Supplementary Table 2. Conserved alterations in the basal gene expression levels of radiation sensitive primary human fibroblasts

Gene ontology group Sequence Name	Accession #	Fold Change	Sequence Description
Response to DNA damage			
DDIT4	NM_019058	-2.01	DNA-damage-inducible transcript 4 (DDIT4),
Programmed cell death			
PDCD5	NM_004708	+1.585	programmed cell death 5 (PDCD5),
ANGPTL4	NM_139314	+1.93	angiopoietin-like 4, transcript variant 1,
TP53I3	NM_004881	-1.62	tumor protein p53 inducible protein 3
SULF1	NM_015170	-3.71	sulfatase 1 (SULF1),
UNC5B	NM_170744	-2.995	unc-5 homolog B (C. elegans) (UNC5B),
NUDT2	NM_001161	-1.62	nucleoside diphosphate linked moiety-type motif 2
SGK	NM_005627	-1.76	serum/glucocorticoid regulated kinase (SGK),
Regulation of cell cycle			
NM_015714	NM_015714	-3.105	putative lymphocyte G0/G1 switch gene (G0S2),
NM_006455	NM_006455	-2.48	synaptonemal complex protein SC65 (SC65),
AK130930	AK130930	-1.74	cDNA FLJ27420 fis, clone WMC07143
Regulation of cell proliferation and growth			
TOB1	NM_005749	+1.58	transducer of ERBB2, 1 (TOB1),
NOV	NM_002514	+2.555	nephroblastoma overexpressed gene (NOV),
CYR61	NM_001554	-3.22	cysteine-rich, angiogenic inducer, 61 (CYR61),
WARS	NM_004184	-1.435	Unknown
ADAMTS1	NM_006988	-1.615	metalloprotease with thrombospondin type 1 motif
CSRP2	NM_001321	-2.335	cysteine and glycine-rich protein 2 (CSRP2),
Defense response			
DF	NM_001928	-2.455	D component of complement (adipsin) (DF),
Z33459	Z33459	-2.955	H.sapiens for MHC class I HLA-C allele
BC020891	BC020891	-1.595	Homo sapiens, clone IMAGE:4694038,
MICA	NM_000247	-1.71	MHC class I polypeptide-related sequence A
IFITM3	NM_021034	-1.68	interferon induced transmembrane protein 3
HLA-F	NM_018950	-2.28	major histocompatibility complex, class I, F
C2	NM_000063	-1.55	complement component 2 (C2),
NM_015892	NM_015892	-3.3	B cell RAG associated protein
X56841	X56841	-1.53	H.sapiens HLA-E gene
SERPING1	NM_000062	-2.785	serine (or cysteine) proteinase inhibitor, clade G,
CRLF1	NM_004750	-3.305	cytokine receptor-like factor 1 (CRLF1),
HLA-B	NM_005514	-2.355	major histocompatibility complex, class I, B
ADA	NM_000022	-1.635	Unknown
Intracellular signaling cascade			
ADAM9	NM_003816	+1.295	a disintegrin and metalloproteinase domain 9
RASSF2	NM_014737	+2.21	Ras association domain family 2 variant
TENS1	NM_022748	-2.015	tensin-like SH2 domain containing 1 (TENS1),
PRKAR1A	NM_002734	-1.49	Unknown
AK027294	AK027294	-1.915	cDNA FLJ14388 fis, clone HEMBA1002716
Cell surface receptor linked signal transduction			
GNG11	NM_004126	+1.66	G protein, gamma 11
AL162032	AL162032	-2.62	cDNA DKFZp434B1272
FZD2	NM_001466	-1.6	frizzled homolog 2 (Drosophila) (FZD2),
AGT	NM_000029	-7.53	angiotensinogen proteinase inhibitor,
GPR124	NM_032777	-2.085	G protein-coupled receptor 124 (GPR124),
NM_017526	NM_017526	-1.745	leptin receptor gene-related protein (OBRGRP),

Gene ontology group **Sequence Name**	**Accession #**	**Fold Change**	**Sequence Description**
Protein metabolism			
PAM	NM_000919	+2.53	peptidylglycine alpha-amidating monooxygenase
