Supplementary Information

Table S1. Gene Ontology analysis of affected biological processes/pathways/themes in H1 hESCs based on sets of statistically significant differentially expressed genes.

Exposures	Overrepresented Categories (Upregulation)	EASE Score
5 cGy, 2 h	Negative regulation of cell differentiation	0.0049
	Lipid biosynthetic process	0.015
	Negative regulation of cell proliferation	0.02
	Transcription factor binding	0.037
	Regulation of apoptosis	0.038
	Positive regulation of anti-apoptosis	0.048
1 Gy, 2 h	P53 signaling pathway	4.2×10^{-10}
	Positive regulation of apoptosis	7.5×10^{-8}
	Response to DNA damage stimulus	1.5×10^{-6}
	Cellular response to stress	9.6×10^{-6}
	Negative regulation of cell proliferation	9.8×10^{-6}
	Cell cycle arrest	7.0×10^{-4}
	Negative regulation of cell differentiation	1.5×10^{-3}
	Regulation of protein kinase activity	0.011
	I-kappaB kinase/NF-kappaB cascade	0.025
1 Gy, 16 h	Metallothionein superfamily	9.9×10^{-18}
	Induction of apoptosis	8.8×10^{-5}
	DNA damage response	2.6×10^{-4}
	Positive regulation of anti-apoptosis	0.001
	Positive regulation of cell death	0.005
	Cellular response to stress	0.012
Exposures	**Overrepresented Categories (Downregulation)**	**EASE Score**
1 Gy, 2 h	Alternative splicing	0.016
	Chromatin organization	0.020
1 Gy, 16 h	Chromatin assembly	2.0×10^{-6}
	Cholesterol biosynthesis	5.1×10^{-5}
	Macromolecular complex assembly	9.3×10^{-4}
	PPAR signaling pathway	0.007
	Hemopoietic organ development	0.033
	Immune system development	0.040

Table S2. Gene Ontology analysis of affected biological processes/pathways/themes in H7 based on sets of statistically significant differentially expressed genes.

Exposures	Overrepresented Categories (Upregulation)	EASE Score
1 Gy, 2 h	Regulation of programmed cell death	2.8×10^{-10}
	Apoptosis	3.8×10^{-10}
	P53 signaling pathway	5.0×10^{-10}
	Response to DNA damage stimulus	1.6×10^{-7}
	Cellular response to stress	8.9×10^{-6}
	Negative regulation of cell proliferation	1.7×10^{-5}
	Negative regulation of apoptosis	2.9×10^{-4}
	Negative regulation of mitotic cell cycle	9.1×10^{-4}
	Activation of caspase activity	0.001
	Cell cycle arrest	0.002
	Protein import into nucleus	0.003
	Positive regulation of hydrolase activity	0.005
	Response to radiation	0.008
	Transcription repressor activity	0.009
	Negative regulation of cell size	0.011
	Negative regulation of cell differentiation	0.012
	Intracellular signaling cascade	0.013
	Positive regulation of gene expression	0.032
	DNA binding	0.034
	DNA repair	0.039
1 Gy, 16 h	P53 signaling pathway	3.4×10^{-8}
	Metallothionein superfamily	1.5×10^{-7}
	Positive regulation of apoptosis	6.1×10^{-7}
	Negative regulation of cell proliferation	3.8×10^{-6}
	Response to steroid hormone stimulus	6.6×10^{-6}
	Negative regulation of cell differentiation	2.2×10^{-5}
	Cell motion	3.8×10^{-5}
	Response to glucocorticoid stimulus	6.1×10^{-5}
	Enzyme linked receptor protein signaling pathway	1.3×10^{-4}
	Actin cytoskeleton	2.2×10^{-4}
	Positive regulation of cell proliferation	2.8×10^{-4}
	Positive regulation of cell differentiation	7.3×10^{-4}
	TGF-beta signaling pathway	0.001
	Blood vessel development	0.001
	Muscle organ development	0.002
	Response to hypoxia	0.002
	Cell migration	0.003
	Cellular response to stress	0.006
	Neurotrophin signaling pathway	0.009
	Negative regulation of apoptosis	0.02
	Response to oxidative stress	0.02
	Response to DNA damage	0.02
	Cytoskeleton organization	0.02
	Cell adhesion	0.03

