.02	1.45
Nucleolar complex protein 2 homolog	NOC2L	Q9H9J5	1.04	0.94	1.45
Surfeit locus protein 4	SURF4	Q5T8U5	0.87	1.05	1.45
Large neutral amino acids transporter small subunit 1	SLC7A5	Q01650	1.02	1.11	1.45
Probable ATP-dependent RNA helicase DDX52	DDX52	B3KM65	0.98	1.10	1.45
Gamma-glutamyl hydrolase	GGH	A8K335	0.78	0.96	1.45
Inorganic pyrophosphatase 2, mitochondrial	PPA2	Q9H2U2	0.83	1.13	1.45
Dihydropyrimidinase-related protein 2	DPYSL2	Q53ET2	1.41	1.19	1.45
Probable ATP-dependent RNA helicase DDX46	DDX46	D3DQA6	1.10	1.02	1.44
G-rich sequence factor 1	GRSF1	B7Z2D8	1.01	0.92	1.44
ADP-ribosylation factor 5	ARF5	A4D0Z3	1.19	1.40	1.44

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	P36551	1.30	1.10	1.44
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	Q9BTT5	1.04	0.97	1.44
Alkylidihydroxyacetonephosphate synthase, peroxisomal	AGPS	O00116	0.95	1.03	1.44
Integrator complex subunit 3	INTS3	Q68E01-2	1.37	1.39	1.44
Transmembrane emp24 domain-containing protein 9	TMED9	B2R8A2	0.96	1.00	1.44
Catenin beta-1	CTNNB1	A0A2R8Y804	1.01	1.07	1.44
Ras-related protein Rab-35	RAB35	F5H157	1.02	1.24	1.44
Mimitin, mitochondrial	NDUFAF2	A0A0S2Z5U1	1.05	1.05	1.44
Guanine nucleotide-binding protein-like 3	GNL3	A0A024R2Z6	1.09	1.01	1.44
Vesicle-associated membrane protein-associated protein A	VAPA	A8KA83	1.03	1.20	1.44
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	Q59FN3	1.06	0.71	1.44
Pre-mRNA-processing factor 40 homolog A	PRPF40A	B4DPY2	0.77	1.14	1.44
Serine/threonine-protein phosphatase	PPP6C	A0A024R861	2.08	2.07	1.44
28S ribosomal protein S35, mitochondrial	MRPS35	P82673	1.00	1.02	1.44
Galectin-3-binding protein	LGALS3BP	B4DVE1	0.93	0.94	1.43
Ras-related protein R-Ras2	RRAS2	P62070	0.87	0.93	1.43
Ribosome biogenesis regulatory protein homolog	RRS1	Q15050	1.09	1.07	1.43
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	Q6IAL5	1.00	1.08	1.43
Putative ATP-dependent RNA helicase DHX30	DHX30	H7BXY3	0.81	0.96	1.43
Uncharacterized protein C4orf32	C4orf32	Q8N8J7	1.15	0.91	1.43
39S ribosomal protein L41, mitochondrial	MRPL41	Q8IXM3	0.93	0.86	1.43
Cation-independent mannose-6-phosphate receptor	IGF2R	Q59EZ3	1.29	1.38	1.43
Protein S100	S100A9	B2R4M6	0.77	1.45	1.43
Heterogeneous nuclear ribonucleoprotein R	HNRPR	Q0VGD6	1.00	0.92	1.43
Spliceosome RNA helicase DDX39B	hCG_2005638	A0A024RCM3	1.09	1.08	1.43
Prohibitin	PHB	A8K401	0.91	0.98	1.43
Glutamate dehydrogenase	GLUD1	B4DMF5	0.84	1.00	1.43
Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	Q70UQ0	0.86	0.95	1.43
Pannexin	PANX1	B6ETL5	0.72	0.88	1.43
Anoctamin	ANO10	H7C3N6	0.73	0.82	1.43
E3 ubiquitin-protein ligase TRIM23	TRIM23	A8K9U9	1.00	1.38	1.43
Transmembrane and TPR repeat-containing protein 3	TMTC3	A8K321	1.02	0.92	1.43
Acylpyruvase FAHD1, mitochondrial	FAHD1	Q6P587	0.90	0.94	1.42
Pre-mRNA-splicing factor SYF2	SYF2	B4E0Y8	0.94	0.89	1.42
Nuclear pore complex protein Nup205	NUP205	Q92621	1.00	1.12	1.42
Arfaptin-2	ARFIP2	B4DXH2	1.19	2.22	1.42
Myoferlin	MYOF	Q9NZM1-6	0.97	1.06	1.42

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
28S ribosomal protein S5, mitochondrial	MRPS5	P82675	0.74	1.08	1.42
Dynamin-like 120 kDa protein, mitochondrial	OPA1	E5KLM2	0.93	0.96	1.42
Cornifin-B	SPRR1B	P22528	1.05	1.55	1.42
Cation-dependent mannose-6-phosphate receptor	M6PR	H0YF90	1.36	1.67	1.42
Lamin-B1	LMNB1	P20700	1.29	1.34	1.42
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	B2RB06	0.87	0.97	1.42
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	B2R6U8	1.05	1.19	1.42
Adenylate kinase 2, mitochondrial	AK2	F8W1A4	0.83	1.03	1.42
Peroxisomal multifunctional enzyme type 2	HSD17B4	A0A2R8YD50	0.96	0.94	1.42
Lamin-B2	LMNB2	A0A384NPH0	1.48	1.25	1.42
28S ribosomal protein S18b, mitochondrial	MRPS18B	A0A0G2JIC6	0.90	0.88	1.42
Fibroblast growth factor-binding protein 1	FGFBP1	Q14512	1.06	1.05	1.42
Stomatin-like protein 2, mitochondrial	STOML2	Q9UJZ1	0.90	0.93	1.41
Conserved oligomeric Golgi complex subunit 3	COG3	Q96JB2	1.05	1.16	1.41
Translational activator of cytochrome c oxidase 1	TACO1	Q9BSH4	0.87	0.80	1.41
ATP synthase F(0) complex subunit B1, mitochondrial	hCG_39985	Q53GB3	0.93	0.97	1.41
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3G	Q59GA3	0.89	0.94	1.41
ATP synthase subunit O, mitochondrial	ATP5O	P48047	0.87	0.92	1.41
Nuclear pore complex protein Nup85	NUP85	J3QS63	1.03	1.51	1.41
3-ketodihydrosphingosine reductase	KDSR	K7ERC8	1.07	1.12	1.41
Ribosome biogenesis protein BOP1	BOP1	B2RDN4	0.97	1.06	1.41
DnaJ homolog subfamily B member 11	DNAJB11	Q9UBS4	1.12	0.95	1.41
Kalirin	KALRN	A0A1S5UZ29	1.49	1.50	1.41
28S ribosomal protein S2, mitochondrial	MRPS2	A0A024R8D4	0.93	1.04	1.41
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	O43143	1.15	1.07	1.41
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	O75643	1.00	1.11	1.41
Replication protein A 14 kDa subunit	RPA3	A4D105	1.28	0.55	1.41
28S ribosomal protein S26, mitochondrial	MRPS26	Q9BYN8	0.95	0.79	1.41
Ras-related protein Rab-18	RAB18	Q9NP72	0.99	1.16	1.41
Protein transport protein Sec61 subunit beta	SEC61B	S4R3B5	1.00	1.04	1.41
Ribonucleases P/MRP protein subunit POP1	POP1	Q96F88	1.12	1.21	1.40
Protein SOX-15	SOX26	O95130	1.47	1.28	1.40
Non-POU domain-containing octamer-binding protein	NONO	A8K525	1.12	1.05	1.40
Nucleolar GTP-binding protein 1	GTPBP4	O60747	1.24	0.94	1.40
RRP12-like protein	RRP12	B3KY97	0.95	1.17	1.40
Torsin-1A-interacting protein 1	TOR1AIP1	A0A0A0MSK5	1.13	0.92	1.40
Signal peptidase complex catalytic subunit SEC11	SEC11A	H0YNG3	0.96	0.87	1.40
FAST kinase domain-containing protein 2	FASTKD2	B3KMB8	0.95	1.01	1.40
Apoptosis inhibitor 5	API5	G3V1C3	1.02	1.12	1.40

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	A8K761	0.94	0.85	1.40
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	Q96ID4	0.97	0.90	1.40
28S ribosomal protein S7, mitochondrial	MRPS7	J3QKW2	1.27	1.16	1.40
39S ribosomal protein L44, mitochondrial	MRPL44	A1MA90	0.89	1.05	1.40
Phosphatidylinositol phosphatase SAC1	SACM1L	E9PGZ4	1.00	0.70	1.40
Nucleolin	NCL	B3KM80	1.01	1.05	1.40
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	B4DFY7	0.99	1.04	1.40
Cathepsin D	HEL-S-130P	A0A1B0GW44	0.84	1.06	1.40
Splicing factor 3B subunit 6	SF3B6	Q9Y3B4	1.02	0.92	1.40
Serine hydroxymethyltransferase	SHMT2	A0A024RB99	0.84	0.91	1.40
ATPase family AAA domain-containing protein 1	ATAD1	B4E2J1	0.89	1.04	1.40
Lysosome-associated membrane glycoprotein 2	LAMP2	B7Z2R9	0.73	0.98	1.39
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	A0A384NL58	1.11	1.13	1.39
Mitochondrial glutamate carrier 1	SLC25A22	A0A0D9SFE1	0.79	0.87	1.39
Isochorismatase domain-containing protein 2, mitochondrial	ISOC2	Q96AB3	0.81	0.92	1.39
Voltage-dependent calcium channel gamma-6 subunit	CACNG6	Q9BXT2	0.99	1.04	1.39
Cytochrome c oxidase subunit 6B1	COX6B1	P14854	0.94	0.97	1.39
Sulfide:quinone oxidoreductase, mitochondrial	hCG_2001986	Q9UHS8	0.87	0.95	1.39
Polypeptide N-acetylgalactosaminyltransferase	GALNT3	C9J388	1.08	0.88	1.39
GrpE protein homolog 1, mitochondrial	GRPEL1	Q9HAV7	0.99	1.00	1.39
Superoxide dismutase	SOD2	Q7Z7M4	0.81	0.91	1.39
DNA topoisomerase 1	TOP1	B9EG90	0.98	1.05	1.39
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	Q53FM7	0.88	0.93	1.39
[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial	BCKDK	A0A024QZA9	0.81	0.96	1.39
PHD finger-like domain-containing protein 5A	PHF5A	A0A024R1U2	1.15	1.05	1.39
39S ribosomal protein L39, mitochondrial	MRPL39	C9JG87	0.91	1.08	1.39
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	Q6NTA2	1.07	1.04	1.38
Small nuclear ribonucleoprotein-associated protein	SNRPN	J3QLE5	1.05	1.06	1.38
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	B4DY35	0.68	0.69	1.38
RNA-binding protein Raly	RALY	Q9UKM9-2	1.03	1.04	1.38
Small nuclear ribonucleoprotein Sm D3	SNRPD3	P62318-2	1.07	1.09	1.38
Ras-related protein Rab-3D	RAB3D	A0A024R7G2	0.85	1.03	1.38
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	A0A384MTR2	0.84	0.94	1.38
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1	H3BN72	1.08	1.00	1.38
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH	B8ZZZ0	0.82	0.95	1.38

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Neuroguidin	NGDN	Q8NEJ9-2	0.97	1.10	1.38
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	A0A1X7SBS1	1.06	1.05	1.38
MICOS complex subunit MIC60	IMMT	B9A067	1.01	1.00	1.38
Erythrocyte band 7 integral membrane protein	STOM	B4E2V5	0.87	1.04	1.38
Junction plakoglobin	JUP	A0A0S2Z487	0.99	1.24	1.38
DNA-directed RNA polymerase I subunit RPA2	POLR1B	Q9H9Y6-5	1.01	0.96	1.38
Isoleucine--tRNA ligase, mitochondrial	IARS2	A8K5W7	0.82	0.92	1.38
Thioredoxin domain-containing protein 12	TXNDC12	O95881	1.06	1.17	1.38
Transferrin receptor protein 1	TFRC	A8K6Q8	1.00	0.97	1.38
Malate dehydrogenase	MDH2	Q0QF37	0.87	0.92	1.38
Heat shock protein 75 kDa, mitochondrial	TRAP1	Q59EK6	0.81	0.98	1.37
Nucleophosmin	NPM1	A0A0S2Z4G7	1.10	0.97	1.37
Solute carrier family 25 member 40	SLC25A40	Q8TBP6	0.67	0.84	1.37
Mitochondrial dicarboxylate carrier	SLC25A10	Q9UBX3	0.90	0.92	1.37
Major facilitator superfamily domain-containing protein 10	MFSD10	D6RIZ4	0.89	0.96	1.37
Vesicle-fusing ATPase	NSF	I3L2G1	0.94	1.05	1.37
Ras-related protein Rab-10	RAB10	P61026	1.21	1.30	1.37
Protein kish-A	TMEM167A	Q8TBQ9	0.92	1.20	1.37
Williams-Beuren syndrome chromosomal region 16 protein	WBSCR16	B2RXG5	0.93	0.80	1.37
LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	D3DVQ1	0.89	0.93	1.37
Extended synaptotagmin-1	FAM62A	B3KMV5	0.97	1.01	1.37
Small nuclear ribonucleoprotein Sm D2	SNRPD2	P62316	1.05	1.12	1.37
Thioredoxin-related transmembrane protein 2	TMX2	Q9Y320-2	1.02	1.01	1.37
Splicing factor 3B subunit 3	SF3B3	A8K6V3	1.04	1.00	1.37
U1 small nuclear ribonucleoprotein A	SNRPA	M0R221	0.99	1.00	1.37
Succinyl-CoA:3-ketoacid-coenzyme A transferase	OXCT	Q6IAV5	0.80	0.96	1.37
Histone H1.4	HIST1H1E	Q4VB24	1.17	1.16	1.37
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	A0A384MDT2	1.13	1.12	1.37
RNA-binding protein 34	RBM34	Q5TCT4	1.45	1.32	1.37
39S ribosomal protein L1, mitochondrial	MRPL1	A0PJ79	0.85	1.02	1.37
Transmembrane emp24 domain-containing protein 7	TMED7-TICAM2	A0A0A6YYA0	1.04	0.99	1.36
Alpha/beta hydrolase domain-containing protein 11	ABHD11	H0YC52	0.77	0.94	1.36
Protein RER1	RER1	Q5T093	1.03	1.09	1.36
U3 small nucleolar RNA-interacting protein 2	RRP9	O43818	0.99	0.90	1.36
Signal peptidase complex subunit 2	SPCS2	E9PL01	1.06	0.87	1.36
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	G1UI16	0.91	0.96	1.36
60 kDa heat shock protein, mitochondrial	HSPD1	A0A024R3X4	0.92	0.95	1.36
Probable ATP-dependent RNA helicase DDX23	DDX23	B3KY11	1.13	1.02	1.36
Serine/arginine-rich splicing factor 6	HEL-S-91	A0A590UJK4	1.08	0.96	1.36

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Bcl-2-like protein 13	BCL2L13	B2RB43	1.14	1.15	1.36
Structural maintenance of chromosomes protein	SMC3	Q86VX4	0.92	1.04	1.36
Protein ERGIC-53	LMAN1	Q53FS4	1.10	1.11	1.36
Sorting and assembly machinery component 50 homolog	SAMM50	Q9Y512	0.91	0.88	1.36
Granulins	GRN	K7EMR1	1.75	1.63	1.36
Epididymal secretory protein E1	NPC2	G3V2V8	0.94	0.95	1.36
28S ribosomal protein S6, mitochondrial	MRPS6	P82932	0.90	0.90	1.36
Protocadherin Fat 1	FAT1	A0A087WVP1	1.25	1.76	1.36
ATP synthase subunit e, mitochondrial	ATP5I	P56385	0.84	1.01	1.36
ATP synthase subunit beta	HEL-S-271	V9HW31	0.87	0.93	1.35
[F-actin]-monooxygenase MICAL2	MICAL-2	O94851	1.13	1.59	1.35
WD repeat-containing protein 3	WDR3	Q5TDG3	0.86	1.04	1.35
Syntaxin-binding protein 2	STXBP2	B4DY46	1.69	1.94	1.35
OCIA domain-containing protein 1	OCIAD1	A0A024R9U3	0.91	0.92	1.35
Serine-protein kinase ATM	ATM	E9PRG7	0.95	0.98	1.35
Protein QIL1	QIL1	A0A140TA86	0.88	0.87	1.35
Ras-related protein Rab-1B	RAB1B	Q9H0U4	0.93	1.01	1.35
2,4-dienoyl-CoA reductase, mitochondrial	DECR1	A0A024R9D7	0.81	0.98	1.35
28S ribosomal protein S30, mitochondrial	MRPS30	Q9BUN6	0.81	0.84	1.35
Acetolactate synthase-like protein	ILVBL	Q59GP4	0.87	0.88	1.35
ATPase family AAA domain-containing protein 3A	ATAD3A	Q9NVI7-2	0.90	0.86	1.35
28S ribosomal protein S11, mitochondrial	MRPS11	Q53GJ8	1.04	1.08	1.35
10 kDa heat shock protein, mitochondrial	HSPE1	A0A384N6A4	0.83	0.93	1.35
Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	B7ZB41	0.80	0.95	1.35
Succinyl-CoA ligase subunit beta	SUCLA2	B4DY87	0.82	0.85	1.34
Epithelial splicing regulatory protein 1	ESRP1	H0YBR2	1.14	0.85	1.34
DnaJ homolog subfamily C member 11	DNAJC11	Q9UMU8	0.71	0.90	1.34
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	Q13151	1.06	0.93	1.34
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	Q5FWY2	0.84	1.05	1.34
Ras-related protein Rab-1A	RAB1A	Q5U0I6	0.94	0.99	1.34
ADP-ribosylation factor-related protein 1	ARFRP1	B7ZKY8	0.97	0.91	1.34
Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3	Q5JWS1	0.80	0.86	1.34
Ribosome-recycling factor, mitochondrial	MRRF	A0A024R850	1.14	1.15	1.34
Sorting nexin-3	SNX3	O60493	1.78	1.51	1.34
Cytochrome b5 type B	DKFZp686M0619	Q5HYD9	0.99	0.88	1.33
Heat shock protein beta-1	HEL-S-102	V9HW43	0.97	1.81	1.33
39S ribosomal protein L14, mitochondrial	MRPL14	A0A024RD78	0.88	1.06	1.33
DAZ-associated protein 1	DAZAP1	K7EQ02	1.12	1.14	1.33

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
DNA replication licensing factor MCM4	MCM4	A0A3B3IU45	0.99	0.93	1.33
Translocon-associated protein subunit delta	SSR4	P51571	0.98	0.91	1.33
Sigma non-opioid intracellular receptor 1	SIGMAR1	Q99720	0.94	0.98	1.33
Beta-hexosaminidase	HEXB	Q5URX0	0.89	0.97	1.33
Sphingosine-1-phosphate lyase 1	SGPL1	H0Y3V8	1.09	0.75	1.33
116 kDa U5 small nuclear ribonucleoprotein component	SNRP116	Q8IXJ3	0.97	1.09	1.33
Protein SCAF11	SFRS2IP	Q05BS8	1.23	1.47	1.33
Nuclear pore complex protein Nup50	hCG_1989366	B4E2D3	1.08	1.15	1.33
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	P31930	0.93	0.89	1.33
Probable ergosterol biosynthetic protein 28	C14orf1	Q86TW5	0.83	1.01	1.33
High mobility group protein B2	HMGB2	D6R9A6	1.23	1.30	1.33
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	E9PN51	0.86	0.86	1.33
Core histone macro-H2A.1	H2AFY	O75367-2	0.89	0.92	1.33
Keratin, type I cytoskeletal 18	KRT18	B2RA03	1.09	0.95	1.33
Probable ATP-dependent RNA helicase DDX10	DDX10	A0A3B3ISR7	0.83	0.81	1.33
Translocon-associated protein subunit gamma	SSR3	C9JA28	1.01	0.96	1.33
Protein S100-A16	S100A16	Q96FQ6	0.92	1.21	1.33
Eukaryotic initiation factor 4A-III	EIF4A3	I3L3H2	1.09	1.07	1.33
Pre-mRNA-processing factor 19	PRPF19	Q9UMS4	0.98	1.04	1.33
Cell division control protein 42 homolog	CDC42	A0A024RAA5	1.04	1.24	1.33
Mitochondrial-processing peptidase subunit alpha	PMPCA	Q10713	0.85	0.93	1.33
RNA-binding protein EWS	EWSR1	B0QYK0	1.11	1.19	1.33
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	A0A384NPZ7	1.00	1.05	1.33
Stress-70 protein, mitochondrial	HEL-S-124m	B7Z4V2	0.87	0.92	1.32
Elongation factor Tu, mitochondrial	TUFM	A0A384ME17	0.90	0.96	1.32
3-hydroxyisobutyrate dehydrogenase	HIBADH	A0A024RA75	0.82	0.99	1.32
THO complex subunit 4	ALYREF	Q86V81	1.06	1.16	1.32
Lysosome membrane protein 2	SCARB2	A0A1W2PRF6	0.88	0.98	1.32
E3 SUMO-protein ligase RanBP2	RANBP2	P49792	1.18	1.18	1.32
ATP-dependent RNA helicase DDX54	DDX54	Q8TDD1	1.06	1.05	1.32
Translocator protein	TSPO	B1AH87	0.89	0.99	1.32
B-cell receptor-associated protein 31	BCAP31	C9JSP1	1.05	1.07	1.32
39S ribosomal protein L10, mitochondrial	MRPL10	B4DEH0	0.78	0.83	1.32
Amino acid transporter	Slc38a1	Q9JM15	0.89	1.02	1.32
Receptor protein-tyrosine kinase	EPHA2	A0A024QZA8	1.10	1.01	1.32
Cystatin-A	CSTA	P01040	0.87	1.49	1.32
Transmembrane protein 205	TMEM205	K7EM09	0.65	1.14	1.32
Golgi apparatus protein 1	GLG1	Q92896	1.16	1.31	1.32
Catenin alpha-2	CTNNA2	P26232-2	0.97	1.26	1.32

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Mitochondrial Rho GTPase 2	RHOT2	Q8IXI1	1.10	0.88	1.32
Ganglioside GM2 activator	GM2A	P17900	0.67	0.95	1.31
Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2	Q96ME4	0.96	0.99	1.31
MICOS complex subunit MIC19	CHCHD3	A4D1N4	1.18	1.06	1.31
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	A0A384MEJ3	1.03	1.09	1.31
Casein kinase I isoform alpha	HEL-S-77p	V9HW00	0.97	1.18	1.31
Ras-related protein Rab-7a	RAB7A	A0A158RFU6	0.98	1.05	1.31
4F2 cell-surface antigen heavy chain	SLC3A2	F5GZS6	0.95	0.98	1.31
Very-long-chain enoyl-CoA reductase	TECR	B3KM97	1.04	0.96	1.31
Mitochondrial import receptor subunit TOM70	TOMM70A	O94826	0.97	1.06	1.31
Enhancer of rudimentary homolog	ERH	A0A024R6D4	1.11	1.10	1.31
Protein sel-1 homolog 1	SEL1L	Q9UBV2	1.31	1.27	1.31
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	A0A140VJX1	0.82	0.96	1.31
Ubiquitin carboxyl-terminal hydrolase	USP7	B7Z855	0.94	1.04	1.31
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P54886-2	0.95	0.94	1.31
Pre-mRNA-splicing factor SPF27	BCAS2	Q53HE3	0.90	0.88	1.31
Mitochondrial import inner membrane translocase subunit Tim23	TIMM23	B1APJ0	0.76	0.77	1.31
Delta(24)-sterol reductase	Nbla03646	Q3LIE7	0.75	0.90	1.31
Aconitate hydratase, mitochondrial	ACO2	A0A0K0K1H7	0.79	0.83	1.31
Pyruvate dehydrogenase E1 component subunit alpha	PDHA1	A0A024RBX9	0.84	0.89	1.31
mRNA turnover protein 4 homolog	C1orf33	A0A024RAE1	0.99	1.00	1.31
Vesicular integral-membrane protein VIP36	LMAN2	B4DWN1	0.90	0.91	1.31
39S ribosomal protein L47, mitochondrial	MRPL47	Q9HD33-2	0.91	0.87	1.31
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3B	A0A087X2E5	1.03	0.98	1.31
Mitochondrial-processing peptidase subunit beta	PMPCB	B4DM90	0.88	0.89	1.31
ELAV-like protein 1	ELAVL1	Q15717	1.09	0.96	1.31
Histone H3	H3F3B	K7EK07	0.88	0.83	1.31
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	H0YLC3	0.72	0.72	1.31
Ras-related protein Rab-2A	RAB2	A0A024R7V6	1.03	1.01	1.30
EH domain-containing protein 2	EHD2	B4DLA1	1.12	1.25	1.30
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	E5KNY5	0.84	0.90	1.30
Target of Myb protein 1	TOM1	Q6UW50	0.88	0.93	1.30
ATP synthase subunit a	ATP6	D2Y6Y7	0.93	0.90	1.30
Tetraspanin	CD63	F8VNT9	0.90	0.90	1.30
WD repeat-containing protein 36	WDR36	A0A0A0MTB8	1.18	1.15	1.30
Lon protease homolog, mitochondrial	LONP1	K7EKE6	0.87	0.88	1.30
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	hCG_2032701	A0A024R3J7	0.90	0.82	1.30
ATP synthase subunit g, mitochondrial	ATP5L	O75964	0.89	0.88	1.30

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	B7Z9L2	1.00	0.94	1.30
NADPH--cytochrome P450 reductase	DKFZp686G04235	Q63HL4	0.95	0.95	1.30
Elongation factor G, mitochondrial	GFM1	E5KND7	1.05	0.89	1.30
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	D6RFM5	0.89	0.93	1.30
Transmembrane protein 126A	TMEM126A	Q9H061	0.84	0.71	1.30
Cytochrome c oxidase subunit 7C, mitochondrial	COX7C	P15954	1.18	0.85	1.30
Thioredoxin-related transmembrane protein 1	TMX1	Q9H3N1	1.02	1.02	1.30
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	A0A0S2Z4Y5	0.83	0.95	1.30
Polymerase I and transcript release factor	PTRF	B4DPZ5	1.08	1.05	1.30
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	P22695	0.89	0.88	1.30
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRCF1	A0A384NPX8	0.76	0.90	1.30
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	P54709	0.89	0.85	1.29
Dehydrogenase/reductase SDR family member 7B	DHRS7B	J3KRS1	0.81	1.02	1.29
tRNA (guanine(37)-N1)-methyltransferase	TRMT5	Q32P41	1.08	0.96	1.29
Transmembrane 9 superfamily member 2	TM9SF2	A0A024QYR8	1.12	0.93	1.29
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	P30837	0.74	0.85	1.29
High affinity cationic amino acid transporter 1	SLC7A1	B2R728	1.03	0.98	1.29
Translocon-associated protein subunit alpha	SSR1	C9J3L8	0.81	1.09	1.29
Receptor protein-tyrosine kinase	MST1R	J3KQS7	0.90	0.99	1.29
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	Q6IBS5	0.85	0.88	1.29
Neural cell adhesion molecule 2	NCAM2	L0R512	1.05	1.14	1.29
Integrin beta-1	ITGB1	P05556	0.93	1.01	1.29
DNA-directed RNA polymerase	POLR1A	B9ZVN9	1.04	0.82	1.29
Pyruvate carboxylase	PC	A0A024R5C5	0.93	0.98	1.29
Integrin alpha-V	ITGAV	L7RXH0	1.35	1.10	1.29
FAS-associated factor 2	FAF2	Q96CS3	1.04	1.13	1.29
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	Q9Y5L4	0.88	0.97	1.29
Catenin delta-1	CTNND1	Q7KZJ3	1.00	1.20	1.29
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	A0A2R8YFY5	1.03	1.14	1.29
Dihydrolipoyl dehydrogenase	DLD	B4DFL1	0.91	1.00	1.29
Guanine nucleotide-binding protein subunit gamma	GNG12	Q53GD1	0.83	0.92	1.29
Transmembrane 9 superfamily member 4	TM9SF4	B4DYH6	1.38	1.10	1.29
ATP synthase subunit gamma	ATP5C1	Q8TAS0	1.07	1.00	1.29
ATP synthase subunit alpha	HEL-S-123m	V9HW26	0.87	0.86	1.29
Serpin H1	SERPINH1	A0A024R5K8	0.94	0.90	1.29
Ras-related protein Rab-14	RAB14	A0A024R845	0.85	0.96	1.29

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
HIG1 domain family member 2A, mitochondrial	HIGD2A	A0A024R7Q3	0.74	1.08	1.28
Protein Red	CSA2	B4DEH2	0.91	1.08	1.28
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	B7ZAX9	1.24	1.10	1.28
HIG1 domain family member 1A, mitochondrial	HIGD1A	C9JAW5	0.91	0.77	1.28
Catenin alpha-1	CTNNA1	A0A384MDY0	1.01	1.12	1.28
RNA polymerase II subunit A C-terminal domain phosphatase SSU72	SSU72	B4DMK6	1.07	1.12	1.28
Basigin	hEMMPRIN	B4DY23	0.85	1.04	1.28
Transducin beta-like protein 2	TBL2	B4DY59	1.00	0.96	1.28
FACT complex subunit SPT16	SUPT16H	Q9Y5B9	0.92	0.97	1.28
Poly [ADP-ribose] polymerase 1	PARP1	B2R5W3	0.98	0.93	1.28
Transcription factor A, mitochondrial	TFAM	Q6LES8	0.13	2.22	1.28
Serine protease HTRA2, mitochondrial	HTRA2	A0A0C4DG44	0.88	1.00	1.28
Serine/arginine repetitive matrix protein 1	SRRM1	M0QXG5	1.25	1.30	1.28
NAD-dependent malic enzyme, mitochondrial	ME2	P23368	0.72	0.80	1.28
Cytoskeleton-associated protein 4	CKAP4	A0A024RBH2	0.93	0.85	1.28
Persulfide dioxygenase ETHE1, mitochondrial	ETHE1	A0A0S2Z5B3	0.94	0.87	1.28
Endoplasmic reticulum resident protein 29	HEL-S-107	V9HW71	0.98	0.92	1.28
Amine oxidase [flavin-containing] A	MAOA	Q53YE7	0.93	1.01	1.28
Beta-hexosaminidase	HEXA	H3BU85	1.16	1.16	1.28
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	Q08J23-2	1.10	0.99	1.28
Microsomal glutathione S-transferase 1	MGST1	Q6LET6	0.92	1.06	1.28
FACT complex subunit SSRP1	SSRP1	A0A024R4Z6	0.93	0.90	1.28
28S ribosomal protein S31, mitochondrial	MRPS31	Q92665	0.98	0.95	1.27
Unconventional myosin-Ib	MYO1B	E9PDF6	1.03	1.02	1.27
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	Q9Y305-2	0.85	0.86	1.27
X-ray repair cross-complementing protein 6	XRCC6	A0A024R1N4	1.03	1.03	1.27
Acyl-coenzyme A thioesterase 13	ACOT13	Q9NPJ3-2	0.90	1.04	1.27
Far upstream element-binding protein 3	hCG_31253	A0A024R8A7	1.29	1.24	1.27
26S proteasome non-ATPase regulatory subunit 10	PSMD10	B1AJY6	1.22	1.09	1.27
Ras-related protein Rap-1b	RAP1B	A0A024RB87	0.88	0.89	1.27
Cleavage stimulation factor subunit 3	CSTF3	B4DFQ5	0.91	0.88	1.27
Leucine-rich repeat-containing protein 59	LRRC59	Q96AG4	1.03	1.03	1.27
Nitrilase homolog 1	NIT1	B7Z410	1.53	1.53	1.27
AP-2 complex subunit alpha-2	AP2A2	B7Z5S9	0.90	0.98	1.27
Polyadenylate-binding protein 2	PABPN1	Q86U42-2	0.99	0.98	1.27
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	Q6FHM2	0.90	0.93	1.27
Cytochrome c oxidase subunit 2	COX2	A0A346M047	0.93	0.90	1.27

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Derlin-1	DERL1	E5RGY0	1.47	1.11	1.27
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	F5GXX5	0.94	1.00	1.27
Elongation of very long chain fatty acids protein	ELOVL1	Q502X7	0.85	0.85	1.27
Glycerol-3-phosphate dehydrogenase	GPD2	Q53T76	0.71	0.72	1.27
Superkiller viralicidic activity 2-like 2	SKIV2L2	A8K6I4	0.93	1.04	1.27
N-acylneuraminate cytidyltransferase	CMAS	Q53GF0	1.11	1.16	1.27
Glutaminase kidney isoform, mitochondrial	GLS	A8K132	0.94	0.90	1.27
Protein lifeguard 3	TMBIM1	C9JEN3	0.97	0.99	1.27
Citrate synthase	CS	B3KTN4	0.89	0.92	1.27
Atlastin-2	ATL2	H7C3A2	0.88	1.06	1.26
Tetraspanin	CD9	B4DPP0	0.88	0.89	1.26
Neutral alpha-glucosidase AB	HEL-S-164nA	V9HWJ0	0.89	0.94	1.26
Presequence protease, mitochondrial	PITRM1	B4DRW8	0.94	0.89	1.26
39S ribosomal protein L15, mitochondrial	MRPL15	E5RIZ4	0.88	0.79	1.26
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	Q05CW0	0.75	0.79	1.26
Mitotic checkpoint protein BUB3	BUB3	B4DDM6	1.20	1.13	1.26
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	B3KWD9	0.85	0.95	1.26
Oligosaccharyltransferase complex subunit OSTC	OSTC	A0A087WUD3	0.91	0.83	1.26
Retinol dehydrogenase 11	RDH11	A0A0S2Z583	0.86	0.86	1.26
2-oxoglutarate dehydrogenase, mitochondrial	OGDH	B4DF00	0.88	0.85	1.26
Microsomal glutathione S-transferase 3	MGST3	Q53GB9	0.85	0.93	1.26
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	B3KQQ3	0.72	0.73	1.26
Serine palmitoyltransferase 1	SPTLC1	A0A024R277	0.82	0.98	1.26
Proline-, glutamic acid- and leucine-rich protein 1	PELP1	A8K548	0.87	1.08	1.26
SUN domain-containing protein 1	SUN1	Q5S4N2	0.84	1.56	1.26
Mitochondrial ornithine transporter 1	SLC25A15	B4DL63	0.46	0.41	1.26
PRA1 family protein 3	ARL6IP5	B4DZZ0	0.91	0.85	1.26
SNW domain-containing protein 1	SNW1	Q0D2M5	1.00	1.08	1.26
Torsin-1A	TOR1A	B3KPA1	0.72	0.89	1.26
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	P05023-3	0.92	0.90	1.26
Carboxylic ester hydrolase	CES2	Q6IPK9	0.83	1.01	1.26
Protein FAM3C	FAM3C	Q92520	0.96	0.99	1.26
ADP/ATP translocase 3	SLC25A6	Q619V5	0.92	0.86	1.26
Ribosome production factor 2 homolog	RPF2	Q5VXN0	1.02	0.91	1.26
Splicing factor 3A subunit 3	SF3A3	B4DW90	1.04	1.00	1.26
CLIP-associating protein 2	CLASP2	B3KR06	1.09	1.08	1.26
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	Q496I0	0.83	0.94	1.26
NADH-cytochrome b5 reductase	CYB5R3	A0A024R4X0	0.95	1.00	1.25
Small nuclear ribonucleoprotein Sm D1	SNRPD1	P62314	1.01	0.91	1.25

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Serine/arginine-rich splicing factor 2	SRSF2	J3QL05	0.93	1.00	1.25
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	A0A384P5S9	1.08	1.17	1.25
Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	P20674	0.84	0.92	1.25
Endoplasmic reticulum aminopeptidase 1	ERAP1	A8K6H1	0.91	1.05	1.25
Voltage-dependent anion-selective channel protein 3	VDAC3	Q9Y277	1.05	1.04	1.25
Calcium-transporting ATPase	DKFZp686M088	Q68DH9	1.34	1.20	1.25
Fatty acid desaturase 2	FADS2	O95864	1.11	0.97	1.25
Integrin beta	ITGB6	E9PEE8	1.10	1.04	1.25
Voltage-dependent anion-selective channel protein 2	VDAC2	A0A0A0MR02	0.86	0.92	1.25
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	Q96EY7	0.90	0.90	1.25
Serine/arginine-rich splicing factor 11	SFRS11	Q05BU6	1.05	1.14	1.25
DnaJ homolog subfamily C member 3	DNAJC3	A8KA82	0.96	1.00	1.25
Erlin-2	ERLIN2	E5RHW4	0.68	0.84	1.25
OCIA domain-containing protein 2	OCIAD2	Q56VL3	1.09	0.86	1.25
Nucleoplasmin-3	NPM3	O75607	0.95	0.93	1.25
NHP2-like protein 1	NHP2L1	A0A3B3IUA2	0.85	1.08	1.25
Adipocyte plasma membrane-associated protein	APMAP	Q9HDC9	1.01	1.03	1.25
Polypyrimidine tract-binding protein 1	PTBP1	A0A0U1RRM4	1.01	1.04	1.25
Hexokinase	HK1	B4DG62	0.87	0.97	1.25
Protein SCO1 homolog, mitochondrial	SCO1	O75880	1.14	1.04	1.25
Cathepsin B	CTSB	B4DL49	0.87	0.82	1.25
Aspartate aminotransferase	GOT2	A0A024R6W0	0.92	0.83	1.24
Voltage-dependent anion-selective channel protein 1	VDAC1	A0A1L1UHR1	0.85	0.93	1.24
RNA-binding protein 14	RBM14	A0A0S2Z4Z0	0.90	0.87	1.24
Amino acid transporter	SLC1A5	Q71UA6	1.03	1.06	1.24
Krueppel-like factor 16	KLF16	D6W5Z8	1.29	1.06	1.24
Neutral cholesterol ester hydrolase 1	NCEH1	H7C046	1.32	1.13	1.24
Lysosome-associated membrane glycoprotein 1	LAMP1	B3KRY3	0.83	0.99	1.24
Creatine kinase U-type, mitochondrial	CKMT1A	P12532	0.78	0.92	1.24
C-terminal-binding protein 2	CTBP2	A0A087WYL1	0.82	1.07	1.24
Nucleolysin TIA-1 isoform p40	TIA1	C9JTN7	0.91	1.10	1.24
Cytochrome c oxidase subunit NDUF44	NDUF44	A0A024R9Z0	0.84	0.89	1.24
Exocyst complex component 3	FLJ00339	B2RE06	1.01	0.96	1.24
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	A0A384MDR8	0.85	0.83	1.24
CAAX prenyl protease 1 homolog	ZMPSTE24	O75844	0.78	0.83	1.24
Unconventional myosin-Ic	MYO1C	F5H6E2	0.95	0.99	1.24
DNA damage-binding protein 1	DDB1	Q16531	1.01	1.13	1.24
Histone H1.5	HIST1H1B	P16401	1.07	0.95	1.24

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Cytochrome b-c1 complex subunit 9	UQCR10	Q9P012	1.07	1.11	1.23
PRA1 family protein 2	PRAF2	B3KN29	0.86	0.98	1.23
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM	B4DJE7	0.78	0.77	1.23
Prohibitin-2	PHB2	J3KPX7	0.87	0.86	1.23
Fumarate hydratase, mitochondrial	FH	A0A0S2Z4C3	0.87	0.95	1.23
Histone deacetylase 2	HDAC2	Q92769-3	0.87	0.86	1.23
Transmembrane emp24 domain-containing protein 10	TMED10	A0A024R6I3	1.05	0.94	1.23
Exocyst complex component 6B	EXOC6B	Q9H8D6	0.90	1.16	1.23
Glucosidase 2 subunit beta	PRKCSH	A0A024R7F1	0.89	0.89	1.23
Branched-chain-amino-acid aminotransferase	BCAT2	B3KSI3	0.67	0.75	1.23
Intron-binding protein aquarius	AQR	B0AZM4	1.09	1.15	1.23
Ras-related protein Rab-21	RAB21	A0A024RBA9	1.31	1.30	1.23
Zinc finger protein 185	DKFZp686B22130	Q6MZQ8	1.11	1.42	1.23
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	J3QQY2	0.94	0.84	1.23
Malectin	MLEC	F5H1S8	0.90	0.83	1.23
Peptidyl-prolyl cis-trans isomerase	FKBP8	M0R1Q0	0.92	1.00	1.23
Negative elongation factor A	NELFA	F8W954	1.00	1.07	1.23
7-dehydrocholesterol reductase	DHCR7	A8K0D2	0.85	0.98	1.23
Transmembrane protein 33	TMEM33	D6RAA6	0.93	1.03	1.23
Cytochrome b-c1 complex subunit 8	UQCRQ	O14949	0.99	2.29	1.23
Heme oxygenase 2	HMOX2	Q6IBP2	0.97	0.96	1.22
Histone H2A type 2-C	HIST2H2AC	Q16777	0.84	0.91	1.22
Desmoplakin	DSP	P15924	0.95	1.35	1.22
Low-density lipoprotein receptor	LDLR	Q9UH51	1.01	0.97	1.22
Histone-binding protein RBBP7	RBBP7	E9PC52	1.00	1.02	1.22
ATP synthase subunit f, mitochondrial	ATP5J2	P56134-3	0.88	0.86	1.22
28S ribosomal protein S9, mitochondrial	MRPS9	Q86WV4	0.74	0.94	1.22
DNA-directed RNA polymerase II subunit RPB3	POLR2C	B7Z377	1.05	0.97	1.22
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	Q96HX3	0.91	0.89	1.22
ADP/ATP translocase 2	SLC25A5	P05141	0.96	0.87	1.22
Torsin-1A-interacting protein 2	TOR1AIP2	Q8NFQ8	1.04	0.98	1.22
ER lumen protein-retaining receptor	KDELRL1	Q96H29	0.91	1.04	1.22
Disks large homolog 1	DLG1	A0A590UJ08	1.31	1.28	1.22
Small nuclear ribonucleoprotein E	SNRPE	P62304	1.02	0.96	1.22
Histone H2B	HIST1H2BJ	A0A024RCJ2	0.74	0.82	1.22
Unconventional myosin-Va	MYO5A	Q59FF5	1.64	1.97	1.22
Endoplasmic reticulum resident protein 44	ERP44	A0A384MEE7	0.94	0.87	1.22

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
E3 ubiquitin-protein ligase DTX3L	DTX3L	Q8TDB6	0.70	0.72	1.22
Lamina-associated polypeptide 2, isoforms beta/gamma	TMPO	A0A024RBE7	1.28	1.13	1.21
Hexokinase	HK2	A8K2U2	1.01	0.99	1.21
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	E5KRK5	0.85	0.78	1.21
DNA helicase	MCM5	B1AHB1	1.04	1.03	1.21
Transcription elongation factor SPT5	SUPT5H	B4DJK4	0.72	0.99	1.21
Ferritin	FTH1	A0A024R525	1.09	1.00	1.21
Protein tweety homolog	TTYH3	A0A024R816	0.88	0.77	1.21
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	B7Z2E2	0.90	0.81	1.21
Inverted formin-2	INF2	Q27J81-2	0.95	1.01	1.21
Beta-2-microglobulin	B2M	A6XMH5	0.91	0.87	1.21
Spectrin beta chain, non-erythrocytic 1	SPTBN1	D6W5C0	0.96	1.05	1.21
General transcription factor IIF subunit 1	GTF2F1	B4DXY2	1.01	1.31	1.21
Protein disulfide-isomerase A3	PDIA3	H7BZJ3	0.79	0.72	1.21
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	Q6IBH0	0.78	0.81	1.21
Amyloid-like protein 2	APLP2	B4E3I5	1.00	0.54	1.21
Protein disulfide-isomerase	P4HB	A0A024R8S5	0.90	0.86	1.21
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	Q9UEH5	0.90	0.90	1.21
Protein NipSnap homolog 1	NIPSNAP1	C9JDV8	0.85	0.86	1.21
All-trans-retinol 13,14-reductase	RETSAT	B4DKE1	0.95	0.85	1.21
CDGSH iron-sulfur domain-containing protein 2	CISD2	D6RCF4	0.87	0.96	1.21
Squalene synthase	FDFT1	Q6IAX1	0.89	0.89	1.21
Laminin subunit beta-1	LAMB1	G3XAI2	0.70	0.69	1.21
Rho-related GTP-binding protein RhoG	ARHG	Q6ICQ8	1.13	1.19	1.21
Coiled-coil domain-containing protein 47	CCDC47	Q96A33-2	0.83	0.78	1.21
Unhealthy ribosome biogenesis protein 2 homolog	URB2	A8K4P8	1.01	0.93	1.21
MICOS complex subunit MIC10	MINOS1	A0A3B3IRY5	0.84	0.99	1.21
Cell growth-regulating nucleolar protein	LYAR	A8K3Y5	1.17	0.97	1.21
Putative HLA class I histocompatibility antigen chain	HLA-C	Q9MYI2	0.90	0.81	1.21
V-type proton ATPase subunit F	ATP6V1F	A4D1K0	1.05	1.08	1.21
Long-chain-fatty-acid--CoA ligase 3	ACSL3	B3KN05	0.92	0.88	1.20
Transitional endoplasmic reticulum ATPase	HEL-S-70	V9HW80	1.06	1.01	1.20
Alpha-N-acetylgalactosaminidase	NAGA	A0A024R1Q5	0.84	0.78	1.20
SAP domain-containing ribonucleoprotein	CIP29	Q567R9	1.27	1.20	1.20
NF-X1-type zinc finger protein NFXL1	URCC5	B1Q2B0	1.10	1.64	1.20
Acyl-CoA dehydrogenase family member 11	ACAD11	D6RDI8	0.93	1.00	1.20
Integrin alpha-2	ITGA2	E7ESP4	0.93	0.87	1.20
Mesencephalic astrocyte-derived neurotrophic factor	MANF	A8K878	0.97	0.87	1.20

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Heterogeneous nuclear ribonucleoprotein F	HNRPF	A0A024R7T3	1.10	1.12	1.20
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	P49419-2	0.89	1.08	1.20
Terpene cyclase/mutase family member	LSS	B2R694	0.96	0.90	1.20
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	M0R3F1	1.10	1.01	1.20
X-ray repair cross-complementing protein 5	XRCC5	P13010	0.99	1.06	1.20
2,5-phosphodiesterase 12	PDE12	F6T1Q0	0.98	1.00	1.20
3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	EBP	C9J719	0.84	0.87	1.20
Minor histocompatibility antigen H13	HM13	A0A0S2Z5V7	0.88	0.91	1.20
Receptor expression-enhancing protein	REEP5	B7Z332	0.92	0.97	1.20
Fibronectin	DKFZp686L11144	B4DU16	1.16	0.80	1.20
Splicing factor U2AF 35 kDa subunit	U2AF1	P0DN76	0.98	0.98	1.20
28S ribosomal protein S23, mitochondrial	MRPS23	J3QLR8	0.85	0.74	1.19
Nucleolar protein 11	NOL11	Q9H8H0	1.07	0.91	1.19
Histone-binding protein RBBP4	RBBP4	Q09028-3	1.03	1.07	1.19
Transmembrane protein 43	TMEM43	A0A024R2F9	0.94	0.83	1.19
Dipeptidyl peptidase 1	CTSC	B4DJQ8	0.89	0.75	1.19
Histone H3.2	HIST2H3A	Q71DI3	0.80	0.89	1.19
5(3)-deoxyribonucleotidase, cytosolic type	NT5C	J3KRC4	1.17	1.49	1.19
Atlastin-3	ATL3	F5H6I7	0.93	0.91	1.19
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	B4DQF2	0.66	0.74	1.19
Peptidyl-prolyl cis-trans isomerase	FKBP2	Q53XJ5	0.81	0.73	1.19
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	B3KPA6	0.60	0.69	1.19
Integrin beta	ITGB4	B7ZLD8	1.00	0.89	1.19
Transgelin	TAGLN	Q5U0D2	0.91	2.11	1.19
LDLR chaperone MESD	MESDC2	Q14696	0.75	0.76	1.19
Dystonin	DST	E9PHM6	1.16	0.99	1.19
Protein disulfide-isomerase A6	PDIA6	A0A384NPU5	0.88	0.84	1.18
Thioredoxin domain-containing protein 5	TXNDC5	Q86UY0	0.97	0.86	1.18
Aspartyl/asparaginyl beta-hydroxylase	ASPH	Q12797-10	0.80	0.77	1.18
Zinc phosphodiesterase ELAC protein 2	ELAC2	H7C2I4	0.88	1.09	1.18
Pyrroline-5-carboxylate reductase 2	PYCR2	A0A087WTV6	0.73	0.74	1.18
Nuclear mitotic apparatus protein 1	NUMA1	A0A024R5G4	1.33	1.07	1.18
5-nucleotidase	NT5E	Q6NZX3	0.91	0.84	1.18
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	P04844	0.84	0.88	1.18
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	A0A0C4DGS1	0.88	0.86	1.18
Involucrin	IVL	P07476	0.96	1.17	1.18
Chromodomain-helicase-DNA-binding protein 4	CHD4	B3KY63	0.99	0.98	1.18