RPS4Y	NM_001008	+2.47	ribosomal protein S4, Y-linked (RPS4Y),
DNAJD1	NM_013238	+1.56	DnaJ (Hsp40) homolog, subfamily D, member 1
RPS4Y2	NM_138963	+2.42	ribosomal protein S4, Y-linked 2 (RPS4Y2),
OXA1L	NM_005015	-1.82	oxidase (cytochrome c) assembly 1-like
AK074645	AK074645	-3.625	cDNA FLJ90164 fis,
NM_007173	NM_007173	-1.55	protease, serine, 23 (SPUVE),
CPZ	NM_003652	-4.08	carboxypeptidase Z (CPZ),
SULF2	NM_018837	-2.62	sulfatase 2 (SULF2), transcript variant 1,
FBXO32	NM_058229	-1.92	F-box only protein 32, transcript variant 1,
BLMH	NM_000386	-1.815	bleomycin hydrolase (BLMH),
CTSF	NM_003793	-1.865	cathepsin F (CTSF),
ADAMTS2	NM_014244	-1.885	metalloprotease with thrombospondin motif
ADAM12	NM_003474	-2.22	metalloproteinase domain 12, transcript variant 1,
PGRMC2	NM_006320	-1.56	progesterone receptor membrane component 2
X75311	X75311	-1.86	Hepatitis B virus fusion for mevalonate kinase
MMP11	NM_005940	-1.8	matrix metalloproteinase 11
BC026270	BC026270	-1.875	phosphodiesterase 4D interacting protein
AF419616	AF419616	-1.775	clone DKFZp564A057 AG02 , partial cds
EEF2	NM_001961	-4.455	eukaryotic translation elongation factor 2 (EEF2),
SIAT4A	NM_003033	-1.695	sialyltransferase 4^{a}, transcript variant 1,
MMP14	NM_004995	-2.47	matrix metalloproteinase 14 (membrane-inserted)
Nucleotide, nucleic acid metabolism			
NR0B1	NM_000475	+2.15	nuclear receptor subfamily 0, group B, member 1
BHLHB3	NM_030762	+2.095	basic helix-loop-helix domain containing, class B
ACYP2	NM_138448	+1.56	acylphosphatase 2, muscle type (ACYP2),
TALDO1	NM_006755	-1.38	transaldolase 1 (TALDO1),
AB058765	AB058765	-2.285	for KIAA1862 protein, partial cds
PYCR1	NM_153824	-1.47	pyrroline-5-carboxylate reductase 1
U2AF1L2	NM_005089	-1.54	small nuclear RNA auxiliary factor 1-like 2
Generation of precursor metabolites and energy			
MT1X	NM_005952	+1.92	metallothionein 1X (MT1X),
PC	NM_000920	-1.56	pyruvate carboxylase, transcript variant A,
GAA	NM_000152	-1.585	glucosidase, alpha; acid
NXN	NM_022463	-2.805	nucleoredoxin (NXN),
Cell communication			
NPTX1	NM_002522	+4.255	neuronal pentraxin I (NPTX1),
AL133035	AL133035	-1.755	cDNA DKFZp434G171
AL359062	AL359062	-2.205	cDNA clone EUROIMAGE 1913076
LAMB3	NM_000228	-2.35	laminin, beta 3 (LAMB3),
COL8A1	NM_001850	-2.765	collagen, type VIII, alpha 1, transcript variant 1,
DPT	NM_001937	-1.805	dermatopontin (DPT),
GLUL	NM_002065	-1.655	glutamate-ammonia ligase (glutamine synthase)
Cell-cell adhesion			
CDH13	NM_001257	+1.98	cadherin 13, H-cadherin (heart) (CDH13),
BX648591	BX648591	+2.365	cDNA DKFZp686G14198
CD36	NM_000072	+2.285	CD36 antigen
Y11711	Y11711	+1.575	extracellular matrix protein collagen type XIV
Oxygene and reactive oxygene species metabolism			
OSR1	NM_005109	+1.40	oxidative-stress responsive 1 (OSR1),

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Transport			
SLC20A2	NM_006749	+1.73	solute carrier family 20 (phosphate transporter),
KCNJ2	NM_000891	+1.775	potassium inwardly-rectifying channel, subfamily
SLC16A3	NM_004207	-2.45	solute carrier family 16, member 3
NPC1	NM_000271	-1.51	Niemann-Pick disease, type C1 (NPC1),