Table S2. *Cont.*

Exposures	Overrepresented Categories (Downregulation)	EASE Score
5 cGy, 2 h	M phase (of cell cycle)	3.9×10^{-5}
	DNA repair	4.6×10^{-4}
	Mitosis	7.9×10^{-4}
	Organelle fission	0.001
	Response to radiation	0.002
	Response to DNA damage stimulus	0.002
	DNA recombination	0.014
	Regulation of translation	0.038
	Mismatch repair	0.044
1 Gy, 2 h	Chromosome organization	2.2×10^{-4}
	Vasculogenesis	6.1×10^{-4}
	Skeletal system development	9.5×10^{-4}
	Regulation of cell cycle	0.001
	Negative regulation of macromolecule metabolic process	0.002
	Hemopoietic organ development	0.003
	Regulation of Notch signaling pathway	0.005
	Positive regulation of cell proliferation	0.006
	Positive regulation of apoptosis	0.008
	Positive regulation of transcription	0.009
	Negative regulation of cell communication	0.01
	Protein catabolic process	0.02
	Negative regulation of gene expression	0.02
	Alternative splicing	0.04
1 Gy, 16 h	DNA packaging	1.7×10^{-12}
	Chromosome organization	1.8×10^{-9}
	Histone H2B	1.1×10^{-8}
	Histone H2A	0.001
	Histone H1/H5	0.01
	Regulation of neurological system process	0.02
	Negative regulation of apoptosis	0.04
	Positive regulation of hydrolase activity	0.04

Table S3. Gene Ontology analysis of affected biological processes/pathways/themes in H9 based on sets of statistically significant differentially expressed genes.

Exposures	Overrepresented Categories (Upregulation)	EASE Score
5 cGy, 2 h	Regulation of apoptosis	0.0012
	Response to DNA damage stimulus	0.0015
	Cellular response to stress	0.0051
	Negative regulation of cell proliferation	0.023
	P53 signaling pathway	0.05
1 Gy, 2 h	Positive regulation of apoptosis	2.4×10^{-10}
	P53 signaling pathway	1.2×10^{-9}
	DNA damage response	1.3×10^{-8}
	Cellular response to stress	6.3×10^{-7}
	Activation of caspase activity	4.1×10^{-4}
	Cell cycle arrest	5.5×10^{-4}
	DNA repair	2.5×10^{-3}
	DNA damage checkpoint	3.7×10^{-3}
	Positive regulation of macromolecule biosynthesis	3.3×10^{-3}
1 Gy, 16 h	Metallothionein superfamily	8.3×10^{-14}
	Positive regulation of apoptosis	1.0×10^{-5}
	P53 signaling pathway	6.4×10^{-5}
	TGF-beta signaling pathway	6.6×10^{-5}
	Extracellular matrix	1.2×10^{-4}
	Negative regulation of cell proliferation	3.0×10^{-4}
	Response to oxidative stress	6.5×10^{-4}
	Cytoskeleton organization	0.0049
Exposures	**Overrepresented Categories (Downregulation)**	**EASE Score**
5 cGy, 2 h	Nucleosome	1.7×10^{-5}
	Histone H2A	2.2×10^{-5}
	Nucleosome assembly	1.1×10^{-4}
	DNA packaging	3.8×10^{-4}
	Cytoplasmic vesicle	0.021
1 Gy, 2 h	Negative regulation of cell communication	5.4×10^{-7}
	Skeletal system development	4.4×10^{-4}
	Regulation of cell proliferation	4.8×10^{-3}
	Negative regulation of macromolecule biosynthesis	4.8×10^{-3}
	Regulation of transcription	7.5×10^{-3}
	Positive regulation of cell differentiation	0.011
	Protein kinase cascade	0.04
1 Gy, 16 h	mRNA processing	5.7×10^{-4}
	Sterol biosynthetic process	8.4×10^{-4}
	RNA splicing	0.0012
	Cholesterol biosynthesis	0.0068
	RNA export from nucleus	0.011
	M phase of mitotic cell cycle	0.023
	DNA packaging	0.04