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Calreticulin	HEL-S-99n	Q53G71	1.01	0.95	1.18
UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	Q9NYU2-2	0.84	0.88	1.18
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	A0A024R745	0.98	0.88	1.18
Calumenin	CALU	Q6IAW5	0.81	0.91	1.18
Synaptic vesicle membrane protein VAT-1 homolog	VAT1	A0A024R1Z6	0.90	0.94	1.18
Protein FAM83B	FAM83B	Q5T0W9	0.95	1.11	1.18
ATP-dependent DNA helicase Q1	RECQL	A0A024RAV2	0.95	1.05	1.18
C-terminal-binding protein 1	CTBP1	X5D7T7	1.02	1.20	1.18
Epiplakin	EPPK1	A0A075B730	0.95	1.48	1.18
Transmembrane emp24 domain-containing protein 5	TMED5	Q49AG2	0.78	0.91	1.17
Histone H2A.V	H2AFV	Q71UI9	0.96	0.92	1.17
AP-1 complex subunit gamma-1	AP1G1	B4DDL1	0.87	1.05	1.17
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	A0A0S2Z410	0.76	0.85	1.17
GPI transamidase component PIG-T	PIGT	A0A1W2PSC5	0.72	0.79	1.17
Endoplasmic reticulum-Golgi intermediate compartment protein 2	ERGIC2	H0YHJ8	0.92	1.03	1.17
RNA-binding protein 25	RBM25	P49756	1.12	1.06	1.17
Probable 28S rRNA (cytosine-C(5))-methyltransferase	NSUN5	B2RD09	0.94	0.96	1.17
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUFB9	E9PH64	0.80	0.81	1.17
RNA-binding motif protein, X chromosome	RBMX	P38159	1.18	1.17	1.17
Cleft lip and palate transmembrane protein 1	CLPTM1	A0A0S2Z3H2	1.20	1.44	1.17
Synaptophysin-like protein 1	SYPL1	A0A0U1RQT9	2.08	2.14	1.17
Phenylalanine--tRNA ligase, mitochondrial	FARS2	A0A3B3ITR6	0.83	0.86	1.17
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	P52272	1.05	0.98	1.17
Plectin	PLEC	Q15149-4	1.08	1.11	1.17
Long-chain-fatty-acid--CoA ligase 4	FACL4	Q8TAF6	0.81	0.86	1.17
DnaJ homolog subfamily C member 10	DNAJC10	B4DP04	0.83	0.79	1.17
General transcription factor 3C polypeptide 1	DKFZp686A111	Q6AHZ7	0.94	0.92	1.17
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	Q8TCJ2	1.09	0.92	1.17
Lupus La protein	SSB	B5BUB5	1.10	1.10	1.17
Protein disulfide-isomerase	HEL-S-269	B3KQT9	0.96	0.85	1.16
Dephospho-CoA kinase domain-containing protein	DKAKD	K7ESP4	0.48	0.76	1.16
Emerin	EMD	Q5HY57	0.92	1.11	1.16
Histone H2B	HIST1H2BC	Q0D2M2	0.88	0.80	1.16
DNA helicase	MCM7	B2RBA6	1.01	1.02	1.16
Cullin-4A	CUL4A	B2RBV7	0.86	0.97	1.16
Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	B3KQJ0	0.89	0.88	1.16

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Apoptosis-inducing factor 1, mitochondrial	AIFM1	O95831-3	0.70	0.72	1.16
Bystin	BYSL	Q13895	1.13	1.06	1.16
rRNA methyltransferase 3, mitochondrial	RNMTL1	Q9HC36	0.73	0.77	1.16
ADP/ATP translocase 1	SLC25A4	A0A0S2Z3H3	0.86	0.78	1.16
Peroxiredoxin-5, mitochondrial	HEL-S-55	V9HW35	0.90	1.18	1.16
Protein TBRG4	TBRG4	D3DVL7	0.87	0.97	1.16
TAR DNA-binding protein 43	TARDBP	B1AKP7	0.93	1.03	1.16
Peroxisomal membrane protein PEX14	PEX14	B7Z4Z4	0.99	0.93	1.16
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	B2R6K4	0.89	0.82	1.16
Protein cornichon homolog 4	CNIH4	A6NLH6	0.74	0.87	1.16
Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	P04899	0.96	0.86	1.16
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	B4DGK8	0.72	0.68	1.16
Signal recognition particle subunit SRP72	HEL103	V9HWK0	1.23	1.26	1.16
ADP-ribosylation factor-like protein 1	ARL1	P40616-2	0.91	1.05	1.16
26S proteasome non-ATPase regulatory subunit 4	PSMD4	A6PVX3	1.12	1.11	1.16
DNA fragmentation factor subunit alpha	DFFA	A0A024R4H5	1.00	2.06	1.16
Rabankyrin-5	DKFZp686M19106	Q5H9P4	1.22	1.51	1.15
Protein disulfide-isomerase A4	ERP70	A0A090N8Y2	0.92	0.87	1.15
Alpha-actinin-4	ACTN4	A0A0S2Z3G9	1.01	1.06	1.15
U6 snRNA-associated Sm-like protein LSM4	LSM4	V9GZ56	1.02	1.09	1.15
Hepatoma-derived growth factor	HDGF	B2RDE8	0.88	1.08	1.15
Chromobox protein homolog 3	CBX3	A4D177	1.00	0.97	1.15
Heat shock 70 kDa protein 6	HSPA6	Q53FC7	1.22	1.39	1.15
28S ribosomal protein S27, mitochondrial	MRPS27	Q8N6F2	0.71	0.87	1.15
Acyl-CoA desaturase	SCD	Q59GX7	0.67	0.59	1.15
DNA topoisomerase 2-alpha	TOP2A	P11388	0.84	0.84	1.15
Scaffold attachment factor B1	SAFB	B7Z2Z1	0.92	0.96	1.15
ER membrane protein complex subunit 1	EMC1	Q8N766-3	1.12	0.94	1.15
UBX domain-containing protein 4	UBXN4	F8WB86	0.91	1.06	1.15
Nicotinamide-nucleotide adenylyltransferase	NMNAT1	Q53GL1	1.16	1.09	1.15
TATA-binding protein-associated factor 2N	TAF15	Q92804-2	1.11	1.11	1.15
DNA-directed RNA polymerase	POLR2B	C9J4M6	0.88	0.98	1.15
Replication protein A 32 kDa subunit	RPA2	Q5TEJ7	0.93	1.07	1.15
Nucleolar and coiled-body phosphoprotein 1	NOLC1	B2RAU8	0.84	0.79	1.14
Scavenger receptor class B member 1	SCARB1	A0A0S2Z3I2	1.07	0.83	1.14
Chromatin complexes subunit BAP18	C17orf49	F8W038	1.38	1.51	1.14
Golgin subfamily A member 3	GOLGA3	Q08378-2	0.85	0.95	1.14
Probable cysteine--tRNA ligase, mitochondrial	CARS2	F5H579	0.81	0.84	1.14

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	C9JLU1	1.02	1.15	1.14
Vesicle-trafficking protein SEC22b	SEC22B	O75396	1.13	1.01	1.14
Peroxiredoxin-4	HEL-S-97n	V9HW63	0.87	0.80	1.14
General transcription factor 3C polypeptide 4	GTF3C4	Q05CN7	0.97	1.01	1.14
Sortilin-related receptor	SORL1	A0A024R3H2	1.17	0.78	1.14
Cytochrome c oxidase subunit 6C	COX6C	A0A024R9B7	0.93	0.83	1.14
Stimulator of interferon genes protein	TMEM173	A0A494C0W5	1.20	1.11	1.14
Nck-associated protein 1	NCKAP1	B3KMK7	1.12	1.19	1.14
Nucleolar and coiled-body phosphoprotein 1	NOLC1	B2RAU8	0.92	1.00	1.14
Hypoxia up-regulated protein 1	HYOU1	A0A087X054	0.93	0.80	1.14
DDRGK domain-containing protein 1	DDRGK1	Q96HY6	1.17	1.31	1.14
Calnexin	CANX	P27824	0.93	0.90	1.14
Signal peptidase complex subunit 3	SPCS3	D3DP46	0.95	0.95	1.14
Exosome complex component MTR3	EXOSC6	Q5RKV6	0.92	0.88	1.14
39S ribosomal protein L4, mitochondrial	MRPL4	K7ES61	1.19	1.08	1.14
SWI/SNF complex subunit SMARCC1	SMARCC1	Q05CR1	0.73	0.94	1.14
Nuclear pore complex protein Nup93	NUP93	A8K897	1.11	1.21	1.14
GDP-fucose protein O-fucosyltransferase 1	POFUT1	Q9H488	0.83	0.75	1.14
AP-2 complex subunit alpha-1	AP2A1	O95782-2	1.00	1.02	1.14
Endoplasmic	TRA1	Q5CAQ5	0.91	0.81	1.13
Pleckstrin homology domain-containing family O member 2	PLEKHO2	B3KTW8	1.40	1.29	1.13
Calpastatin	CAST	A0A1S5UZ18	1.15	1.16	1.13
Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	QRSL1	B2RBJ8	0.84	0.96	1.13
Actin, alpha cardiac muscle 1	ACTC1	P68032	2.07	1.10	1.13
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	A0A0S2Z3L2	0.94	0.85	1.13
Actin, cytoplasmic 1	PS1TP5BP1	Q1KLZ0	0.94	0.85	1.13
U2 snRNP-associated SURP motif-containing protein	U2SURP	E7ET15	1.54	1.34	1.13
Protein MON2 homolog	MON2	B7ZM73	1.29	1.61	1.13
Vesicle-associated membrane protein 3	VAMP3	Q6FGG2	0.97	0.98	1.13
Tripartite motif-containing protein 29	TRIM29	Q53G41	1.03	1.39	1.13
WD repeat-containing protein 5	WDR5	V9GYQ5	1.17	1.02	1.12
Keratin, type II cytoskeletal 1	KRT1	H6VRG2	1.44	1.40	1.12
Prolyl 3-hydroxylase 1	LEPRE1	Q32P28-4	0.98	0.92	1.12
Sec1 family domain-containing protein 1	SCFD1	B7Z5N7	1.02	1.01	1.12
Cytochrome c	CYCS	C9JFR7	0.98	0.81	1.12
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	O96008-2	0.75	0.81	1.12
Thyroid hormone receptor-associated protein 3	THRAP3	A0A3B3ITZ9	1.45	1.49	1.12
ERO1-like protein alpha	ERO1L	Q96HE7	0.90	0.81	1.12

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Guanine nucleotide-binding protein subunit alpha-11	GNA11	Q59FM5	0.95	0.99	1.12
Retinoblastoma-binding protein 5	RBBP5	A0A024R9B5	1.23	0.89	1.12
Nodal modulator 2	NOMO3	J3KN36	0.90	0.87	1.12
26S proteasome non-ATPase regulatory subunit 7	PSMD7	P51665	1.01	1.17	1.12
Beta-catenin-like protein 1	CTNNBL1	A0A087WUB9	1.44	1.19	1.12
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	Q05CK9	1.03	0.94	1.12
Cyclin-H	CCNH	D6RHI7	0.85	0.84	1.12
60S ribosomal protein L31	RPL31	Q76N53	1.21	0.94	1.12
ADP-ribosylation factor 6	ARF6	Q5U025	0.90	1.04	1.12
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	B2RD24	0.84	0.77	1.12
Heterogeneous nuclear ribonucleoprotein K	HNRPK	A0A024R228	1.06	1.00	1.12
Raftlin	RFTN1	C9JHG2	1.48	1.11	1.12
Alpha-2-macroglobulin receptor-associated protein	LRPAP1	B2R6S9	0.92	0.99	1.12
Laminin subunit beta-3	LAMB3	A0A0S2Z3R6	0.98	0.74	1.12
Mannosyl-oligosaccharide glucosidase	MOGS	A0A384MDR6	0.75	0.85	1.11
Protein disulfide-isomerase TMX3	TMX3	Q3B7X1	1.12	1.18	1.11
Eukaryotic translation initiation factor 3 subunit J	EIF3J	H0YGY7	0.86	0.89	1.11
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	Q7LD69	0.78	0.77	1.11
Nuclear pore complex protein Nup133	NUP133	A0A024R3R6	0.89	0.63	1.11
78 kDa glucose-regulated protein	HEL-S-89n	V9HWP4	0.96	0.80	1.11
Secretory carrier-associated membrane protein 2	SCAMP2	H3BV04	0.96	1.17	1.11
SUMO-activating enzyme subunit 1	SAE1	A0A024R0R4	1.02	0.99	1.11
Probable ATP-dependent RNA helicase DDX20	DDX20	Q8TDR3	1.05	1.52	1.11
Proteasome subunit alpha type	PSMA3	Q6IB71	1.10	1.06	1.11
DNA replication licensing factor MCM6	MCM6	Q14566	0.78	1.01	1.10
Serine palmitoyltransferase 2	SPTLC2	A0A024R6H1	0.74	0.82	1.10
Histone H4	HIST1H4H	B2R4R0	0.84	0.79	1.10
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	B3KM81	0.83	0.88	1.10
Zinc transporter SLC39A7	SLC39A7	B4DZZ8	0.98	1.09	1.10
Translocation protein SEC63 homolog	SEC63	B3KQF0	0.88	0.87	1.10
E3 ubiquitin-protein ligase RBBP6	RBBP6	A0A2R8Y880	1.03	1.89	1.10
Peptidyl-prolyl cis-trans isomerase	HEL-S-39	V9HWC6	0.89	0.80	1.10
Quinone oxidoreductase	CRYZ	C9JH92	0.39	1.01	1.10
WD40 repeat-containing protein SMU1	SMU1	A0MNN4	0.09	1.88	1.10
Poly(U)-binding-splicing factor PUF60	PUF60	Q9UHX1-6	1.12	1.12	1.10
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	O00425	1.17	1.16	1.10
RNA-binding protein 8A	RBM8	A0A023T787	0.99	0.93	1.10
EF-hand domain-containing protein D2	EFHD2	A0A024QZ77	1.12	1.10	1.10
Anaphase-promoting complex subunit 7	ANAPC7	B3KMP2	0.81	0.99	1.10

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Mitochondrial import inner membrane translocase subunit TIM14	DNAJC19	A0A0S2Z5X1	0.73	0.88	1.10
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	PLOD2	E7ETU9	0.69	0.62	1.10
U6 snRNA-associated Sm-like protein LSm7	LSM7	O75243	0.95	1.06	1.09
Katanin p60 ATPase-containing subunit A-like 2	KATNAL2	K7EM02	1.03	0.92	1.09
Signal recognition particle 9 kDa protein	SRP9	P49458	1.08	1.02	1.09
Myeloid-derived growth factor	MYDGF	M0QXF7	0.66	0.77	1.09
Extended synaptotagmin-2	ESYT2	A0A499FIX8	2.04	0.84	1.09
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	Q53SW4	0.99	0.77	1.09
Cytochrome b-c1 complex subunit 7	UQCRB	B2R4A2	0.83	0.72	1.09
Ras-related protein Rab-39A	RAB39A	Q14964	0.82	0.97	1.09
Ras GTPase-activating-like protein IQGAP1	IQGAP1	A4QPB0	1.05	1.08	1.09
Armadillo repeat-containing protein 8	ARMC8	G5E9V7	1.15	1.16	1.09
GTP-binding protein SAR1a	SAR1A	Q8NG23	0.87	1.17	1.09
Signal recognition particle 14 kDa protein	SRP14	P37108	0.93	0.88	1.09
U2 small nuclear ribonucleoprotein B	SNRPB2	Q86YK2	0.99	0.85	1.09
Proteolipid protein 2	PLP2	A0A024QYW3	0.82	0.98	1.09
Sodium-coupled neutral amino acid transporter 1	SLC38A1	Q8NCD8	0.84	0.72	1.09
Ubiquitin carboxyl-terminal hydrolase	USP14	B3KTG4	0.96	1.45	1.09
Procollagen galactosyltransferase 1	COLGALT1	Q8NB5	0.82	0.68	1.09
UBE2L3/KRAS fusion protein	UBE2L3/KRAS	#N/A	1.19	1.19	1.09
Histone H3.1	HIST1H3A	P68431	0.84	0.74	1.09
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	S4R3H4	1.17	1.20	1.09
Clathrin heavy chain	CLTC	A0A087WVQ6	1.01	1.02	1.09
CUGBP Elav-like family member 1	CELF1	G5EA30	1.23	1.02	1.08
Fructose-bisphosphate aldolase	ALDOC	B7Z1N6	1.06	1.56	1.08
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	B4DSU9	0.83	0.81	1.08
Barrier-to-autointegration factor	BANF1	B2R4V4	0.82	1.02	1.08
Pituitary tumor-transforming gene 1 protein-interacting protein	PTTG1IP	A8MZH8	0.83	0.88	1.08
4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	B4DYY1	0.97	0.95	1.08
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	F5H669	0.98	0.92	1.08
Renin receptor	ATP6AP2	A0A1B0GVC7	1.25	1.54	1.08
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	Q07021	0.76	1.23	1.08
Lanosterol 14-alpha demethylase	CYP51A1	A0A0C4DFL7	0.80	0.86	1.08
S-phase kinase-associated protein 1	SKP1	E5RI56	0.89	1.04	1.08
Gamma-interferon-inducible protein 16	IFI16	D3DUZ3	1.05	1.05	1.08
Proteasome subunit alpha type	PSMA6	A0A140VK44	0.98	1.15	1.08

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Dynein light chain 1, cytoplasmic	DNCL1	Q6FGH9	1.06	1.35	1.08
60S acidic ribosomal protein P2	RPLP2	A0A024RCA7	0.94	1.03	1.08
Splicing factor 3A subunit 1	SF3A1	A0A024R1K8	0.89	0.79	1.08
Peroxisomal membrane protein PEX16	PEX16	Q9Y5Y5	1.13	0.85	1.08
Ribosomal RNA processing protein 1 homolog B	RRP1B	Q14684-2	1.42	1.37	1.08
Methionine aminopeptidase 1	DKFZp781C0419	Q5CZ91	1.38	1.12	1.07
DNA helicase	MCM2	B4DSV5	1.05	0.91	1.07
Far upstream element-binding protein 2	KHSRP	A0A384P5V3	1.00	0.96	1.07
Transformer-2 protein homolog beta	DKFZp686F18120	Q8N1H4	1.46	0.96	1.07
Treacle protein	TCOF1	Q13428-2	0.94	0.87	1.07
WD repeat-containing protein 61	WDR61	H0YMF9	0.91	0.96	1.07
Kidney mitochondrial carrier protein 1	SLC25A30	E5RIS9	0.80	0.88	1.07
Ras-related protein Rab-8A	RAB8A	A0A024R7I3	1.45	1.29	1.07
Glucosamine-6-phosphate isomerase	GNPDA1	B3KMV2	0.66	0.66	1.07
Protein NDRG1	TRG14	Q597H1	1.15	1.28	1.07
Unconventional myosin-Ic	MYO1C	F5H6E2	0.86	0.95	1.07
60S ribosomal protein L12	RPL12	P30050	1.05	1.02	1.07
Double-strand break repair protein MRE11A	MRE11A	F8W7U8	1.58	1.24	1.07
Proteasome subunit beta type-2	PSMB2	A0A140VJS6	1.08	1.16	1.07
Importin subunit alpha	KPNA3	Q53F09	1.08	1.11	1.07
Phosphatidylinositol-binding clathrin assembly protein	PICALM	B5BU72	1.01	1.10	1.07
MICAL-like protein 1	MICALL1	Q8N3F8	1.00	1.04	1.06
Single-stranded DNA-binding protein	SSBP1	Q567R6	0.91	0.96	1.06
Dystonin	DST	E9PHM6	0.97	1.25	1.06
Integrin alpha-6	ITGA6	P23229-4	0.85	0.71	1.06
26S protease regulatory subunit 6A	PSMC3	R4GNH3	0.97	0.91	1.06
E3 UFM1-protein ligase 1	UFL1	B7ZAY8	1.06	1.07	1.06
RILP-like protein 1	RILPL1	A0A1B0GVV3	0.74	0.91	1.06
39S ribosomal protein L23, mitochondrial	MRPL23	H7C2P7	0.60	0.44	1.06
NADH-ubiquinone oxidoreductase chain 5	ND5	A0A0N7BBR4	0.91	0.67	1.06
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	B4DGN8	0.87	1.00	1.06
N-acetylglucosamine-6-sulfatase	GNS	F5H4C6	0.88	0.74	1.06
Myosin-10	MYH10	P35580	1.16	1.25	1.06
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	FNTA	B3KVN2	0.97	1.20	1.06
Protein AATF	AATF	Q9NY61	0.95	1.09	1.06
Ribose-phosphate pyrophosphokinase 1	PRPS1	B1ALA9	1.49	1.78	1.06
CD44 antigen	CD44	H0YE40	1.05	0.78	1.06
Signal recognition particle subunit SRP68	SRP68	Q9UHB9-4	1.14	1.31	1.06
Carbonic anhydrase 2	HEL-76	V9HW21	0.98	1.76	1.05

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Filamin-B	FLNB	O75369-2	1.07	1.00	1.05
Phosphatidylinositol glycan anchor biosynthesis class U protein	PIGU	B4DXB6	0.73	0.87	1.05
Erlin-1	ERLIN1	B2RDK6	0.85	0.90	1.05
Secretory carrier-associated membrane protein 4	SCAMP4	Q969E2-2	0.68	0.71	1.05
DNA repair protein RAD50	RAD50	A0A494C1B7	0.17	0.71	1.05
Reticulon-4	RTN4	Q9NQC3-2	0.98	0.91	1.05
Proteasome subunit beta type-4	PSMB4	A0A140VK46	0.88	0.98	1.05
Rho GTPase-activating protein 1	ARHGAP1	Q07960	1.00	0.98	1.05
H/ACA ribonucleoprotein complex non-core subunit NAF1	NAF1	Q96HR8-2	0.85	0.94	1.05
NEDD8	NEDD8	Q15843	1.06	1.03	1.05
Lysophospholipid acyltransferase 7	MBOAT7	B4DDH8	0.89	0.95	1.05
Transcription intermediary factor 1-beta	TRIM28	Q13263	0.92	0.91	1.05
Dynactin subunit 1	DKFZp686I0746	Q6MZZ3	1.39	1.22	1.05
Alpha-2-macroglobulin-like protein 1	A2ML1	A8K2U0	0.76	0.35	1.05
NAD(P)H-hydrate epimerase	APOA1BP	B4DP80	1.02	1.26	1.05
NEDD4 family-interacting protein 1	NDFIP1	Q9BT67-2	0.99	0.96	1.04
26S proteasome non-ATPase regulatory subunit 6	PSMD6	Q15008	1.18	1.22	1.04
Neuroblastoma-amplified sequence	NBAS	H7BZU5	0.95	0.92	1.04
Matrin-3	DKFZp686K23100	Q68D11	1.04	0.92	1.04
DNA mismatch repair protein Msh2	MSH2	V9H023	1.02	1.06	1.04
Protein SET	SET	Q5VXV3	1.06	1.09	1.04
Phosphate carrier protein, mitochondrial	SLC25A3	Q8NCF7	0.88	0.74	1.04
E3 ubiquitin-protein ligase KCMF1	KCMF1	Q9P0J7	0.95	1.35	1.04
Mixed lineage kinase domain-like protein	DKFZp667E1714	Q5JPC5	1.11	1.01	1.04
Thymidine phosphorylase	TYMP	A0A494C1N7	0.81	1.34	1.04
Calmodulin-3	CALM3	P0DP25	0.88	1.08	1.04
Peptidyl-prolyl cis-trans isomerase	PPIF	B2R6X6	0.82	0.60	1.04
Protein transport protein Sec24C	SEC24C	B4DSN3	0.82	1.19	1.04
Proteasome subunit beta type-5	PSMB5	P28074	1.07	1.15	1.04
Alpha-actinin-1	ACTN1	A0A024R694	1.03	1.02	1.04
Filamin-A	FLNA	P21333-2	1.03	1.06	1.04
Serine/threonine-protein phosphatase 4 regulatory subunit 1	PPP4R1	A8K923	1.75	1.38	1.04
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	B3KNF6	0.75	0.86	1.04
Fragile X mental retardation syndrome-related protein 2	FXR2	P51116	1.42	1.24	1.04
DnaJ homolog subfamily C member 8	DNAJC8	O75937	1.08	0.95	1.04
Protein canopy homolog 2	CNPY2	F8VXJ7	0.73	0.71	1.04
39S ribosomal protein L3, mitochondrial	MRPL3	E9PF06	0.88	0.98	1.03
Actin, cytoplasmic 2	ACTG1	P63261	0.99	0.93	1.03
Tissue factor	F3	B2R6M5	0.97	0.80	1.03

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Mitochondrial fission 1 protein	FIS1	Q9Y3D6	0.69	1.14	1.03
Proteasome subunit beta type	PSMB7	Q86U62	1.00	1.05	1.03
Nucleoporin NDC1	NDC1	B4DZG6	0.84	0.91	1.03
Signal recognition particle receptor subunit beta	SRPRB	Q549N5	0.97	0.99	1.03
Sodium-coupled neutral amino acid transporter 2	SLC38A2	F8VUY8	0.95	0.89	1.03
Aldehyde dehydrogenase, mitochondrial	ALDH2	Q53FB6	0.76	0.91	1.03
Laminin subunit gamma-2	LAMC2	Q13753	1.03	0.74	1.03
60S ribosomal protein L14	RPL14	E7EPB3	1.12	1.07	1.03
Glutathione peroxidase	GPX1	A0A087WUQ6	0.90	1.00	1.03
Peptidyl-prolyl cis-trans isomerase	PPIL1	A0A024RCX8	1.03	1.08	1.03
Cysteine dioxygenase type 1	CDO1	Q16878	0.72	1.22	1.03
Nuclear protein localization protein 4 homolog	NPLOC4	A0A024R8R4	1.11	1.20	1.03
39S ribosomal protein L28, mitochondrial	MRPL28	A2IDC7	0.86	0.86	1.03
Proteasome subunit beta type	PSMB6	Q6IAT9	1.00	0.91	1.03
Ubiquitin carboxyl-terminal hydrolase 10	USP10	Q14694	1.32	1.04	1.02
AP-2 complex subunit sigma	AP2S1	M0R0N4	0.98	1.06	1.02
Prostaglandin E synthase	hCG_30600	A0A024R8D5	0.68	0.62	1.02
Porphobilinogen deaminase	PBGD	Q68Y91	1.15	1.33	1.02
Ras-related protein Rab-5C	RAB5C	A0A024R1U4	0.92	0.95	1.02
DNA mismatch repair protein Msh6	MSH6	A0A087WWJ1	0.95	1.08	1.02
Catechol O-methyltransferase	COMT	A0A140VJG8	0.90	0.88	1.02
Importin subunit alpha	KPNA1	B3KXZ2	0.98	1.17	1.02
Heterogeneous nuclear ribonucleoprotein K	HNRNPK	B4DUQ1	0.99	0.90	1.02
Vacuolar protein sorting-associated protein 35	VPS35	Q96QK1	1.11	1.19	1.02
cAMP-dependent protein kinase type I-alpha regulatory subunit	DKFZp779L0468	Q68DQ4	1.91	1.35	1.02
Ragulator complex protein LAMTOR5	LAMTOR5	O43504	0.82	0.97	1.02
Tropomyosin alpha-1 chain	TPM1	D9YZV5	1.36	1.19	1.02
Far upstream element-binding protein 1	FUBP1	B4E0X8	0.99	0.93	1.02
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	Q9NPF4	1.00	1.25	1.02
Heat shock 70 kDa protein 4L	HSPA4L	E9PDE8	0.85	1.02	1.02
Exosome complex component RRP42	EXOSC7	B2RDZ9	0.82	1.02	1.02
Superoxide dismutase [Cu-Zn]	HEL-S-44	V9HWC9	1.34	1.45	1.02
Actin-related protein 10	ACTR10	Q53HF6	1.06	1.12	1.02
Ornithine aminotransferase, mitochondrial	OAT	A0A140VJQ4	0.90	0.68	1.02
TOM1-like protein 2	TOM1L2	Q6ZVM7-5	0.92	1.03	1.01
Probable ATP-dependent RNA helicase DDX56	DDX56	G3V0G3	0.89	0.84	1.01
Ribosome-binding protein 1	RRBP1	A7BI36	1.27	1.15	1.01
Nucleolysin TIAR	TIAL1	Q2TSD2	1.02	1.09	1.01
26S protease regulatory subunit 4	PSMC1	Q53XL8	0.97	1.01	1.01

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
UPF0568 protein C14orf166	C14orf166	Q5RLJ0	1.11	1.11	1.01
Casein kinase II subunit alpha	CSNK2A1	A0A2R8YF43	0.94	0.92	1.01
60S ribosomal protein L35	RPL35	F2Z388	1.12	1.04	1.01
26S protease regulatory subunit 6B	PSMC4	A8K2M0	1.01	1.01	1.01
Polymerase delta-interacting protein 2	POLDIP2	B4DEM9	0.96	1.10	1.01
Nuclear autoantigen Sp-100	SP100	C9JBL0	0.90	1.07	1.01
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR	H3BQG3	0.66	0.92	1.01
Vesicle-associated membrane protein 8	VAMP8	Q9BV40	1.40	1.05	1.01
AP-2 complex subunit mu	AP2M1	B4DJB1	0.96	0.91	1.01
Protein AHNAK2	AHNAK2	Q8IVF2-3	1.13	1.42	1.01
Nucleobindin-1	NUCB1	C9JKZ2	0.91	1.26	1.01
V-type proton ATPase catalytic subunit A	ATP6V1A	P38606-2	0.86	1.01	1.01
Histone H2A	HIST1H2AH	A3KPC7	0.48	1.52	1.00
Signal peptidase complex subunit 1	SPCS1	A0A5F9YFS9	1.09	0.85	1.00
Reticulocalbin-1	HEL-S-84	V9HW95	0.67	0.70	1.00
60S ribosomal protein L18	RPL18	Q0QEW2	0.96	0.98	1.00
Small nuclear ribonucleoprotein F	SNRPF	P62306	1.00	0.71	1.00
Clathrin light chain B	CLTB	A0A024R7S3	0.91	1.05	1.00
60S ribosomal protein L22	RPL22	Q7Z4W8	1.08	1.04	1.00
Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1	H0YIY8	0.91	0.77	1.00
Nucleoporin NUP188 homolog	NUP188	Q5SRE5-2	0.68	0.98	1.00
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	B4DRZ6	0.94	1.13	1.00
Histone H1.2	HIST1H1C	P16403	1.06	1.01	1.00
Sorting nexin-27	SNX27	A0A2R8Y3S6	0.82	1.01	1.00
ATP-dependent RNA helicase DDX1	DDX1	A3RJH1	0.90	0.89	1.00
60S ribosomal protein L10a	RPL10A	P62906	1.05	1.01	1.00
Serine/threonine-protein phosphatase	HEL-S-80p	V9HW04	0.95	1.07	1.00
Ubiquitin carboxyl-terminal hydrolase	UCHL5	B2RB07	1.04	1.15	1.00
Sialic acid synthase	HEL-S-100	V9HW39	1.31	1.22	1.00
Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	O14745	1.24	1.18	0.99
Ras GTPase-activating protein-binding protein 2	G3BP2	D6RBM9	1.87	1.14	0.99
Peptidyl-prolyl cis-trans isomerase	FKBP3	Q53GD8	1.10	1.27	0.99
Protein transport protein Sec23A	SEC23A	F5H365	1.16	1.13	0.99
Keratin, type II cytoskeletal 6B	KRT6B	P04259	0.73	1.55	0.99
Flap endonuclease 1	FEN1	B4DWZ4	1.01	1.03	0.99
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	CHCHD2	Q9Y6H1	0.98	1.01	0.99

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Major vault protein	MVP	B4DXN0	1.04	1.02	0.99
COP9 signalosome complex subunit 4	COPS4	Q53FV3	1.11	1.12	0.99
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	H3BPE1	0.93	1.12	0.99
26S proteasome non-ATPase regulatory subunit 13	PSMD13	A0A024R201	0.91	1.05	0.99
Prefoldin subunit 5	PFDN5	Q99471	0.78	0.91	0.99
Transcription elongation factor B polypeptide 1	TCEB1	A0A024R7Y5	1.06	1.34	0.99
60S ribosomal protein L13a	RPL13A	Q5QTS3	1.00	0.98	0.99
Proteasome activator complex subunit 3	HEL-S-283	V9HWJ8	1.03	0.97	0.98
E3 ubiquitin-protein ligase HUWE1	HUWE1	A0A024R9Y3	0.89	0.98	0.98
26S proteasome non-ATPase regulatory subunit 11	PSMD11	O00231	0.97	1.03	0.98
Ras GTPase-activating protein 1	RASA1	B4DTL8	0.96	1.04	0.98
Protein RCC2	RCC2	A5PLK7	1.22	1.23	0.98
Heterogeneous nuclear ribonucleoprotein H3	HNRPH3	Q53F48	1.09	0.93	0.98
Reticulocalbin-2	RCN2	Q14257	0.80	0.84	0.98
V-type proton ATPase subunit B, brain isoform	ATP6V1B2	B4DFM5	0.93	0.88	0.98
Partner of Y14 and mago	WIBG	Q9BRP8-2	1.07	1.40	0.98
Fatty aldehyde dehydrogenase	ALDH3A2	J3QRD1	0.52	0.79	0.98
Proteasome subunit alpha type-1	PSMA1	P25786	1.05	1.08	0.98
60S ribosomal protein L27	RPL27	B2R4D8	0.97	0.94	0.98
AP complex subunit beta	AP2B1	H0UID5	0.98	0.95	0.98
Nuclear cap-binding protein subunit 1	NCBP1	A0A024R179	1.00	1.37	0.98
Prolyl 4-hydroxylase subunit alpha-2	P4HA2	Q05DA4	0.89	0.82	0.98
26S proteasome non-ATPase regulatory subunit 1	PSMD1	B2R6D0	0.97	0.97	0.98
Transaldolase	TALDO1	A0A140VK56	1.10	1.17	0.98
60S ribosomal protein L6	RPL6	Q8TBK5	1.05	0.99	0.97
Methionine adenosyltransferase 2 subunit beta	MAT2B	H7C0X7	1.15	0.64	0.97
26S proteasome non-ATPase regulatory subunit 8	PSMD8	K7EJR3	0.89	1.13	0.97
DNA-(apurinic or apyrimidinic site) lyase	APEX1	Q5TZP7	0.99	1.00	0.97
60S ribosomal protein L7	RPL7	A0A024R814	1.06	1.03	0.97
Signal recognition particle receptor subunit alpha	SRPR	Q6IAX9	1.02	0.92	0.97
Protein S100-A3	S100A3	P33764	1.20	1.24	0.97
Polypyrimidine tract-binding protein 3	ROD1	A0A024R163	0.71	1.07	0.97
Putative 60S ribosomal protein L39-like 5	RPL39P5	Q59GN2	1.11	1.18	0.97
Proteasome subunit alpha type	PSMA4	H0YMZ1	0.91	1.01	0.97
Splicing factor 1	SF1	A0A024R588	0.96	0.87	0.97
Importin subunit alpha-3	KPNA4	O00629	1.10	1.01	0.97
Protein S100-A6	S100A6	P06703	0.96	1.26	0.97
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	A0A024R983	0.92	0.82	0.97
WD repeat-containing protein 13	WDR13	B2RBN3	1.51	1.02	0.97

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Vacuolar protein sorting-associated protein 26A	VPS26A	A8K3C1	0.96	1.01	0.97
Tyrosine-protein phosphatase non-receptor type	PTPN1	A8K3M3	1.36	0.99	0.97
Differentially expressed in FDCP 6 homolog	DEF6	H0Y7V7	0.87	1.05	0.96
GMP synthase [glutamine-hydrolyzing]	GMPS	A0A140VJK6	0.93	0.94	0.96
60S ribosomal protein L35a	RPL35A	P18077	0.95	1.05	0.96
Coatomer subunit gamma	COPG2	Q9H9B7	0.88	1.05	0.96
Protein S100-A10	S100A10	Q6FGE5	0.95	1.12	0.96
Proteasome subunit alpha type	PSMA2	A0A024RA52	0.93	0.99	0.96
Dr1-associated corepressor	DRAP1	E9PNC7	0.85	0.90	0.96
Glyoxalase domain-containing protein 4	GLOD4	B3KV49	0.92	1.07	0.96
Oligoribonuclease, mitochondrial	REXO2	H0YG54	0.88	1.00	0.96
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	D6RBD7	1.00	1.01	0.96
CTTNBP2 N-terminal-like protein	CTTNBP2NL	B1AMN7	1.17	1.36	0.96
Low molecular weight phosphotyrosine protein phosphatase	ACP1	F2Z2Q9	0.97	1.00	0.96
Tax1-binding protein 3	TAX1BP3	O14907	1.05	1.16	0.96
Putative helicase MOV-10	MOV10	Q5JR04	1.13	1.20	0.96
26S protease regulatory subunit 8	PSMC5	A0A140VJS3	0.95	0.94	0.96
Cullin-1	CUL1	B3KU45	1.31	1.24	0.96
ADP-ribosylation factor-binding protein GGA2	GGA2	H3BMN6	0.71	1.26	0.96
Protein arginine N-methyltransferase 1	PRMT1	A0A3Q8AM27	0.97	0.89	0.96
Coronin	CORO1C	Q53G58	0.95	0.96	0.96
Vimentin	HEL113	V9HWE1	1.11	0.89	0.95
tRNA-splicing ligase RtcB homolog	RTCB	Q9Y3I0	0.97	0.99	0.95
60S ribosomal protein L3	RPL3	P39023	1.03	0.98	0.95
SAFB-like transcription modulator	SLTM	H0YKH2	1.42	0.78	0.95
Omega-amidase NIT2	HEL-S-8a	V9HW91	0.93	1.06	0.95
Galectin	LGALS3	Q86TY5	1.21	1.27	0.95
Cytosol aminopeptidase	HEL-S-106	V9HW38	0.91	1.01	0.95
RuvB-like 1	RUVBL1	B5BUB1	0.99	0.97	0.95
Histone acetyltransferase type B catalytic subunit	HAT1	O14929-2	1.22	1.31	0.95
26S protease regulatory subunit 10B	HEL-S-73	V9HW24	0.95	0.97	0.95
60S ribosomal protein L9	RPL9	Q53Z07	1.05	0.99	0.95
Golgi phosphoprotein 3	GOLPH3	B3KQJ9	0.91	1.07	0.95
Inosine triphosphate pyrophosphatase	ITPA	A0A0S2Z423	1.13	1.29	0.95
Alpha-centractin	ACTR1A	B4DM97	1.04	1.13	0.95
MOB kinase activator 1A	MOB1A	Q9H8S9	1.08	2.15	0.95
Transcription elongation factor B polypeptide 2	TCEB2	Q15370	0.95	1.07	0.95
Replication protein A 70 kDa DNA-binding subunit	RPA1	P27694	0.96	1.01	0.95
Cleavage stimulation factor subunit 2	CSTF2	B4DUD5	0.95	0.96	0.95

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Non-specific serine/threonine protein kinase	CDC42BPB	A0A024R6N2	1.57	1.73	0.95
Serine/threonine-protein phosphatase	PPP3CA	Q9UMM5	0.94	0.97	0.95
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	A0A384N605	0.87	0.92	0.95
Splicing factor 3B subunit 2	SF3B2	Q13435	1.00	0.85	0.95
Transportin-1	TNPO1	A0A024RAM0	1.02	1.01	0.95
Tumor protein D54	DKFZp686A1765	Q68E05	0.93	1.01	0.95
DnaJ homolog subfamily C member 7	DNAJC7	A0A6I8PRZ0	1.46	1.32	0.95
Fibrillin-2	FBN2	P35556	1.10	0.77	0.95
60S ribosomal protein L13	RPL13	Q6NZ55	1.15	1.11	0.95
RuvB-like 2	RUVBL2	Q9Y230	0.98	0.96	0.95
COP9 signalosome complex subunit 3	COPS3	Q9UNS2	1.06	1.00	0.95
Protein FAM83H	FAM83H	J3KPS2	1.17	1.39	0.94
Tropomodulin-3	DKFZp686E1899	Q5HYL6	0.97	1.10	0.94
Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	O00154-6	0.92	0.96	0.94
Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	H0YD97	0.80	1.05	0.94
DnaJ homolog subfamily B member 1	DNAJB1	Q6FI51	1.06	1.12	0.94
Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	Q53F35	0.99	1.20	0.94
COP9 signalosome complex subunit 1	GPS1	C9JFE4	0.98	1.03	0.94
Septin-7	SEPT7	B4DNE4	1.25	1.15	0.94
Dehydrogenase/reductase SDR family member 7	DKFZp564H1664	Q659E8	0.59	0.65	0.94
Thyroid hormone receptor-associated protein 3	THRAP3	A0A3B3ITZ9	1.05	1.04	0.94
Non-specific serine/threonine protein kinase	PAK2	A8K5M4	1.01	0.89	0.94
Isoleucine--tRNA ligase, cytoplasmic	IARS	J3KR24	0.97	1.05	0.94
Protein transport protein Sec23B	SEC23B	B4DRA5	1.12	1.03	0.93
High mobility group protein B1	HMGB1	Q5T7C4	1.07	1.06	0.93
60S ribosomal protein L26-like 1	RPL26	J3QRI7	1.28	1.15	0.93
Matrix metalloproteinase-14	MMP14	K4RH61	0.94	0.64	0.93
Proteasome subunit alpha type	PSMA7	Q05DH1	1.01	0.94	0.93
60S ribosomal protein L36	RPL36	Q9Y3U8	0.94	0.98	0.93
Quinone oxidoreductase PIG3	TP53I3	Q53FA7-2	0.97	0.95	0.93
Sorting nexin-6	SNX6	A8K885	1.11	1.20	0.93
Galectin-1	LGALS1	A0A384MR27	0.97	1.10	0.93
Fatty acid-binding protein, epidermal	FABP5	E7DVW5	1.03	1.20	0.93
Proteasome subunit alpha type	PSMA5	Q5U0A0	1.01	1.03	0.93
Clathrin interactor 1	CLINT1	A0A0S2Z4Y4	1.17	1.23	0.93
Syntenin-1	SDCBP	B4DHN5	1.32	1.23	0.93
Unconventional myosin-IId	DKFZp686A01173	Q7Z3N6	1.17	1.00	0.93
Down syndrome critical region protein 3	DSCR3	A8MY26	1.09	1.11	0.93

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Heat shock 70 kDa protein 1B	HEL-S-103	A8K5I0	0.95	1.03	0.93
Eukaryotic translation initiation factor 4 gamma 2	AAG1	Q2TU89	1.05	1.33	0.93
26S proteasome non-ATPase regulatory subunit 14	PSMD14	A0A140VKF2	0.91	0.91	0.93
Egl nine homolog 1	EGLN1	R4SCQ0	1.30	1.04	0.93
U6 snRNA-associated Sm-like protein LSm5	LSM5	B8ZZF8	0.87	0.84	0.93
Importin-8	IPO8	O15397-2	1.73	0.52	0.93
Serrate RNA effector molecule homolog	SRRT	Q9BXP5-4	1.38	1.27	0.93
U6 snRNA-associated Sm-like protein LSm2	LSM2	Q9Y333	1.12	1.23	0.93
EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	A0A0U1RQV3	0.64	0.86	0.93
60S ribosomal protein L4	RPL4	P36578	1.03	0.97	0.93
Rotatin	RTTN	J3KTD2	1.09	1.06	0.93
E3 ubiquitin-protein ligase RBX1	RBX1	P62877	1.00	1.06	0.93
COP9 signalosome complex subunit 2	COPS2	B4DIH5	0.87	1.00	0.92
Proteasome subunit beta type-3	PSMB3	A0A087WUL2	0.79	0.91	0.92
Leucine--tRNA ligase, cytoplasmic	LARS	A0A6I8PRS0	1.03	1.13	0.92
ADP-ribosylation factor 1	ARF3	A0A024R3Q0	0.92	0.95	0.92
Phenylalanine--tRNA ligase beta subunit	FARSB	Q9BR63	0.97	1.02	0.92
Rho guanine nucleotide exchange factor 7	ARHGEF7	E7EUY6	1.27	1.20	0.92
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	A0A669KB10	0.83	0.97	0.92
Transmembrane protein 209	TMEM209	A0A140VJX5	0.82	0.98	0.92
Four and a half LIM domains protein 1	FHL1	A0A0D9SGB2	1.27	1.28	0.92
F-actin-capping protein subunit beta	CAPZB	B2R7T8	1.02	1.12	0.92
26S protease regulatory subunit 7	PSMC2	A0A140VK70	0.98	0.95	0.92
Proteasome assembly chaperone 1	PSMG1	F8WBH7	1.11	1.21	0.92
Integrin alpha-2	ITGA2	E7ESP4	0.97	0.86	0.92
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	B7ZKK7	1.03	0.98	0.92
60S ribosomal protein L7a	RPL7A	P62424	1.00	0.92	0.92
Protein Dr1	DKFZp666G145	Q658N3	0.92	0.82	0.92
Histone H1.3	HIST1H1D	P16402	0.86	0.84	0.92
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	Q12904	1.22	1.15	0.92
Fragile X mental retardation syndrome-related protein 1	FXR1	B4DM78	1.20	1.14	0.92
Tubulin beta-3 chain	TUBB3	Q9BV28	1.39	0.91	0.92
Protein phosphatase 1G	PPM1G	Q6IAU5	0.85	0.99	0.92
Actin-related protein 2/3 complex subunit 5	ARPC5L	B3KPC7	0.89	0.97	0.92
26S proteasome non-ATPase regulatory subunit 3	PSMD3	B3KNN7	1.04	1.04	0.91
Echinoderm microtubule-associated protein-like 2	EML2	K7EKG3	0.96	1.07	0.91
Importin subunit alpha	KPNA6	B4DWX3	0.89	0.95	0.91

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Caveolin	CAV1	Q2TNI1	1.04	0.88	0.91
ATPase ASNA1	ASNA1	O43681	0.92	0.90	0.91
Plakophilin-3	PKP3	Q9Y446	0.97	1.12	0.91
Laminin subunit alpha-3	LAMA3	A0A0A6YYF2	1.14	0.74	0.91
Ubiquitin-like modifier-activating enzyme 1	UBE1	A0A024R1A3	0.95	1.02	0.91
Macrophage-capping protein	HEL-S-66	B4DU58	0.99	1.16	0.91
Protein SCAF8	SCAF8	B7Z876	0.90	0.90	0.91
Transforming acidic coiled-coil-containing protein 1	TACC1	E5RJG6	0.91	0.75	0.91
Activated RNA polymerase II transcriptional coactivator p15	PC4	Q6IBA2	0.99	0.79	0.91
Nucleolar protein 16	NOP16	Q9Y3C1	0.16	1.89	0.91
Protein arginine N-methyltransferase 5	PRMT5	B2RDD7	1.01	1.01	0.91
Peptidyl-prolyl cis-trans isomerase	PPIE	E9PIB0	1.27	1.17	0.91
Unconventional myosin-Ie	MYO1E	Q4KMR3	0.88	1.01	0.91
Mitogen-activated protein kinase	MAPK1	Q499G7	1.17	1.16	0.91
60S ribosomal protein L32	RPL32	D3YTB1	1.11	0.94	0.91
Acetoacetyl-CoA synthetase	AACS	A0A024RBV2	1.24	1.41	0.91
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	P08243-2	0.87	1.08	0.91
60S ribosomal protein L23	RPL23	Q9BTQ7	1.00	0.98	0.91
Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	A0A140VJL6	0.80	0.70	0.91
Myotrophin	DKFZp761E1322	Q69YG1	1.02	1.12	0.91
Acyl-protein thioesterase 1	LYPLA1	Q6IAQ1	0.93	1.04	0.90
Methylosome protein 50	WDR77	H0Y711	1.01	0.85	0.90
60S ribosomal protein L17	RPL17	A0A087WXM6	1.14	0.99	0.90
Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1	PAPSS1	Q4W5H3	0.94	0.97	0.90
Ribosomal protein L15	RPL15	A0A2R8YEM3	1.09	0.98	0.90
DNA primase	PRIM1	F8VSB2	0.99	0.77	0.90
S-adenosylmethionine synthase isoform type-2	MAT2A	A0A140VJP5	1.17	1.00	0.90
Ubiquitin-conjugating enzyme E2 D1	UBE2D1	A0A087WW00	0.90	1.23	0.90
Anterior gradient protein 2 homolog	AGR2	H7C3Z9	0.76	0.71	0.90
Ribosomal protein S6 kinase	RPS6KA1	B7Z2K7	1.16	1.08	0.90
26S proteasome non-ATPase regulatory subunit 5	PSMD5	A8K4T6	1.12	1.12	0.90
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	Q9NZB2-4	1.45	1.20	0.90
Keratin, type II cytoskeletal 5	KRT5	B4E1T1	1.18	0.44	0.90
40S ribosomal protein S21	RPS21	Q8WVC2	0.96	0.91	0.90
Alpha-soluble NSF attachment protein	NAPA	M0R0Y2	1.35	1.03	0.90
Acyl-CoA-binding protein	DBI	P07108	0.94	1.18	0.90
Protein FAM49B	FAM49B	A0A024R9G4	0.92	1.03	0.90
DnaJ homolog subfamily A member 2	DNAJA2	A0A024R6S1	1.05	0.89	0.90
Bleomycin hydrolase	BLMH	K7ES02	1.16	1.33	0.90

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Pleckstrin homology-like domain family B member 1	PHLDB1	Q96D60	1.37	1.16	0.90
CWF19-like protein 1	CWF19L1	A0A286YF56	1.36	1.18	0.90
BH3-interacting domain death agonist	BID	A8ASI8	0.93	1.28	0.90
Aspartate--tRNA ligase, cytoplasmic	DARS	A0A140VJW5	0.99	0.96	0.90
Dynein light chain Tctex-type 1	DYNLT1	P63172	0.88	0.90	0.89
60S acidic ribosomal protein P0	RPLP0	Q53HW2	0.92	0.94	0.89
Multifunctional methyltransferase subunit TRM112-like protein	TRMT112	F5GX77	1.03	1.03	0.89
60S ribosomal protein L23a	RPL23A	H7BY10	1.08	0.91	0.89
60S ribosomal protein L11	RPL11	Q5VVD0	1.13	1.09	0.89
Filamin-binding LIM protein 1	FBLIM1	Q8WUP2-3	0.99	0.90	0.89
Exportin-5	XPO5	Q9H8N6	0.95	0.99	0.89
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	A0A3B3IUB1	1.08	0.97	0.89
Rho-related GTP-binding protein RhoC	RHOC	E9PQH6	0.80	1.15	0.89
Cullin-3	CUL3	B7Z600	0.74	0.95	0.89
60S ribosomal protein L28	RPL28	H0YMF4	1.07	0.91	0.89
Septin-10	SEPT10	E7EW69	1.28	1.28	0.89
Septin-2	SEPTIN2	Q15019	1.00	1.03	0.89
Lysine--tRNA ligase	KARS	Q15046	1.01	0.96	0.89
Deoxycytidylate deaminase	DCTD	P32321	1.15	1.35	0.89
U1 small nuclear ribonucleoprotein C	SNRPC	Q5TAL4	0.96	0.82	0.89
Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	H0YN26	0.90	0.99	0.89
40S ribosomal protein S30	FAU	E9PR30	1.10	1.10	0.89
Dipeptidyl peptidase 3	DKFZp686O1117	B4E357	1.16	1.16	0.89
Phenylalanine--tRNA ligase alpha subunit	FARSLA	Q6IBR2	1.03	1.03	0.89
Bifunctional glutamate/proline--tRNA ligase	EPRS	P07814	1.01	1.02	0.89
RNA-binding protein 39	DKFZp686A11192	Q6N037	0.86	0.81	0.89
Cyclin-G-associated kinase	GAK	Q59HA5	1.02	1.10	0.89
60S ribosomal protein L21	RPL21	Q6IAX2	1.07	0.94	0.88
Vacuolar protein sorting-associated protein 52 homolog	VPS52	B4E225	1.01	1.19	0.88
Proteasome assembly chaperone 2	PSMG2	Q9P1R6	0.97	0.89	0.88
NEDD8-conjugating enzyme Ubc12	UBE2M	A0A024R4T4	0.99	1.09	0.88
Ubiquitin-40S ribosomal protein S27a	RPS27A	A0A248RGE3	0.98	0.91	0.88
Proteasome subunit beta type	PSMB1	Q53FT8	0.92	0.89	0.88
EH domain-containing protein 4	EHD4	A8K9B9	1.04	1.01	0.88
Filamin-A	FLNA	P21333-2	1.07	1.04	0.88
Interferon-related developmental regulator 2	IFRD2	H7C2Z4	0.94	1.06	0.88
Glutathione reductase, mitochondrial	HEL-75	V9HW90	0.96	1.15	0.88
Interferon-induced GTP-binding protein Mx1	MX1	H9KVC7	1.01	1.11	0.88

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
D-tyrosyl-tRNA(Tyr) deacylase	DTD1	Q496C9	1.15	1.29	0.88
40S ribosomal protein S13	RPS13	P62277	1.11	0.98	0.88
40S ribosomal protein S15a	RPS15A	P62244	0.79	0.76	0.88
Exportin-1	XPO1	O14980	0.85	0.91	0.88
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	A8MU58	0.87	1.24	0.88
Septin-11	SEPTIN11	Q9NVA2	0.90	0.87	0.88
40S ribosomal protein S12	RPS12	P25398	1.00	0.98	0.88
Translin-associated protein X	TSNAX	A0A024R3V8	0.96	1.00	0.88
GTP-binding protein 1	GTPBP1	B2RDW9	0.84	0.92	0.88
26S proteasome non-ATPase regulatory subunit 2	PSMD2	Q13200	1.03	0.95	0.88
UV excision repair protein RAD23 homolog B	RAD23B	Q53F10	1.01	1.18	0.88
Lysophosphatidylcholine acyltransferase 1	AYTL2	D3DTC2	0.78	0.78	0.87
Myosin-14	MYH14	Q7Z406	1.03	1.17	0.87
Ladinin-1	LAD1	Q6IPJ9	1.30	1.30	0.87
Malignant T-cell-amplified sequence 1	MCTS1	Q9ULC4	0.97	1.11	0.87
Tubulin-specific chaperone D	TBCD	J3KR97	1.09	1.17	0.87
ATP-binding cassette sub-family F member 2	ABCF2	A0A090N7X1	1.12	1.19	0.87
Cysteine and glycine-rich protein 1	CSRP1	B4DY28	1.21	1.16	0.87
Tensin-4	TNS4	A0A2Z4HJF2	1.03	1.04	0.87
Cytoplasmic dynein 1 light intermediate chain 2	DKFZp686J08252	Q63HJ8	1.02	1.06	0.87
Vacuolar protein sorting-associated protein 51 homolog	VPS51	Q9UID3-2	0.92	0.98	0.87
S-phase kinase-associated protein 1	SKP1	E5RI56	0.90	1.46	0.87
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	Q14204	0.99	0.97	0.87
Protein SEC13 homolog	SEC13	P55735	0.90	0.86	0.87
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	F8W930	1.32	1.32	0.87
Urotensin-2	UTS2	A0AVP6	0.97	0.66	0.87
Ras-related C3 botulinum toxin substrate 1	RAC1	A4D2P2	1.03	0.95	0.87
Serpin B5	SERPINB5	A0A024R2B6	0.98	1.15	0.87
Eukaryotic translation initiation factor 3 subunit K	EIF3K	B4DVD7	0.96	1.12	0.87
RNA-binding protein 3	RBM3	A0A024QYX3	1.05	0.82	0.87
Synapse-associated protein 1	SYAP1	Q53GS5	1.23	1.07	0.87
Prostaglandin E synthase 3	PTGES3	A0A024RB32	1.07	1.14	0.87
DnaJ homolog subfamily C member 17	DNAJC17	S4R343	1.06	0.99	0.87
Peroxisomal biogenesis factor 19	PEX19	B7Z6I5	1.00	1.50	0.87
Glycylpeptide N-tetradecanoyltransferase	NMT1	Q96HI4	0.94	0.93	0.86
NEDD8-activating enzyme E1 catalytic subunit	UBE1C	J3JZZ9	1.00	1.05	0.86
Septin-9	SEPTIN9	Q9UHD8	1.00	1.07	0.86
60S ribosomal protein L34	RPL34	A1LUY1	1.04	1.07	0.86
60S acidic ribosomal protein P1	RPLP1	Q7Z612	0.92	0.90	0.86

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Cancer-related nucleoside-triphosphatase	C1orf57	Q5TDE9	0.75	0.96	0.86
Arginine--tRNA ligase, cytoplasmic	RARS	P54136-2	1.04	0.99	0.86
Thioredoxin-like protein 1	HEL-S-114	V9HW51	1.19	1.03	0.86
Absent in melanoma 1 protein	AIM1	A0A0J9YWL0	1.20	1.30	0.86
Rab3 GTPase-activating protein catalytic subunit	RAB3GAP1	D3DP75	1.30	1.14	0.86
182 kDa tankyrase-1-binding protein	TNKS1BP1	A0A024R542	0.98	1.24	0.86
40S ribosomal protein S14	RPS14	A0A2R8Y811	1.00	0.97	0.86
AP-1 complex subunit beta-1	AP1B1	Q10567-4	0.85	0.93	0.86
Copine-1	CPNE1	A6PVH9	0.98	0.98	0.86
Proteasome inhibitor PI31 subunit	PSMF1	B4DFK1	1.02	1.14	0.86
Protein transport protein Sec31A	SEC31L1	A0A1S5UZ19	1.15	1.17	0.86
Uroporphyrinogen decarboxylase	UROD	A0A494C085	1.11	1.12	0.86
40S ribosomal protein S19	RPS19	B0ZBD0	1.01	0.90	0.86
Tight junction protein ZO-2	TJP2	A0A3B3IRV6	0.87	0.93	0.86
Huntingtin-interacting protein K	hCG_2003792	A0A024R5Q1	0.98	1.23	0.86
Transforming protein RhoA	RHOA	A0A024R324	0.87	1.00	0.86
Plastin-1	PLS1	Q14651	1.09	1.12	0.86
Caldesmon	CALD1	E7EX44	1.19	1.21	0.86
SUMO-conjugating enzyme UBC9	UBE2I	P63279	0.92	0.74	0.86
Aminoacylase-1	HEL-S-5	A0A1B0GU86	0.89	1.09	0.86
Myosin regulatory light chain 12B	MYL12B	O14950	0.92	1.07	0.86
Golgi reassembly-stacking protein 2	GORASP2	B4DEI4	0.95	0.97	0.85
Heat shock cognate 71 kDa protein	HEL-S-72p	V9HW22	1.03	0.93	0.85
Tyrosine--tRNA ligase, cytoplasmic	YARS	A0A0S2Z4R1	0.93	1.16	0.85
Mannose-1-phosphate guanyltransferase beta	GMPPB	A0A024R329	0.79	1.11	0.85
N-acetylserotonin O-methyltransferase-like protein	ASMTL	B4DN81	1.31	1.29	0.85
Charged multivesicular body protein 3	CHMP3	Q9Y3E7-2	0.97	1.14	0.85
Glycogen debranching enzyme	AGL	G1UI17	0.87	0.73	0.85
Thioredoxin	TXN	H9ZYJ2	1.06	1.08	0.85
Dedicator of cytokinesis protein 9	DOCK9	X6RGR3	1.00	0.80	0.85
Glutamine--tRNA ligase	QARS	Q53HS0	0.96	1.00	0.85
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	P41091	1.01	0.97	0.85
60S ribosomal protein L5	RPL5	A0A2R8Y6J3	0.96	0.86	0.85
Phosphatidylinositol transfer protein beta isoform	PITPNB	B3KYB6	1.30	1.05	0.85
Serine/arginine repetitive matrix protein 2	KIAA0324	O60382	0.99	0.75	0.85
Protein flightless-1 homolog	FLII	Q13045-2	0.74	0.94	0.85
60S ribosomal protein L27a	RPL27A	Q6NZ52	1.03	0.90	0.85
Transketolase	HEL107	V9HWD9	1.01	1.00	0.85
Protein DPCD	DPCD	Q5JQQ4	1.18	1.15	0.85

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Casein kinase II subunit beta	CSNK2B	N0E466	0.93	0.84	0.85
Zinc finger RNA-binding protein	ZFR	B2RNR6	0.84	0.82	0.85
Eukaryotic translation initiation factor 3 subunit C	EIF3C	B4DVU3	1.05	1.01	0.85
Interferon regulatory factor 6	IRF6	G0Z349	1.07	1.18	0.85
Proteasome-associated protein ECM29 homolog	KIAA0368	J3KN16	1.00	1.00	0.85
Acetyl-coenzyme A transporter 1	SLC33A1	O00400	1.12	1.22	0.85
40S ribosomal protein S25	RPS25	P62851	1.07	1.00	0.85
COP9 signalosome complex subunit 7a	COPS7A	F5H7C6	0.91	1.08	0.85
BRCA2 and CDKN1A-interacting protein	BCCIP	B4E318	0.93	0.88	0.85
Valine--tRNA ligase	VAR5	A0A1U9X9D5	0.90	0.94	0.85
Origin recognition complex subunit 5	ORC5L	B4DXT8	0.88	0.96	0.85
L-lactate dehydrogenase	HEL-S-133P	V9HWB9	1.06	1.14	0.85
40S ribosomal protein S18	RPS18	P62269	1.05	0.98	0.85
Profilin	PFN2	C9JQ45	1.05	1.18	0.85
Proliferating cell nuclear antigen	PCNA	Q6FI35	0.95	0.91	0.85
SEC23-interacting protein	SEC23IP	B3KN10	1.07	1.33	0.85
PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	F8WCD5	1.10	1.30	0.84
Diacylglycerol kinase	DGKA	A0A024RB23	0.94	1.06	0.84
40S ribosomal protein S4	RPS4X	Q96IR1	1.01	0.95	0.84
Rhotekin	RTKN	Q9BST9-3	1.16	1.24	0.84
DIS3-like exonuclease 2	DIS3L2	B4DI15	1.54	1.27	0.84
40S ribosomal protein S7	RPS7	P62081	1.11	1.02	0.84
Exportin-T	XPOT	A0A024RB67	1.00	1.50	0.84
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	Q8NC51-2	1.38	1.21	0.84
Phosphoserine aminotransferase	PSAT1	A0A024R222	0.92	1.25	0.84
Eukaryotic translation initiation factor 3 subunit I	EIF3I	Q5U0F4	1.06	1.00	0.84
Tumor susceptibility gene 101 protein	TSG101	D3DQY6	0.19	0.68	0.84
Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	PIP4K2C	Q8TBX8-2	1.12	1.26	0.84
Small ubiquitin-related modifier	SUMO2	A0A024R8S3	1.62	1.09	0.84
Proteasomal ubiquitin receptor ADRM1	ADRM1	A0A087WUX6	1.03	0.89	0.84
Gephyrin	GPHN	H0YJ30	0.99	0.75	0.84
40S ribosomal protein S4, Y isoform 2	RPS4Y2	Q8TD47	1.23	0.61	0.84
Collagen alpha-1(XVII) chain	COL17A1	A0A3B3ITM2	0.98	0.97	0.84
5-AMP-activated protein kinase subunit gamma-1	PRKAG1	H0YIC9	0.91	1.29	0.84
Cystatin-B	CSTB	Q76LA1	0.97	1.12	0.84
Coatomer subunit alpha	COPA	P53621	1.00	0.95	0.84
Protein phosphatase 1F	PPM1F	B5MCT7	0.97	1.04	0.84
Proline synthase co-transcribed bacterial homolog protein	PROSC	H0YBG2	0.90	0.85	0.84
Peroxiredoxin-2	HEL-S-2a	V9HW12	1.07	1.12	0.84

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein Niban	FAM129A	Q9BZQ8	0.99	1.19	0.84
40S ribosomal protein S3	RPS3	P23396	1.03	0.94	0.84
40S ribosomal protein S8	RPS8	Q5JR94	1.09	0.92	0.84
Putative RNA-binding protein Luc7-like 2	LUC7L2	B3KSL5	0.94	0.99	0.84
Peptidyl-prolyl cis-trans isomerase	PPIH	Q6FH57	0.86	0.97	0.84
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	HEL-S-90n	V9HWJ5	1.19	1.73	0.84
Nuclear autoantigenic sperm protein	NASP	Q5T626	0.92	0.82	0.84
Actin-related protein 2/3 complex subunit 4	ARPC4-TTLL3	F8WCF6	0.94	1.02	0.83
Cullin-associated NEDD8-dissociated protein 1	CAND1	A8K8U1	0.91	0.98	0.83
Inosine-5-monophosphate dehydrogenase 2	IMPDH2	A0A384N6C2	0.99	1.04	0.83
Eukaryotic translation initiation factor 6	EIF6	P56537	0.94	0.87	0.83
Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1	G3V4W4	1.10	1.10	0.83
Lysophosphatidylcholine acyltransferase 2	LPCAT2	H3BU68	0.97	1.09	0.83
Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	X6RAC9	0.95	1.01	0.83
N-alpha-acetyltransferase 50	NAA50	E7EQ69	1.17	0.91	0.83
Poly(rC)-binding protein 2	PCBP2	Q15366-3	0.95	0.95	0.83
40S ribosomal protein S17	RPS17	H3BNC9	1.12	1.00	0.83
Nuclease-sensitive element-binding protein 1	YBX1	P67809	1.23	1.13	0.83
Microtubule-associated protein 1S	MAP1S	A8K940	1.07	0.86	0.83
Tropomyosin alpha-4 chain	HEL-S-108	V9HW56	1.12	0.99	0.83
Dynein light chain roadblock-type 1	DYNLRB2	H3BNG9	0.87	0.89	0.83
Y-box-binding protein 3	CSDA	Q96GD7	1.34	1.10	0.83
Oxysterol-binding protein	OSBPL8	F8VZ43	0.73	0.72	0.83
Ubiquitin-conjugating enzyme E2 K	HIP2	B3KSH4	0.92	0.99	0.83
Coatomer subunit delta	ARCN1	B0YIW5	1.01	0.97	0.83
40S ribosomal protein S15a	hCG_1994130	B2R4W8	1.05	0.93	0.83
Nuclear pore complex protein Nup214	NUP214	A0A494C1F2	1.03	1.03	0.83
Eukaryotic translation initiation factor 3 subunit E	EIF3E	Q6IAX5	1.02	0.98	0.83
Peptidyl-prolyl cis-trans isomerase	FKBP11	F8VU90	0.99	0.83	0.83
Acylamino-acid-releasing enzyme	APEH	C9JIF9	1.14	1.08	0.83
60S ribosomal protein L10	RPL10	X5D2T3	0.97	0.93	0.83
E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	A0A3B3IUA7	1.18	1.06	0.83
Proliferation-associated protein 2G4	PA2G4	A8K6Y1	1.03	1.00	0.83
NEDD8-activating enzyme E1 regulatory subunit	NAE1	Q13564-3	0.92	0.93	0.83
Nicotinate phosphoribosyltransferase	NAPRT	C9J8U2	0.73	1.45	0.83
40S ribosomal protein S2	RPS2	Q3KQT6	1.01	0.90	0.83
60S ribosomal protein L22-like 1	RPL22L1	C9JYQ9	1.21	0.84	0.83
14-3-3 protein beta/alpha	YWHAB	P31946-2	1.05	1.06	0.83
40S ribosomal protein S5	RPS5	M0R0F0	0.96	0.98	0.82

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
60S ribosomal protein L30	RPL30	E5RI99	1.03	0.97	0.82
40S ribosomal protein S3a	RPS3A	Q6NXR8	1.07	0.94	0.82
Polyadenylate-binding protein	PABPC1	A0A024R9C1	1.00	0.89	0.82
Methylthioribose-1-phosphate isomerase	MRI1	Q9BV20-2	0.85	1.05	0.82
Serine/threonine-protein kinase 3	STK3	A0A384MR07	1.08	1.09	0.82
Cytoskeleton-associated protein 5	CKAP5	Q14008-2	1.28	1.16	0.82
Protein kinase C delta-binding protein	PRKCDBP	E9PIE3	0.76	0.65	0.82
Exportin-7	XPO7	A8K607	0.81	0.95	0.82
U6 snRNA-associated Sm-like protein LSM6	LSM6	P62312	1.01	0.96	0.82
Dynactin subunit 2	HEL-S-77	A0A384MDU9	1.02	0.91	0.82
Proteasome activator complex subunit 2	PSME2	Q86SZ7	1.06	1.08	0.82
Protein-L-isoaspartate O-methyltransferase	PCMT1	B7Z972	0.91	0.95	0.82
Elongation factor 1-beta	EEF1B2	A0A024R3W7	0.93	1.04	0.82
Nucleobindin-2	NUCB2	E9PKG6	0.71	0.80	0.82
4F2 cell-surface antigen heavy chain	SLC3A2	F5GZS6	1.15	0.91	0.82
Protein S100-A2	S100A2	P29034	0.89	1.17	0.82
C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	A0A087X2D8	1.18	1.11	0.82
Importin-7	IPO7	O95373	0.99	1.02	0.82
Cytoplasmic FMR1-interacting protein 1	CYFIP1	B3KVV6	1.04	1.03	0.82
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	Q53XC0	0.95	0.94	0.82
D-3-phosphoglycerate dehydrogenase	PHGDH	A0A286YF22	0.93	1.21	0.82
40S ribosomal protein S10	RPS10	P46783	1.04	0.90	0.82
Elongation factor 1-delta	EEF1D	E9PK01	0.85	1.05	0.82
1-Phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	PLCB3	Q01970-2	0.82	0.99	0.82
F-actin-capping protein subunit alpha-1	CAPZA1	P52907	0.99	0.89	0.82
Tubulin alpha-4A chain	TUBA4A	P68366-2	0.99	1.05	0.82
Eukaryotic translation initiation factor 3 subunit A	EIF3A	Q7Z5T5	1.04	0.96	0.82
Niban-like protein 1	C9orf88	A0A024R872	0.92	0.93	0.82
SRSF protein kinase 1	SRPK1	A8K8B2	1.12	1.02	0.81
Redox-regulatory protein FAM213A	FAM213A	Q9BRX8-2	0.77	0.99	0.81
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	B4DFY5	1.17	0.96	0.81
26S proteasome non-ATPase regulatory subunit 12	PSMD12	A0A0S2Z489	0.92	0.90	0.81
UTP-glucose-1-phosphate uridylyltransferase	UGP2	Q53QE9	0.98	0.99	0.81
E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	A0A3B3IUA7	1.33	0.68	0.81
14-3-3 protein zeta/delta	YWHAZ	D0PNI1	1.01	1.16	0.81
Carbonyl reductase [NADPH] 1	CBR1	A0A384NL53	0.98	1.05	0.81
40S ribosomal protein S16	RPS16	M0R210	1.07	0.94	0.81
Signal transducer and activator of transcription	STAT1	J3KPM9	0.93	1.04	0.81
Pyruvate kinase	PKM2	A0A024R5Z9	1.07	0.83	0.81

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
40S ribosomal protein SA	RPSA	C9J9K3	0.99	0.92	0.81
Eukaryotic translation initiation factor 3 subunit M	EIF3M	Q7L2H7	1.05	1.03	0.81
40S ribosomal protein S28	RPS28	B2R4R9	1.03	1.01	0.81
Glucose-6-phosphate 1-dehydrogenase	G6PD	Q2VF42	1.02	1.14	0.81
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	E9KL35	0.96	0.96	0.81
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	B4DDF7	0.97	0.96	0.81
6-phosphogluconolactonase	PGLS	A0A0K0K1K7	0.96	1.05	0.81
Actin-related protein 2/3 complex subunit 2	ARPC2	Q53R19	1.11	1.11	0.81
LIM domain and actin-binding protein 1	LIMA1	F8VQE1	1.05	0.92	0.81
Maleylacetoacetate isomerase	GSTZ1	G3V267	0.96	0.18	0.81
Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	B4E1E2	1.10	0.98	0.81
Bifunctional purine biosynthesis protein ATIC	ATIC	P31939	1.25	1.03	0.81
Endophilin-A2	SH3GL1	Q9UQD4	1.04	1.18	0.81
Protein LZIC	LZIC	K7ES95	0.79	0.93	0.81
Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	A0A087WY55	0.99	0.97	0.81
Elongation factor 1-gamma	EEF1G	Q53YD7	0.97	0.98	0.81
Asparagine--tRNA ligase, cytoplasmic	NARS	O43776	1.02	1.00	0.81
Aldose reductase	AKR1B1	A0A024R7A8	1.18	1.29	0.80
Eukaryotic translation initiation factor 2 subunit 2	EIF2S2	Q6IBR8	1.17	1.22	0.80
Signal transducer and activator of transcription	STAT3	G8JLH9	1.04	0.88	0.80
Eukaryotic translation initiation factor 5	EIF5	Q6IBU0	1.09	1.01	0.80
Importin subunit beta-1	KPNB1	B2RBR9	0.98	0.96	0.80
40S ribosomal protein S24	RPS24	E7ETK0	1.01	0.90	0.80
Serine/threonine-protein kinase 26	STK26	Q8NBY1	0.99	1.06	0.80
Coatomer subunit zeta-1	COPZ1	Q53FU3	0.97	0.89	0.80
Tripeptidyl-peptidase 2	TPP2	A0A494C1B8	1.09	0.99	0.80
Cyclic nucleotide-gated cation channel beta-3	CNGB3	H0YAZ4	0.97	0.98	0.80
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	Q93008-1	0.90	1.09	0.80
Importin-11	IPO11	D6RCN7	0.73	0.87	0.80
Prefoldin subunit 3	VBP1	D3DWY7	0.96	0.92	0.80
Nucleoredoxin	NXN	Q6DKJ4	0.97	1.05	0.80
Eukaryotic translation initiation factor 5A-1	EIF5A	P63241	1.04	1.06	0.80
40S ribosomal protein S6	RPS6	Q96DV6	1.19	1.02	0.80
Apoptosis-associated speck-like protein containing a CARD	PYCARD	B2RAZ4	1.06	1.28	0.80
Staphylococcal nuclease domain-containing protein 1	SND1	B2R5U1	0.97	0.94	0.80
Nicotinamide phosphoribosyltransferase	PBEF1	A0A024R718	0.85	0.96	0.80
Fumarylacetoacetase	FAH	A0A384P5L6	0.86	0.96	0.80
T-complex protein 1 subunit eta	CCT7	Q53HV2	0.98	0.98	0.80
Apoptosis regulator BAX	BAX	Q07812-5	0.94	0.95	0.80

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	C7DUW4	1.61	1.16	0.80
Uncharacterized protein C10orf62	C10orf62	Q5T681	1.47	0.83	0.80
14-3-3 protein gamma	YWHAG	P61981	1.01	1.12	0.80
DnaJ homolog subfamily A member 1	DNAJA1	P31689	1.14	1.01	0.80
Glutathione synthetase	HEL-S-64p	B7Z1C5	0.95	1.08	0.80
High mobility group protein B3	HMGB3	E9PES6	1.39	0.77	0.80
F-box only protein 44	FBXO44	B7Z1X4	0.98	1.31	0.80
Programmed cell death protein 6	PDCD6	Q53FC3	0.96	0.93	0.80
V-type proton ATPase subunit C 1	ATP6V1C1	A0A024R9I0	0.96	0.97	0.80
Coatomer subunit beta	COPB1	P53618	1.02	0.99	0.79
Acetyl-CoA carboxylase 1	hCG_30204	A0A024R0Y2	1.18	1.01	0.79
Protein S100	HEL-S-43	V9HWH9	1.09	1.20	0.79
tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	C14orf172	A0A024R6Q2	0.22	0.89	0.79
Charged multivesicular body protein 1a	CHMP1A	B4DXN3	1.01	1.03	0.79
Glycogen phosphorylase, brain form	PYGB	P11216	0.97	0.94	0.79
N-acetyl-D-glucosamine kinase	NAGK	H7C286	0.81	2.50	0.79
60S ribosomal protein L18a	RPL18A	M0R1A7	1.03	0.82	0.79
Copine-3	CPNE3	A0A024R994	0.88	1.02	0.79
Cellular nucleic acid-binding protein	CNBP	A0A0S2Z4Q3	1.34	1.10	0.79
ATP-citrate synthase	ACLY	A0A024R1T9	1.03	0.95	0.79
Vigilin	HDLBP	B2R5V9	1.08	0.99	0.79
Stress-induced-phosphoprotein 1	HEL-S-94n	V9HW72	1.08	1.01	0.79
Tropomyosin alpha-3 chain	TPM3	A0A0S2Z4I4	1.10	0.98	0.79
Sorting nexin-2	SNX2	Q53GG3	1.23	1.77	0.79
Exonuclease 3-5 domain-containing protein 2	EXD2	B3KP95	1.15	0.96	0.79
Eukaryotic translation initiation factor 3 subunit B	EIF3B	B4DV79	1.02	0.94	0.79
Peroxiredoxin-6	HEL-S-128m	V9HWC7	0.91	1.07	0.79
ATP-dependent 6-phosphofructokinase	PFKM	B4E162	0.95	0.98	0.79
Protein deglycase DJ-1	HEL-S-67p	V9HWC2	0.95	1.02	0.79
Coatomer subunit beta	COPB2	P35606-2	1.00	0.96	0.79
40S ribosomal protein S11	RPS11	P62280	1.09	0.97	0.79
PEST proteolytic signal-containing nuclear protein	PCNP	Q8WW12-2	1.39	1.04	0.79
ARF GTPase-activating protein GIT2	GIT2	F8W822	1.15	1.16	0.79
Malic enzyme	ME1	A8K168	0.95	1.08	0.79
Ubiquitin carboxyl-terminal hydrolase 5	USP5	A0A140VJZ1	0.97	0.98	0.79
Plasminogen activator inhibitor 2	SERPINB2	P05120	0.99	0.86	0.79
Ras suppressor protein 1	RSU1	Q32Q10	1.03	0.99	0.79
Phosphoglucomutase-2	PGM2	Q96G03	0.88	1.03	0.79
General vesicular transport factor p115	USO1	O60763	0.95	0.99	0.79

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Serine/threonine-protein phosphatase	PPP2CA	B3KUN1	0.93	1.16	0.79
PDZ and LIM domain protein 1	HEL-S-112	V9HW92	1.07	1.03	0.79
Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	B4DEA6	0.92	0.97	0.79
ADP-ribosylation factor 4	ARF4	P18085	0.95	0.94	0.78
Protein FAM98A	FAM98A	Q05CT2	0.87	0.84	0.78
T-complex protein 1 subunit gamma	CCT3	B3KX11	0.99	0.94	0.78
Isocitrate dehydrogenase [NADP]	HEL-216	V9HW78	1.04	1.07	0.78
Methionine--tRNA ligase, cytoplasmic	MARS	A8K492	0.98	0.86	0.78
Tubulin-folding cofactor B	TBCB	K7EK42	0.94	0.87	0.78
Transmembrane protein 97	TMEM97	J3KTD1	0.89	0.49	0.78
Carbonyl reductase [NADPH] 3	HEL-S-25	V9HW40	1.05	1.23	0.78
Annexin	ANXA1	Q5TZZ9	0.99	0.98	0.78
Gasdermin-A	GSDMA	Q96QA5	0.84	0.95	0.78
Annexin	ANXA8	B4DQE1	0.90	1.02	0.78
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2	O43678-2	0.86	0.53	0.78
Eukaryotic translation initiation factor 3 subunit G	EIF3G	O75821	1.05	1.05	0.78
40S ribosomal protein S20	RPS20	P60866	1.07	1.02	0.78
Adenine phosphoribosyltransferase	APRT	P07741	0.93	1.15	0.78
Tripartite motif-containing protein 16	TRIM16	B3KMJ2	0.97	0.93	0.78
Serine hydroxymethyltransferase	SHMT1	Q53ET7	0.91	1.28	0.78
Protein unc-45 homolog A	UNC45A	Q9H3U1-2	0.87	1.02	0.78
Gem-associated protein 5	GEMIN5	B7ZLC9	0.87	0.79	0.78
Plastin-3	PLS3	P13797	0.93	1.02	0.78
Histidine triad nucleotide-binding protein 1	HINT1	A0A384NPU2	0.99	0.93	0.78
40S ribosomal protein S9	RPS9	A0A024R4M0	1.07	0.92	0.78
Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	A0A3B3ISQ4	0.90	1.08	0.78
AP-3 complex subunit delta-1	AP3D1	O14617-4	0.85	0.81	0.78
Caprin-1	CAPRIN1	Q14444-2	1.13	0.87	0.78
T-complex protein 1 subunit epsilon	HEL-S-69	V9HW37	0.95	0.93	0.78
Actin-related protein 3	ACTR3	A0A024RAI1	0.96	0.95	0.78
Ribosomal protein L19	RPL19	Q8IWR8	1.07	0.90	0.78
Eukaryotic translation initiation factor 3 subunit L	EIF3L	B3KPB9	1.01	0.99	0.78
T-complex protein 1 subunit zeta	CCT6A	Q59ET3	1.01	0.95	0.78
40S ribosomal protein S26	RPS26	A0A024RB14	1.29	1.09	0.78
Nucleoside diphosphate kinase	NME1-NME2	Q32Q12	1.03	1.00	0.78
Basic leucine zipper and W2 domain-containing protein 1	BZW1	Q53FN7	0.98	0.94	0.78
Ubiquitin-protein ligase E3C	UBE3C	B4DHJ9	1.08	0.75	0.78

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Phosphoglycerate mutase	PGAM1	Q6FHU2	0.96	1.05	0.78
Hsp70-binding protein 1	HSPBP1	K7EMM7	0.93	1.12	0.78
60S ribosomal protein L8	RPL8	E9PKZ0	1.03	0.89	0.78
Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	B4DPZ3	1.08	0.97	0.78
Wiskott-Aldrich syndrome protein family member 2	WASF2	Q05BU7	0.76	0.84	0.78
UPF0505 protein C16orf62	C16orf62	H3BVG8	0.63	0.76	0.78
40S ribosomal protein S23	RPS23	A8K517	1.04	0.87	0.77
N-terminal Xaa-Pro-Lys N-methyltransferase 1	C9orf32	A0A024R8E4	1.00	1.12	0.77
Translational activator GCN1	PRIC295	E1NZA1	0.95	0.95	0.77
Protein CutA	CUTA	O60888-3	0.90	0.91	0.77
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	Q9Y237	1.59	1.61	0.77
Transcriptional repressor p66-beta	GATAD2B	A0A0U1RRM1	1.56	1.02	0.77
Vacuolar protein sorting-associated protein 4B	VPS4B	A8K5D8	1.10	0.99	0.77
STE20-like serine/threonine-protein kinase	SLK	Q9H2G2-2	1.79	1.53	0.77
PDZ and LIM domain protein 4	PDLIM4	A0A0S2Z4P0	1.19	1.11	0.77
Condensin complex subunit 3	NCAPG	Q6NUR1	0.75	0.93	0.77
NudC domain-containing protein 1	NUDCD1	Q96RS6-2	1.16	0.59	0.77
Actin-related protein 2/3 complex subunit 3	ARPC3	Q2LE71	0.97	0.96	0.77
Prolyl endopeptidase	PREP	Q9UM02	0.99	1.13	0.77
EH domain-containing protein 1	EHD1	B2R5U3	1.06	0.88	0.77
UDP-glucose 4-epimerase	GALE	A0A384NL38	0.90	0.91	0.77
Alpha-enolase	ENO1	A0A024R4F1	1.00	0.99	0.77
Kinesin-like protein	HEL-S-61	V9HW29	1.20	1.02	0.77
DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	M4VP52	0.33	0.63	0.77
Profilin-1	PFN1	P07737	0.95	1.00	0.77
Phosphoglycerate kinase	HEL-S-68p	V9HWF4	0.99	0.98	0.77
Myosin-9	MYH9	A0A024R1N1	1.05	0.97	0.77
Protein transport protein Sec24A	SEC24A	B4E205	0.84	1.11	0.77
Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	P62942	1.18	1.16	0.77
Programmed cell death 6-interacting protein	DRIP4	Q4W4Y1	0.98	1.06	0.77
Heat shock 70 kDa protein 4	HSPA4	P34932	0.96	0.92	0.77
Protein diaphanous homolog 1	DIAPH1	A0A2R8Y5N1	0.94	0.97	0.77
T-complex protein 1 subunit delta	CCT4	B7Z9L0	0.89	0.87	0.77
Aspartyl aminopeptidase	DNPEP	Q9BSS9	0.56	0.94	0.77
Coactosin-like protein	COTL1	A0A384MTY2	0.88	1.02	0.77
Eukaryotic translation initiation factor 5B	EIF5B	Q8N5A0	0.92	1.01	0.77
Phosphoglucomutase-1	PGM1	B4DFP1	0.95	1.03	0.77
Myosin light polypeptide 6	MYL6	P60660	0.93	0.90	0.77
Small ubiquitin-related modifier 1	SUMO1	B8ZZJ0	1.14	0.93	0.77

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Chloride intracellular channel protein	CLIC4	Q6FIC5	1.03	1.02	0.76
Glycogen phosphorylase, liver form	PYGL	P06737-2	0.96	0.97	0.76
Ubiquitin carboxyl-terminal hydrolase 15	USP15	Q9Y4E8-2	0.79	0.98	0.76
Ribonuclease inhibitor	RNH1	A0A024RC87	0.91	1.01	0.76
Eukaryotic translation initiation factor 3 subunit F	EIF3F	B4DMT5	0.98	0.89	0.76
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	A0A140VJS9	0.86	0.92	0.76
A-kinase anchor protein 2	AKAP2	C9JVV5	1.80	1.28	0.76
14-3-3 protein sigma	SFN	P31947	1.00	1.05	0.76
SHC-transforming protein 1	SHC1	Q5T187	0.80	1.00	0.76
T-complex protein 1 subunit theta	CCT8	P50990	0.95	0.95	0.76
Coatomer subunit gamma-1	COPG1	Q9Y678	1.00	0.89	0.76
Transcription factor BTF3	BTF3L4	E9PL10	0.83	0.96	0.76
Fermitin family homolog 1	FERMT1	Q49AC8	0.96	0.91	0.76
Gelsolin	GSN	B7Z4U6	0.95	1.02	0.76
Probable ATP-dependent RNA helicase DDX6	DDX6	B2R858	0.99	0.93	0.76
Alpha-ketoglutarate-dependent dioxygenase FTO	FTO	A0A1B0GTZ8	0.99	0.99	0.76
Proteasome activator complex subunit 1	PSME1	A0A384NQ35	1.01	1.32	0.76
Bcl-2-associated transcription factor 1	BCLAF1	Q9NYF8-4	1.03	0.87	0.76
Translationally-controlled tumor protein	TPT1	A0A0P1J1R0	1.03	1.09	0.76
Transportin-3	TNPO3	E9PFH4	0.73	0.81	0.76
5-Nucleotidase domain-containing protein 1	NT5DC1	A8K2Z3	0.73	0.75	0.76
Adenylosuccinate lyase	ADSL	B4DUM2	0.80	0.96	0.76
ATP-dependent RNA helicase DDX3Y	DDX3Y	A0A024R9A4	0.81	0.82	0.76
Puromycin-sensitive aminopeptidase	NPEPPS	B7Z4B2	1.13	1.02	0.76
Cytosolic non-specific dipeptidase	CNDP2	B4DV28	1.04	1.03	0.76
Coatomer subunit epsilon	COPE	Q7Z4Z1	0.93	0.94	0.76
Dynamin-1-like protein	DNM1L	O00429-4	0.90	0.95	0.76
Microtubule-associated protein	MAP4	E7EVA0	1.12	1.07	0.76
Malate dehydrogenase	HEL-S-32	V9HWF2	0.98	0.94	0.76
Receptor-interacting serine/threonine-protein kinase 1	RIPK1	B3KU53	0.84	0.94	0.76
Peroxiredoxin-1	PRDX1	A0A384NPQ2	0.99	1.00	0.76
Clustered mitochondria protein homolog	CLUH	I3L2B0	1.04	0.93	0.76
Interleukin-18	IL18	A0A024R3E0	1.01	0.98	0.76
14 kDa phosphohistidine phosphatase	HEL-S-132P	V9HWC4	0.85	1.05	0.75
Thimet oligopeptidase	THOP1	K7EP46	1.12	1.13	0.75
Protein S100-A13	S100A13	D3DV53	0.59	1.18	0.75
Ubiquitin-conjugating enzyme E2 N	HEL-S-71	V9HW41	1.07	1.17	0.75
Eukaryotic translation initiation factor 3 subunit H	EIF3H	Q5BKY2	0.98	1.03	0.75
GTP-binding nuclear protein Ran	RAN	B5MDF5	0.99	0.91	0.75

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
GSK3-beta interaction protein	GSKIP	G3V368	1.07	1.21	0.75
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	A0A140VJT0	1.03	0.95	0.75
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	V9GZ78	0.96	0.95	0.75
Centrosomal protein of 164 kDa	DKFZp434O2413	Q9NTH6	0.82	0.81	0.75
Gamma-tubulin complex component 2	TUBGCP2	F2Z2B9	0.91	0.94	0.75
Peptidyl-prolyl cis-trans isomerase	HEL-S-69p	V9HWF5	0.94	1.00	0.75
14-3-3 protein epsilon	HEL2	V9HW98	0.91	0.97	0.75
Thyroid adenoma-associated protein	THADA	H7BYZ4	0.99	1.26	0.75
Basic leucine zipper and W2 domain-containing protein 2	BZW2	E7ETZ4	0.84	0.78	0.75
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	B7Z6P0	1.15	1.02	0.75
Importin-5	RANBP5	A0A024RDY0	1.04	0.96	0.75
ATP-dependent RNA helicase DDX3X	DDX3X	A0A0D9SFB3	0.93	0.88	0.75
Neuroblast differentiation-associated protein AHNAK	AHNAK	Q09666	1.06	1.11	0.75
Eukaryotic translation initiation factor 4B	EIF4B	B4DEP6	1.11	1.03	0.75
Protein phosphatase 1 regulatory subunit	PPP1R12A	F8VZN8	0.92	1.05	0.75
Developmentally-regulated GTP-binding protein 1	DRG1	Q9Y295	1.14	1.01	0.75
Src substrate cortactin	CTTN	A0A024R5M3	1.10	1.21	0.75
Pleckstrin-2	PLEK2	Q9NYT0	1.06	0.84	0.75
F-actin-capping protein subunit alpha-2	CAPZA2	Q53GE2	1.07	0.87	0.75
Acetyl-coenzyme A synthetase	ACSS2	Q4G0E8	0.91	1.12	0.75
S-(hydroxymethyl)glutathione dehydrogenase	ADH5	H0YAG8	1.08	1.06	0.75
Cofilin-1	HEL-S-15	V9HWI5	1.05	0.96	0.75
NudC domain-containing protein 3	NUDCD3	Q8IVD9	1.03	1.14	0.75
ATP-binding cassette sub-family F member 1	ABCF1	Q59F96	1.14	0.96	0.75
Protein kinase C	PRKCI	B5BUK7	1.00	1.00	0.75
Exportin-2	CSE1L	A0A384NKW7	0.94	0.88	0.75
Eukaryotic translation initiation factor 1	SUI1	Q6IAV3	0.97	0.88	0.75
Polyadenylate-binding protein-interacting protein 2	PAIP2	Q9BPZ3	1.40	1.50	0.75
Importin-4	IPO4	B3KQ33	1.03	0.90	0.75
cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	A0A0S2Z472	0.79	0.84	0.75
Talin-1	TLN1	A0A1S5UZ07	1.01	1.00	0.75
Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	A0M8W4	1.11	0.94	0.75
Heat shock protein 105 kDa	HSPH1	A0A024RDQ0	0.99	0.89	0.75
WD repeat-containing protein 1	WDR1	Q53H17	1.00	1.01	0.75
Translin	TSN	Q15631	1.23	1.26	0.74
40S ribosomal protein S15	RPS15	K7ELC2	1.06	0.91	0.74
ADP-sugar pyrophosphatase	NUDT5	A6NFX8	1.12	1.12	0.74
Hematological and neurological expressed 1-like protein	HN1L	H3BU16	1.48	1.18	0.74

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Spermidine synthase	SRM	P19623	1.10	1.08	0.74
Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	B4DF38	0.87	0.92	0.74
40S ribosomal protein S27	RPS27L	C9JLI6	0.90	0.84	0.74
Hsp90 co-chaperone Cdc37	CDC37	A0A024R7B7	1.10	0.90	0.74
Glutathione S-transferase P	HEL-S-22	V9HWE9	0.93	0.94	0.74
T-complex protein 1 subunit beta	HEL-S-100n	V9HW96	0.97	0.94	0.74
Caspase-4	CASP4	H0YD34	0.85	0.81	0.74
Signal transducer and activator of transcription	STAT2	B4DHI1	1.01	1.24	0.74
Eukaryotic translation initiation factor 4H	EIF4H	Q15056-2	1.02	1.10	0.74
Osteoclast-stimulating factor 1	OSTF1	A8K646	0.94	0.96	0.74
Histidine--tRNA ligase, cytoplasmic	HARS	P12081-3	1.04	1.12	0.74
Luc7-like protein 3	LUC7L3	C9JL41	0.78	0.67	0.74
Alcohol dehydrogenase [NADP(+)]	HEL-S-165mP	V9HWI0	0.89	0.98	0.74
Macrophage migration inhibitory factor	MIF	I4AY87	0.86	1.11	0.74
SUMO-activating enzyme subunit 2	UBA2	B3KMZ6	0.84	0.76	0.74
Calponin	CNN2	B4DDF4	1.03	0.98	0.74
Elongation factor 1-delta	EEF1D	E9PK01	0.93	0.91	0.74
Triosephosphate isomerase	HEL-S-49	V9HWK1	1.02	1.01	0.74
UMP-CMP kinase	CMPK1	P30085	0.99	0.98	0.74
Annexin A8-like protein 2	ANXA8L2	Q5VT79	1.00	1.04	0.74
ARF GTPase-activating protein GIT1	DKFZp686G1540	Q7Z2E5	0.92	0.86	0.74
Tubulin gamma-2 chain	TUBG2	A0A1B4Z394	0.85	0.91	0.74
Exportin-4	XPO4	F2Z2X4	0.82	0.83	0.74
Kinesin-like protein	KIF21A	H0YIM7	1.12	1.06	0.74
BTB/POZ domain-containing protein KCTD12	KCTD12	B3KY04	1.21	0.89	0.74
Costars family protein ABRACL	ABRACL	Q9P1F3	1.02	1.00	0.74
Nuclear receptor-binding protein	NRBP1	B4DW31	0.96	0.90	0.74
Acetyl-CoA acetyltransferase, cytosolic	ACAT2	A8K4W5	0.93	0.99	0.74
T-complex protein 1 subunit alpha	TCP1	P17987	0.94	0.91	0.74
Actin-related protein 2/3 complex subunit 5	ARPC5	O15511	0.93	0.97	0.74
Suppressor of G2 allele of SKP1 homolog	SUGT1	A8K7W3	1.15	1.14	0.74
Vinculin	VCL	A0A384NYN5	0.96	1.01	0.73
Regulator of nonsense transcripts 1	UPF1	A0A024R7L5	0.93	1.04	0.73
V-type proton ATPase subunit E 1	ATP6V1E1	C9J8H1	0.80	0.93	0.73
Poly(rC)-binding protein 1	PCBP1	Q53SS8	0.94	0.94	0.73
Nascent polypeptide-associated complex subunit alpha	NACA	F8VZJ2	0.93	0.97	0.73
Ezrin	EZR	Q6NUR7	0.96	0.98	0.73
Adenosylhomocysteinase	AHCY	A0A384MTQ3	0.98	0.98	0.73
Radixin	RDX	Q6PKD3	1.18	1.12	0.73