Table S4. Gene Ontology analysis of affected biological processes/pathways/themes in H14 based on sets of statistically significant differentially expressed genes.

Exposures	**Overrepresented Categories (Upregulation)**	**EASE Score**
5 cGy, 2 h	Response to DNA damage stimulus	0.00033
	P53 signaling pathway	0.0026
	Cell cycle arrest	0.0042
	Wnt signaling pathway	0.012
	Response to radiation	0.015
	DNA repair	0.029
	Negative regulation of apoptosis	0.044
1 Gy, 2 h	P53 signaling pathway	1.0×10^{-12}
	Positive regulation of apoptosis	2.0×10^{-9}
	DNA damage response	5.3×10^{-7}
	Release of cytochrome c from mitochondria	4.6×10^{-5}
	Activation of caspase activity	8.9×10^{-5}
	Cell cycle arrest	2.0×10^{-4}
	Cell migration	1.2×10^{-3}
	MAPK signaling pathway	0.0073
1 Gy, 16 h	Positive regulation of apoptosis	5.2×10^{-10}
	P53 signaling pathway	2.3×10^{-6}
	DNA damage response	2.7×10^{-5}
	Negative regulation of cell differentiation	6.7×10^{-4}
	Negative regulation of cell proliferation	7.7×10^{-4}
	Response to wounding	9.1×10^{-4}
	Inflammatory response	0.0066
Exposures	**Overrepresented Categories (Downregulation)**	**EASE Score**
1 Gy, 2 h	Blood vessel development	0.0018
	Neural crest development	0.034
1 Gy, 16 h	DNA packaging	1.2×10^{-17}
	Citrullination	3.7×10^{-15}
	Histone H2A	8.1×10^{-13}
	Hemopoiesis	0.016

Table S5. Genes upregulated in all hESC lines (H1, H7, H9 and H14) after 1 Gy IR exposures (2 h post IR). $p < 0.001$.

GDF15
BTG2
PLK2
CDKN1A
PHLDA3
SESN1
BBC3
GADD45A
TP53INP1
DRAM1
PLK3

GRHL3
ZNF79
PPM1D
TNFRSF10B
KITLG
FAM212B
ASCC3
SERTAD1
FDXR
TNFRSF10A
POLH
TOB1
PDE4A
C12orf5
RGS16
TRIM22
AEN
ARC
BCL3
DDB2
IER5
FOSL1
PTP4A1
UFM1
HES1
IKBIP
PMAIP1
STK17A
VWCE
SESN2
BDNF
E2F7
TRIAP1
BRMS1L
DDIT4
ARL4A
ANKRA2
CHADL
EPHA2

Genes upregulated in all hESC lines (H1, H7, H9 and H14) after 1 Gy IR exposures (16 h post IR). $p < 0.001$.

GDF15
BBS9
BTG2
ACTA2
PHLDA3
PLK2
CDKN1A
EPS8L2
TNFRSF10C
FDXR
RPS27L
INPP5D
GNA14
SULF2
DRAM1
ITIH5

Genes downregulated in all hESC lines (H1, H7, H9 and H14) after 1 Gy IR exposures (16 h post IR). $p < 0.001$.

SEMG1
HIST1H1D
LEAP2
ATP8B3
PNMA2
USP3
SLC1A3
NPTX1