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Unconventional myosin-XVIIIa	MYO18A	A0A0D9SFK2	1.30	1.31	0.73
Xaa-Pro dipeptidase	PEPD	J3K000	0.91	0.89	0.73
Serine-threonine kinase receptor-associated protein	STRAP	Q9Y3F4	1.02	0.91	0.73
Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	Q02790	1.00	1.00	0.73
Ras GTPase-activating protein-binding protein 1	DKFZp686L1159	Q5U0Q1	1.05	0.91	0.73
Afadin	MLLT4	Q5TIG5	0.65	0.60	0.73
MMS19 nucleotide excision repair protein homolog	MMS19	Q96T76-9	0.90	0.98	0.73
Isopentenyl-diphosphate Delta-isomerase 1	IDI1	Q13907	0.95	1.00	0.73
E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	Q9C0C9	1.39	0.96	0.73
Ubiquitin thioesterase OTUB1	OTUB1	F5GYN4	0.99	1.00	0.73
Epithelial membrane protein 3	EMP3	M0QXS0	0.79	0.56	0.73
Importin subunit alpha	KPNA2	A8K7D9	1.14	0.91	0.73
60S ribosomal protein L37a	RPL37A	C9J4Z3	1.12	0.90	0.73
Thioredoxin domain-containing protein 17	TXNDC17	A0A140VJY7	1.01	1.11	0.73
Zinc finger protein 462	ZNF462	H3BLX4	0.50	0.56	0.73
Annexin	ANXA2	A0A024R5Z7	0.95	0.87	0.73
Eukaryotic translation initiation factor 3 subunit D	EIF3D	O15371-2	1.01	0.93	0.73
Pyruvate kinase	HEL-S-30	V9HWB8	1.02	0.97	0.73
Protein HGH1 homolog	HGH1	Q9BTY7	0.91	0.92	0.73
Adenylosuccinate synthetase isozyme 2	ADSS	B4E1L0	0.95	1.20	0.73
Tryptophan--tRNA ligase, cytoplasmic	WARS	A0A024R6K8	0.99	0.96	0.73
Annexin	ANXA4	Q6LES2	1.01	1.07	0.73
NAD(P)H dehydrogenase [quinone] 1	NQO1	P15559-2	1.07	1.05	0.73
Dihydropyrimidinase-related protein 2	DPYSL2	Q53ET2	0.93	0.95	0.73
Glutaredoxin-3	GLRX3	A0A140VJK1	0.96	0.97	0.73
ATP-dependent 6-phosphofructokinase, liver type	PFKL	P17858	0.87	1.01	0.73
CAD protein	CAD	F8VPD4	0.93	0.93	0.73
Microtubule-associated protein RP/EB family member 1	MAPRE1	Q15691	0.98	0.98	0.72
Bifunctional purine biosynthesis protein PURH	HEL-S-70p	V9HWH7	1.00	0.97	0.72
Focal adhesion kinase 1	PTK2	Q59GN8	0.80	0.77	0.72
Farnesyl pyrophosphate synthase	FDPS	P14324-2	0.94	0.91	0.72
Non-syndromic hearing impairment protein 5	DFNA5	A4FVA8	0.93	1.00	0.72
Transgelin-2	TAGLN2	A0A384MTL2	1.03	1.01	0.72
Tubulin beta-6 chain	TUBB6	Q2NKY5	1.18	0.99	0.72
Nucleosome assembly protein 1-like 4	NAP1L4	A0A024RCC9	0.93	0.92	0.72
Fatty acid synthase	FASN	P49327	0.96	0.95	0.72
La-related protein 1	LARP1	H0YC73	0.88	0.79	0.72
PDZ and LIM domain protein 5	PDLIM5	B7Z8X5	1.24	1.17	0.72
L-lactate dehydrogenase	LDHB	Q5U077	1.00	1.06	0.72

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein transport protein Sec16A	SEC16A	A0A0C4DH09	0.85	0.79	0.72
Glutamate--cysteine ligase catalytic subunit	GCLC	B4E2I4	1.15	1.14	0.72
Polyadenylate-binding protein	PABPC4	B1ANR0	0.97	0.93	0.72
Heat shock protein HSP 90-beta	HSP90AB1	A0A024RD80	1.02	0.93	0.72
Telomere length regulation protein TEL2 homolog	TELO2	Q9Y4R8	0.92	0.88	0.72
Inhibitor of nuclear factor kappa-B kinase subunit beta	IKBKB	E5RGW5	0.79	0.89	0.72
SH3 domain-binding glutamic acid-rich-like protein 3	HEL-S-297	Q86Z22	1.13	1.02	0.72
Palladin	PALLD	Q8WX93-4	1.12	1.02	0.72
Methylosome subunit pICln	CLNS1A	E9PMI6	0.83	0.93	0.72
Multifunctional protein ADE2	PAICS	P22234	0.88	0.97	0.72
14-3-3 protein theta	YWHAQ	P27348	0.96	0.94	0.72
Annexin	ANXA11	Q6ICS0	0.98	0.98	0.72
Protein TFG	TFG	Q7Z426	1.01	0.92	0.72
Nuclear transport factor 2	NUTF2	A0A024R6Y2	1.06	0.97	0.72
Methylsterol monooxygenase 1	MSMO1	D6RDP9	0.76	0.71	0.72
Actin-related protein 2/3 complex subunit 1B	ARPC1B	A4D275	1.03	0.91	0.71
Alanine--tRNA ligase, cytoplasmic	AARS	P49588	1.00	1.05	0.71
RelA-associated inhibitor	PPP1R13L	A0A024R0Q5	1.03	1.02	0.71
BolA-like protein 2	BOLA2B	H3BV85	1.35	1.06	0.71
Ubiquitin-conjugating enzyme E2 L3	UBE2L3	A8K4W8	0.95	0.82	0.71
Annexin	HEL-S-7	V9HWE0	0.98	1.04	0.71
Protein CDV3 homolog	CDV3	Q9UKY7-2	1.07	1.16	0.71
Leucine zipper protein 1	LUZP1	A0A024RAC0	0.96	0.94	0.71
Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	C9J168	0.58	1.13	0.71
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	Q9H2M9	0.89	0.68	0.71
S-methyl-5-thioadenosine phosphorylase	MTAP	A0A384ME80	1.02	1.01	0.71
Calpain-1 catalytic subunit	CAPN1	A0A024R5A3	0.99	1.05	0.71
Heat shock protein HSP 90-alpha	EL52	K9JA46	0.99	0.89	0.71
Myosin light chain 1/3, skeletal muscle isoform	MYL1	Q53R15	0.92	0.74	0.71
Ribose-phosphate pyrophosphokinase 2	PRPS2	A0A140VK41	0.94	0.99	0.71
Elongation factor 1-alpha	EEF1A1	Q6IPT9	1.00	0.90	0.71
Dynein assembly factor 5, axonemal	DNAAF5	Q86Y56	0.84	0.97	0.71
Tubulin alpha-1C chain	TUBA1C	Q53GA7	1.04	0.90	0.71
Pyridoxal kinase	HEL-S-1a	V9HWC3	0.98	0.98	0.71
1,4-alpha-glucan-branching enzyme	GBE1	E9PGM4	1.42	1.39	0.71
RNA 3-terminal phosphate cyclase	RTCA	O00442	1.27	0.81	0.70
Annexin A3	ANXA3	P12429	1.01	0.93	0.70
Tubulin beta-6 chain	TUBB6	Q2NKY5	1.02	0.92	0.70
Purine nucleoside phosphorylase	HEL-S-156an	V9HWH6	0.99	0.95	0.70

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Fructose-bisphosphate aldolase	HEL-S-87p	V9HWN7	1.01	0.90	0.70
Actin-related protein 2	ACTR2	P61160	0.94	0.92	0.70
Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	A0A0F7NGI8	1.22	1.21	0.70
Ubiquitin-fold modifier 1	UFM1	P61960	0.96	0.95	0.70
Trifunctional purine biosynthetic protein adenosine-3	GART	Q3B7A7	0.97	0.95	0.70
Integrin-linked protein kinase	HEL-S-28	V9HWF0	1.08	0.95	0.70
BAG family molecular chaperone regulator 3	BAG3	Q53GY1	1.04	1.03	0.70
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	G3V438	1.08	1.05	0.70
Moesin	HEL70	V9HWC0	0.97	0.92	0.70
Tubulin--tyrosine ligase-like protein 12	TTLL12	A0A024R4U3	0.94	0.96	0.70
Calpain small subunit 1	CAPNS1	A0A0C4DGQ5	1.01	1.00	0.70
Branched-chain-amino-acid aminotransferase	BCAT1	A0A024RAV0	1.08	0.90	0.70
Transcription factor BTF3	BTF3	P20290-2	0.97	0.91	0.70
Peptidyl-prolyl cis-trans isomerase FKBP5	FKBP5	B7Z8G2	1.19	1.16	0.70
Aspartate aminotransferase	GIG18	Q2TU84	0.77	0.97	0.70
Inosine-5-monophosphate dehydrogenase	IMPDH1	A0A024R725	1.22	0.93	0.70
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	A0A0B4J1W3	1.07	0.85	0.70
Destrin	HEL32	V9HWA6	0.97	0.98	0.70
Enolase-phosphatase E1	ENOPH1	A0A0C4DGY8	0.99	0.91	0.70
Alpha-parvin	PARVA	E9PS97	0.92	1.01	0.70
Pseudouridine-5-phosphatase	HDHD1	Q08623	0.72	0.87	0.70
Glucose-6-phosphate isomerase	GPI	P06744	0.97	0.95	0.70
Serine--tRNA ligase, cytoplasmic	SARS	Q0VGA5	1.02	0.89	0.70
Phosphoacetylglucosamine mutase	PGM3	A0A494C0G1	1.01	0.82	0.70
Protein lin-7 homolog C	LIN7A	H0YI92	0.60	0.81	0.70
60S ribosomal protein L38	RPL38	A0A024R8P8	0.96	0.98	0.70
Fascin	FSCN1	A0A384MEG1	0.98	0.94	0.70
Nucleosome assembly protein 1-like 1	NAP1L1	F5H4R6	1.05	0.92	0.70
14-3-3 protein eta	YWHAH	A0A024R1K7	1.03	1.03	0.70
Glucose-6-phosphate 1-dehydrogenase X	G6PD	Q2VF42	0.79	0.82	0.70
Glycine--tRNA ligase	GARS	A0A090N8G0	0.93	0.94	0.70
ATP-dependent 6-phosphofructokinase, platelet type	PFKP	Q01813	0.94	0.89	0.70
Peflin	PEF1	A0A384MQX5	0.89	0.63	0.70
Polyadenylate-binding protein-interacting protein 1	PAIP1	A0A024R094	0.62	0.88	0.69
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	A0A6I8PRN4	1.11	0.89	0.69
Coronin	DKFZp762I166	Q9NSK3	0.82	1.05	0.69
Ubiquitin carboxyl-terminal hydrolase	UCHL3	A0A087WTB8	1.16	1.05	0.69
Rab GDP dissociation inhibitor beta	GDI2	Q6IAT1	0.99	0.92	0.69
Eukaryotic translation initiation factor 4E	EIF4E	Q32Q75	0.89	0.89	0.69

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	Q6LET3	0.89	0.86	0.69
Leukotriene A-4 hydrolase	LTA4H	A0A140VK27	0.91	1.05	0.69
Platelet-activating factor acetylhydrolase IB subunit beta	HEL-S-303	V9HW44	0.99	1.00	0.69
Ubiquitin-conjugating enzyme E2 D2	UBE2D2	D6RFM0	0.94	0.97	0.69
Zinc finger CCCH domain-containing protein 15	ZC3H15	B7Z592	1.14	1.17	0.69
Elongation factor 2	EEF2	A0A384N6H1	0.99	0.93	0.69
Alpha-synuclein	SNCA	Q4W5L2	1.29	1.32	0.69
Ubiquitin-associated protein 2-like	UBAP2L	B4DZJ6	1.15	0.98	0.69
Fructose-2,6-bisphosphatase TIGAR	TIGAR	Q9NQ88	1.03	0.96	0.69
CTP synthase 1	CTPS1	A0A3B3IRI2	0.96	0.91	0.69
Sorbitol dehydrogenase	HEL-S-95n	V9HW89	0.92	1.41	0.69
ATP synthase subunit epsilon, mitochondrial	ATP5E	P56381	1.98	0.68	0.69
N-alpha-acetyltransferase 10	NAA10	P41227-2	1.10	0.95	0.69
Spermine synthase	SMS	P52788	0.98	0.87	0.69
Eukaryotic peptide chain release factor subunit 1	ETF1	P62495	1.04	0.97	0.69
Adenylate kinase isoenzyme 1	AK1	H0YID2	1.07	0.99	0.69
Dual specificity mitogen-activated protein kinase kinase 4	MAP2K4	B7ZA62	0.81	0.84	0.69
Importin-9	IPO9	Q96P70	0.97	0.89	0.69
Cyclin-dependent kinase 1	CDK1	A0A087WZZ9	0.81	0.72	0.69
Tubulin beta chain	TUBB	Q5JP53	1.04	0.86	0.69
Condensin complex subunit 1	NCAPD2	E7EN77	0.92	0.75	0.68
Ras and Rab interactor 1	RIN1	B4DN44	0.97	0.97	0.68
YTH domain-containing family protein 2	YTHDF2	B5BU99	0.87	0.80	0.68
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	E7EX73	1.04	0.96	0.68
Structural maintenance of chromosomes protein	SMC2	Q6P712	0.92	0.71	0.68
Perilipin-3	PLIN3	A0A140VJN8	0.97	0.98	0.68
Phostensin	hCG_1821276	A0A1U9X8D3	1.23	1.12	0.68
Glyceraldehyde-3-phosphate dehydrogenase	HEL-S-162eP	V9HVZ4	0.96	0.85	0.68
60S ribosomal protein L24	RPL24	C9JXB8	0.93	0.86	0.68
Serine/threonine-protein kinase 24	STK24	B4DR80	0.96	1.12	0.68
AP-3 complex subunit beta	AP3B1	Q3MNE1	1.02	0.94	0.68
S-formylglutathione hydrolase	ESD	A0A140VJJ2	0.94	0.91	0.68
ATP-binding cassette sub-family E member 1	ABCE1	P61221	0.99	0.90	0.68
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	Q59EF0	0.86	0.78	0.68
Ubiquilin-1	UBQLN1	B3KNI8	0.95	1.01	0.68
Eukaryotic initiation factor 4A-I	EIF4A1	P60842	0.96	0.90	0.68
60S ribosomal protein L36a-like	RPL36A	B2R4V2	0.88	0.77	0.68
Phosphomannomutase	PMM2	H3BR08	0.86	0.80	0.68
Vasodilator-stimulated phosphoprotein	VASP	A0A0S2Z4I9	1.05	0.90	0.68

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
DNA-directed RNA polymerase I subunit RPA49	POLR1E	Q9GZS1	0.84	0.75	0.68
Diphosphomevalonate decarboxylase	MVD	P53602	0.95	0.95	0.68
Tubulin alpha-1B chain	TUBA1B	P68363	0.98	0.83	0.68
Adenylyl cyclase-associated protein 1	CAP1	D3DPU2	0.98	0.87	0.68
Protein O-GlcNAcase	MGEA5	O60502-2	0.71	0.84	0.67
Adenosine kinase	ADK	A0A140VJE0	0.87	0.88	0.67
Transmembrane protein 40	TMEM40	Q8WWA1-2	1.18	1.02	0.67
E3 ubiquitin-protein ligase UBR4	UBR4	Q5T4S7-3	0.85	0.80	0.67
Ataxin-10	ATXN10	Q9UBB4	1.01	0.85	0.67
Prefoldin subunit 2	PFDN2	B1AQP2	0.85	0.83	0.67
Ubiquitin-like modifier-activating enzyme 6	UBA6	B3KSS1	1.00	1.05	0.67
Obg-like ATPase 1	OLA1	J3KQ32	1.06	1.02	0.67
Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	Q9Y3C8	0.85	1.00	0.67
14-3-3 protein beta/alpha	HEL-S-1	V9HWD6	0.94	1.08	0.67
BRO1 domain-containing protein BROX	BROX	Q5VW33	1.24	1.23	0.67
Glutathione S-transferase omega-1	HEL-S-21	V9HWG9	1.03	0.93	0.67
Thymosin beta-4	TMSB4X	A2VCK8	1.18	1.60	0.67
Mothers against decapentaplegic homolog	SMAD3	H3BQ00	0.87	0.87	0.67
dCTP pyrophosphatase 1	DCTPP1	Q9H773	0.74	0.94	0.67
COP9 signalosome complex subunit 8	COPS8	A0A024R4D1	1.08	0.86	0.67
UBX domain-containing protein 1	UBXN1	E9PJ81	0.96	1.29	0.67
6-phosphogluconate dehydrogenase, decarboxylating	PGD	P52209-2	0.94	0.86	0.67
Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	A0A0C4DGL3	0.99	0.71	0.67
Ashwin	C2orf49	C9J4K0	0.33	1.12	0.67
Serpin B8	SERPINB8	C9JVA8	1.03	0.83	0.67
Lactoylglutathione lyase	GLO1	X5DNM4	0.99	0.92	0.67
Calcyclin-binding protein	CACYBP	Q6NVY0	1.00	0.83	0.67
COP9 signalosome complex subunit 7b	COPS7B	B3KW51	0.78	1.28	0.66
Calcium-binding protein 39	CAB39	A0A087X0K1	1.06	0.98	0.66
Signal recognition particle 54 kDa protein	SRP54	P61011	0.93	0.83	0.66
Translation initiation factor eIF-2B subunit alpha	EIF2B1	Q14232	1.05	0.95	0.66
E3 ubiquitin-protein ligase NEDD4	NEDD4	A0A3B3IUC1	0.55	0.73	0.66
Drebrin-like protein	DBNL	B4DKZ4	1.16	1.13	0.66
Tubulin beta-4B chain	TUBB2C	Q8IZ29	1.00	0.85	0.66
PDZ and LIM domain protein 7	PDLIM7	Q9NR12-2	1.29	1.08	0.66
Programmed cell death protein 2-like	PDCD2L	Q9BRP1	0.98	0.80	0.66
LanC-like protein 1	LANCL1	E9PHS0	0.65	0.82	0.66
Glia maturation factor beta	GMFB	G3V4P8	1.00	0.88	0.66
Mothers against decapentaplegic homolog	SMAD4	K7EIU8	0.72	0.76	0.66

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Aldo-keto reductase family 1 member C1	AKR1C2	S4R3P0	1.31	0.97	0.66
UDP-glucose 6-dehydrogenase	UGDH	O60701-3	0.81	0.89	0.66
Hsc70-interacting protein	ST13	Q0IJ56	0.82	0.92	0.66
Adenylyl cyclase-associated protein	CAP1	D3DPU2	1.04	0.86	0.66
Phosphatidylethanolamine-binding protein 1	HEL-S-34	D9IAI1	0.94	0.90	0.65
Annexin	ANXA7	B4DT77	0.86	0.89	0.65
Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	B7Z4M5	0.88	0.88	0.65
EKC/KEOPS complex subunit LAGE3	LAGE3	Q14657	0.93	0.86	0.65
Threonine--tRNA ligase, cytoplasmic	TARS	Q5M7Z9	0.99	0.97	0.65
Condensin complex subunit 2	NCAPH	H7C415	1.15	0.84	0.65
Kinetochore protein Spc24	SPC24	K7ERQ7	0.93	0.88	0.65
Phosphotriesterase-related protein	PTER	Q96BW5-2	0.98	0.78	0.65
Glucose-6-phosphate isomerase	GPI	P06744	0.55	0.82	0.65
Zyxin	ZYX	Q15942	1.00	1.02	0.65
Protein MEMO1	MEMO1	A8K3Y8	0.94	0.89	0.65
Plasminogen activator inhibitor 2	SERPINB2	P05120	1.00	0.63	0.65
Nucleoside diphosphate kinase A	NME1	A0A384MTW7	1.07	1.18	0.65
SH3 domain-binding protein 1	SH3BP1	Q6ZTJ5	1.38	1.12	0.65
Inorganic pyrophosphatase	HEL-S-66p	V9HWB5	0.95	1.01	0.65
Leucine-rich repeat-containing protein 47	LRRC47	Q8N1G4	0.77	0.81	0.65
LIM and SH3 domain protein 1	LASP1	A0A024R1S8	1.21	1.10	0.65
Switch-associated protein 70	SWAP70	E9PJM7	0.96	1.37	0.65
Uridine 5-monophosphate synthase	UMPS	E9PFD2	0.86	0.90	0.64
Programmed cell death protein 5	PDCD5	K7EQA1	0.90	0.94	0.64
Protein SON	SON	Q3SWV4	1.01	0.87	0.64
A-kinase anchor protein 1, mitochondrial	AKAP1	A0A140VK05	0.91	0.91	0.64
Vacuolar protein-sorting-associated protein 25	VPS25	K7EP45	0.62	1.39	0.64
Coiled-coil domain-containing protein 124	LOC115098	A0A024R7M8	1.02	1.32	0.64
Platelet-activating factor acetylhydrolase IB subunit gamma	PAFAH1B3	M0R389	0.83	0.83	0.64
Biliverdin reductase A	BLVRA	A0A140VJF4	0.82	1.00	0.64
Transcriptional repressor CTCF	CTCF	A0A2R8Y6Z6	0.80	0.76	0.64
Testin	TES	Q53GU1	1.18	1.00	0.64
Transportin-2	TNPO2	B4DRY5	0.75	0.95	0.64
Chloride intracellular channel protein	CLIC1	Q5SRT3	0.97	0.85	0.64
Tubulin beta-8 chain	TUBB8	Q3ZCM7	0.96	0.87	0.63
Aminopeptidase B	RNPEP	Q9H4A4	0.92	1.08	0.63
Calpain-2 catalytic subunit	CAPN2	Q59EF6	0.94	0.88	0.63
CCR4-NOT transcription complex subunit 1	CNOT1	A5YKK6-4	0.93	0.75	0.63
Elongator complex protein 1	DKFZp781H1425	Q68DI5	47.19	41.85	0.63

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Putative heat shock protein HSP 90-beta 2	HSP90AB2P	Q58FF8	0.90	0.77	0.63
Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	I3L4G9	0.78	1.13	0.63
Guanine nucleotide exchange factor VAV2	VAV2	P52735-3	1.00	1.01	0.63
Nucleoporin Nup37	NUP37	Q8NFB4	0.82	0.85	0.62
Thyroid receptor-interacting protein 6	TRIP6	Q15654	1.11	1.11	0.62
Prothymosin alpha	PTMA	Q15203	0.80	0.95	0.62
Calponin-3	CNN3	Q15417	1.17	0.84	0.62
Cytosolic purine 5-nucleotidase	NT5C2	Q5JUV6	0.73	1.02	0.62
Developmentally-regulated GTP-binding protein 2	DRG2	J3QKW7	0.87	0.82	0.62
Rho GDP-dissociation inhibitor 1	ARHGDIA	J3KTF8	0.86	0.90	0.61
Ran-specific GTPase-activating protein	RANBP1	C9JJ34	0.92	0.92	0.61
Gem-associated protein 4	GEMIN4	Q8WUM5	0.84	0.82	0.61
Pachytene checkpoint protein 2 homolog	TRIP13	Q15645	1.12	1.13	0.61
Nuclear migration protein nudC	NUDC	Q9Y266	0.93	0.93	0.61
Thymosin beta-10	TMSB10	P63313	1.15	1.18	0.61
Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	Q8TCS8	0.45	0.82	0.61
Protein PBDC1	PBDC1	Q9BVG4	1.30	1.48	0.61
Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	ARAP1	Q96P48-3	0.80	0.73	0.61
Ataxin-2-like protein	ATXN2L	A0A024QZC0	1.08	1.04	0.61
PDZ domain-containing protein GIPC1	GIPC1	A8K2I7	1.18	1.28	0.61
Paxillin	PXN	A0A140VJQ8	1.03	0.88	0.61
UDP-N-acetylhexosamine pyrophosphorylase	UAP1	A0A140VKC0	1.04	0.82	0.61
Thioredoxin reductase 1, cytoplasmic	TXNRD1	E9PIR7	0.97	0.78	0.60
Glutathione S-transferase Mu 3	GSTM3	A4UJ43	0.93	1.18	0.60
Annexin	ANXA6	A0A0S2Z377	1.06	0.90	0.60
Plastin-2	HEL-S-37	V9HWJ7	0.81	0.88	0.60
Serine/threonine-protein phosphatase 6 regulatory subunit 3	SAPS3	A0A024R5F3	0.91	0.80	0.60
Rho guanine nucleotide exchange factor 1	ARHGEF1	A0A2X0SFA4	0.96	0.75	0.60
Cysteine and histidine-rich domain-containing protein 1	CHORDC1	A0A024R394	0.90	0.75	0.59
NSFL1 cofactor p47	NSFL1C	Q53FF5	0.97	1.47	0.59
Astrocytic phosphoprotein PEA-15	PEA15	B1AKZ5	1.03	0.91	0.59
Immunoglobulin-binding protein 1	IGBP1	P78318	1.38	1.00	0.59
Rho GDP-dissociation inhibitor 2	ARHGDIB	A0A024RAS5	0.87	0.95	0.59
Xaa-Pro aminopeptidase 1	XPNPEP1	Q5T6H7	1.01	0.78	0.59
FAS-associated death domain protein	FADD	Q6LCG1	0.96	0.88	0.59
La-related protein 4	LARP4	Q71RC2-6	0.82	0.66	0.59
MAP7 domain-containing protein 1	MAP7D1	Q6NX58	1.13	0.99	0.58
Interleukin-1 alpha	IL1A	P01583	1.29	0.61	0.58
Cytoglobin	CYGB	K7EIM9	0.99	0.80	0.58

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Eukaryotic translation initiation factor 2A	EIF2A	F8WAE5	1.02	1.09	0.58
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1	P15170-2	1.05	0.92	0.58
TPR and ankyrin repeat-containing protein 1	TRANK1	A0A2R8Y7N6	0.97	1.81	0.57
Actin filament-associated protein 1-like 2	AFAP1L2	B7Z2Q0	0.63	1.10	0.57
Density-regulated protein	DENR	F8VVL1	0.98	1.00	0.57
Large proline-rich protein BAG6	BAT3	A0A0G2JL47	0.78	0.62	0.57
Translation initiation factor eIF-2B subunit gamma	EIF2B3	Q9NR50-3	0.89	0.83	0.57
Tight junction protein ZO-1	DKFZp686M05161	B4DZK4	1.35	1.14	0.57
Microtubule-associated protein 4	MAP4	E7EVA0	0.82	0.70	0.56
Sepiapterin reductase	SPR	B4DSF0	0.99	0.33	0.56
Kelch repeat and BTB domain-containing protein 8	KBTBD8	Q8NFX9	0.61	2.74	0.56
Synembryn-A	RIC8A	E9PSI0	1.01	0.79	0.55
Glycogen [starch] synthase, muscle	GYS1	B7Z255	0.91	0.82	0.55
Specifically androgen-regulated gene protein	SARG	Q9BW04-2	0.95	1.01	0.55
Sorcin	SRI	C9J0K6	0.92	1.07	0.55
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	Q8N995	1.00	0.72	0.55
U6 snRNA-associated Sm-like protein LSM3	LSM3	P62310	1.39	0.98	0.55
Parathymosin	PTMS	F5H7R9	0.82	0.76	0.54
Ran GTPase-activating protein 1	RANGAP1	A0A024R1U0	0.90	0.70	0.54
Copper transport protein ATOX1	ATOX1	E5RGN3	1.38	1.13	0.54
Zinc finger protein 36, C3H1 type-like 2	ZFP36L2	P47974	0.99	0.93	0.53
Eukaryotic initiation factor 4A-II	EIF4A2	Q14240	1.01	0.91	0.53
Stathmin	STMN1	A2A2D0	0.88	0.87	0.52
GTP-binding protein SAR1b	SAR1B	D6RDB2	0.61	0.62	0.52
Phosphorylated adapter RNA export protein	PHAX	B4DPU2	1.02	0.98	0.51
Phosphoribosylformylglycinamide synthase	PFAS	A8K9T9	0.83	0.76	0.51
COMM domain-containing protein 1	C2orf5	Q53QP8	2.13	0.92	0.51
Neural Wiskott-Aldrich syndrome protein	WASL	A4D0Y1	1.28	1.01	0.50
Translation initiation factor eIF-2B subunit beta	EIF2B2	Q9BPX4	0.95	0.89	0.50
Protein PML	PML	Q59GQ8	0.61	1.59	0.50
Glycogen synthase kinase-3 beta	GSK3B	Q6FI27	1.08	1.23	0.50
Endothelial differentiation-related factor 1	EDF1	O60869-2	1.94	0.66	0.49
Protein phosphatase 1 regulatory subunit 7	PPP1R7	H7C003	0.67	1.03	0.49
Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	I3L209	0.75	0.81	0.49
Methionine aminopeptidase 2	MEAP2	A0A140VJE3	1.27	0.98	0.49
Mevalonate kinase	MVK	F5H8H2	0.76	0.79	0.49
Serine/threonine-protein kinase OSR1	OXSRI	O95747	0.69	0.75	0.48
Hematological and neurological expressed 1 protein	HN1	J3KT51	0.80	0.82	0.48

Table S1. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Prostaglandin reductase 1	LTB4DH	A0A024R172	0.90	0.59	0.48
ATP-dependent RNA helicase DDX19A	DKFZp762C1313	Q69YM2	0.94	1.10	0.47
Aldo-keto reductase family 1 member C3	AKR1C3	S4R3Z2	1.10	0.71	0.47
Acyl-protein thioesterase 2	LYPLA2	A0A140VJC9	1.32	1.55	0.47
Cold-inducible RNA-binding protein	CIRBP	Q53XX5	0.88	0.51	0.46
Tubulin-specific chaperone A	TBCA	E5RIW3	0.81	0.61	0.45
Phosducin-like protein 3	PDCL3	B7Z6S0	0.54	0.87	0.45
Thymidylate synthase	TYMS	Q53Y97	0.73	0.64	0.45
ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	E9PMR9	0.62	0.75	0.45
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	G3V576	1.17	0.71	0.42
Four and a half LIM domains protein 2	FHL2	Q53T40	1.59	0.41	0.41
Mitochondrial import receptor subunit TOM34	TOMM34	Q6ZPD0	1.27	0.51	0.39
Serine/threonine-protein phosphatase	PPP1CC	Q9UPN1	2.11	1.67	0.35
Rab GDP dissociation inhibitor alpha	GDI1	B4DHX4	0.26	0.59	0.35
Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	TSTD1	Q8NFI3-3	0.45	0.88	0.35
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	E7EU94	0.47	0.91	0.30
Centrosomal protein of 170 kDa	CEP170	B4DL23	0.93	0.84	0.27
ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1	F8W1U7	0.53	0.54	0.27
Myosin light polypeptide 6	MYL6	P60660	0.97	0.59	0.26
Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	H3BPZ1	0.12	0.76	0.17
Immortalization up-regulated protein	IMUP	Q9GZP8-2	2.09	0.34	0.14
Nuclear factor NF-kappa-B p105 subunit	NFKB1	D6RF93	0.55	0.20	0.13
2-deoxynucleoside 5-phosphate N-hydrolase 1	DNPH1	H0Y8X4	0.78	1.02	0.07
Guanylate kinase	GUK1	Q96IN2	0.44	0.06	0.07
Protein bicaudal D homolog 2	BICD2	Q8TD16	0.49	0.63	0.01

Table S2. Proteomic changes on day 2 after irradiation

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Polymerase delta-interacting protein 3	POLDIP3	Q96DI9	12.63	11.95	30.72
Keratin, type II cytoskeletal 6B	KRT6B	P04259	1.37	3.45	10.34
HLA class I histocompatibility antigen, alpha chain G	HLA-B	P01889	29.62	24.35	9.32
Microsomal glutathione S-transferase 2	MGST2	Q99735-2	1.46	1.82	8.97
Keratin, type I cytoskeletal 18	KRT1	H6VRG2	1.54	2.43	6.49
DNA damage-binding protein 2	DDB2	Q92466	1.74	1.61	5.68
Alpha-N-acetylgalactosaminidase	NAGA	P17050	1.22	1.49	5.60
Serine/threonine-protein kinase MARK2	MARK2	F5H6N2	0.87	0.78	5.09
High mobility group protein B2	HMGB2	Q5U071	0.83	0.84	4.54

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Nucleolar MIF4G domain-containing protein 1	NOM1	Q5C9Z4	0.68	0.89	4.43
Elongation factor Ts, mitochondrial	TSFM	P43897	2.34	3.36	4.30
Keratin, type I cytoskeletal 15	KRT15	P19012	1.21	1.28	4.20
Kinesin light chain 3	KLC3	K7EL76	6.62	1.29	3.86
Branched-chain-amino-acid aminotransferase	BCAT2	B3KSI3	3.25	3.01	3.24
Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	Q8WYJ5	1.87	1.96	3.22
Sorting nexin-33	SNX33	H3BPR3	1.13	2.02	2.93
Keratinocyte differentiation-associated protein	KRTDAP	P60985-2	1.67	1.94	2.82
Afadin	MLLT4	Q5TIG5	2.77	2.60	2.73
von Willebrand factor	VWF	L8E853	1.00	1.78	2.55
Protein PML	promyelocytic leukemia rotein	A0A2Z5DI29	0.80	0.21	2.45
Regulator of microtubule dynamics protein 3	RMDN3	H0YMB1	1.28	1.67	2.38
Ganglioside GM2 activator	GM2A	P17900	1.34	1.70	2.37
Actin, alpha cardiac muscle 1	ACTC1	P68032	1.18	1.29	2.37
p53 apoptosis effector related to PMP-22	PERP	Q96FX8	2.73	3.71	2.34
Galectin-7	LGALS7	P47929	1.84	2.43	2.29
tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	C14orf172	A0A024R6Q2	1.38	1.70	2.26
Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	E9PAM4	1.42	1.50	2.25
[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial	BCKDK	A0A024QZA9	1.42	1.92	2.23
Multiple inositol polyphosphate phosphatase 1	MINPP1	B4E394	1.35	1.45	2.21
Ly6/PLAUR domain-containing protein 3	DKFZp686D0114	Q5JPJ9	1.27	2.10	2.19
Ras-related protein Rab-27B	RAB27B	O00194	1.60	2.05	2.17
Cocaine esterase	CES2	O00748	1.58	1.94	2.16
Protein FAM3C	FAM3C	C9JP35	2.01	1.89	2.14
Protein SON	SON	P18583	1.36	1.67	2.13
COMM domain-containing protein 1	C2orf5	Q53Q75	1.12	2.17	2.11
Fermitin family homolog 2	FERMT2	A8K6S3	0.65	1.57	2.10
Tumor protein D52	TPD52	H0YC42	1.79	2.49	2.05
Protein scribble homolog	SCRIB	A0A0G2JNZ2	2.00	2.29	2.05
Catalase	CAT	A0A384P5Q0	1.25	1.73	2.03
Gap junction protein	GJB2	A8DU55	1.69	2.12	2.02
Extended synaptotagmin-2	ESYT2	A0A499FIX8	1.14	1.41	2.01
ADP/ATP translocase 1	SLC25A4	A0A0S2Z3H3	1.35	1.50	2.01
E3 SUMO-protein ligase RanBP2	RANBP2	P49792	2.29	1.97	1.99
Syntaxin-5	STX5	H7C3X5	1.47	2.30	1.99
Protein lifeguard 3	RECS1	Q969X1	0.92	1.12	1.98
Syntaxin-binding protein 3	STXBP3	O00186	1.47	1.74	1.95
Transmembrane emp24 domain-containing protein 5	TMED5	Q49AG2	1.17	1.23	1.94

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Plakophilin-1	PKP1	A0A024R952	1.75	2.11	1.94
Bystin	BYSL	H7BY94	1.41	1.92	1.93
Serine protease HTRA2, mitochondrial	HTRA2	A0A0C4DG44	1.25	1.57	1.93
Alpha-mannosidase	MAN2B1	B4E0K9	1.38	1.79	1.92
Dynamin-like 120 kDa protein, mitochondrial	OPA1	A0A2R8Y4G4	1.71	2.79	1.92
Protein NipSnap homolog 2	GBAS	O75323-2	1.57	1.49	1.91
Translation initiation factor eIF-2B subunit beta	EIF2B2	Q9BPX4	1.71	1.84	1.89
Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	H3BPZ1	1.56	0.94	1.84
Carbonic anhydrase 2	HEL-76	V9HW21	1.61	1.87	1.84
Splicing factor 3A subunit 3	SF3A3	B4DW90	1.39	1.65	1.82
Desmoglein-1	DSG1	Q02413	1.18	1.41	1.82
Histone H3	H3F3B	K7EK07	1.11	1.19	1.82
Alpha-2-macroglobulin-like protein 1	A2ML1	A8K2U0	1.51	1.88	1.82
Prostaglandin F2 receptor negative regulator	PTGFRN	A0A024R0J4	1.42	1.45	1.81
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	Q9NPF4	1.41	1.60	1.77
GTP:AMP phosphotransferase AK3, mitochondrial	AK3	B3KWD9	1.17	1.15	1.77
Nicastrin	NCSTN	H0Y3Z4	1.32	1.59	1.76
U3 small nucleolar RNA-associated protein 18 homolog	UTP18	J3QLD6	1.08	0.89	1.76
Prolyl 4-hydroxylase subunit alpha-2	P4HA2	Q05DA4	1.17	1.21	1.76
Beta-2-microglobulin	B2M	A6XMH5	0.58	0.11	1.74
Williams-Beuren syndrome chromosomal region 16 protein	WBSCR16	B2RXG5	1.28	1.37	1.74
ADP-ribosylation factor-like protein 8B	ARL8B	B4DQT8	1.59	1.58	1.74
Protein S100-A16	S100A16	Q96FQ6	1.26	1.32	1.73
Serpin B3	SCCA1	Q9BYH9	1.42	1.96	1.73
SUN domain-containing protein 1	SUN1	H7C2K3	1.49	1.24	1.72
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	B4DGK8	1.24	1.29	1.71
Cornifin-B	SPRR1B	P22528	1.38	1.84	1.70
Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3	Q5JWS1	1.39	1.37	1.69
RNA-binding protein 42	RBM42	K7EQ03	2.48	1.59	1.69
Copper homeostasis protein cutC homolog	CUTC	Q5TCZ7	1.34	1.92	1.68
Phosphoribosylformylglycinamide synthase	PFAS	A8K9T9	1.33	1.62	1.68
Coiled-coil domain-containing protein 47	CCDC47	Q96A33-2	1.37	1.60	1.68
28S ribosomal protein S6, mitochondrial	MRPS6	P82932	1.19	1.27	1.67
Cleavage stimulation factor subunit 2 tau variant	CSTF2T	Q9H0L4	1.58	1.64	1.67
Probable cysteine--tRNA ligase, mitochondrial	CARS2	F5H579	1.09	1.65	1.66
Dehydrogenase/reductase SDR family member 1	DHRS1	Q96LJ7	1.25	1.36	1.66
Tumor-associated calcium signal transducer 2	TACSTD2	C5IX07	1.41	1.57	1.66
Integrator complex subunit 1	DKFZP586J0619	A4D212	2.22	1.95	1.65
Protein-tyrosine-phosphatase	PTPRF	B3KXJ7	1.30	1.50	1.65

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH	B8ZZZ0	1.46	1.53	1.65
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	DKFZp586J151	Q9H072	1.56	1.84	1.65
CDKN2AIP N-terminal-like protein	CDKN2AIPNL	Q96HQ2-2	0.31	1.60	1.65
SPRY domain-containing protein 4	SPRYD4	B4DUC9	1.38	1.75	1.64
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	DKFZp566O173	Q5JVG7	0.63	0.48	1.64
PRA1 family protein 3	ARL6IP5	B4DZZ0	0.97	0.74	1.63
Protein Dr1	DKFZp666G145	Q658N3	1.93	2.10	1.63
SWI/SNF complex subunit SMARCC2	SMARCC2	Q59G16	1.20	1.57	1.63
Golgi SNAP receptor complex member 1	GOSR1	B4DQA8	1.49	1.58	1.63
Junction plakoglobin	JUP	A0A0S2Z487	1.39	1.58	1.63
HIG1 domain family member 1A, mitochondrial	HIGD1A	C9JAW5	1.28	1.47	1.62
SH3 domain-binding protein 1	SH3BP1	Q6ZTJ5	2.55	2.19	1.62
Sulfurtransferase	MPST	Q2VEU0	1.30	1.45	1.61
Gamma-glutamyl hydrolase	GGH	A8K335	1.45	1.63	1.61
GPI transamidase component PIG-T	PIGT	A0A1W2PSC5	1.18	1.47	1.60
NADPH:adrenodoxin oxidoreductase, mitochondrial	FDXR	A0A0A0MTR6	1.15	1.44	1.60
Transformer-2 protein homolog alpha	HSU53209	Q549U1	0.99	1.28	1.60
Tripartite motif-containing protein 29	TRIM29	Q53G41	1.23	1.54	1.60
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	P08754	1.08	1.15	1.59
Epithelial splicing regulatory protein 2	ESRP2	Q9H6T0-2	1.57	1.84	1.59
Prosaposin	PSAP	B4DEK5	1.06	1.37	1.59
Serine palmitoyltransferase 1	SPTLC1	A0A024R277	1.44	1.53	1.59
Membrane-associated progesterone receptor component 1	PGRMC1	Q6IB11	1.38	1.57	1.59
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	B3KPA6	1.30	1.28	1.58
RNA-binding protein 25	RBM25	P49756	1.29	1.12	1.58
Ras-related protein Ral-B	RALB	A0A024RAG3	1.14	1.02	1.58
EKC/KEOPS complex subunit LAGE3	LAGE3	Q14657	1.56	1.73	1.57
Haloacid dehalogenase-like hydrolase domain-containing protein 2	HDHD2	K7ER15	1.36	1.40	1.57
Ras-related protein Rab-39A	RAB39A	Q14964	0.80	1.07	1.57
Ribosome biogenesis protein BMS1 homolog	BMS1	Q14692	1.38	1.31	1.57
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	A0A384MR44	1.23	1.33	1.57
Nucleolysin TIAR	TIAL1	Q2TSD2	2.04	1.82	1.57
UBE2L3/KRAS fusion protein	UBE2L3/KRAS	I1SRC5	1.06	1.29	1.56
Cytoplasmic dynein 1 light intermediate chain 2	DKFZp686J08252	Q63HJ8	1.70	2.13	1.56
Basigin	hEMMPRIN	B4DY23	0.94	1.09	1.56
Cytochrome b-c1 complex subunit 8	UQCRCQ	O14949	0.70	0.97	1.56
Kinesin-like protein KIF16B	KIF16B	A0A1B0GTU3	1.19	1.31	1.55
Pinin	PNN	A8K964	0.85	0.95	1.55
ATP synthase subunit e, mitochondrial	ATP5I	P56385	1.29	1.16	1.55

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Peptidyl-prolyl cis-trans isomerase	PPIF	H0Y548	0.98	1.27	1.54
Prostasin	PRSS8	H3BVC8	1.55	1.54	1.54
LDLR chaperone MESD	MESDC2	Q14696	0.96	0.80	1.53
Tripeptidyl-peptidase 2	TPP2	A0A494C1S6	1.40	1.74	1.53
Cytochrome c oxidase subunit 6C	COX6C	A0A024R9B7	0.87	1.01	1.53
Mimitin, mitochondrial	NDUFAF2	A0A0S2Z5U2	1.14	1.26	1.53
Torsin-1A	TOR1A	B3KPA1	1.36	1.66	1.52
Transmembrane protein 126A	TMEM126A	Q9H061	1.14	1.25	1.52
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM	B4DJE7	1.27	1.29	1.52
Pannexin	PANX1	B6ETL5	1.38	1.56	1.52
Orotidine 5-phosphate decarboxylase	UMPS	B5LY70	0.84	1.00	1.52
Cyclin-dependent kinase 13	CDC2L5	Q14004	1.57	1.38	1.52
Exosome complex exonuclease RRP44	DIS3	A8QI98	1.09	1.12	1.52
Ovarian cancer-associated gene 2 protein	OVCA2	Q8WZ82	1.63	3.21	1.51
ATP-binding cassette sub-family D member 3	ABCD3	B4DZ22	1.20	1.28	1.51
Minor histocompatibility antigen H13	HM13	A0A0S2Z6F0	1.36	1.24	1.51
Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	Q9NZB2	0.84	0.97	1.51
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	Q7LD69	1.31	1.51	1.51
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	A0A024RAC7	1.21	1.34	1.51
Integrator complex subunit 2	INTS2	J3KMZ7	1.83	2.29	1.51
CAAX prenyl protease 1 homolog	ZMPSTE24	O75844	1.34	1.54	1.51
WD repeat-containing protein 3	WDR3	Q5TDG3	1.40	1.56	1.51
Testis-expressed sequence 10 protein	TEX10	A0A024R169	1.14	1.54	1.51
mRNA turnover protein 4 homolog	C1orf33	A0A024RAE1	1.51	1.41	1.50
Nuclear pore complex protein Nup107	NUP107	B3KMK0	1.27	1.54	1.50
Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1	G3V5A2	1.17	1.94	1.50
Mitochondrial-processing peptidase subunit alpha	PMPCA	Q10713	1.26	1.19	1.50
Protein S100-A10	S100A10	Q6FGE5	1.09	1.11	1.50
Heat shock protein beta-1	HEL-S-102	V9HW43	1.52	1.83	1.50
ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	A0A0S2Z2W5	1.14	1.54	1.49
Alpha-2-macroglobulin-like protein 1	A2ML1	A8K2U0	1.34	1.55	1.49
Exocyst complex component 6B	EXOC6B	Q9H8D6	1.38	1.47	1.49
3-Hydroxyisobutyrate dehydrogenase	HIBADH	A0A024RA75	1.33	1.21	1.49
High mobility group protein HMG-I/HMG-Y	HMGAI	P17096	1.01	0.93	1.49
Succinyl-CoA ligase subunit beta	SUCLA2	B4DY87	1.18	1.21	1.49
Prostaglandin E synthase	hCG_30600	A0A024R8D5	1.42	1.48	1.49
Histone H3.2	HIST2H3A	Q71DI3	1.35	1.29	1.49
UV excision repair protein RAD23 homolog A	RAD23A	K7ENJ0	0.92	1.15	1.49
Prelamin-A/C	LMNA	A0A384MQX1	1.24	1.40	1.48

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Negative elongation factor A	NELFA	Q53GS8	1.53	1.29	1.48
Non-specific protein-tyrosine kinase	YES1	B2RA70	1.32	1.44	1.48
FXVD domain-containing ion transport regulator 3	FXVD3	S4R445	1.02	1.28	1.48
DnaJ homolog subfamily C member 8	DNAJC8	O75937	1.02	0.75	1.48
E3 UFM1-protein ligase 1	UFL1	B7ZAY8	1.34	1.76	1.48
Torsin-1A-interacting protein 1	TOR1AIP1	A0A0A0MSK5	0.91	0.95	1.48
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	B3KN45	1.03	1.14	1.47
Serum paraoxonase/arylesterase 2	PON2	B4DKM6	1.61	1.63	1.47
Syntaxin-4	STX4	C9JFM5	1.12	1.12	1.47
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	P36551	0.85	0.79	1.47
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	Q96I99	1.10	1.25	1.46
Epiplakin	EPPK1	P58107	1.38	1.63	1.46
General transcription factor 3C polypeptide 4	GTF3C4	Q05CN7	1.25	1.56	1.46
Tripeptidyl-peptidase 1	TPP1	B4DSE2	1.26	0.64	1.46
Retinoid-inducible serine carboxypeptidase	SCPEP1	I3L4Z3	1.32	1.77	1.46
E3 ubiquitin-protein ligase UBR5	UBR5	E7EMW7	1.09	1.20	1.46
Probable leucine--tRNA ligase, mitochondrial	LARS2	A0A499FJL2	1.24	1.37	1.46
G protein-coupled receptor kinase 6	GRK6	D6RHX8	0.53	0.82	1.45
Target of Myb protein 1	TOM1	B0QY01	1.30	1.60	1.45
Mitochondrial ribonuclease P protein 3	KIAA0391	O15091-4	0.83	0.91	1.45
Alpha-endosulfine	ENSA	A0A1W2PRU0	1.36	0.01	1.45
Isoleucine--tRNA ligase, mitochondrial	IARS2	A8K5W7	1.32	1.28	1.45
Protein S100	S100A9	B2R4M6	1.50	1.82	1.45
Cytochrome b-c1 complex subunit 6, mitochondrial	UQCRH	Q567R0	1.05	1.17	1.45
Tumor-associated calcium signal transducer 2	TACSTD2	C5IX07	1.50	1.39	1.45
U3 small nucleolar RNA-interacting protein 2	RRP9	O43818	1.26	1.44	1.45
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	Q6IBH0	1.39	1.58	1.44
Desmoplakin	DSP	P15924	1.35	1.53	1.44
Rab11 family-interacting protein 5	GAF1	Q9SCQ6	0.70	0.66	1.44
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	B2RB06	1.22	1.16	1.44
Zinc finger protein 513	ZNF513	Q8N8E2	1.12	1.39	1.44
Mitochondrial carrier homolog 1	PIG60	A8YXX5	1.31	1.37	1.43
Cathepsin D	HEL-S-130P	A0A1B0GW44	1.08	1.13	1.43
Unconventional myosin-Id	MYO1D	J3KRL0	0.97	1.14	1.43
Aladin	AAAS	H3BU82	1.30	1.35	1.43
Protein S100-A14	S100A14	Q9HCY8	1.18	1.35	1.43
Ribosome production factor 2 homolog	RPF2	Q5VXN0	1.32	1.39	1.43
Carnitine O-palmitoyltransferase 2, mitochondrial	CPT2	Q53G79	1.31	1.32	1.43
Translocator protein	TSPO	B1AH87	1.09	1.36	1.43

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein Mpv17	MPV17	A0A0S2Z469	1.10	1.36	1.43
Exosome complex component RRP41	EXOSC4	E9PPI9	1.28	1.25	1.43
39S ribosomal protein L4, mitochondrial	MRPL4	K7ES61	0.99	0.89	1.43
ADP/ATP translocase 3	SLC25A6	Q6I9V5	1.13	1.12	1.43
Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	B3KVN0	1.10	1.00	1.42
Myeloid-derived growth factor	MYDGF	M0QXF7	1.09	1.18	1.42
Serine-protein kinase ATM	ATM	E9PRG7	1.07	1.03	1.42
NADH-ubiquinone oxidoreductase chain 5	ND5	A0A0N7BBR4	1.19	1.55	1.42
Long-chain-fatty-acid--CoA ligase 1	ACSL1	B7Z3Z9	1.24	1.61	1.42
Replication protein A 32 kDa subunit	RPA2	Q5TEJ7	1.14	1.09	1.41
Vesicle-associated membrane protein 3	VAMP3	Q6FGG2	1.15	1.27	1.41
Trifunctional enzyme subunit beta, mitochondrial	HADHB	P55084-2	1.14	1.21	1.41
Interleukin-1 receptor antagonist protein	IL1RN	A0A024R528	2.11	1.37	1.40
Dipeptidyl peptidase 1	CTSC	B4DJQ8	1.20	1.32	1.40
TPR and ankyrin repeat-containing protein 1	TRANK1	A0A2R8Y7N6	1.17	2.32	1.40
Serine palmitoyltransferase 2	SPTLC2	A0A024R6H1	1.19	0.75	1.40
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	B4DJ81	1.17	1.05	1.40
Tetraspanin	UPK1B	B4E1P0	1.26	1.43	1.40
Zinc finger protein 462	ZNF462	H3BLX4	1.18	1.24	1.40
Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	B4E1E2	1.32	1.53	1.40
2,4-dienoyl-CoA reductase, mitochondrial	DECR1	A0A024R9D7	1.22	1.30	1.40
Dehydrogenase/reductase SDR family member 7B	DHRS7B	J3KRS1	1.26	1.57	1.39
Ras-related protein Rap-2c	RAP2A	F6U784	1.41	1.04	1.39
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	B3KM81	1.19	1.09	1.39
Sulfotransferase family cytosolic 2B member 1	SULT2B1	O00204	1.71	2.28	1.39
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	Q6FHM2	1.06	1.12	1.39
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	A0A0S2Z3S5	1.21	1.18	1.38
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	Q53GL5	1.06	1.17	1.38
Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	Q6FHM4	0.78	0.85	1.38
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	B2R6K4	1.05	1.08	1.38
Cleavage and polyadenylation specificity factor subunit 7	CPSF7	F5H669	1.34	1.52	1.38
Tetraspanin	CD9	B4DPP0	0.99	1.10	1.38
39S ribosomal protein L1, mitochondrial	MRPL1	A0PJ79	1.14	1.19	1.38
Cytochrome c1, heme protein, mitochondrial	CYC1	Q8TBT6	1.11	1.15	1.38
Nuclear pore complex protein Nup160	NUP160	G3V198	1.25	1.16	1.38
RNA-binding protein 14	RBM14	A0A0S2Z4Z0	1.26	1.36	1.38
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUFS4	A0A0S2Z433	1.64	1.51	1.38
Hexokinase	HK1	B4DG62	1.08	1.17	1.38
Polypeptide N-acetylgalactosaminyltransferase	GALNT3	Q14435	0.98	0.77	1.38

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Dipeptidyl peptidase 2	DPP7	R4GN05	1.20	1.40	1.37
Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	P20674	0.99	0.97	1.37
Mannosyl-oligosaccharide glucosidase	GCS1	Q58F09	1.18	1.17	1.37
Saccharopine dehydrogenase-like oxidoreductase	SCCPDH	A0A384NPM7	0.80	1.22	1.37
Acyl-coenzyme A thioesterase 13	ACOT13	Q9NPJ3-2	0.86	1.17	1.37
tRNA (guanine(37)-N1)-methyltransferase	TRMT5	Q32P41	1.29	1.55	1.37
Creatine kinase U-type, mitochondrial	CKMT1A	P12532	1.17	1.26	1.37
Heterochromatin protein 1-binding protein 3	HP1BP3	Q5SSJ5-2	1.03	1.05	1.37
Aconitate hydratase, mitochondrial	ACO2	Q99798	1.19	1.22	1.37
Mitochondrial-processing peptidase subunit beta	PMPCB	O75439	1.15	1.19	1.36
Heme-binding protein 2	HEBP2	Q05DB4	0.95	0.07	1.36
Paraplegin	SPG7	J3KRF6	1.08	1.19	1.36
Hepatoma-derived growth factor	HDGF	B2RDE8	1.19	1.26	1.36
Early endosome antigen 1	EEA1	Q15075	1.06	1.21	1.36
Erythrocyte band 7 integral membrane protein	STOM	B4E2V5	0.99	1.12	1.36
Junction plakoglobin	JUP	A0A0S2Z487	1.40	1.40	1.36
PRA1 family protein 2	PRAF2	B3KN29	0.99	1.30	1.36
Pre-mRNA-splicing factor RBM22	RBM22	E5RJW4	0.92	0.90	1.36
Inorganic pyrophosphatase 2, mitochondrial	PPA2	Q9H2U2	1.12	1.15	1.36
Glia-derived nexin	SERPINE2	C9JN98	1.02	1.07	1.36
Galectin-3-binding protein	LGALS3BP	B4DVE1	0.99	1.05	1.36
Integrin alpha-2	ITGA2	E7ESP4	0.99	0.98	1.36
1-acyl-sn-glycerol-3-phosphate acyltransferase	AGPAT1	Q9HBM8	1.32	1.17	1.36
Pituitary tumor-transforming gene 1 protein-interacting protein	PTTG1IP	A8MZH8	1.02	1.14	1.35
Pre-mRNA-splicing factor SYF2	SYF2	B4E0Y8	1.19	1.42	1.35
ATP synthase subunit beta	HEL-S-271	V9HW31	1.15	1.16	1.35
DnaJ homolog subfamily C member 11	DNAJC11	Q9UMU8	1.00	1.24	1.35
Lysosome-associated membrane glycoprotein 2	LAMP2	B7Z2R9	1.09	0.93	1.35
Histone H2A.V	H2AFV	Q71UI9	0.88	1.00	1.35
Catenin delta-1	CTNND1	Q96FS1	1.19	1.19	1.35
Cathepsin B	CTSB	B4DL49	1.05	1.22	1.35
Serine/arginine-rich splicing factor 7	SRSF7	A0A0B4J1Z1	0.93	1.03	1.35
Dynein light chain roadblock-type 1	DYNLRB2	H3BNG9	1.21	1.64	1.35
Peroxisomal membrane protein PEX14	PEX14	B7Z4Z4	1.32	1.47	1.35
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	Q96EY7	1.30	1.38	1.35
Sideroflexin-1	SFXN1	Q9H9B4	1.09	1.10	1.35
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	D6RFM5	1.07	1.25	1.35
E3 ubiquitin-protein ligase CHIP	STUB1	H3BTA3	1.17	1.19	1.34
Collagen alpha-1(VII) chain	COL7A1	Q02388-2	1.58	2.02	1.34

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Mitochondrial import inner membrane translocase subunit Tim9	TIMM9	A0A024R648	0.96	0.91	1.34
SUMO-activating enzyme subunit 2	UBA2	B3KMZ6	1.18	1.25	1.34
COP9 signalosome complex subunit 8	COPS8	B4DFF9	1.75	1.09	1.34
FAS-associated factor 2	FAF2	Q96CS3	1.21	1.29	1.34
DNA repair protein RAD50	RAD50	A0A494C1B7	1.34	1.02	1.34
Reticulocalbin-1	HEL-S-84	V9HW95	0.98	1.04	1.34
Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	Q53F35	0.97	0.91	1.34
Dystonin	DST	E9PHM6	1.45	1.27	1.34
Ribosome biogenesis regulatory protein homolog	RRS1	Q15050	1.05	0.84	1.33
Histone H3	HIST2H3PS2	Q5TEC6	0.97	1.20	1.33
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	Q53FM7	1.16	1.13	1.33
Cornifin-A	SPRR1A	P35321	1.31	1.98	1.33
Bifunctional epoxide hydrolase 2	EPHX2	B4E1M2	1.74	1.89	1.33
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	G1UI16	0.93	0.91	1.33
Serine beta-lactamase-like protein LACTB, mitochondrial	LACTB	P83111	0.97	1.08	1.33
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR	Q8NCN5	1.02	0.93	1.33
DnaJ homolog subfamily A member 2	DNAJA2	A0A024R6S1	0.97	1.01	1.33
NADH-cytochrome b5 reductase 1	CYB5R1	Q9UHQ9	1.12	1.16	1.33
Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	J3KTL8	1.11	0.73	1.33
Vacuolar protein sorting-associated protein 28 homolog	VPS28	A0A0S2Z5H5	1.12	1.22	1.33
Glycogen debranching enzyme	AGL	G1UI17	1.11	1.19	1.32
Cleavage and polyadenylation specificity factor subunit 6	CPSF6	F8WJN3	1.08	1.15	1.32
N-acetyltransferase 10	NAT10	Q9H0A0	1.10	1.05	1.32
Cytochrome b5 type B	CYB5B	O43169	1.08	0.87	1.32
Cyclin-dependent kinase 1	CDK1	A0A087WZZ9	1.02	1.28	1.32
Dr1-associated corepressor	DRAP1	E9PNC7	1.50	1.37	1.32
Prelamin-A/C	LMNA	A0A384MQX1	1.01	1.13	1.32
NHP2-like protein 1	NHP2L1	Q6FHM6	1.09	1.21	1.32
Cat eye syndrome critical region protein 5	CECR5	A8MYZ9	1.53	1.52	1.32
2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	B4DI06	1.05	1.13	1.32
Histone H1.2	HIST1H1C	P16403	1.05	1.02	1.32
Proline-, glutamic acid- and leucine-rich protein 1	PELP1	E7EV54	1.54	1.29	1.32
Histone H2A type 2-C	HIST2H2AC	Q16777	0.95	1.05	1.32
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2-BSCL2	H3BQZ7	1.05	1.07	1.32
ATP synthase subunit a	ATP6	D2Y6Y7	1.03	1.13	1.32
Protein-glutamine gamma-glutamyltransferase K	TGM1	B0AZN7	1.58	1.69	1.32
Astrocytic phosphoprotein PEA-15	PEA15	B1AKZ5	2.33	1.74	1.32
Cadherin-1	CDH1	D3XNU5	0.77	0.91	1.32

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Tight junction protein ZO-2	TJP2	B7Z2R3	1.24	1.11	1.32
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	E9KL44	1.14	1.16	1.32
Fatty acid-binding protein, epidermal	FABP5	E7D VW5	1.25	1.79	1.32
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1	Q86WV2	1.30	1.00	1.32
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	B4DSM4	1.26	1.25	1.31
Histone H3.1	HIST1H3A	P68431	1.30	1.37	1.31
Poly(U)-binding-splicing factor PUF60	PUF60	Q9UHX1-6	0.98	1.36	1.31
39S ribosomal protein L10, mitochondrial	MRPL10	B4DEH0	1.08	1.20	1.31
CD59 glycoprotein	CD59	A0A3Q8TLE1	0.81	1.07	1.31
Nucleolar protein 56	NOP56	O00567	1.00	1.02	1.31
Serine/arginine-rich splicing factor 2	SRSF2	J3QL05	0.97	0.96	1.31
39S ribosomal protein L40, mitochondrial	MRPL40	Q9NQ50	1.00	1.11	1.31
Remodeling and spacing factor 1	RSF1	Q05DG0	1.28	1.30	1.31
Dehydrogenase/reductase SDR family member 7	DHRS7	H0YJR8	1.38	1.28	1.31
Zinc finger protein 185	ZNF185	O15231	1.17	1.44	1.31
Catenin alpha-1	CTNNA1	A0A384MDY0	1.16	1.22	1.31
rRNA 2-O-methyltransferase fibrillarin	FBL	Q96BS4	1.00	0.99	1.30
V-type proton ATPase subunit C 1	ATP6V1C1	A0A024R9I0	1.36	1.21	1.30
Dynein assembly factor 3, axonemal	DNAAF3	Q8N9W5-7	0.16	0.16	1.30
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	A8K651	1.10	1.11	1.30
General transcription factor II-I repeat domain-containing protein 2A	GTF2IRD2B	A0A087WW90	1.07	1.72	1.30
Xaa-Pro dipeptidase	PEPD	J3K000	1.30	1.46	1.30
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	A0A499FJI4	1.16	0.97	1.30
Superoxide dismutase	SOD2	Q7Z7M4	1.22	1.06	1.30
TOM1-like protein 2	TOM1L2	Q6ZVM7-5	1.18	1.46	1.30
Sulfide:quinone oxidoreductase, mitochondrial	hCG_2001986	Q9UHS8	1.05	1.10	1.30
Stomatin-like protein 2, mitochondrial	STOML2	Q9UJZ1	1.14	1.11	1.30
39S ribosomal protein L12, mitochondrial	MRPL12	B4DLN1	1.05	1.07	1.30
Signal peptidase complex subunit 2	SPCS2	E9PRB9	0.97	0.92	1.30
28S ribosomal protein S18b, mitochondrial	MRPS18B	A0A0G2JIC6	1.06	1.05	1.30
Glutamate dehydrogenase	GLUD1	B4DMF5	1.14	1.12	1.30
WD repeat-containing protein 36	WDR36	A0A0A0MTB8	1.10	1.07	1.29
Integrin alpha-3	ITGA3	Q59F03	1.10	1.04	1.29
Redox-regulatory protein FAM213A	FAM213A	Q9BRX8-2	1.07	0.82	1.29
RRP12-like protein	RRP12	B3KY97	1.31	1.43	1.29
Scaffold attachment factor B1	SAFB	B7Z2Z1	1.13	1.04	1.29
Laminin subunit alpha-3	LAMA3	A0A0A0MTS5	0.98	1.23	1.29
Aspartate aminotransferase	GOT2	A0A024R6W0	1.03	1.05	1.29
ADP/ATP translocase 2	SLC25A5	P05141	0.99	0.99	1.29

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
OClA domain-containing protein 1	OCIAD1	D6RDI5	1.12	1.03	1.29
ATP synthase subunit alpha	HEL-S-123m	V9HW26	1.02	1.06	1.29
Phosphatidylinositol-binding clathrin assembly protein	PICALM	B5BU72	1.12	1.00	1.29
Catenin beta-1	CTNNB1	A0A2R8Y804	1.05	1.08	1.29
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	Q59FN3	1.10	1.22	1.29
Beta-hexosaminidase	HEXB	Q5URX0	1.03	1.05	1.29
NADPH--cytochrome P450 reductase	DKFZp686G04235	Q63HL4	1.29	1.30	1.29
ATP synthase F(0) complex subunit B1, mitochondrial	hCG_39985	Q53GB3	1.00	1.06	1.29
Adenylate kinase 2, mitochondrial	AK2	F8W1A4	1.14	1.13	1.29
Probable ergosterol biosynthetic protein 28	C14orf1	Q86TW5	1.37	1.33	1.29
Thymidine phosphorylase	TYMP	A0A494C0L6	1.64	1.75	1.28
Growth factor receptor-bound protein 2	GRB2	A0A384ME16	1.43	1.80	1.28
Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	Q9Y3C8	1.79	1.75	1.28
Structural maintenance of chromosomes protein	SMC3	Q86VX4	1.44	1.36	1.28
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	A0A1X7SBS1	1.06	1.06	1.28
Pyruvate carboxylase	PC	A0A024R5C5	0.98	1.06	1.28
DNA damage-binding protein 1	DDB1	Q16531	1.01	1.01	1.28
Mitochondrial fission 1 protein	FIS1	Q9Y3D6	1.29	1.14	1.28
ATPase family AAA domain-containing protein 1	ATAD1	B4E2J1	1.28	1.28	1.28
Protein S100-A6	S100A6	P06703	1.29	1.53	1.28
ATP synthase subunit gamma	ATP5C1	Q8TAS0	1.05	0.96	1.28
Exocyst complex component 5	EXOC5	G3V377	1.16	1.49	1.28
Voltage-dependent anion-selective channel protein 3	VDAC3	Q9Y277	1.01	0.99	1.28
Structural maintenance of chromosomes protein	SMC1A	Q7Z4C6	1.04	1.15	1.28
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	Q9P0J0	0.94	0.99	1.28
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	D6RD67	1.24	1.16	1.28
Protein dpy-30 homolog	DPY30	Q9C005	0.91	1.18	1.28
Granulins	GRN	K7EMR1	1.08	1.26	1.28
Prenylcysteine oxidase 1	PCYOX1	F8W8W4	1.05	1.09	1.28
Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	PIP4K2C	Q8TBX8-2	1.51	1.76	1.28
Core histone macro-H2A.1	H2AFY	O75367-2	1.05	1.08	1.27
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	P22695	1.03	1.12	1.27
Small subunit processome component 20 homolog	UTP20	O75691	1.29	1.71	1.27
Long-chain-fatty-acid--CoA ligase 3	ACSL3	B3KN05	0.97	1.06	1.27
Electron transfer flavoprotein subunit beta	ETFB	P38117	1.14	1.11	1.27
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	A0A384MDT2	0.90	0.95	1.27
mRNA cap guanine-N7 methyltransferase	RNMT	K7ERH6	0.73	0.61	1.27
Calcium-binding mitochondrial carrier protein SCA _{MC} -1	SLC25A24	B7ZB41	1.20	1.33	1.27
Periplakin	PPL	K7EKI8	1.42	1.39	1.27

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
60 kDa heat shock protein, mitochondrial	HSPD1	A0A024R3X4	1.12	1.12	1.27
Electron transfer flavoprotein subunit alpha, mitochondrial	ETF A	A0A0S2Z3L0	1.17	1.16	1.27
V-type proton ATPase subunit E 1	ATP6V1E1	Q53Y06	1.22	1.42	1.27
Lysosome-associated membrane glycoprotein 1	LAMP1	B3KRY3	1.17	1.28	1.27
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	A0A384NL63	1.00	1.01	1.27
Pleckstrin homology domain-containing family S member 1	hCG_40992	D3DRC0	1.46	1.75	1.27
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3A	B4DJB4	1.14	1.23	1.27
GrpE protein homolog 1, mitochondrial	GRPEL1	Q9HAV7	0.97	1.03	1.27
U6 snRNA-associated Sm-like protein LSM7	LSM7	A0A087X2I5	1.31	1.25	1.27
Myosin light polypeptide 6	MYL6	P60660	1.50	1.60	1.27
Pyrroline-5-carboxylate reductase 2	PYCR2	A0A087WTV6	0.80	1.06	1.26
Transformer-2 protein homolog beta	TRA2B	H7BXF3	0.93	0.92	1.26
Fumarate hydratase, mitochondrial	FH	A0A0S2Z4C3	1.04	1.05	1.26
Exosome complex component MTR3	EXOSC6	Q5RKV6	1.20	1.66	1.26
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	B2RD24	1.36	1.34	1.26
Mitochondrial import receptor subunit TOM6 homolog	TOMM6	Q96B49	0.84	0.80	1.26
Integrin beta-1	ITGB1	P05556	0.98	0.98	1.26
Coronin	Coronin	A0A024R611	1.38	1.53	1.26
DnaJ homolog subfamily C member 17	DNAJC17	Q9NVM6	1.26	1.25	1.25
Succinyl-CoA:3-ketoacid-coenzyme A transferase	OXCT	Q6IAV5	0.95	0.94	1.25
AP-2 complex subunit mu	AP2M1	B4DJB1	1.04	1.05	1.25
5-nucleotidase	NT5E	Q6NZX3	0.91	0.91	1.25
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	Q496I0	1.00	1.00	1.25
NAD-dependent malic enzyme, mitochondrial	ME2	A0A1W2PPH1	1.07	1.11	1.25
Protein FAM162A	FAM162A	F8W7Q4	0.95	1.05	1.25
39S ribosomal protein L23, mitochondrial	MRPL23	H7C2P7	0.69	0.95	1.25
Integrin alpha-2	ITGA2	E7ESP4	0.83	0.88	1.25
Nucleolar pre-ribosomal-associated protein 1	URB1	O60287	1.49	1.25	1.25
DAZ-associated protein 1	DAZAP1	K7EQ02	1.12	1.07	1.25
Signal recognition particle receptor subunit beta	SRPRB	H7C4H2	1.13	1.20	1.25
THO complex subunit 2	THOC2	Q8NI27	1.04	0.98	1.25
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	B4DRZ6	1.34	1.40	1.25
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	A0A087WXX8	1.06	1.10	1.25
Voltage-dependent anion-selective channel protein 2	VDAC2	A0A0A0MR02	1.00	1.09	1.25
SWI/SNF complex subunit SMARCC1	SMARCC1	Q58EY4	1.63	1.49	1.25
ATP synthase subunit O, mitochondrial	ATP5O	P48047	1.04	1.10	1.24
Non-specific lipid-transfer protein	SCP2	B2R761	0.96	1.10	1.24
Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	H0YN26	1.11	1.15	1.24
Citrate synthase	CS	B4DJV2	1.11	1.06	1.24

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	H0YA96	1.09	1.08	1.24
Pre-mRNA-splicing factor SPF27	BCAS2	Q53HE3	1.15	1.27	1.24
10 kDa heat shock protein, mitochondrial	HSPE1	P61604	0.96	1.00	1.24
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	A0A384MEJ3	1.01	1.06	1.24
Ribosome biogenesis protein WDR12	WDR12	Q53T99	1.12	1.14	1.24
ATP-dependent RNA helicase DDX19B	DKFZp686C21137	Q68DY7	0.92	0.93	1.24
ADP-ribosylation factor 6	ARF6	Q5U025	1.09	1.10	1.24
Histone H2A	HIST1H2AH	A3KPC7	1.32	1.35	1.24
60S ribosomal protein L22	RPL22	Q7Z4W8	0.96	1.05	1.24
Diablo homolog, mitochondrial	DIABLO	A0A024RBT2	1.72	2.19	1.24
Nucleophosmin	NPM1	A0A0S2Z4G7	1.09	1.11	1.24
Unconventional myosin-Ib	MYO1B	E9PDF6	1.11	1.13	1.24
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	Q9Y5L4	0.92	1.12	1.24
Nicotinamide-nucleotide adenyltransferase	NMNAT1	Q53GL1	1.06	0.96	1.24
14-3-3 protein beta/alpha	HEL-S-1	V9HWD6	1.10	1.43	1.24
N-acylneuraminate cytidyltransferase	CMAS	Q53GF0	0.88	1.08	1.24
Cytochrome c	CYCS	C9JFR7	1.06	1.00	1.24
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8	B7Z768	0.91	0.93	1.24
Serine/threonine-protein kinase mTOR	MTOR	B4DZD5	2.51	1.86	1.24
Splicing factor 3B subunit 5	SF3B5	Q9BWJ5	1.05	0.94	1.23
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRRF51	A0A384NPX8	1.07	1.11	1.23
Elongation of very long chain fatty acids protein	ELOVL1	Q502X7	1.38	1.39	1.23
Serine/arginine repetitive matrix protein 1	SRRM1	M0QXG5	1.16	1.56	1.23
Splicing factor U2AF 65 kDa subunit	U2AF2	B5BU25	1.08	1.12	1.23
Ras-related protein Rab-10	RAB10	P61026	0.85	1.20	1.23
Epididymal secretory protein E1	NPC2	G3V2V8	0.97	0.93	1.23
U1 small nuclear ribonucleoprotein 70 kDa	SNRP70	A8KAQ5	1.01	1.03	1.23
Fatty aldehyde dehydrogenase	ALDH3A2	J3QRD1	1.39	1.61	1.23
Tricarboxylate transport protein, mitochondrial	SLC25A1	Q6LAP8	1.20	1.23	1.23
Single-stranded DNA-binding protein	SSBP1	Q567R6	1.06	1.00	1.23
DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	M4VP52	0.90	0.98	1.23
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	A0A384NKJ3	1.21	1.24	1.23
Pre-mRNA-splicing factor 38B	DKFZp434O1172	Q69YH0	1.44	0.68	1.23
Alanine--tRNA ligase, mitochondrial	AARS2	Q5JTZ9	1.16	1.21	1.23
EGF domain-specific O-linked N-acetylglucosamine transferase	EOGT	B3KR71	0.53	0.41	1.23
F-box only protein 22	FBXO22	H3BTH6	1.26	1.12	1.23
Enoyl-CoA hydratase, mitochondrial	ECHS1	A0A384MDW7	1.00	1.08	1.23
Persulfide dioxygenase ETHE1, mitochondrial	ETHE1	A0A0S2Z5B3	1.03	1.08	1.23
Phosphate carrier protein, mitochondrial	SLC25A3	Q8NCF7	1.08	1.09	1.22

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Cleavage stimulation factor subunit 3	CSTF3	B4DFQ5	1.20	1.06	1.22
Thioredoxin-related transmembrane protein 1	TMX1	Q9H3N1	1.07	0.97	1.22
Maleylacetoacetate isomerase	GSTZ1	H0YJN8	1.12	0.93	1.22
X-ray repair cross-complementing protein 5	XRCC5	P13010	1.12	1.08	1.22
Non-POU domain-containing octamer-binding protein	NONO	A8K525	0.96	1.06	1.22
Nucleolin	NCL	B3KM80	0.96	0.92	1.22
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	A0A384MTT2	1.34	1.30	1.22
Nuclear pore complex protein Nup205	NUP205	Q92621	1.21	1.21	1.22
Enhancer of rudimentary homolog	ERH	A0A024R6D4	0.97	1.12	1.22
Protein AATF	AATF	Q9NY61	1.16	1.10	1.22
Nucleolar protein 58	NOP58	Q9Y2X3	1.08	1.19	1.22
Pre-mRNA-processing factor 40 homolog A	PRPF40A	B4DPY2	1.00	0.94	1.22
Wiskott-Aldrich syndrome protein family member 2	WASF2	Q05BU7	1.29	1.38	1.22
Cell growth-regulating nucleolar protein	LYAR	Q9NX58	0.95	0.84	1.22
Protein phosphatase 1F	PPM1F	Q0VGL7	1.38	2.00	1.22
C-terminal-binding protein 1	CTBP1	E9PGB1	1.08	1.45	1.22
Putative ATP-dependent RNA helicase DHX30	DHX30	Q7L2E3-2	1.30	1.28	1.22
AP-2 complex subunit alpha-2	AP2A2	B7Z5S9	1.16	1.13	1.22
Envoplakin	EVPL	A0A024R8L8	1.49	1.85	1.22
Neuropathy target esterase	PNPLA6	A0A384DVU0	1.16	0.88	1.22
Keratin, type I cytoskeletal 18	KRT18	B2RA03	0.99	0.94	1.22
Nucleolar complex protein 4 homolog	NOC4L	Q9BVI4	1.33	1.83	1.22
Solute carrier family 25 member 40	SLC25A40	Q8TBP6	1.13	1.48	1.22
Protein S100	HEL-S-43	V9HWH9	1.22	1.32	1.22
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	H3BPE1	1.14	1.35	1.22
Replication protein A 70 kDa DNA-binding subunit	RPA1	P27694	1.22	0.97	1.22
Exportin-4	XPO4	Q86VC1	1.14	1.36	1.21
Cleavage and polyadenylation specificity factor subunit 5	NUDT21	B2R6U8	0.99	1.00	1.21
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	O75643	1.20	1.19	1.21
Nuclear receptor-binding protein	NRBP1	B4DW31	1.19	1.58	1.21
Endonuclease domain-containing 1 protein	ENDOD1	O94919	1.14	1.19	1.21
39S ribosomal protein L38, mitochondrial	MRPL38	B2R894	0.93	0.74	1.21
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	A0A0S2Z410	1.02	1.05	1.21
Cleavage stimulation factor subunit 2	CSTF2	B4DUD5	1.17	1.30	1.21
Cell cycle and apoptosis regulator protein 2	CCAR2	B3KTJ9	1.02	0.85	1.21
ATP-dependent Clp protease proteolytic subunit	CLPP	M0QXE9	0.94	1.76	1.21
Lysosome membrane protein 2	SCARB2	A0A1W2PPX5	1.21	0.98	1.21
Toll-interacting protein	TOLLIP	Q8N8J5	0.99	0.97	1.21
Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	A0A3B3ISQ4	1.16	1.27	1.21

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Growth hormone-inducible transmembrane protein	GHITM	Q9P099	0.85	1.08	1.21
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	A0A140VJX1	1.01	1.03	1.21
Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	P31930	0.97	0.96	1.21
Methylosome subunit pICln	CLNS1A	E9PMI6	0.86	0.54	1.21
Nuclear pore complex protein Nup50	hCG_1989366	B4E2D3	1.10	1.18	1.21
UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	Q9NYU2-2	1.08	1.15	1.20
Splicing factor 3B subunit 1	SF3B1	O75533	1.05	1.11	1.20
26S proteasome non-ATPase regulatory subunit 14	PSMD14	A0A140VKF2	1.21	1.26	1.20
RNA-binding protein Raly	RALY	Q9UKM9-2	1.05	1.01	1.20
NEDD8-activating enzyme E1 regulatory subunit	NAE1	Q13564-3	1.12	1.13	1.20
Transmembrane protein 43	TMEM43	A0A024R2F9	1.13	1.06	1.20
Malate dehydrogenase	MDH2	Q0QF37	1.01	1.00	1.20
TAR DNA-binding protein 43	TDP43	A0A0A0N0L3	0.92	0.89	1.20
Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP	Q9H0C8	1.08	1.14	1.20
CDGSH iron-sulfur domain-containing protein 2	CISD2	D6RCF4	0.98	0.94	1.20
DNA repair protein complementing XP-C cells	XPC	D2CPJ9	0.82	0.75	1.20
Emerin	EMD	P50402	1.10	1.31	1.20
Tubulin gamma-1 chain	TUBG1	P23258	1.34	1.64	1.20
HIG1 domain family member 2A, mitochondrial	HIGD2A	A0A024R7Q3	0.94	0.94	1.20
Carboxypeptidase D	CPD	B7Z843	1.11	1.69	1.20
Differentially expressed in FDCP 6 homolog	DEF6	H0Y7V7	1.22	1.34	1.20
Very-long-chain enoyl-CoA reductase	TECR	B3KM97	0.80	1.00	1.20
Ras-related protein Rab-35	RAB35	F5H157	1.26	1.51	1.20
L-xylulose reductase	DCXR	A0A384NY14	1.15	1.23	1.20
Elongation factor G, mitochondrial	GFM1	E5KND7	0.90	0.99	1.20
Multifunctional methyltransferase subunit TRM112-like protein	TRMT112	F5GX77	1.43	0.42	1.20
Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	P04899	0.99	1.01	1.20
U6 snRNA-associated Sm-like protein LSM2	LSM2	Q9Y333	0.96	0.96	1.20
Double-stranded RNA-specific adenosine deaminase	ADAR	A0A024DAK3	1.02	0.97	1.20
Presequence protease, mitochondrial	PITRM1	B4DRW8	1.03	0.97	1.20
Serine/arginine-rich splicing factor 6	HEL-S-91	A0A590UJK4	0.86	0.94	1.20
Transmembrane and TPR repeat-containing protein 3	TMTC3	A8K321	0.88	0.84	1.20
Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1	PAPSS1	Q05BW9	1.17	1.27	1.20
28S ribosomal protein S35, mitochondrial	MRPS35	P82673	1.03	0.91	1.20
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	H0YLC3	1.05	1.05	1.20
Transportin-3	TNPO3	E9PFH4	1.32	1.33	1.20
Interleukin enhancer-binding factor 2	ILF2	F4ZW62	1.07	1.05	1.19
Dihydrolipoyl dehydrogenase	DLD	B4DFL1	0.97	0.95	1.19
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	Q86TQ8	0.94	0.93	1.19

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Nuclear autoantigenic sperm protein	NASP	Q5T626	0.94	0.90	1.19
Nucleolar complex protein 2 homolog	NOC2L	Q9H9J5	1.22	1.21	1.19
Probable ATP-dependent RNA helicase DDX17	DDX17	A0A1X7SBZ2	0.99	1.03	1.19
Glycerol-3-phosphate dehydrogenase	GPD2	Q53T76	0.97	0.94	1.19
Secretory carrier-associated membrane protein 4	SCAMP4	Q969E2	1.01	1.10	1.19
Calcium homeostasis endoplasmic reticulum protein	CHERP	Q8IWX8	1.14	0.83	1.19
Histone-binding protein RBBP4	RBBP4	Q09028-3	1.04	1.03	1.19
Sigma non-opioid intracellular receptor 1	SIGMAR1	Q5T1J1	0.89	0.99	1.19
Nucleoside diphosphate kinase A	NME1	A0A384MTW7	1.10	1.28	1.19
Phosphoglucomutase-2	PGM2	Q96G03	1.24	1.33	1.19
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	A0A384MTR2	1.00	0.96	1.19
Cytoskeleton-associated protein 5	CKAP5	Q14008-2	1.16	1.32	1.19
Gasdermin-A	GSDMA	Q96QA5	1.22	1.46	1.19
Glucosidase 2 subunit beta	PRKCSH	A0A024R7F1	0.93	1.00	1.19
Polyadenylate-binding protein 2	PABPN1	B4DEH8	1.15	1.08	1.19
ATP synthase subunit g, mitochondrial	ATP5L	O75964	1.01	1.10	1.19
E3 ubiquitin-protein ligase TRIM23	TRIM23	A8K9U9	1.17	0.97	1.19
Pre-mRNA-processing factor 19	PRPF19	Q9UMS4	1.10	1.01	1.19
Far upstream element-binding protein 2	KHSRP	A0A384P5V3	1.06	1.04	1.19
3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	A0A024R2M6	1.05	1.09	1.19
THO complex subunit 4	ALYREF	Q86V81	1.02	1.00	1.19
Clathrin light chain B	CLTB	A0A024R7S3	0.96	1.09	1.19
Glutathione S-transferase kappa 1	LOC51064	Q6FII1	1.09	0.97	1.19
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3B	A0A087X2E5	1.02	1.07	1.19
Protein TBRG4	TBRG4	D3DVL7	1.07	1.06	1.19
U1 small nuclear ribonucleoprotein A	SNRPA	M0R221	1.12	1.09	1.19
Choline transporter-like protein 2	SLC44A2	A0A088QCU6	1.17	1.19	1.19
Calcium/calmodulin-dependent protein kinase type II subunit delta	CAMK2D	Q92991	1.15	1.20	1.19
Protein RCC2	RCC2	A5PLK7	0.92	0.93	1.18
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	Q9BT'T5	1.01	1.09	1.18
Integrin alpha-V	ITGAV	L7RXH0	0.92	0.90	1.18
Interferon-induced GTP-binding protein Mx1	MX1	F8W8T1	1.22	1.18	1.18
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	E5KNY5	1.10	1.04	1.18
Prohibitin	PHB	A8K401	1.00	1.00	1.18
Radixin	RDX	Q6PKD3	0.77	0.90	1.18
MICOS complex subunit MIC60	IMMT	B9A067	1.02	0.99	1.18
Oxysterol-binding protein	OSBPL8	F8VZ43	1.16	1.47	1.18
28S ribosomal protein S5, mitochondrial	MRPS5	P82675	0.95	1.02	1.18
DNA-dependent protein kinase catalytic subunit	PRKDC	P78527	1.10	1.07	1.18

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
High affinity cationic amino acid transporter 1	SLC7A1	B2R728	1.25	1.30	1.18
MICOS complex subunit MIC19	CHCHD3	A4D1N4	0.98	1.14	1.18
Protein SET	SET	Q5VXV3	0.93	0.91	1.18
Cullin-4B	CUL4B	A0A669KAX4	1.08	0.93	1.18
ATP synthase subunit f, mitochondrial	ATP5J2-PTCD1	C9JJT5	0.88	0.94	1.18
SUMO-activating enzyme subunit 1	SAE1	B4DY66	1.11	1.16	1.17
Acylpyruvase FAHD1, mitochondrial	FAHD1	Q6P587	0.99	1.01	1.17
Microsomal glutathione S-transferase 3	MGST3	Q53GB9	0.99	0.93	1.17
Lon protease homolog, mitochondrial	LONP1	K7EKE6	1.06	1.02	1.17
Protein LZIC	LZIC	K7ES95	1.27	1.98	1.17
Amine oxidase [flavin-containing] A	MAOA	Q53YE7	1.16	1.24	1.17
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	A8K761	0.91	0.89	1.17
Ras-related protein Rap-1b	RAP1B	A0A024RB87	0.95	1.08	1.17
Activated RNA polymerase II transcriptional coactivator p15	PC4	Q6IBA2	1.15	0.97	1.17
Vesicle-fusing ATPase	NSF	Q96D47	1.66	1.55	1.17
COP9 signalosome complex subunit 2	COPS2	B4DIH5	1.19	1.35	1.17
Serine/arginine-rich splicing factor 3	SFRS3	B2R6F3	0.92	0.86	1.17
Transketolase	HEL107	V9HWD9	1.09	1.12	1.17
Negative elongation factor B	NELFB	A0A5H1ZRP4	0.93	0.94	1.17
Splicing factor 3B subunit 3	SF3B3	A8K6V3	1.06	1.01	1.17
Histone H2B	HIST1H2BJ	A0A024RCJ2	1.00	1.10	1.17
General transcription factor IIF subunit 1	GTF2F1	B4DXY2	0.77	0.95	1.17
Transportin-2	TNPO2	B4DRY5	1.40	1.42	1.17
DIS3-like exonuclease 2	DIS3L2	Q8IYB7	1.24	1.70	1.17
Splicing factor 3A subunit 2	SF3A2	K7EMT0	1.01	0.95	1.17
28S ribosomal protein S16, mitochondrial	MRPS16	A6ND22	1.02	1.11	1.17
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	F8W6I7	1.02	0.98	1.17
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3G	Q59GA3	0.08	0.11	1.17
Histone H1.4	HIST1H1E	Q4VB24	0.87	0.89	1.17
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	A0A669KB10	1.17	1.19	1.16
Lysophospholipid acyltransferase 7	MBOAT7	B4DDH8	0.96	0.91	1.16
Peroxisomal multifunctional enzyme type 2	HSD17B4	A0A2R8YD50	1.04	0.92	1.16
Heat shock protein 75 kDa, mitochondrial	TRAP1	Q59EK6	1.05	1.00	1.16
Ras-related protein Rab-6A	RAB6A	B7Z5Z9	1.01	1.03	1.16
Ras-related protein R-Ras2	RRAS2	P62070	0.95	0.86	1.16
Transmembrane glycoprotein NMB	GPNMB	Q14956	1.09	1.25	1.16
Sulfurtransferase	TST	Q53EW8	1.20	1.22	1.16
Protein QIL1	QIL1	A0A140TA86	1.13	1.03	1.16
Vesicle-associated membrane protein 8	VAMP8	C9JXZ5	0.75	0.59	1.16

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
NADH-cytochrome b5 reductase	CYB5R3	A0A024R4X0	1.01	0.89	1.16
Isochorismatase domain-containing protein 2, mitochondrial	ISOC2	Q96AB3	1.17	1.07	1.16
Histone H2B	HIST1H2BC	Q0D2M2	1.05	0.98	1.16
Endoplasmic reticulum-Golgi intermediate compartment protein 2	ERGIC2	H0YHJ8	0.95	0.82	1.16
Ubiquitin-conjugating enzyme E2 D1	UBE2D1	A0A087WW00	1.70	1.43	1.16
Heterogeneous nuclear ribonucleoprotein L	HNRNPL	Q6NTA2	1.02	1.02	1.15
Syntaxin-12	STX12	B1AJQ6	1.17	1.30	1.15
3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	EBP	C9J719	1.00	1.07	1.15
RNA-binding motif protein, X chromosome	RBMX	H0Y6E7	0.88	0.90	1.15
2-oxoglutarate dehydrogenase, mitochondrial	OGDH	Q02218	0.99	0.91	1.15
Protoporphyrinogen oxidase	PPOX	B3KT30	1.08	1.09	1.15
Ribosome-binding protein 1	RRBP1	A7BI36	0.87	0.84	1.15
Lamin-B2	LMNB2	A0A384NPH0	0.89	0.88	1.15
Niban-like protein 1	C9orf88	A0A024R872	1.12	1.16	1.15
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	A0A087X0X3	1.02	1.02	1.15
Protein cornichon homolog 4	CNIH4	A6NLH6	1.08	1.03	1.15
Tyrosine-protein kinase receptor	MPRIP	J3KSW8	1.12	0.96	1.15
Microsomal glutathione S-transferase 1	MGST1	Q6LET6	1.01	1.15	1.15
Major facilitator superfamily domain-containing protein 10	MFSD10	D6RIZ4	1.08	1.08	1.15
Ras-related GTP-binding protein D	RRAGC	B4DQ03	1.34	1.63	1.15
Apoptosis-inducing factor 1, mitochondrial	AIFM1	O95831-3	1.01	0.91	1.15
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	Q08J23-2	1.09	1.08	1.15
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	A0A384NPZ7	0.98	0.89	1.15
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	A0A0C4DGS1	1.00	0.89	1.15
Host cell factor 1	HCFC1	Q05C05	1.06	1.04	1.15
GMP synthase [glutamine-hydrolyzing]	GMPS	A0A140VJK6	1.13	1.11	1.15
Ras-related protein Rab-5C	RAB5C	A0A024R1U4	1.01	1.09	1.15
Monocarboxylate transporter 1	SLC16A1	B4E106	0.97	1.01	1.15
Ras-related protein Rab-11A	RAB11A	H3BMH2	1.11	1.05	1.15
Prohibitin-2	PHB2	J3KPX7	1.04	1.01	1.15
Nuclear pore complex protein Nup93	NUP93	A8K897	1.21	1.20	1.14
Nuclear pore complex protein Nup85	NUP85	J3QS63	1.04	1.22	1.14
Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	M0QXU7	0.86	0.91	1.14
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	D6R9P3	1.03	0.97	1.14
LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	D3DVQ1	1.09	0.96	1.14
Gamma-interferon-inducible protein 16	IFI16	D3DUZ3	0.94	0.92	1.14
39S ribosomal protein L37, mitochondrial	MRPL37	S4R369	1.21	1.00	1.14
Cytochrome b-c1 complex subunit 7	UQCRB	B2R4A2	0.75	0.74	1.14
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	A0A024R745	0.97	1.05	1.14

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Serpin B8	SERPINB8	A0A1B0GU38	1.45	1.57	1.14
Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	Q8TCS8	0.81	0.82	1.14
Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	B7Z2E2	0.97	1.06	1.14
ATP-dependent RNA helicase A	DHX9	Q08211	1.02	1.00	1.14
Alpha-aminoadipic semialdehyde synthase, mitochondrial	AASS	B4DFY7	0.89	0.95	1.14
Metaxin-2	MTX2	C9JAZ1	1.21	1.28	1.14
Translocon-associated protein subunit gamma	SSR3	C9JA28	0.93	0.93	1.14
Activating signal cointegrator 1 complex subunit 3	ASCC3	Q8N3C0	0.71	0.71	1.14
Ras-related protein Rab-5B	RAB5B	A0A024RB09	1.02	0.93	1.14
Transcription elongation factor B polypeptide 2	TCEB2	Q15370	1.04	1.15	1.13
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	A0A384MDR8	1.11	1.02	1.13
Elongation factor Tu, mitochondrial	TUFM	A0A384ME17	0.93	0.91	1.13
Histone H4	HIST1H4H	B2R4R0	0.91	0.96	1.13
Splicing factor 3B subunit 6	SF3B6	Q9Y3B4	1.01	0.99	1.13
COP9 signalosome complex subunit 7a	COPS7A	F5H7C6	1.44	1.58	1.13
V-type proton ATPase subunit a	ATP6V0A1	B7Z2J9	1.13	1.42	1.13
Involucrin	IVL	P07476	1.06	1.45	1.13
Cytochrome c oxidase subunit 2	COX2	A0A346M047	0.97	0.88	1.13
Neuroguidin	NGDN	Q8NEJ9-2	0.97	1.00	1.13
Transaldolase	TALDO1	A0A140VK56	0.96	1.07	1.13
ADP-sugar pyrophosphatase	NUDT5	A6NFX8	0.99	1.12	1.13
28S ribosomal protein S27, mitochondrial	MRPS27	Q8N6F2	1.03	0.97	1.13
39S ribosomal protein L44, mitochondrial	MRPL44	A1MA90	0.91	0.80	1.13
High mobility group protein B1	HMGB1	Q5T7C4	0.90	0.95	1.13
Vesicular integral-membrane protein VIP36	LMAN2	B4DWN1	0.89	0.81	1.13
Acetolactate synthase-like protein	ILVBL	M0R1B5	0.95	0.93	1.13
H/ACA ribonucleoprotein complex subunit 1	GAR1	Q9NY12-2	1.06	0.97	1.13
Nuclear pore complex protein Nup214	NUP214	A0A494C1F2	1.11	1.21	1.13
Cytoskeleton-associated protein 4	CKAP4	A0A024RBH2	0.97	0.92	1.13
Serine hydroxymethyltransferase	DKFZp686P09201	Q5HYG8	1.00	1.04	1.13
Mitochondrial carrier homolog 2	MTCH2	Q9Y6C9	0.96	1.03	1.13
Non-specific serine/threonine protein kinase	PAK4	B4DUG0	1.03	1.01	1.13
ATP-dependent RNA helicase DDX18	DDX18	H7C452	0.93	0.82	1.13
Ubiquitin carboxyl-terminal hydrolase	USP7	B7Z855	1.00	1.03	1.12
Splicing factor U2AF 35 kDa subunit	U2AF1	P0DN76	1.06	1.01	1.12
ADP-ribosylation factor-like protein 1	ARL1	B4DR16	1.17	1.29	1.12
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	F8W930	0.99	0.88	1.12
Splicing factor, proline- and glutamine-rich	SFPQ	Q9BSV4	0.97	0.94	1.12
Dual specificity mitogen-activated protein kinase kinase 4	MAP2K4	B7ZA62	0.94	0.72	1.12

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Prostaglandin E synthase 2	PTGES2	B4DWP1	1.10	0.89	1.12
Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	P49419-2	0.98	0.95	1.12
Trophoblast glycoprotein	TPBG	Q13641	1.00	1.11	1.12
Nuclear-interacting partner of ALK	ZC3HC1	C9J0I9	1.17	1.42	1.12
Guanine nucleotide-binding protein subunit gamma	GNG12	Q53GD1	0.98	0.87	1.12
Nuclear pore complex protein Nup155	NUP155	E9PF10	0.95	0.94	1.12
Alpha-actinin-4	ACTN4	A0A0S2Z3G9	1.09	1.15	1.12
Regulator of chromosome condensation	RCC1	Q5T081	0.93	0.95	1.12
39S ribosomal protein L17, mitochondrial	MRPL17	E9PKV2	0.99	1.03	1.12
Plectin	PLEC	Q15149-4	1.01	1.03	1.12
Transcription factor BTF3	BTF3L4	E9PL10	1.21	1.37	1.12
OCIA domain-containing protein 2	OCIAD2	Q56VL3	0.87	0.94	1.12
Retinol dehydrogenase 11	RDH11	A0A0S2Z583	1.05	1.13	1.12
Cysteine dioxygenase type 1	CDO1	Q16878	0.06	0.40	1.12
39S ribosomal protein L39, mitochondrial	MRPL39	C9JG87	1.00	0.86	1.12
5(3)-deoxyribonucleotidase, cytosolic type	NT5C	J3KRC4	1.36	1.24	1.12
Voltage-dependent anion-selective channel protein 1	VDAC1	A0A1L1UHR1	1.02	1.01	1.12
Pre-mRNA-processing-splicing factor 8	PRPF8	Q6P2Q9	1.04	1.02	1.12
Small nuclear ribonucleoprotein E	SNRPE	P62304	1.12	1.09	1.12
Protein kinase C delta-binding protein	PRKCDBP	E9PIE3	0.96	1.00	1.12
Adipocyte plasma membrane-associated protein	APMAP	Q9HDC9	0.98	1.05	1.12
Protein transport protein Sec23A	SEC23A	F5H365	1.06	1.04	1.12
Polypyrimidine tract-binding protein 1	PTBP1	A0A0U1RRM4	1.07	1.07	1.12
Small nuclear ribonucleoprotein Sm D3	SNRPD3	P62318-2	0.98	1.05	1.12
Guanine nucleotide-binding protein G(q) subunit alpha	GNAQ	P50148	0.86	0.87	1.12
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	B3KNF6	1.23	1.20	1.12
rRNA/tRNA 2-O-methyltransferase fibrillarin-like protein 1	FBLL1	A6NHQ2	1.04	0.94	1.12
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	Q59EF0	1.25	1.34	1.12
Neutral alpha-glucosidase AB	HEL-S-164nA	V9HWJ0	1.03	0.95	1.11
Spectrin beta chain, non-erythrocytic 1	SPTBN1	D6W5C0	1.13	1.15	1.11
Histone H1.5	HIST1H1B	P16401	0.93	0.92	1.11
RNA-binding protein 34	RBM34	Q5TCT4	0.86	0.75	1.11
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	P04844	1.05	1.09	1.11
Glutaminase kidney isoform, mitochondrial	GLS	A8K132	0.97	1.05	1.11
Peroxiredoxin-4	PRDX4	H7C3T4	0.98	0.97	1.11
WD repeat-containing protein 5	WDR5	V9GYQ5	0.84	0.85	1.11
TBC1 domain family member 22A	TBC1D22A	F8WDP1	0.43	1.00	1.11
Protein phosphatase 1 regulatory subunit	PPP1R12A	F8VZN8	1.34	1.35	1.11

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Translocon-associated protein subunit alpha	SSR1	C9J3L8	0.99	1.03	1.11
Unconventional myosin-Ic	MYO1C	F5H6E2	1.00	1.06	1.11
ATP-dependent RNA helicase DDX50	DDX50	Q9BQ39	0.87	0.70	1.11
Mitochondrial import receptor subunit TOM22 homolog	MST065	Q549C5	0.98	1.02	1.11
Protein transport protein Sec61 subunit beta	SEC61B	S4R3B5	1.19	1.18	1.11
Mitochondrial ornithine transporter 1	SLC25A15	B4DL63	0.74	1.70	1.11
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	P54886-2	0.98	0.96	1.11
Ras-related protein Rab-5A	RAB5A	A0A024R2K1	1.82	0.75	1.11
Inosine triphosphate pyrophosphatase	ITPA	A0A0S2Z3W7	1.34	1.30	1.11
Protein disulfide-isomerase	P4HB	A0A024R8S5	0.90	0.88	1.11
2,5-phosphodiesterase 12	PDE12	F6T1Q0	1.12	1.19	1.11
Ribosomal RNA processing protein 1 homolog B	RRP1B	Q14684-2	0.88	1.01	1.11
Calreticulin	HEL-S-99n	Q53G71	0.90	0.84	1.11
Endoplasmic reticulum resident protein 29	HEL-S-107	V9HW71	0.95	0.93	1.10
60S acidic ribosomal protein P1	RPLP1	Q7Z612	1.17	1.18	1.10
Mitotic checkpoint protein BUB3	BUB3	J3QT28	0.97	1.08	1.10
Spliceosome RNA helicase DDX39B	hCG_2005638	A0A024RCM3	0.99	0.95	1.10
Septin-11	SEPTIN11	Q9NVA2	1.00	0.90	1.10
Hexokinase	HK2	A8K2U2	1.26	1.41	1.10
Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	B3KQJ0	0.96	0.93	1.10
Vacuolar protein sorting-associated protein 51 homolog	VPS51	Q9UID3-2	1.18	1.36	1.10
Stress-70 protein, mitochondrial	HEL-S-124m	B7Z4V2	1.01	0.96	1.10
Interleukin enhancer-binding factor 3	ILF3	A0A024R7C7	1.03	1.02	1.10
Mitochondrial import receptor subunit TOM70	TOMM70A	B4DZ87	0.96	0.98	1.10
Small nuclear ribonucleoprotein F	SNRPF	P62306	1.01	0.98	1.10
ATP synthase subunit d, mitochondrial	ATP5H	O75947	1.06	1.03	1.10
Protein unc-45 homolog A	UNC45A	Q9H3U1-2	1.35	1.43	1.10
Nicotinate phosphoribosyltransferase	NAPRT	C9J8U2	1.49	1.75	1.10
Eukaryotic initiation factor 4A-III	EIF4A3	I3L3H2	1.00	1.01	1.10
Reticulocalbin-2	RCN2	A8MXP8	0.98	1.16	1.10
RNA-binding protein 8A	RBM8	A0A023T787	0.85	0.94	1.10
Cytochrome c oxidase subunit 6B1	COX6B1	P14854	0.76	0.89	1.10
Calcium-regulated heat stable protein 1	CARHSP1	Q9Y2V2	0.98	1.29	1.10
Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRPUL1	Q9BUJ2	1.09	0.97	1.10
Up-regulated during skeletal muscle growth protein 5	USMG5	Q96IX5	0.99	1.11	1.10
CD44 antigen	CD44	H0YE40	1.12	1.10	1.10
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	B4E043	0.96	1.02	1.10
Erlin-1	ERLIN1	B2RDK6	0.94	0.92	1.10
Ubiquitin-40S ribosomal protein S27a	RPS27A	A0A248RGE3	0.97	1.07	1.10

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
116 kDa U5 small nuclear ribonucleoprotein component	SNRP116	Q8IXJ3	1.03	1.01	1.10
Cytoplasmic FMR1-interacting protein 1	CYFIP1	B3K WV6	1.07	1.18	1.10
Dolichol-phosphate mannosyltransferase subunit 1	DPM1	A0A0S2Z4Y5	1.14	0.99	1.10
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	B4DTA2	1.08	1.06	1.10
HEAT repeat-containing protein 1	HEATR1	A0A024R3R7	1.23	1.21	1.10
Myoferlin	MYOF	Q9NZM1-6	0.96	0.92	1.10
Ras-related protein Rab-14	RAB14	A0A024R845	1.02	1.07	1.10
Probable ATP-dependent RNA helicase DDX46	DDX46	D3DQA6	1.04	1.01	1.10
Terpene cyclase/mutase family member	LSS	B2R694	0.87	0.85	1.10
Serine/arginine-rich splicing factor 1	SRSF1	J3KTL2	1.06	0.99	1.10
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	A0A384P5S9	1.10	1.13	1.09
28S ribosomal protein S29, mitochondrial	DAP3	P51398-2	1.23	1.27	1.09
Protein Hook homolog 2	HOOK2	K7EJA7	1.39	1.50	1.09
ARF GTPase-activating protein GIT1	DKFZp686G1540	Q7Z2E5	1.15	1.24	1.09
ATP-dependent RNA helicase DDX3Y	DDX3Y	A0A024R9A4	1.03	1.22	1.09
S-adenosylmethionine synthase isoform type-2	MAT2A	A0A140VJP5	0.90	0.88	1.09
Acyl-coenzyme A oxidase	ACOX1	B4DU07	0.87	0.91	1.09
Heme oxygenase 2	HMOX2	Q6IBP2	0.84	0.88	1.09
Nuclear mitotic apparatus protein 1	NUMA1	Q96HN5	0.97	0.85	1.09
ATP-dependent DNA helicase Q1	RECQL	A0A024RAV2	0.91	0.88	1.09
Chromobox protein homolog 3	CBX3	A4D177	0.93	0.95	1.09
BRO1 domain-containing protein BROX	BROX	Q5VW33	1.04	1.07	1.09
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	Q8N1B9	0.96	0.86	1.09
Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	Q9NQG5	0.95	1.03	1.09
Histone H2A	HIST1H2AB	Q08AJ9	0.97	0.83	1.09
Splicing factor 1	SF1	B4DX42	1.22	1.30	1.09
28S ribosomal protein S23, mitochondrial	MRPS23	J3QLR8	1.01	0.94	1.09
Proteasome activator complex subunit 3	HEL-S-283	V9HWJ8	0.79	0.83	1.09
Torsin-1A-interacting protein 2	TOR1AIP2	Q8NFBQ8	1.08	1.44	1.09
Protein-tyrosine-phosphatase	PTPN23	B4DJ12	1.41	1.56	1.09
Carboxypeptidase A1	CPA1	S4R433	0.32	0.92	1.09
Bleomycin hydrolase	BLMH	K7ES02	1.10	0.95	1.09
60S ribosomal protein L27a	RPL27A	Q6NZ52	0.95	0.95	1.09
Mesencephalic astrocyte-derived neurotrophic factor	MANF	A8K878	0.83	0.79	1.09
PHD finger-like domain-containing protein 5A	PHF5A	A0A024R1U2	0.84	0.87	1.09
Glycine cleavage system H protein, mitochondrial	GCSH	A0A1W2PQV2	0.89	0.89	1.09
Focal adhesion kinase 1	PTK2	H0YB99	1.19	1.07	1.09
Protein S100-A3	S100A3	P33764	1.14	1.00	1.09
G-rich sequence factor 1	GRSF1	B7Z2D8	0.91	0.85	1.08

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Serrate RNA effector molecule homolog	SRRT	Q9BXP5-5	0.91	0.79	1.08
Programmed cell death protein 4	PDCD4	B4DKX4	0.90	0.94	1.08
Amino acid transporter	SLC1A5	Q71UA6	0.95	0.91	1.08
Small nuclear ribonucleoprotein Sm D1	SNRPD1	P62314	1.00	0.96	1.08
Protein transport protein Sec61 subunit gamma	SEC61G	A0A024QYZ0	1.06	0.98	1.08
Armadillo repeat-containing protein 1	ARMC1	E9PR92	0.90	0.90	1.08
U4/U6.U5 tri-snRNP-associated protein 2	USP39	B3KPG7	1.06	1.10	1.08
RNA-binding protein EWS	EWSR1	B0QYK0	1.01	1.10	1.08
AP-2 complex subunit alpha-1	AP2A1	O95782-2	1.03	1.02	1.08
Transmembrane emp24 domain-containing protein 9	TMED9	B2R8A2	0.97	1.08	1.08
Heterogeneous nuclear ribonucleoprotein A3	HNRPA3	B4DDB6	0.91	1.11	1.08
Coatomer subunit gamma	COPG2	Q9H9B7	1.31	1.22	1.08
Reticulon-4	RTN4	Q9NQC3-2	1.00	0.97	1.08
Lupus La protein	SSB	B5BUB5	0.91	0.91	1.08
Vacuolar protein sorting-associated protein 26A	VPS26A	A8K3C1	1.14	1.13	1.08
Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	A0A384N605	1.17	1.26	1.08
Inositol monophosphatase 2	IMPA2	Q6PIP6	1.39	2.11	1.08
V-type proton ATPase 16 kDa proteolipid subunit	ATP6V0C	P27449	0.88	1.04	1.08
Dynein light chain 1, cytoplasmic	DNCL1	Q6FGH9	1.08	1.25	1.08
Barrier-to-autointegration factor	BANF1	A0A024R5H0	0.89	0.99	1.08
Thyroid hormone receptor-associated protein 3	THRAP3	A0A3B3ITZ9	0.83	0.79	1.08
ATP synthase-coupling factor 6, mitochondrial	ATP5J	Q61B54	1.07	0.99	1.08
Endoplasmic reticulum resident protein 44	ERP44	A0A384MEE7	0.98	0.83	1.08
Cellular retinoic acid-binding protein 2	CRABP2	P29373	1.31	1.51	1.08
Lamin-B1	LMNB1	P20700	0.90	0.89	1.08
U2 small nuclear ribonucleoprotein A	SNRPA1	H0YKK0	0.89	1.21	1.08
Septin-8	SEPTIN8	Q92599	1.05	0.97	1.08
Protein disulfide-isomerase	HEL-S-269	B3KQT9	0.91	0.86	1.08
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	Q96ID4	0.87	0.96	1.08
Junctional adhesion molecule A	F11R	Q9Y5B2	0.96	1.00	1.08
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	P05023-3	1.02	1.01	1.08
Tubulin-specific chaperone D	TBCD	J3KR97	1.21	1.55	1.08
Fermitin family homolog 1	FERMT1	Q49AC8	1.02	1.13	1.07
NF-X1-type zinc finger protein NFXL1	URCC5	B1Q2B0	0.87	0.58	1.07
Ras-related protein Rab-1A	RAB1A	B7Z8M7	0.97	0.98	1.07
Pyruvate dehydrogenase E1 component subunit alpha	PDHA1	A0A024RBX9	0.97	0.98	1.07
Fibronectin	FN1	Q9H382	0.77	0.75	1.07
Polypeptide N-acetylgalactosaminyltransferase	GALNT2	G3V1S6	0.93	0.73	1.07
Transcription intermediary factor 1-beta	TRIM28	Q13263	0.92	0.91	1.07

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
14-3-3 protein beta/alpha	YWHAB	P31946-2	0.71	1.10	1.07
Atlastin-3	ATL3	F5H6I7	1.12	1.04	1.07
Vimentin	HEL113	V9HWE1	0.95	0.86	1.07
Casein kinase II subunit alpha	CSNK2A1	A0A2R8YF43	1.00	0.93	1.07
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	E9PN51	1.03	0.87	1.07
DnaJ homolog subfamily C member 10	DNAJC10	B4DP04	0.90	0.94	1.07
NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	NDUFS5	O43920	1.07	1.08	1.07
Extended synaptotagmin-1	FAM62A	B3KMOV5	1.04	1.03	1.07
Far upstream element-binding protein 3	hCG_31253	A0A024R8A7	0.80	1.03	1.07
14-3-3 protein gamma	YWHAG	P61981	1.09	1.26	1.07
Integrin alpha-6	ITGA6	P23229-7	1.15	0.93	1.07
Cell division cycle protein 23 homolog	CDC23	D6RBY8	1.94	1.37	1.07
Acyl-CoA synthetase family member 3, mitochondrial	ACSF3	Q4G176	0.88	0.93	1.07
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	Q9Y305-3	0.97	0.98	1.07
Exportin-7	XPO7	A8K607	1.19	1.28	1.07
WD repeat-containing protein 75	WDR75	A8K330	1.07	1.04	1.07
Cytochrome c oxidase subunit 7C, mitochondrial	COX7C	P15954	0.20	0.89	1.07
Protein mago nashi homolog	MAGOH	P61326	0.90	0.91	1.07
ADP-ribosylation factor-related protein 1	ARFRP1	B7ZKY8	1.01	1.18	1.07
AP complex subunit beta	AP2B1	H0UID5	1.06	1.04	1.07
Nucleolysin TIA-1 isoform p40	TIA1	B4E0E5	1.09	1.10	1.07
A-kinase anchor protein 1, mitochondrial	AKAP1	A0A140VK05	1.43	1.25	1.07
Histone H1x	H1FX	Q92522	1.19	1.17	1.07
Sphingosine-1-phosphate lyase 1	SGPL1	H0Y3V8	0.76	0.98	1.06
Aspartate--tRNA ligase, mitochondrial	DARS2	A0A3B3ITK9	1.07	0.72	1.06
Nucleoprotein TPR	TPR	P12270	0.89	0.79	1.06
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	B2R7W4	0.96	0.92	1.06
ATPase family AAA domain-containing protein 3A	ATAD3A	Q9NVI7-2	0.93	0.86	1.06
Protein S100-A8	S100A8	P05109	1.14	1.26	1.06
60S ribosomal protein L35	RPL35	F2Z388	0.94	1.02	1.06
Raftlin	RFTN1	C9JHG2	0.92	0.83	1.06
Enoyl-CoA delta isomerase 2, mitochondrial	ECI2	Q53HG3	0.84	0.88	1.06
tRNA-splicing ligase RtcB homolog	RTCB	Q9Y3I0	0.94	0.99	1.06
U6 snRNA-associated Sm-like protein LSM5	LSM5	B8ZZF8	0.94	1.06	1.06
Ragulator complex protein LAMTOR3	LAMTOR3	Q9UHA4	1.04	0.98	1.06
U2 small nuclear ribonucleoprotein B	SNRPB2	Q86YK2	1.00	0.97	1.06
Lamina-associated polypeptide 2, isoforms beta/gamma	TMPO	A0A024RBE7	0.88	0.95	1.06
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	Q8TCJ2	0.76	0.69	1.06

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein bicaudal D homolog 2	BICD2	Q8TD16	1.21	1.41	1.06
Histone-binding protein RBBP7	RBBP7	E9PC52	0.88	0.88	1.06
Cation-independent mannose-6-phosphate receptor	IGF2R	Q59EZ3	0.86	0.87	1.06
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	A0A0S2Z3L2	0.95	0.91	1.06
F-actin-capping protein subunit alpha-1	CAPZA1	P52907	1.04	1.01	1.06
Integrin beta	ITGB6	E9PEE8	0.64	0.59	1.06
Cancer-related nucleoside-triphosphatase	C1orf57	Q5TDE9	0.98	1.21	1.06
Nck-associated protein 1	NCKAP1	Q9Y2A7	1.03	1.08	1.06
Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	Q70UQ0	1.03	0.86	1.05
Ras-related protein Rab-1B	RAB1B	E9PLD0	1.04	0.87	1.05
Transmembrane emp24 domain-containing protein 7	TMED7-TICAM2	A0A0A6YYA0	0.96	0.88	1.05
F-actin-capping protein subunit alpha-2	CAPZA2	Q53GE2	1.12	1.04	1.05
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	F5GXX5	0.96	1.13	1.05
ATPase ASNA1	ASNA1	O43681	1.25	1.34	1.05
Cytochrome c oxidase assembly factor 6 homolog	COA6	Q5TJ3	1.00	1.00	1.05
Dihydropteridine reductase	QDPR	A0A140VKA9	1.13	0.95	1.05
F-actin-capping protein subunit beta	CAPZB	B2R7T8	1.07	1.13	1.05
Tyrosine-protein phosphatase non-receptor type	PTPN1	A8K3M3	0.90	0.98	1.05
FACT complex subunit SSRP1	SSRP1	A0A024R4Z6	1.07	1.12	1.05
Transmembrane emp24 domain-containing protein 10	TMED10	A0A024R6I3	0.92	0.76	1.05
Actin-related protein 2/3 complex subunit 5	ARPC5L	B3KPC7	1.02	1.22	1.05
Heterogeneous nuclear ribonucleoprotein F	HNRPF	A0A024R7T3	0.97	0.96	1.05
Fragile X mental retardation syndrome-related protein 1	FXR1	B4DM78	1.09	1.24	1.05
Protein S100-A2	S100A2	P29034	1.06	1.19	1.05
Actin, cytoplasmic 1	PS1TP5BP1	Q1KLZ0	1.03	0.95	1.05
Ubiquitin-conjugating enzyme E2 K	UBE2K	P61086	1.06	1.53	1.05
Plakophilin-3	PKP3	Q9Y446	1.09	1.17	1.05
Alkylldihydroxyacetonephosphate synthase, peroxisomal	AGPS	O00116	1.11	0.81	1.05
Brain acid soluble protein 1	BASP1	P80723	0.93	1.06	1.05
ERO1-like protein alpha	ERO1L	Q96HE7	0.91	0.89	1.05
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	A0A024R983	1.00	1.00	1.05
Ribonuclease P protein subunit p30	RPP30	B4DJR3	1.04	1.18	1.05
Omega-amidase NIT2	HEL-S-8a	V9HW91	1.13	1.04	1.05
Ubiquitin carboxyl-terminal hydrolase	UCHL5	B2RB07	1.18	1.33	1.05
Epithelial splicing regulatory protein 1	ESRP1	H0YBR2	1.19	1.25	1.05
Paraspeckle component 1	PSPC1	A0A024RDP4	0.85	0.78	1.05
Ras-related C3 botulinum toxin substrate 1	RAC1	A4D2P2	1.06	1.07	1.05
Ribosomal L1 domain-containing protein 1	RSL1D1	Q32Q62	0.88	0.85	1.05
V-type proton ATPase catalytic subunit A	ATP6V1A	P38606-2	0.95	0.99	1.05

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
DNA-directed RNA polymerase	DKFZp686D10173	Q7Z3R8	1.04	1.52	1.05
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	Q05CK9	0.99	0.91	1.04
Receptor protein-tyrosine kinase	MST1R	J3KQS7	3.32	1.41	1.04
Thyroid hormone receptor-associated protein 3	THRAP3	A0A3B3ITZ9	0.76	0.86	1.04
Serpin B5	SERPINB5	A0A024R2B6	1.12	1.20	1.04
Atlastin-2	ATL2	C9JC25	1.40	1.17	1.04
Protein FAM210A	FAM210A	K7EK00	1.32	1.48	1.04
General transcription factor II-I	GTF2I	A0A1W6S962	0.83	0.79	1.04
Matrin-3	DKFZp686K23100	Q68D11	0.99	0.90	1.04
NEDD8-activating enzyme E1 catalytic subunit	UBE1C	J3JZZ9	0.93	0.86	1.04
Long-chain-fatty-acid--CoA ligase 4	FACL4	B4DH39	0.81	1.13	1.04
Methylthioribose-1-phosphate isomerase	MRI1	Q9BV20-2	1.21	1.22	1.04
DDRKG domain-containing protein 1	DDRKG1	Q96HY6	1.25	1.15	1.04
Splicing factor 3B subunit 4	SF3B4	Q53FG6	1.03	1.11	1.04
Importin subunit alpha	KPNA3	A0A024RDV7	1.18	1.01	1.04
SAP domain-containing ribonucleoprotein	CIP29	Q567R9	1.01	0.97	1.04
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	Q96HX3	0.97	0.89	1.04
X-ray repair cross-complementing protein 6	XRCC6	A0A024R1N4	0.97	0.93	1.04
MICAL-like protein 1	MICALL1	Q8N3F8	0.81	1.19	1.04
RNA-binding protein FUS	FUS	Q59H57	0.94	1.01	1.04
Pyrroline-5-carboxylate reductase	PYCR1	E2QRB3	0.86	0.86	1.04
Periodic tryptophan protein 2 homolog	PWP2	A0A0B4J2E5	0.97	0.94	1.04
40S ribosomal protein S28	RPS28	B2R4R9	0.97	0.97	1.04
26S proteasome non-ATPase regulatory subunit 1	PSMD1	Q05CW6	0.98	1.00	1.04
Proteasome subunit beta type	PSMB6	Q6IAT9	0.91	0.96	1.04
Luc7-like protein 3	LUC7L3	D6RDI2	0.95	0.93	1.04
Rho-related GTP-binding protein RhoC	RHOC	E9PQH6	1.05	1.04	1.04
Transforming protein RhoA	RHOA	A0A024R324	1.38	1.27	1.04
Centrosomal protein of 164 kDa	DKFZp434O2413	Q9NTH6	1.05	1.08	1.04
Protein DEK	DEK	A0A494C198	1.03	1.00	1.04
Cirhin	CIRH1A	A0A0J9YWM9	0.39	0.60	1.04
NAD(P) transhydrogenase, mitochondrial	NNT	D6RHU2	1.02	1.28	1.04
Serine/arginine repetitive matrix protein 2	KIAA0324	O60382	0.70	1.03	1.03
Chloride intracellular channel protein 3	CLIC3	O95833	1.46	1.41	1.03
Ubiquitin carboxyl-terminal hydrolase 15	USP15	Q9Y4E8-2	1.13	1.24	1.03
Signal recognition particle receptor subunit alpha	SRPR	Q6IAX9	1.06	0.96	1.03
N-acetyl-D-glucosamine kinase	NAGK	H7C286	1.00	0.94	1.03
H/ACA ribonucleoprotein complex subunit 2	NHP2	D6RC52	0.90	0.94	1.03
Peptidyl-prolyl cis-trans isomerase FKBP5	FKBP5	B7Z8G2	0.89	0.93	1.03

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein disulfide-isomerase A6	PDIA6	A0A384NPU5	0.85	0.84	1.03
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	P30837	0.90	0.89	1.03
Mitochondrial import inner membrane translocase subunit Tim10	TIMM10	P62072	0.98	0.95	1.03
Arachidonate 15-lipoxygenase B	ALOX15B	O15296	1.12	1.14	1.03
Prothymosin alpha	PTMA	Q15203	1.13	1.18	1.03
Ras GTPase-activating-like protein IQGAP1	IQGAP1	A4QPB0	1.02	1.07	1.03
Proline synthase co-transcribed bacterial homolog protein	PROSC	H0YBG2	1.04	1.14	1.03
Methylosome protein 50	WDR77	A0A024R0H7	1.18	0.99	1.03
Caspase-3	CASP3	P42574	0.71	1.32	1.03
Receptor expression-enhancing protein	REEP5	B7Z332	1.01	1.06	1.03
Splicing factor 3A subunit 1	SF3A1	B4E091	0.92	1.04	1.03
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	O43143	1.03	0.97	1.03
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	Q93008-1	1.31	1.54	1.03
COMM domain-containing protein 9	COMMD9	B4DIH0	1.05	1.06	1.03
Myristoylated alanine-rich C-kinase substrate	MARCKS	P29966	0.97	0.71	1.03
Small nuclear ribonucleoprotein Sm D2	SNRPD2	P62316	0.96	0.85	1.03
AP-1 complex subunit gamma-1	AP1G1	Q8IY97	1.20	1.25	1.03
All-trans-retinol 13,14-reductase	RETSAT	B4DKE1	0.93	1.06	1.03
28S ribosomal protein S2, mitochondrial	MRPS2	Q5T8A0	1.35	0.93	1.03
Protein NDRG1	TRG14	Q597H1	0.99	1.14	1.03
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	A0A2R8YEY5	0.92	0.80	1.03
Apoptosis inhibitor 5	API5	G3V1C3	1.02	0.99	1.03
Serine/arginine-rich splicing factor 11	SFRS11	Q05519	0.86	0.76	1.03
Actin, cytoplasmic 2	ACTG1	P63261	1.02	1.04	1.02
E3 ubiquitin-protein ligase RBX1	RBX1	P62877	0.97	1.01	1.02
COP9 signalosome complex subunit 6	COPS6	B2R514	1.07	1.13	1.02
Acylglycerol kinase, mitochondrial	AGK	E9PG39	1.03	0.87	1.02
SHC-transforming protein 1	SHC1	X6R6D0	0.98	1.18	1.02
Polymerase I and transcript release factor	PTRF	B4DPZ5	0.94	0.89	1.02
U6 snRNA-associated Sm-like protein LSm4	LSM4	U3KQK1	1.05	0.86	1.02
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	A0A1W2PPR9	1.04	1.23	1.02
26S protease regulatory subunit 6A	PSMC3	R4GNH3	1.00	0.98	1.02
Programmed cell death protein 5	PDCD5	K7EQA1	1.06	1.10	1.02
Glutathione peroxidase	GPX1	A0A087WUQ6	0.95	1.01	1.02
Nucleolar protein 6	NOL6	B4DF80	0.90	0.97	1.02
39S ribosomal protein L28, mitochondrial	MRPL28	Q13084	1.07	1.09	1.02
Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	O00154-6	0.96	0.99	1.02
5-3 exoribonuclease 2	XRN2	B4E0B9	0.96	0.92	1.02
Ribosome biogenesis protein BOP1	BOP1	B2RDN4	0.81	0.87	1.02

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Src substrate cortactin	CTTN	Q53HG7	1.02	1.09	1.02
26S proteasome non-ATPase regulatory subunit 7	PSMD7	P51665	1.14	1.08	1.02
Eukaryotic translation initiation factor 6	EIF6	P56537	1.04	1.14	1.02
Heterogeneous nuclear ribonucleoprotein K	HNRPK	A0A024R228	0.94	0.95	1.02
Clathrin heavy chain	CLTC	A0A087WVQ6	1.02	0.99	1.02
Vacuolar protein sorting-associated protein 37B	VPS37B	F5H1F6	0.59	1.49	1.02
28S ribosomal protein S22, mitochondrial	MRPS22	G5E9W7	1.10	0.98	1.02
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	CHCHD2	Q9Y6H1	0.85	1.05	1.02
Importin-9	IPO9	Q96P70	1.19	1.21	1.02
Ornithine aminotransferase, mitochondrial	OAT	A0A140VJQ4	0.89	0.78	1.02
Nitrilase homolog 1	NIT1	B7Z410	0.88	0.78	1.02
Small nuclear ribonucleoprotein-associated protein	SNRPN	J3QLE5	0.94	0.90	1.02
Nuclear protein localization protein 4 homolog	NPLOC4	A0A024R8R4	0.96	1.11	1.02
Ubiquitin thioesterase otulin	OTULIN	Q96BN8	1.13	1.33	1.01
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	hCG_2032701	A0A024R3J7	1.01	0.91	1.01
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	A0A384NL58	0.97	0.95	1.01
Actin-related protein 10	ACTR10	Q53HF6	1.14	1.24	1.01
Laminin subunit gamma-2	LAMC2	B4DLD1	0.63	0.51	1.01
Glutathione S-transferase P	HEL-S-22	V9HWE9	1.13	1.17	1.01
EH domain-containing protein 2	EHD2	B4DLA1	1.05	0.98	1.01
Serine/arginine-rich splicing factor 10	SRSF10	Q5JRI1	1.03	1.03	1.01
Acetyl-coenzyme A synthetase	ACSS2	Q4G0E8	1.15	1.50	1.01
Signal recognition particle 14 kDa protein	SRP14	P37108	1.09	0.88	1.01
60S ribosomal protein L13	RPL13	Q6NZ55	0.97	0.92	1.01
Nucleolar and coiled-body phosphoprotein 1	NOLC1	B2RAU8	1.84	0.84	1.01
Nucleoplasmin-3	NPM3	O75607	0.94	0.98	1.01
Ribosomal protein L19	RPL19	Q8IWR8	0.88	0.92	1.01
Ras-related protein Rab-18	RAB18	Q9NP72	0.76	0.90	1.01
Major vault protein	MVP	B4DXN0	1.08	1.18	1.01
Alpha/beta hydrolase domain-containing protein 11	ABHD11	H0YC52	0.94	0.85	1.01
V-type proton ATPase subunit B, brain isoform	ATP6V1B2	B4DFM5	1.19	1.08	1.01
GTP-binding protein 1	GTPBP1	B2RDW9	1.11	1.36	1.01
40S ribosomal protein S15	RPS15	K7ELC2	1.08	1.13	1.01
MICOS complex subunit MIC10	MINOS1	A0A3B3IRY5	0.95	0.80	1.01
Interferon regulatory factor 6	IRF6	G0Z349	1.20	1.22	1.01
60S ribosomal protein L11	RPL11	Q5VVC8	1.03	1.05	1.01
AP-1 complex subunit sigma-1A	AP1S1	A0A2R8YGH5	1.08	1.04	1.01
Ras-related protein Rab-7a	RAB7A	A0A158RFU6	1.02	0.96	1.01
Myosin-10	MYH10	P35580	0.99	1.04	1.01

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Ubiquitin-like modifier-activating enzyme 1	UBE1	A0A024R1A3	1.07	1.03	1.01
Importin-13	IPO13	O94829	1.01	1.11	1.01
Calpastatin	CAST	A0A1S5UZ18	1.01	1.08	1.01
Ubiquitin-protein ligase E3C	UBE3C	B4DHJ9	1.15	0.93	1.01
Signal recognition particle subunit SRP72	HEL103	V9HWK0	0.96	0.85	1.01
Protein PRRC2A	PRRC2A	A0A1U9X9A9	1.04	1.03	1.01
Calcium-transporting ATPase	DKFZp686M088	Q68DH9	0.92	0.90	1.01
WD repeat-containing protein 61	WDR61	H0YMF9	0.76	1.09	1.01
Polypyrimidine tract-binding protein 3	ROD1	A0A024R163	1.31	1.56	1.01
N-acetylserotonin O-methyltransferase-like protein	ASMTL	B4DN81	1.06	1.11	1.00
Far upstream element-binding protein 1	FUBP1	B4E0X8	1.05	0.96	1.00
Calmodulin-3	CALM3	P0DP25	0.94	1.12	1.00
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	Q6IAL5	0.79	0.80	1.00
Mannose-P-dolichol utilization defect 1 protein	MPDU1	J3KSI4	1.15	0.80	1.00
Tumor necrosis factor receptor superfamily member 6	CD95	Q8IUB7	0.79	0.48	1.00
NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	NDUFV3	P56181	0.83	0.71	1.00
39S ribosomal protein L47, mitochondrial	MRPL47	Q9HD33-3	0.63	0.79	1.00
Importin subunit alpha	KPNA1	B3KXZ2	1.12	1.08	1.00
Treacle protein	DKFZp434G1035	Q9UFD4	0.82	0.76	1.00
Filamin-B	FLNB	O75369-2	0.97	0.99	1.00
Peptidyl-prolyl cis-trans isomerase	HEL-S-39	V9HWC6	0.88	0.87	1.00
Mitochondrial ribonuclease P protein 1	TRMT10C	C9JVB6	1.13	0.92	1.00
Something about silencing protein 10	UTP3	Q9NQZ2	0.90	0.90	1.00
Hsc70-interacting protein	ST13	H7C3I1	1.07	1.03	1.00
Cystatin-A	CSTA	P01040	1.10	1.26	1.00
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	G3V4W0	0.94	0.87	1.00
40S ribosomal protein S16	RPS16	M0R210	0.89	0.96	1.00
Signal transducer and activator of transcription 3	STAT3	P40763-3	1.04	1.15	1.00
Rho GDP-dissociation inhibitor 1	ARHGDI1	J3KTF8	1.09	1.13	1.00
B-cell receptor-associated protein 31	BCAP31	C9JSP1	0.86	0.92	1.00
DnaJ homolog subfamily C member 3	DNAJC3	A8KA82	0.82	0.82	1.00
Abl interactor 1	ABI1	B6VEX5	1.22	1.29	1.00
Peflin	PEF1	A0A384MQX5	1.14	1.15	1.00
Transmembrane protein 14C	TMEM14C	Q53F27	1.05	1.01	1.00
Calnexin	CANX	P27824	0.91	0.83	1.00
Myb-binding protein 1A	MYBBP1A	Q9BQG0	1.01	0.97	1.00
60S ribosomal protein L13a	RPL13A	Q5QTS3	1.02	0.89	1.00
Oligosaccharyltransferase complex subunit OSTC	OSTC	A0A087WUD3	0.99	0.83	1.00
Annexin	ANXA4	Q6LES2	1.06	1.08	0.99

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Unconventional myosin-Ic	MYO1C	F5H6E2	1.00	0.91	0.99
Serine/threonine-protein phosphatase	HEL-S-80p	V9HW04	1.03	1.03	0.99
60S ribosomal protein L7a	RPL7A	P62424	0.96	1.01	0.99
Disco-interacting protein 2 homolog B	DIP2B	Q3UH60	0.93	0.66	0.99
60S ribosomal protein L21	RPL21	Q6IAX2	0.99	0.99	0.99
Annexin	ANXA1	Q5TZZ9	1.05	1.08	0.99
Vacuolar protein sorting-associated protein 18 homolog	VPS18	A0A024R9R3	1.20	1.04	0.99
Oligoribonuclease, mitochondrial	REXO2	H0YG54	0.79	1.02	0.99
Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	B4DJX1	1.03	0.98	0.99
6.8 kDa mitochondrial proteolipid	C14orf2	A0A0A0MTQ5	1.02	0.92	0.99
Thioredoxin domain-containing protein 5	TXNDC5	Q86UY0	0.80	0.74	0.99
ATP-dependent RNA helicase DDX39A	DDX39A	B4DX78	0.96	0.92	0.99
Nuclear cap-binding protein subunit 1	NCBP1	A0A024R179	1.31	1.30	0.99
Bcl-2-associated transcription factor 1	BCLAF1	Q9NYF8-4	1.03	0.87	0.99
Transcriptional adapter 2-beta	TADA2B	B3KX99	1.03	1.12	0.99
Glycogen [starch] synthase, muscle	GYS1	B7Z255	0.86	0.83	0.99
Aminopeptidase N	ANPEP	A0A024RC61	0.91	0.67	0.99
Ras GTPase-activating protein-binding protein 2	G3BP2	A8K6V7	0.91	0.98	0.99
ATP-dependent 6-phosphofructokinase, liver type	PFKL	P17858	1.12	1.30	0.99
Cytochrome c oxidase subunit NDUFA4	NDUFA4	A0A024R9Z0	0.91	0.89	0.99
Zinc phosphodiesterase ELAC protein 2	ELAC2	H7C2I4	1.05	1.05	0.99
Beta-galactosidase	GLB1	Q53H18	0.77	0.64	0.99
Filamin-A	FLNA	P21333-2	1.04	1.06	0.99
28S ribosomal protein S9, mitochondrial	MRPS9	Q86WV4	1.18	1.05	0.99
Proteasome subunit alpha type	PSMA2	A0A024RA52	1.07	0.96	0.99
Programmed cell death protein 2-like	PDCD2L	Q9BRP1	1.02	1.48	0.99
NudC domain-containing protein 3	NUDCD3	Q8IVD9	1.15	1.29	0.99
60S ribosomal protein L23	RPL23	Q9BTQ7	0.97	0.94	0.99
Dipeptidyl peptidase 3	DKFZp686O1117	Q5JPB8	1.11	1.03	0.99
Non-homologous end-joining factor 1	NHEJ1	Q9H9Q4	0.86	0.57	0.99
DNA-(apurinic or apyrimidinic site) lyase	APEX1	Q5TZP7	0.92	0.84	0.99
Coronin	CORO1C	Q53G58	1.03	1.07	0.99
Apoptosis regulator BAX	BAX	Q07812-5	1.14	0.93	0.99
Dehydrogenase/reductase SDR family member 4	DHRS4	F5GWZ1	0.73	0.71	0.99
Calumenin	CALU	Q6IAW5	0.83	0.86	0.98
Kinectin	KTN1	A0A024R663	1.02	0.86	0.98
39S ribosomal protein L50, mitochondrial	MRPL50	Q8N5N7-2	0.81	0.77	0.98
Putative RNA-binding protein Luc7-like 1	LUC7L	Q9NQ29	1.03	1.67	0.98
60S ribosomal protein L18	RPL18	Q0QEW2	1.03	0.99	0.98

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Zinc finger CCCH domain-containing protein 4	ZC3H4	M0QY97	1.00	0.64	0.98
FACT complex subunit SPT16	SUPT16H	Q9Y5B9	1.00	1.06	0.98
Charged multivesicular body protein 3	CHMP3	Q9Y3E7-2	1.11	1.01	0.98
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	Q53HG1	0.94	0.76	0.98
UDP-glucose 4-epimerase	GALE	A0A384NL38	1.11	1.10	0.98
Nicotinamide phosphoribosyltransferase	PBEF1	A0A024R718	1.11	1.09	0.98
EH domain-containing protein 4	EHD4	A8K9B9	1.00	1.09	0.98
Splicing factor 3B subunit 2	SF3B2	E9PPJ0	0.88	0.69	0.98
Proteasome subunit beta type-4	PSMB4	A0A140VK46	1.06	1.04	0.98
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	B4DVV1	1.03	1.11	0.98
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	Q05CP4	0.96	1.00	0.98
Peptidyl-prolyl cis-trans isomerase	FKBP8	M0R1Q0	1.04	1.10	0.98
Mitochondrial import inner membrane translocase subunit TIM14	DNAJC19	G5E9V2	1.37	1.02	0.98
Protein disulfide-isomerase A3	PDIA3	H7BZJ3	0.63	0.86	0.98
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	O96008	1.01	0.89	0.98
28S ribosomal protein S30, mitochondrial	MRPS30	Q9BUN6	0.92	0.87	0.98
40S ribosomal protein S7	RPS7	P62081	0.96	0.95	0.98
Transmembrane 9 superfamily member 3	TM9SF3	Q5TB53	0.95	0.97	0.98
COP9 signalosome complex subunit 3	COPS3	J3QL22	0.97	1.05	0.98
Ragulator complex protein LAMTOR5	LAMTOR5	R4GMU8	0.80	0.91	0.98
Transitional endoplasmic reticulum ATPase	HEL-S-70	V9HW80	0.98	0.99	0.98
AP-2 complex subunit sigma	AP2S1	M0R0N4	0.90	0.91	0.97
Anoctamin-7	ANO7	A0A6I8PRE6	0.93	1.05	0.97
Vesicle-associated membrane protein-associated protein A	VAPA	A8KA83	0.92	0.81	0.97
Transmembrane and coiled-coil domain-containing protein 1	TMCO1	J3QQY2	0.97	0.85	0.97
Glyceraldehyde-3-phosphate dehydrogenase	HEL-S-162eP	V9HVZ4	1.06	1.07	0.97
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	P54709	0.97	0.84	0.97
Hematological and neurological expressed 1 protein	HN1	J3KT51	0.94	1.27	0.97
m7GpppX diphosphatase	DCPS	A0A3B3ITF0	1.23	1.12	0.97
Alpha-centractin	ACTR1A	B4DM97	1.06	0.98	0.97
Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	P46087-2	0.95	0.90	0.97
Peptidyl-prolyl cis-trans isomerase	PPIH	Q6FH57	1.02	1.13	0.97
26S protease regulatory subunit 6B	PSMC4	A8K2M0	1.03	0.99	0.97
cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	A0A0S2Z472	1.02	1.26	0.97
GDP-fucose protein O-fucosyltransferase 1	POFUT1	Q9H488	0.63	0.86	0.97
Transducin beta-like protein 3	TBL3	A0A087WYP7	0.92	0.68	0.97
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	Q9UEH5	1.10	1.02	0.97
28S ribosomal protein S34, mitochondrial	MRPS34	A4UCR9	0.97	0.98	0.97
Proteolipid protein 2	PLP2	A0A024QYW3	0.96	1.05	0.97

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Amino acid transporter	SLC1A5	Q71UA6	1.01	0.94	0.97
Eukaryotic translation initiation factor 3 subunit I	EIF3I	Q5U0F4	1.01	1.14	0.97
Alpha-actinin-1	ACTN1	A0A024R694	0.99	0.99	0.97
3-ketodihydrosphingosine reductase	KDSR	K7ERC8	0.80	0.84	0.97
Proteasome subunit alpha type-1	PSMA1	P25786	0.96	0.89	0.97
Probable ATP-dependent RNA helicase DDX5	DDX5	B4DN41	0.89	0.91	0.97
Protein RRP5 homolog	PDCD11	A0A3B3IUD7	0.96	0.83	0.97
Aspartyl aminopeptidase	DNPEP	Q9BSS9	0.96	1.07	0.97
Myosin light chain 1/3, skeletal muscle isoform	MYL1	Q53R15	1.04	1.20	0.97
Superoxide dismutase [Cu-Zn]	HEL-S-44	V9HWC9	1.15	1.09	0.97
Coatomer subunit epsilon	COPE	O14579	1.04	1.02	0.97
Macrophage-capping protein	HEL-S-66	V9HW69	1.02	1.04	0.97
ELAV-like protein 1	ELAVL1	Q15717	0.86	0.79	0.97
60S ribosomal protein L3	RPL3	B3KS36	0.98	0.90	0.97
RuvB-like 2	RUVBL2	Q9Y230	1.06	0.98	0.97
Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	ARAP1	Q96P48-3	1.08	1.05	0.96
Tetratricopeptide repeat protein 25	TTC25	Q96NG3	1.07	0.96	0.96
26S protease regulatory subunit 7	PSMC2	A0A140VK70	0.96	1.00	0.96
Protein disulfide-isomerase A4	ERP70	A0A090N8Y2	0.82	0.75	0.96
C-terminal-binding protein 2	CTBP2	P56545	0.93	1.06	0.96
Ribosome biogenesis protein BRX1 homolog	BRX1	Q8TDN6	0.90	0.80	0.96
Ribosomal RNA small subunit methyltransferase NEP1	EMG1	Q92979	1.15	1.23	0.96
Cell division control protein 42 homolog	CDC42	A0A024RAA5	1.04	1.01	0.96
SH3 domain-binding glutamic acid-rich-like protein 3	HEL-S-297	Q86Z22	1.02	1.12	0.96
Type-1 angiotensin II receptor-associated protein	AGTRAP	Q6RW13	0.97	0.98	0.96
Annexin	ANXA2	A0A024R5Z7	0.98	0.97	0.96
Proteasome-associated protein ECM29 homolog	KIAA0368	J3KN16	1.07	1.12	0.96
Transmembrane protein 33	TMEM33	D6RAA6	0.99	0.86	0.96
60S ribosomal protein L38	RPL38	A0A024R8P8	0.99	0.98	0.96
40S ribosomal protein S12	RPS12	P25398	1.05	1.00	0.96
40S ribosomal protein S13	RPS13	P62277	0.90	0.85	0.96
Proteasome subunit alpha type	PSMA5	Q5U0A0	0.98	0.88	0.96
Pachytene checkpoint protein 2 homolog	TRIP13	Q15645	1.05	0.97	0.96
Membrane-associated progesterone receptor component 2	PGRMC2	O15173	0.75	1.14	0.96
Synaptic vesicle membrane protein VAT-1 homolog	VAT1	A0A024R1Z6	1.00	1.09	0.96
Serine/threonine-protein phosphatase	PPP2CA	B3KUN1	1.02	1.06	0.96
Lanosterol 14-alpha demethylase	CYP51A1	A0A0C4DFL7	0.87	0.89	0.96
7-dehydrocholesterol reductase	DHCR7	A8K0D2	0.85	0.85	0.96
UPF0568 protein C14orf166	C14orf166	Q5RLJ0	1.07	0.97	0.96

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
DnaJ homolog subfamily B member 11	DNAJB11	Q9UBS4	0.79	0.77	0.96
40S ribosomal protein S21	RPS21	Q8WVC2	1.04	1.06	0.96
Poly [ADP-ribose] polymerase 1	PARP1	B4E0E1	0.94	0.76	0.96
Chromatin target of PRMT1 protein	CHTOP	A0A087X1B7	0.84	0.88	0.96
26S proteasome non-ATPase regulatory subunit 5	PSMD5	A8K4T6	0.97	0.86	0.95
26S protease regulatory subunit 8	PSMC5	Q59GS3	0.99	0.89	0.95
Katanin p60 ATPase-containing subunit A-like 2	KATNAL2	K7EM02	0.99	1.11	0.95
Phosphatidylinositol phosphatase SAC1	SACM1L	Q9NTJ5-2	0.89	0.90	0.95
RILP-like protein 1	RILPL1	A0A1B0GVV3	1.65	1.61	0.95
Catechol O-methyltransferase	COMT	A0A140VJG8	0.99	0.91	0.95
Transcription elongation factor A protein 2	TCEA1	B7Z4S1	0.96	1.04	0.95
Myosin light polypeptide 6	MYL6	P60660	1.01	1.09	0.95
60S ribosomal protein L12	RPL12	P30050	1.05	0.99	0.95
UNC5C-like protein	MUXA	H8YHX0	1.14	1.38	0.95
40S ribosomal protein S6	RPS6	Q96DV6	0.87	0.95	0.95
60S ribosomal protein L4	RPL4	P36578	0.95	0.97	0.95
Ladinin-1	LAD1	Q61PJ9	0.94	1.00	0.95
Casein kinase I isoform alpha	HEL-S-77p	V9HW00	0.96	1.03	0.95
Actin-related protein 3	ACTR3	A0A024RAI1	0.99	1.04	0.95
60S ribosomal protein L23a	RPL23A	H7BY10	0.99	0.98	0.95
WD repeat-containing protein 13	WDR13	B2RBN3	1.00	1.12	0.95
Peptidyl-prolyl cis-trans isomerase	PPIL1	A0A024RCX8	1.09	0.91	0.95
Gem-associated protein 5	GEMIN5	B7ZLC9	0.96	1.00	0.95
Laminin subunit beta-3	LAMB3	A0A0S2Z3R6	0.74	0.69	0.95
Septin-7	SEPT7	B4DUD6	0.94	0.92	0.95
Proteasome subunit alpha type	PSMA7	Q05DH1	1.08	1.03	0.95
Septin-9	SEPTIN9	Q9UHD8	1.00	0.98	0.95
Mevalonate kinase	MVK	F5H8H2	1.16	1.23	0.95
26S proteasome non-ATPase regulatory subunit 10	PSMD10	B1AJY5	1.15	1.05	0.95
Protein-L-isoaspartate O-methyltransferase	PCMT1	B7Z972	1.01	0.94	0.95
Actin-related protein 2/3 complex subunit 4	ARPC4-TTLL3	F8WCF6	1.08	1.17	0.95
Pyridoxal kinase	HEL-S-1a	V9HWC3	1.19	1.21	0.95
Vacuolar protein-sorting-associated protein 25	VPS25	K7EP45	0.91	1.22	0.95
26S proteasome non-ATPase regulatory subunit 13	PSMD13	A0A024R201	0.93	0.97	0.95
Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP	Q9H008	1.05	1.20	0.95
Elongation factor 1-gamma	EEF1G	Q53YD7	1.08	1.10	0.95
Signal peptidase complex subunit 3	SPCS3	D3DP46	0.78	0.99	0.95
Probable ATP-dependent RNA helicase DDX47	E4-DBP	B4DYP6	0.94	0.87	0.95
DNA replication licensing factor MCM4	MCM4	P33991	0.93	0.75	0.95

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Eukaryotic translation initiation factor 3 subunit J	EIF3J	H0YGF7	0.94	1.06	0.95
Leukotriene A-4 hydrolase	LTA4H	A0A140VK27	1.17	1.14	0.95
Zinc finger RNA-binding protein	ZFR	B2RNR6	0.98	1.10	0.95
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	B4DJC7	1.10	1.21	0.95
Quinone oxidoreductase	CRYZ	C9JH92	0.99	0.96	0.95
Protein HGH1 homolog	HGH1	Q9BTY7	0.87	1.14	0.95
26S proteasome non-ATPase regulatory subunit 11	PSMD11	O00231	1.03	1.02	0.95
40S ribosomal protein S19	RPS19	B0ZBD0	0.94	0.95	0.95
E3 ubiquitin-protein ligase HUWE1	HUWE1	A0A024R9Y3	1.22	1.21	0.95
SLIT-ROBO Rho GTPase-activating protein 2B	SRGAP2	A0A075B7C8	0.96	0.99	0.94
Proteasome subunit beta type	PSMB7	Q86U62	1.12	1.10	0.94
AP-1 complex subunit beta-1	AP1B1	Q10567-4	1.04	1.20	0.94
Proteasome subunit alpha type	PSMA6	A0A140VK44	0.95	0.95	0.94
F-box only protein 2	FBXO2	Q80UW2	0.92	0.88	0.94
Plasminogen activator inhibitor 2	SERPINB2	P05120	1.00	1.00	0.94
Replication protein A 14 kDa subunit	RPA3	P35244	0.87	0.87	0.94
Valine--tRNA ligase	VAR5	A0A1U9X9D5	1.07	1.09	0.94
Syntaxin-binding protein 1	STXBP1	A0A1B0GW76	0.78	1.24	0.94
Peroxiredoxin-5, mitochondrial	HEL-S-55	V9HW35	1.08	1.11	0.94
Kinesin-like protein	HEL-S-61	V9HW29	1.09	1.03	0.94
Importin subunit alpha	KPNA6	B4DWX3	1.05	1.25	0.94
Tubulin alpha-4A chain	TUBA4A	P68366-2	1.21	1.22	0.94
Phosphotriesterase-related protein	PTER	Q96BW5-2	1.13	1.07	0.94
Ubiquitin-associated protein 2-like	UBAP2L	B4DYY5	0.86	0.70	0.94
TATA-binding protein-associated factor 2N	TAF15	Q92804-2	0.90	0.89	0.94
60S ribosomal protein L37a	RPL37A	C9J4Z3	0.96	0.98	0.94
Phenylalanine--tRNA ligase alpha subunit	FARSLA	Q6IBR2	0.95	0.84	0.94
Tumor protein D54	TPD52L2	Q6FGS1	1.05	1.07	0.94
AP-3 complex subunit delta-1	AP3D1	O14617-4	0.92	1.00	0.94
60S ribosomal protein L17	RPL17	A0A087WXM6	0.98	0.96	0.94
Utrrophin	UTRN	P46939	1.27	1.18	0.94
182 kDa tankyrase-1-binding protein	TNKS1BP1	A0A024R542	1.00	1.06	0.94
Proteasome subunit alpha type	PSMA4	H0YMZ1	0.99	0.95	0.94
Nodal modulator 2	NOMO3	J3KN36	0.81	0.80	0.94
Ras suppressor protein 1	RSU1	Q32Q10	1.03	1.17	0.94
Serine/threonine-protein kinase 24	STK24	B4DR80	1.14	1.35	0.94
Tropomodulin-3	DKFZp686E1899	Q5HYL6	1.09	1.12	0.94
Endoplasmin	TRA1	Q5CAQ5	0.84	0.79	0.94
Phosphoglycerate kinase	HEL-S-68p	V9HWF4	1.04	1.04	0.94

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
General vesicular transport factor p115	USO1	O60763	0.97	0.94	0.94
Leucine-rich repeat-containing protein 59	LRRC59	Q96AG4	0.92	0.82	0.94
Probable ATP-dependent RNA helicase DDX52	DDX52	Q59H21	0.95	0.88	0.94
ADP-ribosylation factor 1	ARF3	P40994	1.04	0.99	0.94
Ras-related protein Rab-2A	RAB2	A0A024R7V6	0.86	0.92	0.93
Tetraspanin	CD63	F8VNT9	0.86	0.84	0.93
1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	AGPAT5	H0YC22	1.58	1.11	0.93
14-3-3 protein zeta/delta	YWHAZ	D0PNI1	1.03	1.17	0.93
Proteasomal ubiquitin receptor ADRM1	ADRM1	B4DMP7	1.06	0.91	0.93
60S ribosomal protein L27	RPL27	B2R4D8	0.89	0.96	0.93
Protein RER1	RER1	Q5T093	0.91	0.96	0.93
DnaJ homolog subfamily A member 1	DNAJA1	P31689-2	0.84	1.00	0.93
Signal recognition particle 54 kDa protein	SRP54	G3V4F7	0.93	1.06	0.93
DNA-directed RNA polymerase II subunit RPB3	POLR2C	Q6FGR6	1.03	0.87	0.93
Myosin-14	MYH14	Q7Z406	1.06	1.02	0.93
Ribosome maturation protein SBDS	SBDS	A0A0S2Z5I7	1.18	1.92	0.93
Eukaryotic translation initiation factor 5B	EIF5B	Q8N5A0	1.06	1.04	0.93
Elongation factor 1-delta	EEF1D	E9PK01	0.84	0.90	0.93
Serpin H1	SERPINH1	A0A024R5K8	0.87	0.77	0.93
LIM domain and actin-binding protein 1	LIMA1	F8VQE1	0.95	0.96	0.93
60S ribosomal protein L14	RPL14	E7EPB3	0.86	0.78	0.93
Poly(rC)-binding protein 2	PCBP2	Q15366-3	1.04	1.03	0.93
Thioredoxin domain-containing protein 17	TXNDC17	A0A140VJY7	1.03	1.00	0.93
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	S4R3H4	0.96	0.98	0.93
Ferritin	FTH1	A0A024R525	0.94	0.95	0.93
Prolyl 3-hydroxylase 1	P3H1	E2QRI1	0.73	0.77	0.93
Serine--tRNA ligase, mitochondrial	SARS2	B4DJM9	1.00	0.83	0.93
Transforming acidic coiled-coil-containing protein 1	TACC1	E5RJG6	0.86	0.99	0.93
Y-box-binding protein 3	CSDA	A0A024RAV4	0.88	0.84	0.93
Protein CutA	CUTA	O60888-3	0.99	0.93	0.93
Hypoxia up-regulated protein 1	HYOU1	A0A087X054	0.87	0.82	0.93
Telomere length regulation protein TEL2 homolog	TELO2	Q9Y4R8	1.01	0.98	0.93
Aconitate hydratase	HEL60	V9HWB7	0.83	0.90	0.93
Ragulator complex protein LAMTOR1	LAMTOR1	Q6IAA8	0.91	0.92	0.93
Cysteine desulfurase, mitochondrial	NFS1	Q5QP19	0.72	0.70	0.93
Superkiller viralicidic activity 2-like 2	SKIV2L2	A8K6I4	1.00	0.98	0.93
Lysosomal Pro-X carboxypeptidase	PRCP	P42785	0.93	0.89	0.93
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	C9JLU1	1.16	1.20	0.92
Dihydroxyacetone phosphate acyltransferase	GNPAT	Q5TBH6	0.78	0.60	0.92

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
26S protease regulatory subunit 4	PSMC1	Q53XL8	1.04	0.95	0.92
40S ribosomal protein S18	RPS18	P62269	0.96	0.91	0.92
Importin-11	IPO11	F8WDV0	1.06	1.18	0.92
Ribonuclease inhibitor	RNH1	A0A140VJT8	1.07	1.17	0.92
Translation initiation factor eIF-2B subunit gamma	EIF2B3	A0A0D9SEN0	1.06	1.18	0.92
GTP-binding protein SAR1a	SAR1A	Q5SQT9	0.98	0.96	0.92
Translocon-associated protein subunit delta	SSR4	P51571	0.79	0.74	0.92
Cystatin-B	CSTB	Q76LA1	1.08	1.24	0.92
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	Q14204	0.96	0.97	0.92
PEST proteolytic signal-containing nuclear protein	PCNP	Q8WW12-2	0.84	0.67	0.92
Fructose-bisphosphate aldolase	ALDOC	B7Z1N6	1.03	1.12	0.92
Malate dehydrogenase	HEL-S-32	V9HWF2	1.05	1.07	0.92
Ras-related protein Rab-8A	RAB8A	A0A024R7I3	0.59	0.75	0.92
Putative RNA-binding protein Luc7-like 2	LUC7L2	Q9Y383	0.90	0.87	0.92
Guanine nucleotide-binding protein-like 3	GNL3	A0A024R2Z6	1.06	0.93	0.92
Serine/threonine-protein phosphatase	PPP3CA	E7ETC2	1.18	1.11	0.92
Protein transport protein Sec16A	SEC16A	A0A0C4DH09	0.93	1.15	0.92
Phosphatidylinositol transfer protein alpha isoform	PITPNA	I3L3W1	0.85	1.07	0.92
14-3-3 protein theta	YWHAQ	P27348	1.06	1.10	0.92
Histone deacetylase complex subunit SAP18	SAP18	A0A384ME24	0.94	0.90	0.92
Methionine aminopeptidase 2	METAP2	A0A140VJE3	1.00	0.94	0.92
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	O00425	0.84	0.86	0.92
Sorting nexin-6	SNX6	A8K885	0.95	0.92	0.92
Uncharacterized protein C4orf32	C4orf32	Q8N8J7	0.95	0.92	0.92
Oxidoreductase HTATIP2	HTATIP2	Q9BUP3	0.88	0.90	0.92
Integrator complex subunit 3	INTS3	Q68E01-2	0.72	0.74	0.92
Signal recognition particle subunit SRP68	SRP68	Q9UHB9-4	0.91	0.99	0.92
Elongation factor 1-alpha	EEF1A1	Q6IPT9	1.04	1.05	0.92
Polyadenylate-binding protein	PABPC4	B1ANR0	0.90	0.93	0.92
Basic leucine zipper and W2 domain-containing protein 2	BZW2	E7ETZ4	1.09	1.02	0.91
Protein transport protein Sec31A	SEC31L1	A0A1S5UZ19	1.05	1.04	0.91
Uroporphyrinogen decarboxylase	UROD	A0A494BZY8	1.02	1.03	0.91
Septin-2	SEPTIN2	Q15019	1.02	1.05	0.91
LanC-like protein 1	LANCL1	E9PHS0	1.05	0.98	0.91
60S acidic ribosomal protein P0	RPLP0	Q53HW2	0.98	0.95	0.91
40S ribosomal protein S30	FAU	E9PR30	0.76	0.83	0.91
Endoplasmic reticulum aminopeptidase 1	ERAP1	A8K6H1	0.89	0.83	0.91
Exocyst complex component 1	EXOC1	A0A024RDA1	0.64	1.09	0.91
Ubiquitin fusion degradation protein 1 homolog	UFD1L	C9IZG3	0.76	0.98	0.91

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
DnaJ homolog subfamily C member 9	hCG_2024613	A0A024QZN2	0.92	1.08	0.91
Rho GTPase-activating protein 1	ARHGAP1	Q07960	0.96	0.97	0.91
Glutathione S-transferase Mu 3	GSTM3	A4UJ43	1.20	1.57	0.91
Glyoxalase domain-containing protein 4	GLOD4	B3KV49	1.00	0.97	0.91
Dynein light chain Tctex-type 1	DYNLT1	P63172	0.94	1.00	0.91
26S proteasome non-ATPase regulatory subunit 12	PSMD12	A0A0S2Z489	1.08	0.99	0.91
Receptor protein-tyrosine kinase	EPHA2	B4DL04	0.86	0.90	0.91
Tubulin beta-8 chain	TUBB8	Q3ZCM7	1.07	1.07	0.91
Acyl-protein thioesterase 1	LYPLA1	Q6IAQ1	1.09	1.05	0.91
NADP-dependent malic enzyme	ME1	P48163-2	1.22	1.38	0.91
Aminopeptidase B	RNPEP	Q9H4A4	1.07	1.05	0.91
Surfeit locus protein 4	SURF4	Q5T8U5	0.96	0.96	0.91
Signal peptidase complex catalytic subunit SEC11	SEC11A	H0YNG3	0.85	0.85	0.91
40S ribosomal protein S5	RPS5	M0R0F0	1.00	0.92	0.91
Keratin, type II cytoskeletal 5	KRT5	B4E1T1	1.50	1.57	0.91
Transportin-1	TNPO1	A0A024RAM0	1.09	1.04	0.91
Importin subunit beta-1	KPNB1	B2RBR9	0.99	1.02	0.91
Integrin beta	ITGB4	B7ZLD8	0.85	0.76	0.91
UBX domain-containing protein 4	UBXN4	F8WB86	1.02	0.98	0.91
Protein transport protein Sec23B	SEC23B	B4DRA5	0.89	0.94	0.91
E3 ubiquitin-protein ligase NEDD4	NEDD4	A0A3B3IUC1	0.73	0.76	0.91
RelA-associated inhibitor	PPP1R13L	A0A024R0Q5	1.14	1.09	0.91
Niemann-Pick C1 protein	NPC1	A0A0S2A5C8	1.01	0.94	0.91
Glia maturation factor beta	GMFB	G3V4P8	1.13	1.20	0.91
Interferon-induced transmembrane protein 1	IFITM2	H7BYV1	0.83	0.83	0.91
40S ribosomal protein SA	RPSA	C9J9K3	0.95	0.93	0.91
Signal recognition particle 9 kDa protein	SRP9	P49458	0.90	0.88	0.91
Alpha-soluble NSF attachment protein	NAPA	M0R0Y2	0.77	0.93	0.91
40S ribosomal protein S3a	RPS3A	Q6NXR8	0.92	0.92	0.90
Drebrin-like protein	DBNL	B4DKZ4	0.77	1.10	0.90
UPF0505 protein C16orf62	C16orf62	H3BVG8	1.18	1.15	0.90
Ras GTPase-activating protein 1	RASA1	B4DTL8	1.05	1.29	0.90
Actin-related protein 2/3 complex subunit 5	ARPC5	O15511	1.05	1.10	0.90
60S ribosomal protein L7-like 1	RPL7L1	B3KMP5	1.04	0.86	0.90
40S ribosomal protein S15a	hCG_1994130	B2R4W8	0.88	0.87	0.90
Aminoacylase-1	HEL-S-5	A0A1B0GU86	1.06	1.02	0.90
Galectin	LGALS3	Q86TY5	0.94	1.07	0.90
Protein FAM83H	FAM83H	J3KPS2	1.00	1.08	0.90
Heat shock cognate 71 kDa protein	HEL-S-72p	V9HW22	1.00	1.00	0.90

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Eukaryotic translation initiation factor 3 subunit F	EIF3F	B4DMT5	1.04	1.08	0.90
Cathepsin Z	CTSZ	Q5U000	0.92	1.36	0.90
Tropomyosin alpha-1 chain	TPM1	H0YKX5	0.88	0.75	0.90
Prefoldin subunit 3	VBP1	D3DWY7	1.03	1.03	0.90
Non-specific serine/threonine protein kinase	PAK2	A8K5M4	0.81	0.94	0.90
60S ribosomal protein L10	RPL10	X1WI28	0.92	0.89	0.90
E3 ubiquitin-protein ligase DTX3L	DTX3L	Q8TDB6	0.77	0.73	0.90
40S ribosomal protein S29	RPS29	P62273	0.89	0.68	0.90
T-complex protein 1 subunit zeta	CCT6A	Q59ET3	1.03	0.99	0.90
60S acidic ribosomal protein P2	RPLP2	A0A024RCA7	1.10	1.11	0.90
Low-density lipoprotein receptor	LDLR	Q9UH51	0.72	0.70	0.90
Glutamine--tRNA ligase	QARS	Q53HS0	1.07	1.11	0.90
H/ACA ribonucleoprotein complex subunit 4	DKC1	H7C0M1	0.83	0.69	0.90
40S ribosomal protein S24	RPS24	E7ETK0	0.99	0.85	0.90
Protein AHNAK2	AHNAK2	Q8IVF2-3	1.02	1.13	0.90
60S ribosomal protein L9	RPL9	Q53Z07	0.93	0.84	0.90
26S protease regulatory subunit 10B	PSMC6	P62333	0.95	0.94	0.90
Signal transducer and activator of transcription 1-alpha/beta	STAT1	A0A669KB68	1.10	1.13	0.90
Specifically androgen-regulated gene protein	SARG	Q9BW04-2	0.99	1.19	0.90
Cellular nucleic acid-binding protein	CNBP	A0A0S2Z4Q3	0.96	0.75	0.90
Beta-hexosaminidase	HEXA	H3BU85	0.74	0.92	0.90
4F2 cell-surface antigen heavy chain	SLC3A2	P08195-2	1.02	0.99	0.90
Coronin	CORO1B	A0A024R5K1	0.97	0.80	0.90
Nucleolar and coiled-body phosphoprotein 1	NOLC1	B2RAU8	0.96	0.83	0.90
60S ribosomal protein L6	RPL6	Q8TBK5	0.91	0.89	0.90
Thymosin beta-10	TMSB10	P63313	0.77	0.72	0.90
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	P41091	0.97	1.02	0.90
40S ribosomal protein S14	RPS14	A0A2R8Y811	0.97	0.96	0.90
Cullin-associated NEDD8-dissociated protein 1	CAND1	A8K8U1	1.06	1.04	0.90
Mitogen-activated protein kinase 15	MAPK15	A0A1C7CYZ1	0.93	0.94	0.90
40S ribosomal protein S2	RPS2	Q3KQT6	0.97	0.93	0.90
Glycolipid transfer protein	GLTP	F5GZ49	1.82	2.02	0.90
UMP-CMP kinase	CMPK1	P30085	1.04	1.04	0.90
Heat shock 70 kDa protein 4L	HSPA4L	B3KNM0	1.32	1.27	0.90
Gelsolin	GSN	P06396-2	1.01	1.01	0.89
Golgi resident protein GCP60	ACBD3	A0A024R3P9	0.59	0.96	0.89
Basic leucine zipper and W2 domain-containing protein 1	BZW1	Q53FN7	1.13	1.16	0.89
Rhotekin	RTKN	Q9BST9-3	1.05	1.07	0.89
ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1	F8W1U7	0.89	1.12	0.89

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Conserved oligomeric Golgi complex subunit 3	COG3	Q96JB2	0.99	1.00	0.89
Tubulin beta-2A chain	TUBB2A	B2R6L0	0.93	1.04	0.89
Peptidyl-prolyl cis-trans isomerase FKBP9	FKBP9	B7Z230	0.89	1.01	0.89
40S ribosomal protein S8	RPS8	Q5JR94	0.89	0.92	0.89
Developmentally-regulated GTP-binding protein 1	DRG1	Q9Y295	1.00	0.94	0.89
Staphylococcal nuclease domain-containing protein 1	SND1	B2R5U1	0.97	0.94	0.89
Sec1 family domain-containing protein 1	SCFD1	B7Z5N7	0.81	0.69	0.89
Squalene synthase	FDFT1	Q6IAX1	0.93	0.78	0.89
Heterogeneous nuclear ribonucleoprotein H3	HNRPH3	Q53F48	0.90	0.80	0.89
Ribosomal protein L15	RPL15	A0A2R8YEM3	0.96	0.81	0.89
Cysteine--tRNA ligase, cytoplasmic	CARS	P49589	1.03	1.10	0.89
DNA-directed RNA polymerase	POLR2B	C9J4M6	1.13	1.20	0.89
40S ribosomal protein S27	RPS27L	C9JLI6	1.00	0.92	0.89
Casein kinase II subunit beta	CSNK2B	A0A1U9X7J2	0.92	0.93	0.89
Glucose-6-phosphate isomerase	GPI	P06744	1.04	1.06	0.89
40S ribosomal protein S4	RPS4X	Q96IR1	0.91	0.87	0.89
E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	Q14258	0.80	0.79	0.89
Calpain-1 catalytic subunit	CAPN1	A0A024R5A3	1.13	1.11	0.89
Protein Njmu-R1	OK/SW-cl.19	Q8NI83	1.00	0.91	0.89
14-3-3 protein sigma	SFN	P31947	1.00	1.08	0.89
Caldesmon	CALD1	A0A140VKA0	0.96	0.99	0.89
Tubulin--tyrosine ligase-like protein 12	TTLL12	A0A024R4U3	1.00	1.00	0.89
Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	C7DUW4	0.96	1.29	0.89
Copine-1	CPNE1	A6PVH9	1.02	1.08	0.89
Proteasome subunit beta type	PSMB1	Q53FT8	0.97	0.86	0.89
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUFA11	K7EQ77	0.85	0.82	0.89
Heat shock 70 kDa protein 1B	HEL-S-103	A8K5I0	0.95	1.00	0.89
PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	F8WCD5	1.02	0.88	0.89
78 kDa glucose-regulated protein	HEL-S-89n	V9HWB4	0.81	0.78	0.88
Transcription elongation factor B polypeptide 1	TCEB1	E5RHG8	1.03	1.03	0.88
Inhibitor of nuclear factor kappa-B kinase subunit beta	IKBKB	E5RGW5	1.02	1.31	0.88
Puromycin-sensitive aminopeptidase	NPEPPS	E9PLK3	1.12	1.08	0.88
Protein SCAF11	SFRS2IP	Q05BS8	0.55	0.83	0.88
14-3-3 protein epsilon	HEL2	V9HW98	1.04	1.05	0.88
Protein phosphatase 1 regulatory subunit 3A	PPP1R3A	Q16821	4.42	1.83	0.88
Peptidyl-prolyl cis-trans isomerase	HEL-S-69p	V9HWF5	0.99	0.95	0.88
Proliferation-associated protein 2G4	PA2G4	A8K6Y1	0.99	0.98	0.88
Nucleosome assembly protein 1-like 4	NAP1L4	A0A024RCC9	1.04	1.15	0.88
Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	A0A087WY55	0.88	0.96	0.88

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
PDZ and LIM domain protein 1	HEL-S-112	V9HW92	1.04	1.05	0.88
40S ribosomal protein S11	RPS11	P62280	0.92	0.94	0.88
Leucine--tRNA ligase, cytoplasmic	LARS	B4E266	1.03	0.98	0.88
60S ribosomal protein L10a	RPL10A	P62906	0.96	0.99	0.88
Myosin-9	MYH9	A0A024R1N1	0.97	0.97	0.88
Exportin-1	XPO1	O14980	1.04	1.09	0.88
RNA-binding protein 39	DKFZp686A11192	Q6N037	0.66	0.71	0.88
40S ribosomal protein S25	RPS25	P62851	0.95	1.00	0.88
60S ribosomal protein L32	RPL32	D3YTB1	0.96	0.97	0.88
40S ribosomal protein S9	RPS9	A0A024R4M0	0.93	0.90	0.88
NEDD8-conjugating enzyme Ubc12	UBE2M	A0A024R4T4	1.21	1.14	0.88
UTP--glucose-1-phosphate uridylyltransferase	UGP2	Q53QE9	0.99	0.94	0.88
Platelet-activating factor acetylhydrolase IB subunit beta	HEL-S-303	V9HW44	1.07	0.96	0.88
Phenylalanine--tRNA ligase beta subunit	FARSB	Q9BR63	0.94	0.89	0.88
Fructose-bisphosphate aldolase	HEL-S-87p	V9HWN7	0.96	1.00	0.88
Sodium-coupled neutral amino acid transporter 1	SLC38A1	Q8NCD8	1.03	1.06	0.88
Proteasome subunit beta type-5	PSMB5	P28074	0.99	0.95	0.88
Fascin	FSCN1	A0A384MEG1	0.99	0.94	0.88
Annexin	ANXA7	B4DT77	1.00	0.98	0.88
26S proteasome non-ATPase regulatory subunit 8	PSMD8	K7EJR3	0.94	0.93	0.88
Bcl-2-like protein 13	BCL2L13	B2RB43	0.84	0.76	0.88
26S proteasome non-ATPase regulatory subunit 6	PSMD6	Q15008	0.90	0.97	0.88
Guanine nucleotide exchange factor VAV2	VAV2	P52735-3	1.28	1.38	0.88
Peptidyl-prolyl cis-trans isomerase	PPIE	E9PIB0	0.69	0.75	0.88
Peroxiredoxin-2	HEL-S-2a	V9HW12	0.97	0.89	0.88
NSFL1 cofactor p47	NSFL1C	Q53FF5	0.92	0.89	0.88
Macrophage migration inhibitory factor	MIF	I4AY87	1.01	1.14	0.88
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	Q6YN16	0.87	0.79	0.88
Condensin complex subunit 3	NCAPG	Q6NUR1	1.26	1.18	0.88
60S ribosomal protein L35a	RPL35A	P18077	1.00	0.95	0.88
60S ribosomal protein L26-like 1	RPL26	J3QRI7	0.96	0.97	0.88
Adenine phosphoribosyltransferase	APRT	P07741	1.01	1.08	0.88
Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	NUDT2	P50583	1.04	0.86	0.88
Ubiquitin-conjugating enzyme E2 D2	UBE2D2	D6RFM0	1.10	1.11	0.88
Galectin-1	LGALS1	A0A384MR27	0.95	0.88	0.87
Hsp90 co-chaperone Cdc37	CDC37	A0A024R7B7	0.97	1.02	0.87
Protein SEC13 homolog	SEC13	P55735	0.80	0.86	0.87
Ras GTPase-activating protein-binding protein 1	G3BP	Q6FI03	0.82	0.85	0.87
Cytosol aminopeptidase	HEL-S-106	V9HW38	0.92	0.90	0.87

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
ADP-ribosylation factor 4	ARF4	P18085	0.96	0.97	0.87
Actin-related protein 2/3 complex subunit 3	ARPC3	Q2LE71	1.05	0.96	0.87
Coatomer subunit zeta-1	COPZ1	Q53FU3	0.92	0.80	0.87
Putative helicase MOV-10	MOV10	Q5JR04	0.77	0.68	0.87
Fumarylacetoacetase	FAH	A0A384P5L6	0.98	1.14	0.87
D-dopachrome decarboxylase	DDT	Q53Y51	0.95	0.99	0.87
Myotrophin	DKFZp761E1322	Q69YG1	1.02	1.01	0.87
Golgi reassembly-stacking protein 2	GORASP2	B4DEI4	1.02	0.98	0.87
Glycylpeptide N-tetradecanoyltransferase	NMT1	Q96HI4	1.04	1.02	0.87
Phosphoglycerate mutase	PGAM1	Q6FHU2	1.02	1.03	0.87
NADH-ubiquinone oxidoreductase chain 4	NADH4	Q14YI3	1.04	1.00	0.87
WD repeat-containing protein 1	HEL-S-52	V9HWG7	0.99	1.02	0.87
Gem-associated protein 4	GEMIN4	I3L4A4	1.13	0.98	0.87
Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	Q2TAA2	0.93	0.95	0.87
Translation initiation factor eIF-2B subunit delta	DKFZp586J0119	Q9Y3W7	1.17	0.93	0.87
Proteasome subunit beta type-3	PSMB3	A0A087WUL2	0.93	0.71	0.87
Polyglutamine-binding protein 1	PQBP1	Q4VY28	1.18	1.12	0.87
60S ribosomal protein L8	RPL8	P62917	0.89	0.90	0.87
Unconventional myosin-Ie	MYO1E	Q4KMR3	1.04	1.01	0.87
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	A0A140VJS9	0.78	1.33	0.87
Cartilage-associated protein	CRTAP	O75718	0.91	0.87	0.87
Triosephosphate isomerase	HEL-S-49	V9HWK1	0.95	0.99	0.87
T-complex protein 1 subunit epsilon	HEL-S-69	V9HW37	0.96	0.93	0.87
ATP-dependent RNA helicase DDX3X	DDX3X	A0A2R8YDT5	1.03	0.95	0.87
Ubiquitin carboxyl-terminal hydrolase	USP14	B3KTG4	1.03	1.02	0.87
Rabankyrin-5	DKFZp686M19106	Q5H9P4	1.52	1.77	0.87
60S ribosomal protein L30	RPL30	E5RI99	0.94	0.86	0.87
Thioredoxin domain-containing protein 12	TXNDC12	O95881	0.85	0.79	0.87
RuvB-like 1	RUVB1	B5BUB1	0.93	0.88	0.87
Calpain small subunit 1	CAPNS1	A0A0C4DQG5	0.98	1.01	0.86
Bifunctional polynucleotide phosphatase/kinase	PNKP	M0R3C8	0.80	0.64	0.86
ATP-dependent RNA helicase DDX1	DDX1	A3RJH1	0.97	0.94	0.86
Receptor protein-tyrosine kinase	EGFR	Q504U8	0.87	0.87	0.86
Adenylyl cyclase-associated protein	CAP1	D3DPU2	1.03	1.03	0.86
Inverted formin-2	INF2	Q27J81-2	1.08	1.03	0.86
Programmed cell death 6-interacting protein	DRIP4	Q4W4Y1	1.01	1.08	0.86
BAG family molecular chaperone regulator 3	BAG3	Q53GY1	1.01	1.11	0.86
Protein arginine N-methyltransferase 1	PRMT1	A0A3S6H812	0.91	0.88	0.86
Tax1-binding protein 3	TAX1BP3	O14907	1.08	1.06	0.86

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Estradiol 17-beta-dehydrogenase 8	HSD17B8	A0A1U9X7U8	0.82	0.73	0.86
4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	B4DE91	0.87	0.51	0.86
Phosphomannomutase	PMM2	B7Z3M6	1.06	1.20	0.86
UV excision repair protein RAD23 homolog B	RAD23B	P54727	0.96	1.03	0.86
Tropomyosin alpha-4 chain	HEL-S-108	V9HW56	1.00	0.99	0.86
Ezrin	EZR	Q6NUR7	1.04	1.05	0.86
Transgelin-2	TAGLN2	A0A384MTL2	1.00	0.99	0.86
Beta-catenin-like protein 1	CTNBL1	A0A087WUB9	0.95	0.99	0.86
Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	P43034	0.94	1.13	0.86
Ubiquilin-1	UBQLN1	B3KNI8	1.02	1.11	0.86
Ras-related protein Rab-21	RAB21	A0A024RBA9	0.87	0.85	0.86
Twinfilin-2	TWF2	D6RG15	0.88	0.78	0.86
Actin-related protein 2/3 complex subunit 2	ARPC2	Q53R19	1.03	1.02	0.86
Quinone oxidoreductase PIG3	TP53I3	Q53FA7	1.01	0.90	0.86
Nucleolar RNA helicase 2	DDX21	Q9NR30-2	0.89	0.77	0.86
Perilipin-3	PLIN3	A0A140VJN8	0.99	0.97	0.86
Poly(rC)-binding protein 1	PCBP1	Q53SS8	1.02	0.97	0.86
Collagen alpha-1(XVII) chain	COL17A1	D3DRA2	0.91	0.80	0.86
T-complex protein 1 subunit eta	CCT7	Q6IBT3	1.00	0.97	0.86
Adenylate kinase isoenzyme 1	AK1	Q6FGX9	0.93	1.03	0.86
Ribonucleases P/MRP protein subunit POP1	POP1	Q96F88	0.84	0.80	0.86
60S ribosomal protein L5	RPL5	A0A2R8Y6J3	0.91	0.94	0.86
Dynactin subunit 2	HEL-S-77	A0A384MDU9	0.98	0.96	0.86
Tubulin alpha-1B chain	TUBA1B	P68363	1.00	0.99	0.86
Histidine triad nucleotide-binding protein 1	HINT1	A0A384NPU2	0.88	0.96	0.86
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	B4DJ89	1.83	1.77	0.86
Elongation factor 1-delta	EEF1D	E9PK01	0.96	0.98	0.86
Ras and Rab interactor 1	RIN1	B4DN44	1.00	0.94	0.86
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	B4E2T6	0.94	1.01	0.85
Tubulin beta-6 chain	TUBB6	Q2NKY5	0.94	0.96	0.85
MMS19 nucleotide excision repair protein homolog	MMS19	Q96T76-9	1.11	1.19	0.85
40S ribosomal protein S10	RPS10	P46783	0.91	0.82	0.85
UBX domain-containing protein 1	UBXN1	B4DU88	1.20	1.08	0.85
Fructose-2,6-bisphosphatase TIGAR	TIGAR	Q9NQ88	0.88	0.99	0.85
Coatomer subunit delta	ARCN1	B0YIW5	0.96	0.77	0.85
Coatomer subunit alpha	COPA	A0A3B3ISC6	0.96	0.91	0.85
Eukaryotic translation initiation factor 4B	EIF4B	E7EX17	1.10	1.12	0.85
Histone-arginine methyltransferase CARM1	CARM1	Q86X55-1	0.90	0.91	0.85
Polyadenylate-binding protein	PABPC1	A0A024R9C1	0.97	0.95	0.85

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Peroxisredoxin-6	HEL-S-128m	V9HWC7	1.02	0.97	0.85
Protein phosphatase 1 regulatory subunit 14B	PPP1R14B	A0A024R563	0.92	0.91	0.85
Exportin-2	CSE1L	A0A384NKW7	1.02	1.00	0.85
Ubiquitin thioesterase OTUB1	OTUB1	F5GYN4	0.96	0.96	0.85
Urotensin-2	UTS2	A0AVP6	0.65	0.48	0.85
Platelet-activating factor acetylhydrolase IB subunit gamma	PAFAH1B3	M0R389	1.13	0.88	0.85
Sphingomyelin phosphodiesterase 4	SMPD4	Q9NXE4	0.94	0.92	0.85
Mannose-6-phosphate isomerase	MPI	H3BP57	0.92	0.73	0.85
E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	Q14258	1.10	1.01	0.85
ADP-ribosylation factor 5	ARF5	A4D0Z3	1.14	1.05	0.85
Elongation factor 1-beta	EEF1B2	A0A024R3W7	0.96	0.98	0.85
Costars family protein ABRACL	ABRACL	Q9P1F3	1.05	0.96	0.85
40S ribosomal protein S3	RPS3	P23396	0.97	0.95	0.85
Interleukin-18	IL18	A0A024R3E0	1.00	0.96	0.85
Proteasome inhibitor PI31 subunit	PSMF1	Q5QPM7	0.94	1.15	0.85
Phosphoglucomutase-1	PGM1	B4DFP1	1.05	1.07	0.85
Transcription factor BTF3	BTF3	P20290-2	1.01	0.99	0.85
DNA topoisomerase 1	TOP1	B9EG90	0.71	0.80	0.85
Calponin	CNN2	B4DDF4	0.99	0.97	0.85
DNA repair protein XRCC1	XRCC1	M0R0D2	0.78	0.92	0.85
60S ribosomal protein L7	RPL7	A0A024R814	0.93	0.86	0.85
6-phosphogluconolactonase	PGLS	A0A0K0K1K7	0.98	1.00	0.85
Rotatin	RTTN	J3KTD2	0.86	0.83	0.85
Neuroblast differentiation-associated protein AHNAK	AHNAK	Q09666	1.00	1.01	0.85
26S proteasome non-ATPase regulatory subunit 2	PSMD2	Q13200	1.01	1.00	0.85
Importin subunit alpha-3	KPNA4	O00629	1.02	1.02	0.85
Aspartate--tRNA ligase, cytoplasmic	DARS	A0A140VJW5	0.99	0.97	0.85
Acyl-protein thioesterase 2	LYPLA2	A0A140VJC9	0.97	0.84	0.85
5-AMP-activated protein kinase subunit gamma-1	PRKAG1	F8VYY9	1.14	1.22	0.85
Coatomer subunit gamma-1	COPG1	Q9Y678	0.98	0.90	0.85
Carbonyl reductase [NADPH] 1	CBR1	A0A384NL53	0.98	1.03	0.85
Destrin	HEL32	V9HWA6	0.96	0.89	0.85
Small ubiquitin-related modifier 1	SUMO1	B8ZZJ0	0.59	0.73	0.85
Protein flightless-1 homolog	FLII	B4DIX0	0.95	0.78	0.85
60S ribosomal protein L24	RPL24	C9JXB8	1.01	0.89	0.85
Adenosine kinase	ADK	A0A140VJE0	0.98	0.94	0.85
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	B4DDF7	1.00	0.99	0.84
T-complex protein 1 subunit delta	CCT4	B7Z9L0	0.98	0.94	0.84
Biliverdin reductase A	BLVRA	A0A140VJF4	1.04	1.09	0.84

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
26S proteasome non-ATPase regulatory subunit 3	PSMD3	Q6IBN0	0.93	0.83	0.84
Glucose-6-phosphate isomerase	GPI	P06744	1.05	0.94	0.84
Plastin-3	PLS3	P13797	1.10	1.08	0.84
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	Q12904	0.91	0.93	0.84
L-lactate dehydrogenase	HEL-S-133P	V9HWB9	1.02	1.10	0.84
Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	Q8NC51-2	0.92	0.86	0.84
SUMO-conjugating enzyme UBC9	UBE2I	P63279	1.10	0.87	0.84
NudC domain-containing protein 1	NUDCD1	Q96RS6-2	1.15	0.88	0.84
Peptidyl-prolyl cis-trans isomerase	FKBP3	Q53GD8	0.87	0.89	0.84
39S ribosomal protein L24, mitochondrial	MRPL24	Q96A35	0.93	1.07	0.84
Huntingtin-interacting protein K	hCG_2003792	A0A024R5Q1	0.98	1.07	0.84
Glucose-6-phosphate 1-dehydrogenase	G6PD	Q2VF42	0.88	0.47	0.84
Cytokine receptor-like factor 3	CRLF3	Q8IUI8	0.98	1.04	0.84
Vigilin	HDLBP	A0A024R4E5	0.84	0.87	0.84
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	Q53XC0	0.91	0.96	0.84
40S ribosomal protein S23	RPS23	A8K517	0.97	1.02	0.84
ER lumen protein-retaining receptor	KDELR1	Q96H29	1.11	1.12	0.84
40S ribosomal protein S26	RPS26	A0A024RB14	0.84	0.77	0.84
Translation initiation factor eIF-2B subunit alpha	EIF2B1	Q14232	1.30	0.95	0.84
WD repeat-containing protein 18	WDR18	U3KQC1	0.96	0.77	0.84
2-deoxynucleoside 5-phosphate N-hydrolase 1	DNPH1	H0Y8X4	0.99	0.98	0.84
Chromodomain-helicase-DNA-binding protein 4	CHD4	B3KY63	1.04	0.91	0.84
Lactoylglutathione lyase	GLO1	X5DNM4	1.08	1.06	0.84
Sorting nexin-1	SNX1	H0YK42	0.98	0.96	0.84
T-complex protein 1 subunit gamma	CCT3	B3KX11	0.97	0.96	0.84
Myeloid leukemia factor 2	MLF2	F5H7L5	0.85	0.81	0.84
Density-regulated protein	DENR	A0A024RBR3	0.87	0.94	0.84
Tubulin-folding cofactor B	TBCB	K7EK42	1.64	1.24	0.84
Profilin-1	PFN1	P07737	0.92	0.90	0.84
Vacuolar protein sorting-associated protein 52 homolog	VPS52	B4E225	0.63	1.07	0.84
Moesin	HEL70	V9HWC0	0.98	0.99	0.84
Chloride intracellular channel protein	CLIC1	Q5SRT3	0.87	0.87	0.83
Actin-related protein 2	ACTR2	P61160	1.04	1.00	0.83
Importin-4	IPO4	B3KQ33	1.02	0.99	0.83
Echinoderm microtubule-associated protein-like 2	EML2	K7EKG3	1.03	1.05	0.83
Plasminogen activator inhibitor 2	SERPINB2	P05120	1.00	0.92	0.83
Heat shock protein HSP 90-alpha	EL52	K9JA46	0.96	0.98	0.83
Sialic acid synthase	HEL-S-100	V9HW39	0.91	0.90	0.83
Solute carrier family 35 member F2	SLC35F2	E9PKZ2	0.69	0.83	0.83

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein kish-A	TMEM167A	Q8TBQ9	0.81	0.72	0.83
Non-syndromic hearing impairment protein 5	DFNA5	A0A024RA58	1.01	0.86	0.83
Prefoldin subunit 5	PFDN5	Q99471	1.12	1.25	0.83
Proteasome subunit beta type-2	PSMB2	A0A140VJS6	0.92	0.90	0.83
Eukaryotic translation initiation factor 3 subunit B	EIF3B	B4DV79	0.95	0.93	0.83
Methionine aminopeptidase 1	DKFZp781C0419	Q5CZ91	0.80	0.60	0.83
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	Q6FHF7	2.33	2.16	0.83
Serine/threonine-protein kinase 25	STK25	C9JDH9	0.98	1.05	0.83
RNA polymerase II subunit A C-terminal domain phosphatase SSU72	SSU72	B4DMK6	0.99	1.05	0.83
60S ribosomal protein L28	RPL28	H0YMF4	0.96	0.89	0.83
Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	B7Z6P0	1.07	1.01	0.83
T-complex protein 1 subunit beta	HEL-S-100n	V9HW96	0.94	0.91	0.83
Heat shock 70 kDa protein 4	HSPA4	B4DH02	0.97	1.00	0.83
Alpha-parvin	PARVA	E9PS97	1.02	1.11	0.83
Eukaryotic translation initiation factor 3 subunit C	EIF3C	B4DVU3	0.98	0.85	0.83
Spermidine synthase	SRM	P19623	0.99	0.94	0.83
Zinc finger CCCH domain-containing protein 18	FLJ00419	Q86YU5	0.53	0.70	0.83
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	PLCB3	Q01970-2	1.07	0.92	0.83
E3 ubiquitin-protein ligase KCMF1	KCMF1	Q9P0J7	0.98	1.05	0.83
Nuclear pore glycoprotein p62	hCG_19665	A0A024QZF1	0.95	1.06	0.83
Tubulin alpha-1C chain	TUBA1C	Q53GA7	1.06	1.01	0.83
Heat shock protein 105 kDa	HSPH1	A0A024RDQ0	0.94	0.96	0.83
Unconventional myosin-XVIIIa	MYO18A	A0A0D9SFK2	0.86	0.86	0.83
Thioredoxin-related transmembrane protein 2	TMX2	B2R7I0	0.81	0.89	0.82
CTP synthase 1	CTPS1	A0A3B3IRI2	1.04	0.88	0.82
Serine-threonine kinase receptor-associated protein	STRAP	Q9Y3F4	0.94	0.92	0.82
Copine-3	CPNE3	A0A024R994	0.97	0.89	0.82
Probable ATP-dependent RNA helicase DDX6	DDX6	B2R858	0.96	0.88	0.82
Eukaryotic initiation factor 4A-II	EIF4A2	Q14240	1.11	1.14	0.82
Eukaryotic translation initiation factor 3 subunit D	EIF3D	O15371-2	0.93	0.89	0.82
LIM and senescent cell antigen-like-containing domain protein 1	LIMS1	P48059-2	0.85	0.98	0.82
Eukaryotic translation initiation factor 3 subunit H	EIF3H	Q5BKY2	1.04	1.03	0.82
Protein deglycase DJ-1	HEL-S-67p	V9HWC2	0.97	0.97	0.82
Inosine-5-monophosphate dehydrogenase 2	IMPDH2	A0A384N6C2	0.96	0.92	0.82
Tubulin beta chain	TUBB	Q5JP53	1.01	0.91	0.82
Glutathione S-transferase omega-1	HEL-S-21	V9HWG9	0.91	0.87	0.82
Microtubule-associated protein	MAP4	E7EVA0	1.01	1.00	0.82
Methylsterol monooxygenase 1	MSMO1	D6RDP9	0.79	0.74	0.82
Eukaryotic translation initiation factor 2 subunit 2	EIF2S2	Q6IBR8	0.94	0.88	0.82

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
5-nucleotidase domain-containing protein 1	NT5DC1	Q5QPD0	0.94	0.93	0.82
Translin-associated protein X	TSNAX	A0A024R3V8	1.05	1.23	0.82
PDZ and LIM domain protein 4	PDLIM4	A0A0S2Z4N4	0.93	0.98	0.82
Eukaryotic translation initiation factor 3 subunit E	EIF3E	Q6IAX5	0.97	0.99	0.82
COP9 signalosome complex subunit 4	COPS4	A0A0S2Z5H7	0.98	0.80	0.82
N-alpha-acetyltransferase 10	NAA10	P41227-2	0.72	0.84	0.82
Arginine--tRNA ligase, cytoplasmic	RARS	P54136	0.96	0.93	0.82
Thioredoxin	TXN	H9ZYJ2	0.99	1.00	0.82
Leucyl-cystinyl aminopeptidase	LNPEP	B2RAK1	0.98	0.94	0.82
Rho-related GTP-binding protein RhoG	ARHG	Q6ICQ8	0.84	0.96	0.82
T-complex protein 1 subunit alpha	TCP1	P17987	0.93	0.96	0.82
Eukaryotic translation initiation factor 3 subunit M	EIF3M	Q7L2H7	1.05	0.98	0.82
DnaJ homolog subfamily B member 1	DNAJB1	Q6FI51	0.97	0.88	0.82
SNW domain-containing protein 1	SNW1	Q0D2M5	1.01	1.18	0.82
Prostaglandin E synthase 3	PTGES3	A0A024RB32	0.91	0.95	0.82
Eukaryotic translation initiation factor 3 subunit G	EIF3G	O75821	0.95	0.86	0.82
Heat shock protein HSP 90-beta	HSP90AB1	A0A024RD80	0.93	0.92	0.82
Isoleucine--tRNA ligase, cytoplasmic	IARS	Q59G75	1.00	0.93	0.82
Sepiapterin reductase	SPR	B4DSF0	0.90	0.73	0.82
Vacuolar protein sorting-associated protein 35	VPS35	Q96QK1	0.94	0.98	0.82
Actin-related protein 2/3 complex subunit 1B	ARPC1B	A4D275	0.89	0.90	0.82
Pleckstrin-2	PLEK2	Q9NYT0	0.93	0.82	0.82
Porphobilinogen deaminase	PBGD	Q68Y91	0.83	0.79	0.82
Tubulin beta-4B chain	TUBB2C	Q8IZ29	0.94	0.94	0.82
C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	A0A087X2D8	0.72	0.89	0.82
Transcriptional coactivator YAP1	YAP1	B4E2Y3	0.95	0.89	0.81
Putative 60S ribosomal protein L39-like 5	RPL39P5	Q59GN2	0.82	0.80	0.81
60S ribosomal protein L36	RPL36	Q9Y3U8	1.02	1.04	0.81
Glutathione synthetase	HEL-S-64p	B7Z1C5	0.97	0.92	0.81
Activating signal cointegrator 1 complex subunit 2	ASCC2	Q53H58	0.96	0.99	0.81
Alcohol dehydrogenase [NADP(+)]	HEL-S-165mP	V9HWI0	1.01	0.82	0.81
L-lactate dehydrogenase	LDHB	Q5U077	1.03	1.01	0.81
Egl nine homolog 1	EGLN1	Q9GZT9	0.83	0.91	0.81
Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	P62942	0.87	0.94	0.81
Coatomer subunit beta	COPB2	P35606-2	0.96	0.95	0.81
Eukaryotic translation initiation factor 5	EIF5	Q6IBU0	1.01	0.87	0.81
Actin-like protein 6A	BAF53A	O96019	0.82	0.81	0.81
Serine/threonine-protein phosphatase 4 regulatory subunit 1	PPP4R1	A8K923	0.85	0.60	0.81
Bifunctional purine biosynthesis protein PURH	HEL-S-70p	V9HWH7	0.96	0.95	0.81

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Signal peptidase complex subunit 1	SPCS1	A0A5F9YFS9	0.64	0.61	0.81
Ubiquitin-like modifier-activating enzyme 6	UBA6	B3KSS1	1.09	1.13	0.81
Dynamin-2	DNM2	P50570-2	0.95	0.78	0.81
Proteasome activator complex subunit 4	PSME4	Q14997-3	0.98	0.74	0.81
Purine nucleoside phosphorylase	HEL-S-156an	V9HWH6	0.98	0.95	0.81
Flap endonuclease 1	FEN1	Q6FHX6	1.01	0.82	0.81
Clustered mitochondria protein homolog	CLUH	K7EIG1	1.15	1.28	0.81
S-formylglutathione hydrolase	ESD	A0A140VJJ2	1.05	0.98	0.81
Serine--tRNA ligase, cytoplasmic	SARS	Q0VGA5	1.01	1.06	0.81
Aflatoxin B1 aldehyde reductase member 2	AKR7A2	H3BLU7	1.04	1.04	0.81
Lysine--tRNA ligase	KARS	Q15046	0.97	0.90	0.81
Pescadillo homolog	PES1	B3KXD6	0.68	0.69	0.81
Bifunctional glutamate/proline--tRNA ligase	EPRS	P07814	1.03	0.93	0.81
Phosphatidylethanolamine-binding protein 1	HEL-S-34	D9IAI1	0.96	0.96	0.80
Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	E9KL35	0.94	0.93	0.80
Ran-specific GTPase-activating protein	RANBP1	C9JJ34	0.96	0.97	0.80
Proteasome subunit alpha type	PSMA3	Q6IB71	0.79	0.88	0.80
Eukaryotic translation initiation factor 5A-1	EIF5A	P63241	1.01	1.03	0.80
Translational activator GCN1	PRIC295	E1NZA1	1.01	1.02	0.80
Putative heat shock protein HSP 90-beta 2	HSP90AB2P	Q58FF8	0.90	0.88	0.80
ATP-binding cassette sub-family E member 1	ABCE1	P61221	1.02	1.00	0.80
Annexin	ANXA8	B4DQE1	1.03	1.07	0.80
Mitochondrial import receptor subunit TOM34	TOMM34	Q6ZPD0	0.80	0.79	0.80
Bifunctional purine biosynthesis protein ATIC	ATIC	P31939	0.95	1.01	0.80
T-complex protein 1 subunit theta	CCT8	P50990-2	0.93	0.94	0.80
Proteasome activator complex subunit 2	PSME2	Q86SZ7	0.94	0.86	0.80
40S ribosomal protein S17	RPS17	H3BNC9	0.85	0.84	0.80
Osteoclast-stimulating factor 1	OSTF1	A8K646	1.00	0.99	0.80
BRCA2 and CDKN1A-interacting protein	BCCIP	Q9P287	0.94	0.77	0.80
Adenylyl cyclase-associated protein 1	CAP1	D3DPU2	1.03	0.97	0.80
1,4-alpha-glucan-branching enzyme	GBE1	Q04446	0.94	0.72	0.80
CD99 antigen	CD99	B2R932	0.85	0.73	0.80
Histidine--tRNA ligase, cytoplasmic	HARS	P12081-3	0.99	0.96	0.80
NEDD8	NEDD8	Q15843	0.92	0.88	0.80
TIP41-like protein	TIPRL	O75663	0.89	0.75	0.80
Alpha-enolase	ENO1	A0A024R4F1	0.92	0.89	0.80
Clathrin interactor 1	CLINT1	A0A0S2Z4Y4	0.85	0.78	0.80
Small ubiquitin-related modifier	SUMO2	A0A024R8S3	0.84	0.74	0.80
GTP-binding nuclear protein Ran	RAN	B5MDF5	0.94	0.93	0.80

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
PDZ and LIM domain protein 7	PDLIM7	D6RH06	0.73	0.90	0.80
Diacylglycerol kinase	DGKA	A0A024RB23	1.05	1.12	0.79
Cdc42-interacting protein 4	TRIP10	M0R2H7	0.75	0.85	0.79
Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	FNTA	E9PPM9	1.00	0.97	0.79
Ran GTPase-activating protein 1	RANGAP1	B4E0U0	0.97	0.92	0.79
Inorganic pyrophosphatase	HEL-S-66p	V9HWB5	1.06	1.08	0.79
Cysteine and histidine-rich domain-containing protein 1	CHORDC1	A0A024R394	0.88	0.84	0.79
Glycogen phosphorylase, brain form	PYGB	P11216	0.98	0.94	0.79
Mannose-1-phosphate guanyltransferase beta	GMPPB	A0A024R329	0.91	0.67	0.79
Profilin	PFN2	C9JQ45	1.06	1.07	0.79
28 kDa heat- and acid-stable phosphoprotein	PDAP1	Q13442	1.09	0.90	0.79
60S ribosomal protein L18a	RPL18A	M0R3D6	0.88	0.84	0.79
14 kDa phosphohistidine phosphatase	HEL-S-132P	V9HWC4	1.09	1.09	0.79
Ubiquitin-protein ligase E3A	UBE3A	A0A0D9SG77	0.93	0.84	0.79
Dynactin subunit 1	DCTN1	E7EX90	0.83	0.93	0.79
Programmed cell death protein 6	PDCD6	Q53FC3	0.86	0.96	0.79
Farnesyl pyrophosphate synthase	FDPS	P14324-2	1.01	0.97	0.79
Pseudouridine-5-phosphatase	HDHD1	Q08623-2	1.22	1.40	0.79
Protein O-GlcNAcase	MGEA5	O60502	1.46	1.09	0.79
14-3-3 protein eta	YWHAH	A0A024R1K7	0.93	0.90	0.79
Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	E7EX73	0.95	0.98	0.79
Protein sel-1 homolog 1	SEL1L	G3V3B3	0.59	0.62	0.79
SET and MYND domain-containing protein 5	SMYD5	Q6GMV2	0.61	0.82	0.79
Ubiquilin-4	UBQLN4	Q9NRR5	0.80	0.84	0.79
Protein lin-7 homolog C	LIN7A	H0YI92	0.72	0.64	0.79
Eukaryotic initiation factor 4A-I	EIF4A1	P60842	0.92	0.93	0.79
Dynamin-1-like protein	DNM1L	O00429-4	1.01	0.97	0.78
Proteasome activator complex subunit 1	PSME1	A0A384NQ35	0.94	0.97	0.78
Spermine synthase	SMS	P52788	1.08	0.95	0.78
WD repeat and FYVE domain-containing protein 1	WDFY1	Q9H8N9	0.88	1.01	0.78
Eukaryotic translation initiation factor 4E	EIF4E	Q32Q75	0.94	0.80	0.78
Protein TFG	TFG	Q7Z426	0.91	0.93	0.78
Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	A0A140VJZ4	0.85	0.89	0.78
Carboxymethylenebutenolidase homolog	CMBL	B2RD36	0.71	0.77	0.78
Vinculin	VCL	A0A384NYN5	1.02	1.03	0.78
Methionine--tRNA ligase, cytoplasmic	MARS	A8K492	0.86	0.74	0.78
Large neutral amino acids transporter small subunit 1	SLC7A5	Q01650	0.88	0.86	0.78
Nucleoredoxin	NXN	Q6DKJ4	0.83	1.00	0.78

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	JTV1	B2R7M3	0.98	0.97	0.78
Leucine-rich repeat-containing protein 47	LRRC47	Q8N1G4	1.06	1.06	0.78
Eukaryotic translation initiation factor 1	SUI1	Q6IAV3	1.02	0.84	0.78
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	E7EU94	1.34	0.65	0.78
Cofilin-1	HEL-S-15	V9HWI5	0.95	0.90	0.78
Ubiquitin carboxyl-terminal hydrolase 5	USP5	P45974-2	1.00	1.00	0.78
Aldose reductase	AKR1B1	A0A024R7A8	0.95	0.89	0.78
Pyruvate kinase	HEL-S-30	V9HWB8	1.00	0.94	0.78
UDP-glucose 6-dehydrogenase	UGDH	O60701-3	0.93	0.93	0.78
Eukaryotic translation initiation factor 3 subunit A	EIF3A	Q7Z5T5	0.90	0.86	0.78
Acetyl-CoA acetyltransferase, cytosolic	ACAT2	A8K4W5	0.91	0.82	0.78
Flavin reductase (NADPH)	BLVRB	M0R192	0.76	1.01	0.78
Armadillo repeat-containing protein 8	ARMC8	G5E9V7	0.96	1.09	0.78
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	A0A590UJY3	0.92	0.95	0.77
Eukaryotic translation initiation factor 3 subunit L	EIF3L	B3KPB9	0.93	0.89	0.77
Protein DPCD	DPCD	Q5JQQ4	1.11	1.09	0.77
Peptidyl-prolyl cis-trans isomerase	FKBP2	Q53XJ5	0.61	0.65	0.77
Coatomer subunit beta	COPB1	P53618	0.92	0.88	0.77
DnaJ homolog subfamily C member 7	DNAJC7	A0A6I8PRZ0	0.70	0.79	0.77
Glycogen phosphorylase, liver form	PYGL	P06737-2	0.96	0.90	0.77
Ubiquitin-like modifier-activating enzyme ATG7	ATG7	C9JE55	1.00	1.05	0.77
Rab GDP dissociation inhibitor beta	GDI2	Q6IAT1	0.94	0.88	0.77
Sorbitol dehydrogenase	HEL-S-95n	V9HW89	1.06	0.98	0.77
Histone deacetylase 2	HDAC2	Q92769-3	0.72	0.75	0.77
Peroxiredoxin-1	PRDX1	A0A384NPQ2	0.99	0.99	0.77
EH domain-containing protein 1	EHD1	B2R5U3	0.93	0.93	0.77
Isocitrate dehydrogenase [NADP]	HEL-216	V9HW78	0.96	0.88	0.77
RNA-binding protein 3	RBM3	A0A024QYX3	0.80	0.71	0.77
Ethanolamine-phosphate cytidylyltransferase	PCYT2	I3L2Q1	0.95	0.91	0.77
Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1	G3V4W4	0.87	0.89	0.77
Branched-chain-amino-acid aminotransferase	BCAT1	A0A024RAV0	1.07	0.86	0.77
NAD(P)H-hydrate epimerase	APOA1BP	B4DP80	0.94	0.85	0.77
Glutaredoxin-3	GLRX3	A0A140VJK1	1.06	0.99	0.77
Rootletin	CROCC	A0A4D6DSY5	1.09	1.03	0.77
PDZ and LIM domain protein 5	PDLIM5	A0A024RDE8	0.89	0.88	0.77
Protein NipSnap homolog 3A	NIPSNAP3A	B4DW81	0.70	0.81	0.77
ATP-dependent RNA helicase DDX54	DDX54	Q8TDD1	0.76	0.68	0.77
Erlin-2	ERLIN2	E5RHW4	0.73	0.69	0.76

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	Q02790	0.93	0.97	0.76
Stress-induced-phosphoprotein 1	HEL-S-94n	V9HW72	0.96	0.91	0.76
60S ribosomal protein L34	RPL34	A1LUY1	0.87	0.85	0.76
Xaa-Pro aminopeptidase 1	XPNPEP1	Q5T6H7	1.03	0.99	0.76
E3 ubiquitin-protein ligase UBR4	UBR4	Q5T4S7-3	1.07	1.22	0.76
Transgelin	TAGLN	Q5U0D2	1.25	1.37	0.76
Acyl-CoA-binding protein	DBI	P07108	0.76	0.98	0.76
GDP-L-fucose synthase	TSTA3	E9PP14	1.05	0.70	0.76
Tight junction protein ZO-1	DKFZp686M05161	B4DZK4	0.65	0.71	0.76
Elongation factor 2	EEF2	A0A384N6H1	0.97	0.94	0.76
Malignant T-cell-amplified sequence 1	MCTS1	Q9ULC4	1.03	0.97	0.76
Aspartate aminotransferase	GIG18	Q2TU84	1.09	1.11	0.76
Annexin	HEL-S-7	V9HWE0	0.93	0.88	0.76
Caspase-4	CASP4	P49662-2	1.06	1.33	0.76
Testin	TES	Q53GU1	0.87	0.77	0.76
Rab3 GTPase-activating protein catalytic subunit	RAB3GAP1	D3DP75	0.77	0.59	0.76
Vacuolar protein sorting-associated protein 29	DKFZp667O202	Q5JPE4	0.78	0.69	0.76
Prefoldin subunit 2	PFDN2	B1AQP2	0.90	0.99	0.76
Importin-7	IPO7	O95373	0.95	0.94	0.76
HBS1-like protein	HBS1L	D9YZV0	0.87	0.85	0.76
Ubiquitin-fold modifier 1	UFM1	P61960	0.97	0.91	0.76
Phosphatidylinositol transfer protein beta isoform	PITPNB	A0A0A0MSW4	0.66	0.66	0.76
Stromelysin-1	MMP3	P08254	0.04	0.28	0.76
S-phase kinase-associated protein 1	SKP1	P63208	1.03	0.97	0.76
Calpain-2 catalytic subunit	CAPN2	Q59EF6	0.98	0.95	0.76
ER lumen protein-retaining receptor	KDELR2	A0A024QZT7	1.10	0.91	0.76
Microtubule-associated protein RP/EB family member 1	MAPRE1	Q15691	0.92	0.93	0.76
Prolactin regulatory element-binding protein	PREB	B5MC98	0.73	0.97	0.76
Coiled-coil domain-containing protein 58	CCDC58	Q4VC31	1.00	0.78	0.76
ATP-dependent 6-phosphofructokinase	PFKM	F8VZI0	0.84	1.01	0.76
Tyrosine-protein phosphatase non-receptor type 11	PTPN11	A0A6C0W8I3	0.86	0.82	0.76
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	Q06210-2	1.15	1.17	0.76
Glycine--tRNA ligase	GARS	A0A090N8G0	1.00	0.93	0.76
Mitochondrial import inner membrane translocase subunit Tim23	TIMM23	O14925	0.91	1.32	0.76
Caveolin	CAV1	Q2TNI1	0.85	0.88	0.76
26S proteasome non-ATPase regulatory subunit 4	PSMD4	A6PVX3	0.62	0.99	0.75
Plastin-2	HEL-S-37	V9HWJ7	1.13	1.25	0.75
Nucleoside diphosphate kinase	NME1-NME2	Q32Q12	0.94	0.93	0.75
Fatty acid synthase	FASN	P49327	0.92	0.91	0.75

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Apoptosis-associated speck-like protein containing a CARD	PYCARD	B2RAZ4	0.85	0.89	0.75
CAD protein	CAD	F8VPD4	0.86	0.80	0.75
Interferon regulatory factor 3	IRF3	Q14653-5	1.09	1.02	0.75
U1 small nuclear ribonucleoprotein C	SNRPC	Q5TAL4	1.06	0.97	0.75
Aldo-keto reductase family 1 member C1	AKR1C1	Q04828	0.78	0.85	0.75
Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	Q0VAB1	1.11	0.94	0.75
Synembryn-A	RIC8A	E9PSI0	0.83	0.82	0.75
Mitogen-activated protein kinase	MAPK1	Q499G7	1.03	1.15	0.75
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	D6RBD7	0.83	0.70	0.75
Vasodilator-stimulated phosphoprotein	VASP	A0A0S2Z4I9	0.93	1.00	0.75
Metastasis-associated protein MTA2	MTA2	A0A024R534	0.67	0.69	0.75
Syntaxin-binding protein 2	STXBP2	M0R376	0.75	0.56	0.75
LIM and SH3 domain protein 1	LASP1	A0A024R1S8	0.88	0.84	0.75
Tropomyosin alpha-3 chain	TPM3	A0A087WWU8	0.86	0.81	0.75
Filamin-A	FLNA	P21333-2	0.90	0.86	0.75
Msx2-interacting protein	SPEN	Q96T58	0.61	0.59	0.75
Non-specific serine/threonine protein kinase	CDC42BPB	A0A024R6N2	0.69	0.72	0.75
Leucine zipper protein 1	LUZP1	A0A024RAC0	0.82	0.64	0.74
Calcyclin-binding protein	CACYBP	Q6NVY0	0.88	0.80	0.74
La-related protein 1	LARP1	H0YC73	1.10	0.81	0.74
Prolyl endopeptidase	PREP	Q9UM02	1.02	0.94	0.74
ATP-dependent 6-phosphofructokinase, platelet type	PFKP	Q01813	0.93	0.86	0.74
Myosin regulatory light chain 12B	MYL12B	O14950	1.05	0.96	0.74
Nascent polypeptide-associated complex subunit alpha	NACA	F8VZJ2	1.01	1.02	0.74
BolA-like protein 2	BOLA2	Q9H3K6	0.92	0.77	0.74
COP9 signalosome complex subunit 7b	COPS7B	B3KW51	0.84	0.84	0.74
Tetraspanin	CD81	E9PJK1	1.17	0.77	0.74
Eukaryotic peptide chain release factor subunit 1	ETF1	B7Z7P8	0.88	0.97	0.74
DNA mismatch repair protein Msh6	MSH6	A0A087WWJ1	0.81	0.80	0.74
Septin-10	SEPTIN10	Q9P0V9	0.85	0.76	0.74
Tryptophan--tRNA ligase, cytoplasmic	WARS	A0A024R6K8	0.98	0.97	0.74
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	G3V438	0.99	0.75	0.74
Chloride intracellular channel protein	CLIC4	Q6FIC5	0.96	0.92	0.74
CUGBP Elav-like family member 1	CELF1	G5EA30	0.76	0.82	0.74
Ragulator complex protein LAMTOR2	LAMTOR2	Q9Y2Q5	0.91	1.75	0.74
TLD domain-containing protein 1	KIAA1609	B4DTA9	1.14	1.12	0.74
DNA replication licensing factor MCM6	MCM6	Q14566	0.76	0.67	0.74
Paxillin	PXN	A0A140VJQ8	1.00	0.89	0.74
H/ACA ribonucleoprotein complex non-core subunit NAF1	NAF1	Q96HR8-2	1.09	0.80	0.74

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Protein diaphanous homolog 1	DIAPH1	A0A2R8Y5N1	1.01	1.00	0.74
Sorcin	SRI	C9J0K6	0.98	0.88	0.74
Antigen peptide transporter 1	TAP1*0102N	O94774	0.84	0.95	0.74
Cytosolic non-specific dipeptidase	CNDP2	B4DV28	0.93	0.83	0.74
6-phosphogluconate dehydrogenase, decarboxylating	PGD	P52209-2	0.95	0.88	0.73
Transmembrane emp24 domain-containing protein 2	TMED2	F5GX39	0.91	0.80	0.73
Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	B4DPZ3	0.81	0.79	0.73
U2 snRNP-associated SURP motif-containing protein	U2SURP	E7ET15	0.72	0.72	0.73
UBX domain-containing protein 6	UBXN6	K7EP32	1.04	0.97	0.73
Ubiquitin-conjugating enzyme E2 N	HEL-S-71	V9HW41	0.90	0.87	0.73
Acylamino-acid-releasing enzyme	APEH	C9JIF9	0.91	0.82	0.73
Heat shock 70 kDa protein 6	HSPA6	Q53FC7	0.69	0.85	0.73
S-(hydroxymethyl)glutathione dehydrogenase	ADH5	Q6IRT1	1.01	0.97	0.73
Polyadenylate-binding protein-interacting protein 1	PAIP1	A0A024R094	0.95	0.97	0.73
Diphosphomevalonate decarboxylase	MVD	P53602	0.93	0.90	0.73
Adenosylhomocysteinase	AHCY	A0A384MTQ3	0.94	0.95	0.73
Talin-1	TLN1	A0A1S5UZ07	0.93	0.89	0.73
Neural Wiskott-Aldrich syndrome protein	WASL	A4D0Y1	0.88	0.95	0.73
Exportin-5	XPO5	Q9H8N6	0.93	0.89	0.73
Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	B7Z2V8	0.95	1.04	0.73
Multifunctional protein ADE2	PAICS	P22234	0.97	0.96	0.73
Annexin	ANXA11	B4DPJ2	0.99	0.92	0.73
Protein FAM98A	FAM98A	I6L9E8	0.74	0.78	0.73
Palladin	PALLD	Q8WX93-4	0.84	0.90	0.73
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	B1AK13	0.62	0.63	0.73
Glucose-6-phosphate 1-dehydrogenase	G6PD	Q2VF42	0.92	0.88	0.72
Chorionic somatomammotropin hormone 2	CSH1	A0A087WUG6	1.06	1.05	0.72
Catenin alpha-2	CTNNA2	P26232-3	1.25	0.40	0.72
Protein arginine N-methyltransferase 5	PRMT5	B2RDD7	0.98	0.87	0.72
Guanylate kinase	DKFZp666D023	Q658U3	0.35	0.96	0.72
Argininosuccinate synthase	ASS1	Q5T6L5	1.28	1.20	0.72
Exportin-T	XPOT	A8KA19	0.85	0.98	0.72
Cysteine and glycine-rich protein 1	CSRP1	B3KVC9	1.02	0.97	0.72
Prostaglandin reductase 1	LTB4DH	A0A024R172	1.16	1.46	0.72
Cullin-3	CUL3	B7Z600	1.18	1.05	0.72
Cullin-1	CUL1	B3KTW0	1.02	1.03	0.72
Methionine adenosyltransferase 2 subunit beta	MAT2B	A0A140VJP2	1.00	1.11	0.72
DNA helicase	MCM7	P33993	0.75	0.75	0.72
Dihydropyrimidinase-related protein 2	DPYSL2	Q53ET2	0.89	0.95	0.72

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
D-3-phosphoglycerate dehydrogenase	PHGDH	A0A286YF22	0.97	0.97	0.72
40S ribosomal protein S20	RPS20	P60866	0.76	0.76	0.72
Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	TSTD1	Q8NFI3-3	1.02	1.03	0.72
Unconventional myosin-VI	MYO6	A0A590UK22	1.05	1.30	0.72
Fragile X mental retardation syndrome-related protein 2	FXR2	P51116	0.77	0.72	0.72
Nucleosome assembly protein 1-like 1	NAP1L1	F8VY35	0.93	0.87	0.71
Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2	Q96ME4	0.70	0.62	0.71
Trifunctional purine biosynthetic protein adenosine-3	GART	Q3B7A7	0.95	0.84	0.71
Deoxycytidylate deaminase	DCTD	D6RAD7	0.76	0.75	0.71
Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	Q5TB19	0.90	0.68	0.71
Translationally-controlled tumor protein	TPT1	A0A0P1J1R0	0.96	0.95	0.71
Laminin subunit beta-1	LAMB1	Q8TAS6	0.56	0.54	0.71
Eukaryotic translation initiation factor 3 subunit K	EIF3K	Q9UBQ5	1.13	0.99	0.71
Importin-5	RANBP5	A0A024RDY0	0.95	0.88	0.71
Eukaryotic translation initiation factor 4H	EIF4H	Q15056-2	0.88	1.06	0.71
C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	V9GYY3	0.96	0.86	0.71
Cytoglobin	CYGB	K7EIM9	1.04	0.76	0.71
A-kinase anchor protein 2	AKAP2	C9JYV5	0.76	0.74	0.71
Annexin A3	ANXA3	P12429	0.93	0.89	0.71
Caprin-1	CAPRIN1	E9PLA9	1.31	1.07	0.71
Charged multivesicular body protein 1a	CHMP1A	B4DXN3	0.81	0.87	0.71
Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2	B4DQ43	1.00	0.93	0.71
Protein CDV3 homolog	CDV3	Q9UKY7-2	0.86	0.90	0.70
Glutathione reductase, mitochondrial	HEL-75	V9HW90	0.93	1.19	0.70
Oxysterol-binding protein	OSBP	H0YCV6	0.81	1.04	0.70
Asparagine--tRNA ligase, cytoplasmic	NARS	O43776	0.92	0.93	0.70
Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	X6RAC9	0.83	0.87	0.70
Rho GDP-dissociation inhibitor 2	ARHGDIB	A0A024RAS5	0.86	0.82	0.70
Obg-like ATPase 1	OLA1	J3KQ32	0.89	0.88	0.70
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	Q13151	0.87	0.77	0.70
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	B4DFY5	1.00	0.97	0.70
Ubiquitin-conjugating enzyme E2 L3	UBE2L3	A8K4W8	0.88	0.89	0.70
Stathmin	STMN1	A2A2D0	0.92	0.85	0.70
Suppressor of G2 allele of SKP1 homolog	SUGT1	A8K7W3	0.73	0.82	0.70
Protein transport protein Sec24A	SEC24A	B4E205	1.04	1.18	0.70
Eukaryotic translation initiation factor 4 gamma 2	AAG1	Q2TU89	1.04	0.90	0.69
S-methyl-5-thioadenosine phosphorylase	MTAP	A0A140CZL4	0.83	0.78	0.69
Nuclease-sensitive element-binding protein 1	YBX1	P67809	0.88	0.85	0.69
Protein transport protein Sec24B	SEC24B	B4E2E1	1.06	0.98	0.69

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Small integral membrane protein 13	SMIM13	P0DJ93	0.74	0.73	0.69
Nuclear transport factor 2	NUTF2	A0A024R6Y2	0.95	0.85	0.69
Secernin-1	SCRN1	A0A024RA21	0.96	1.02	0.69
Lipoma-preferred partner	LPP	B7Z871	1.01	0.69	0.69
ATP-citrate synthase	ACLY	A0A024R1Y2	0.85	0.79	0.69
Coactosin-like protein	COTL1	A0A384MTY2	0.88	0.85	0.69
Serine hydroxymethyltransferase	SHMT1	D3DXC9	0.77	0.76	0.69
Zyxin	ZYX	H0Y2Y8	0.99	0.99	0.69
Threonine--tRNA ligase, cytoplasmic	TARS	Q5M7Z9	0.98	0.91	0.69
Ribose-phosphate pyrophosphokinase 1	PRPS1	B1ALA9	0.95	0.93	0.69
ATP-binding cassette sub-family F member 2	ABCF2	A0A090N7X1	0.74	0.80	0.68
RNA-binding protein MEX3D	MEX3D	S4R446	0.68	1.06	0.68
Sorting nexin-12	SNX12	Q9UMY4	0.83	0.65	0.68
Glycogen synthase kinase-3 beta	GSK3B	Q6FI27	0.91	0.97	0.68
Protein FAM83B	FAM83B	Q5T0W9	1.05	0.95	0.68
Disks large homolog 1	DLG1	A0A590UJ08	0.83	0.77	0.68
28S ribosomal protein S7, mitochondrial	MRPS7	J3KSI8	0.95	0.80	0.68
Translin	TSN	Q15631	0.93	0.85	0.68
Phosphoacetylglucosamine mutase	PGM3	A0A494C0G1	0.86	0.70	0.68
Parathymosin	PTMS	F5H7R9	0.68	0.75	0.68
FAS-associated death domain protein	FADD	Q6LCG1	1.23	1.40	0.68
Actin filament-associated protein 1-like 2	AFAP1L2	B7Z2Q0	1.01	0.92	0.68
Thioredoxin reductase 1, cytoplasmic	TXNRD1	E9PIR7	0.92	0.75	0.68
Eukaryotic translation initiation factor 2A	EIF2A	H7C5R5	1.25	1.28	0.68
Adapter molecule crk	CRK	L7RT18	1.10	1.05	0.68
Tyrosine--tRNA ligase, cytoplasmic	YARS	A0A0S2Z4R1	0.94	0.85	0.67
Zinc finger protein 36, C3H1 type-like 2	ZFP36L2	P47974	0.99	1.01	0.67
Heme-binding protein 1	HEBP1	F5GWX2	1.03	1.04	0.67
Integrin-linked protein kinase	HEL-S-28	V9HWF0	0.86	0.76	0.67
Tripartite motif-containing protein 16	TRIM16	B3KMJ2	0.83	1.00	0.67
Down syndrome critical region protein 3	DSCR3	A8MY26	0.84	0.93	0.67
Alanine--tRNA ligase, cytoplasmic	AARS	P49588	0.98	0.89	0.67
CDK5 regulatory subunit-associated protein 3	CDK5RAP3	J3QL86	1.12	0.47	0.67
UDP-N-acetylhexosamine pyrophosphorylase	UAP1	A0A140VKC0	0.90	0.76	0.67
Phostensin	hCG_1821276	A0A1U9X8D3	0.83	0.83	0.66
EF-hand domain-containing protein D2	EFHD2	A0A024QZ77	0.79	0.66	0.66
Vacuolar protein sorting-associated protein 4B	VPS4B	A8K5D8	0.98	0.88	0.66
Protein ERGIC-53	LMAN1	Q53FS4	0.87	0.85	0.66
Deoxyhypusine hydroxylase	DOHH	Q9BU89	0.80	0.91	0.65

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Interferon-related developmental regulator 2	IFRD2	H7C2Z4	0.80	0.91	0.65
Coiled-coil domain-containing protein 124	LOC115098	A0A024R7M8	0.92	0.61	0.65
Protein-glutamate O-methyltransferase	ARMT1	Q9H993	0.86	0.91	0.65
Protein transport protein Sec24C	SEC24C	B4DSN3	0.88	0.81	0.65
Inositol monophosphatase 1	IMPA1	E5RG13	1.01	1.06	0.65
Protein FAM49B	FAM49B	A0A024R9G4	1.02	0.95	0.65
Thymidylate kinase	DTYMK	G5E9E9	0.81	0.78	0.64
NAD(P)H dehydrogenase [quinone] 1	NQO1	P15559-2	0.77	0.79	0.64
Tubulin beta-6 chain	TUBB6	Q2NKY5	0.71	0.54	0.64
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1	P15170-2	0.87	0.92	0.64
Sorting nexin-2	SNX2	B3KN57	0.69	0.74	0.64
AP-3 complex subunit beta	AP3B1	A8K586	1.00	1.05	0.64
Cytosolic purine 5-nucleotidase	NT5C2	A8K6K2	0.74	0.71	0.64
Aldo-keto reductase family 1 member C3	AKR1C3	S4R3Z2	0.71	0.89	0.64
Histone H1.3	HIST1H1D	P16402	0.94	0.73	0.64
Mothers against decapentaplegic homolog	SMAD4	K7EIU8	0.88	0.87	0.63
Protein MEMO1	MEMO1	A8K3Y8	0.82	0.68	0.63
Serine/threonine-protein phosphatase 2A activator	PPP2R4	A6PVN8	1.10	0.88	0.63
BH3-interacting domain death agonist	BID	B2ZP79	0.96	1.01	0.63
Annexin A8-like protein 2	ANXA8L2	Q5VT79	1.03	1.11	0.63
Immunoglobulin-binding protein 1	IGBP1	P78318	0.84	0.94	0.63
Malate dehydrogenase, cytoplasmic	MDH1	C9JRL4	1.46	1.08	0.62
Neural cell adhesion molecule 2	NCAM2	L0R512	0.78	0.72	0.62
Regulator of nonsense transcripts 1	UPF1	A0A024R7L5	0.67	0.70	0.62
Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	A0A0F7NGI8	0.80	0.79	0.62
cAMP-dependent protein kinase type I-alpha regulatory subunit	DKFZp779L0468	Q68DQ4	0.69	0.70	0.62
Absent in melanoma 1 protein	AIM1	A0A0J9YWL0	0.80	0.71	0.62
Serine/threonine-protein kinase 3	STK3	A0A384MR07	0.78	0.77	0.62
Protein phosphatase 1G	PPM1G	Q6IAU5	0.65	0.59	0.61
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	HEL-S-90n	V9HWJ5	0.89	0.75	0.61
DNA helicase	MCM2	Q9BWF4	0.67	0.54	0.61
Isopentenyl-diphosphate Delta-isomerase 1	IDI1	Q13907	0.88	0.75	0.61
Zinc finger CCCH domain-containing protein 15	ZC3H15	B7Z592	0.72	0.60	0.61
RNA 3-terminal phosphate cyclase	RTCA	A8K8K1	0.85	0.90	0.61
Glutamate--cysteine ligase catalytic subunit	GCLC	B4E2I4	1.08	1.19	0.61
Transferrin receptor protein 1	TFRC	F8WBE5	0.66	0.63	0.61
Ubiquitin-conjugating enzyme E2 variant 1	TMEM189-UBE2V1	I3L0A0	0.51	0.84	0.61
Protein S100-A13	S100A13	D3DV53	0.84	0.81	0.61
Ataxin-10	ATXN10	A0A1W2PQD2	0.72	0.78	0.60

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Rho guanine nucleotide exchange factor 2	ARHGEF2	Q5VY93	1.09	0.71	0.60
BTB/POZ domain-containing protein KCTD12	KCTD12	B3KY04	0.90	0.73	0.60
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	Q8N995	0.74	0.64	0.60
Tissue factor	F3	Q86SE7	0.75	0.58	0.60
Four and a half LIM domains protein 1	FHL1	A0A0D9SFZ9	0.80	0.68	0.60
Phosphoserine aminotransferase	PSAT1	A0A024R222	0.96	0.94	0.60
Cystathionine gamma-lyase	CTH	P32929-2	1.54	1.47	0.60
Phosphoinositide phospholipase C	DKFZp686K101	B3KXR5	1.53	1.39	0.60
Kinetochore protein Spc24	SPC24	K7ERQ7	0.63	0.67	0.60
Endophilin-B1	SH3GLB1	A0A140VJU5	1.08	0.95	0.59
Transmembrane protein 40	TMEM40	Q8WWA1-2	0.82	0.82	0.59
Helicase SKI2W	SKIV2L	A0A024RCU1	0.61	0.64	0.59
dCTP pyrophosphatase 1	DCTPP1	Q9H773	0.89	1.06	0.59
Dystonin	DST	E9PHM6	0.91	0.81	0.59
Phosphatidate cytidyltransferase, mitochondrial	TAMM41	A0A0G2JQ92	0.65	1.36	0.59
RNA-binding protein 28	RBM28	A0A0S2Z5E5	0.55	0.51	0.59
Plastin-1	PLS1	Q14651	0.86	0.82	0.58
Thimet oligopeptidase	THOP1	K7EP46	1.11	1.29	0.58
GPI transamidase component PIG-S	PIGS	A0A024QZ14	1.35	0.41	0.58
Non-histone chromosomal protein HMG-14	HMGN1	A6NL93	0.81	0.67	0.58
Mitochondrial glutamate carrier 1	SLC25A22	A0A0D9SFE1	1.30	1.29	0.58
Annexin	ANXA6	B7Z582	0.78	0.66	0.58
Serine/threonine-protein kinase OSR1	OXSR1	C9JIG9	0.98	0.99	0.58
E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	Q9C0C9	0.70	0.64	0.57
Thyroid receptor-interacting protein 6	TRIP6i1	F2ZC06	0.68	0.73	0.57
Filamin-binding LIM protein 1	FBLIM1	Q8WUP2	1.55	1.52	0.57
Hematological and neurological expressed 1-like protein	HN1L	H3BU16	0.77	0.80	0.57
Proteasome assembly chaperone 1	PSMG1	F8WBH7	0.82	0.74	0.57
N-terminal Xaa-Pro-Lys N-methyltransferase 1	C9orf32	A0A024R8E4	0.73	0.56	0.56
Phosphatidylinositol 4-kinase beta	PI4KB	A0A0A0MSL0	0.64	0.58	0.55
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	Q9Y6G9	0.97	0.92	0.55
Condensin complex subunit 1	NCAPD2	Q15021	0.89	0.82	0.55
Large proline-rich protein BAG6	BAG6	F6TC96	0.67	0.62	0.55
D-tyrosyl-tRNA(Tyr) deacylase	DTD1	Q496C9	0.72	0.78	0.54
Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	B4E0N6	0.51	0.81	0.54
Serine/threonine-protein phosphatase 6 regulatory subunit 3	SAPS3	A0A024R5F3	0.77	0.84	0.54
Twinfilin-1	TWF1	Q12792	0.79	0.72	0.54
Mannose-1-phosphate guanyltransferase alpha	GMPPA	A0A384MDS7	0.68	0.62	0.53
Golgi apparatus protein 1	GLG1	H3BM42	0.74	0.64	0.53

Table S2. Continued

Protein names	Gene names	Uniprot ID	Fold-change compared to control		
			0.1 Gy	0.5 Gy	2 Gy
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	Q6LET3	0.80	0.67	0.53
Nuclear migration protein nudC	NUDC	A0A0A0MSS4	0.71	0.54	0.52
Thymosin beta-4	TMSB4X	A2VCK8	0.59	0.68	0.51
Adenylosuccinate synthetase isozyme 2	ADSS	B4E1L0	0.93	0.83	0.51
Calcium-binding protein 39	CAB39	A0A087X0K1	0.83	0.75	0.51
Thioredoxin-like protein 1	HEL-S-114	V9HW51	0.73	0.57	0.50
Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	A0A0C4DGL3	0.46	0.29	0.50
Synaptophysin-like protein 1	SYPL1	A0A0U1RQT9	1.20	0.97	0.49
Protein disulfide-isomerase TMX3	TMX3	Q3B7X1	0.89	1.21	0.48
Proliferating cell nuclear antigen	PCNA	Q6FI35	0.04	0.07	0.47
Protein PBDC1	PBDC1	Q9P0N4	0.68	0.57	0.47
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	P08243-2	0.87	0.78	0.46
Ribosomal protein S6 kinase	RPS6KA1	B7Z2K7	0.75	0.76	0.46
STE20-like serine/threonine-protein kinase	SLK	B4DZC9	0.60	0.58	0.45
Ethylmalonyl-CoA decarboxylase	ECHDC1	Q9NTX5-6	0.52	0.68	0.45
Putative deoxyribonuclease TATDN1	TATDN1	E5RG62	0.50	0.64	0.43
Alpha-synuclein	SNCA	Q4W5L2	0.61	0.50	0.43
Exocyst complex component 4	EXOC4	B7Z689	0.97	0.67	0.43
Transforming growth factor beta-1-induced transcript 1 protein	TGFB1I1	I3L209	0.92	0.59	0.42
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	Q9Y237	0.77	0.70	0.42
Enolase-phosphatase E1	ENOPH1	A0A0C4DGY8	0.94	0.79	0.42
Non-specific protein-tyrosine kinase	PTK2	H0YB99	1.44	0.84	0.41
Developmentally-regulated GTP-binding protein 2	DRG2	J3QR71	0.65	0.76	0.41
Rho guanine nucleotide exchange factor 1	ARHGEF1	Q49AN3	0.57	0.42	0.41
Tubulin beta-3 chain	TUBB3	Q9BV28	0.66	0.43	0.37
Sodium-coupled neutral amino acid transporter 2	SLC38A2	A8K6H9	0.75	0.65	0.37
Dynein assembly factor 5, axonemal	DNAAF5	Q86Y56	1.23	0.91	0.34
Small proline-rich protein 2B	SPRR2B	P35325	1.17	1.31	0.28
Acetyl-CoA carboxylase 1	ACACA	Q13085	0.51	0.63	0.24
Pleckstrin homology-like domain family B member 1	PHLDB1	Q96D60	0.40	0.29	0.23
E3 ubiquitin-protein ligase listerin	LTN1	S4R3T2	0.68	0.56	0.22
COMM domain-containing protein 4	COMMD4	A0A0B4J287	0.75	0.46	0.19
High mobility group protein B3	DKFZp779G118	Q7Z684	1.00	0.63	0.12
Immortalization up-regulated protein	IMUP	Q9GZP8-2	1.68	1.19	0.09
Alpha-mannosidase	MAN2A1	A5PKX5	0.01	1.59	0.08
ATP synthase subunit delta, mitochondrial	ATP5D	P30049	1.17	1.17	0.05

Table S3. Metabolomic changes on day 0 after irradiation

Metabolites	Fold-change		
	0.1 Gy	0.5 Gy	2 Gy
Deoxyuridine	0.89	0.49	0.71
Glucose	0.89	0.50	0.91
Thiamine	0.65	0.45	0.47
Cytidine	1.00	0.58	0.67
Thymine	0.66	0.37	0.58
Deoxyadenosine	0.91	0.88	1.02
Riboflavin	0.50	0.43	0.33
Nicotinamide	1.12	0.78	0.38
Cytosine	0.59	0.33	0.53
Adenosine	0.99	0.72	0.59
Uridine	0.76	0.67	1.19
Deoxyguanosine	0.90	0.65	0.53
Choline	0.65	0.68	0.87
Glucosamine	0.39	0.35	0.49
Adenine	0.54	0.32	0.39
Carnitine	0.93	1.09	1.14
Hypoxanthine	0.55	0.29	0.35
Phenylalanine_13C9	0.99	0.49	0.62
Trehalose	0.66	0.44	0.58
Guanine	0.87	0.92	1.60
Leucine	0.74	0.61	0.67
Threonine	1.37	1.13	1.30
Pyridoxine	0.43	0.26	0.32
Homoserine	1.56	1.24	1.50
Inosine	1.05	1.35	1.37
Valine	0.73	0.64	0.73
Proline	0.86	0.72	0.66
Guanosine	1.01	1.18	1.88
Taurine	1.41	0.85	1.31
Arginine	0.65	0.53	0.73
Citruline	0.66	0.50	0.68
Lysine	0.97	0.74	0.85
Acetoacetate	1.23	0.61	0.83
Glutamine	0.93	0.69	0.78
Lactic acid	0.92	1.59	1.46
Xanthine	1.18	1.58	1.38
s-Adenosyl-methionine	1.35	1.27	1.24
Diglydoorotate	0.44	1.08	1.55
Orotate	0.67	1.23	0.92
Dihydroxy benzoate	0.52	0.31	0.36
N-acetyl glutamine	0.61	0.47	0.79
Asparagine	1.11	1.07	1.31
Histidine	0.91	0.74	0.85
Pantothenate	0.64	0.50	1.21

Table S3. Continued

Metabolites	Fold-change		
	0.1 Gy	0.5 Gy	2 Gy
S-Adenosyl-L-homocysteine	1.16	1.18	1.64
Shikimate	1.09	0.43	0.53
Cystathionine	1.10	1.07	1.14
alpha-ketoglutarate	0.97	0.55	0.73
Homocysteic acid	1.25	0.88	1.12
D-Fructose-6-phosphate	1.02	1.05	1.44
D-glucose-6-phosphate	0.88	1.02	1.15
NAD+	1.00	1.04	1.02
dAMP	0.53	0.67	1.27
Glutamate	0.89	0.75	0.88
Aspartate	0.85	0.37	0.77
Glucosamine-6-P	0.71	0.44	0.75
Reduced glutathione	0.85	1.04	1.12
Malate	1.00	1.13	1.05
Fumaric acid	1.23	1.16	1.19
UMP	1.17	0.90	1.16
D-Rib(ul)ose-5-phosphate	0.38	0.66	1.25
UDP-D-glucose	0.93	0.82	0.83
CMP	0.95	0.63	0.66
UDP-N-acetyl-D-glucosamine	0.87	0.85	0.84
Carbomoyl-phosphate	0.98	0.83	1.02
Succinic acid	0.75	1.10	0.87
5-Methyl-THF	0.97	0.55	0.73
FAD	0.84	0.72	0.77
6-phospho-D-gluconate	0.64	0.37	0.57
AMP	0.69	0.73	1.39
Citrate	0.95	0.51	0.27
Aconitate	1.07	0.49	0.31
GMP	0.73	0.64	1.20
UDP-D-glucuronate	0.86	0.69	0.68
IMP	0.70	0.76	1.30
D(+)-2-phosphoglyceric acid	0.57	0.70	0.91
Fuctose-1,6-bisphosphate	0.29	0.54	0.83
GDP	1.00	0.83	0.98
IDP	1.00	1.11	1.06
ADP	0.96	1.12	1.06
UDP	1.09	0.97	0.95
Acetyl-CoA	0.69	0.76	0.77
Succinyl-CoA	1.40	1.03	1.21
CoA	1.13	1.38	1.35
ITP	0.97	0.91	0.56
ATP	0.97	0.98	0.58
CTP	1.12	0.80	0.50
UTP	1.02	0.74	0.44

Table S4. Metabolomic changes on day 2 after irradiation

Metabolites	Fold-change		
	0.1 Gy	0.5 Gy	2 Gy
Deoxyuridine	1.40	0.50	0.81
Glucose	0.98	1.07	1.13
Thiamine	0.95	1.11	1.20
Cytidine	0.96	0.99	1.02
Thymine	1.08	1.11	1.06
Deoxyadenosine	41.46	0.71	0.97
Riboflavin	1.05	1.06	1.15
Nicotinamide	0.75	0.44	0.50
Uracil	1.59	1.76	1.63
Cytosine	3.40	1.25	1.21
Adenosine	1.03	0.96	1.17
Uridine	1.19	1.19	1.48
Deoxyguanosine	0.95	0.91	1.12
Choline	1.74	2.42	3.64
Glucosamine	0.99	0.96	1.20
Adenine	1.11	1.02	1.21
Carnitine	0.83	0.71	0.95
Hypoxanthine	0.72	0.68	1.07
Trehalose	1.74	0.84	1.02
Guanine	1.06	0.92	1.65
Leucine	0.74	0.71	1.28
Threonine	0.81	0.81	1.50
Pyridoxine	1.41	1.27	2.38
Homoserine	0.81	0.86	1.60
Inosine	0.97	0.87	1.13
Valine	0.80	0.81	1.42
Proline	0.65	0.55	0.98
Guanosine	1.23	1.27	1.57
Taurine	0.69	0.47	1.33
Arginine	1.02	1.11	1.90
Citruline	1.10	1.12	1.87
Lysine	0.60	0.58	1.50
Acetoacetate	0.92	0.91	1.12
Glutamine	0.67	0.67	1.58
Lactic acid	0.94	1.09	1.16
Xanthine	1.02	0.53	1.56
s-Adenosyl-methionine	0.74	1.01	0.97
Digydroorotate	9.28	0.38	0.26
Orotate	0.94	0.26	0.15
Dihydroxy benzoate	1.04	1.19	1.48
N-acetyl glutamine	1.20	0.92	1.37
Asparagine	0.63	0.66	1.13
Histidine	0.75	0.76	1.27
Biotin	0.87	1.00	1.15

Table S4. Continued

Metabolites	Fold-change		
	0.1 Gy	0.5 Gy	2 Gy
Pantothenate	1.67	0.48	1.35
Homocysteine	0.95	0.54	0.90
S-Adenosyl-L-homocystein	0.82	1.05	1.19
Shikimate	0.75	0.65	0.96
Cystathionine	0.59	0.43	0.51
alpha-ketoglutarate	0.79	0.80	0.99
D-Fructose-6-phosphate	1.02	1.05	0.70
D-glucose-6-phosphate	1.04	1.13	0.94
NAD+	0.87	0.81	0.81
dAMP	0.82	0.78	0.77
Glutamate	0.64	0.61	0.93
Aspartate	1.07	1.07	2.07
Glucosamine-6-P	1.08	1.00	0.69
Reduced glutathione	0.69	0.62	0.72
D-glucarate	0.95	0.97	1.61
Malate	0.99	1.10	1.58
Fumaric acid	1.02	1.10	1.49
UMP	1.21	1.50	2.92
dCMP	0.96	1.13	1.46
CMP	0.88	0.87	1.13
UDP-N-acetyl-D-glucosamine	0.97	0.69	0.42
Carbomoyl-phosphate	0.89	0.83	1.57
Succinic acid	1.05	1.07	1.21
5-Methyl-THF	0.89	1.05	1.08
FAD	1.03	1.05	0.97
6-phospho-D-gluconate	0.83	0.85	1.17
AMP	1.05	0.75	1.53
Citrate	0.87	0.77	0.70
Aconitate	0.75	0.74	0.83
GMP	1.26	1.31	2.33
UDP-D-glucuronate	0.88	0.76	0.75
IMP	1.15	1.00	0.99
D(+)-2-phosphoglyceric acid	1.18	1.26	1.00
Fuctose-1,6-bisphosphate	1.42	1.40	0.73
GDP	0.87	0.93	1.19
IDP	0.90	0.85	1.04
ADP	0.89	0.84	1.03
UDP	0.91	1.00	1.36
Acetyl-CoA	0.95	0.95	0.77
CoA	0.91	0.95	1.09
ITP	0.71	0.65	0.50
ATP	0.73	0.66	0.49
CTP	0.76	0.69	0.51
UTP	0.85	0.89	0.81