SLC12A7	NM_006598	-1.43	solute carrier family 12, member 7
C1QTNF5	NM_015645	-2.46	C1q and tumor necrosis factor related protein 5
COL4A1	NM_001845	-1.905	collagen, type IV, alpha 1 (COL4A1),
PTGDS	NM_000954	-2.895	prostaglandin D2 synthase 21kDa (brain)
Organic acid metabolism			
CPT1C	NM_152359	-1.605	carnitine palmitoyltransferase 1C (CPT1C),
SEPHS2	NM_012248	-1.635	selenophosphate synthetase 2 (SEPHS2),
Lipid metabolism			
RARRES2	NM_002889	-10.785	retinoic acid receptor responder
DHCR7	NM_001360	-1.66	7-dehydrocholesterol reductase (DHCR7),
Not-annotated			
TMEM16C	NM_031418	+4.55	transmembrane protein 16C (TMEM16C),
MT2A	NM_005953	+1.915	metallothionein 2A (MT2A),
DDX3Y	NM_004660	+2.34	DEAD box polypeptide 3, Y-linked
DDX3X	NM_024005	+1.72	DEAD box polypeptide 3, X-linked
BX460058	BX460058	+1.865	Unknown
AF085871	AF085871	+1.855	full length insert cDNA clone YO11A01
PDGFRL	NM_006207	+2.39	platelet-derived growth factor receptor-like
SERPINE2	NM_006216	+1.87	serine (or cysteine) proteinase inhibitor member 2
BC007034	BC007034	+2.34	metallothionein 2A,
D50683	D50683	+1.935	TGF-betaIIR alpha, complete cds
AL133052	AL133052	+1.655	cDNA DKFZp434G2415
A_24_P238386	A_24_P238386	+2.45	Unknown
FJX1	NM_014344	+1.89	four jointed box 1 (Drosophila) (FJX1),
AL133118	AL133118	+3.91	cDNA DKFZp586N0121
A_32_P56415	A_32_P56415	+2.095	Unknown
ETHE1	NM_014297	+1.415	ethylmalonic encephalopathy 1 (ETHE1),
BX640636	BX640636	+1.525	cDNA DKFZp779H2259
CWF19L1	NM_018294	+1.45	CWF19-like 1, cell cycle control (S. pombe)
MOXD1	NM_015529	+1.805	monooxygenase, DBH-like 1 (MOXD1),
AB002384	AB002384	+2.76	for KIAA0386 gene, partial cds
C6orf139	NM_018132	+2.005	chromosome 6 open reading frame 139
PLA2G4A	NM_024420	+1.655	phospholipase A2, group IVA
TFPI	NM_006287	+1.705	tissue factor pathway inhibitor
THC1945691	THC1945691	+2.09	Unknown
SVIL	NM_021738	+1.885	supervillin (SVIL), transcript variant 2,
NM_016448	NM_016448	+2.25	RA-regulated nuclear matrix-associated protein
LMO2	NM_005574	+1.47	LIM domain only 2 (rhombotin-like 1)
BG436185	BG436185	+2.1	Unknown
RTN3	NM_006054	+1.41	reticulon 3 (RTN3), transcript variant 1,
SEC3L1	NM_018261	+1.325	SEC3-like 1 (S. cerevisiae), transcript variant 1,
BC043603	BC043603	+1.85	Similar to hypothetical protein FLJ33215
FAM29A	NM_017645	+1.43	family with sequence similarity 29, member A
ENST00000308092	ENST00000308092	+1.98	Unknown
THC1869247	THC1869247	+1.705	Unknown
BM550834	BM550834	+1.76	Unknown
A_32_P225328	A_32_P225328	+3.05	Unknown

Gene ontology group			
Sequence Name	**Accession #**	**Fold Change**	**Sequence Description**
IL13RA2	NM_000640	+2.05	interleukin 13 receptor, alpha 2 (IL13RA2),
NR_000039	NR_000039	-1.745	RAB9, member RAS oncogene family,
PSG6	NM_002782	-3.815	pregnancy specific beta-1-glycoprotein 6
AK092921	AK092921	-1.65	cDNA FLJ35602 fis,
CENTB2	NM_012287	-1.34	centaurin, beta 2 (CENTB2),
AK027191	AK027191	-3.005	cDNA: FLJ23538 fis
A_24_P254933	A_24_P254933	-1.77	Unknown
A_24_P101426	A_24_P101426	-1.41	Unknown
NM_032762	NM_032762	-2.35	hypothetical protein MGC16121
NM_025268	NM_025268	-1.72	hole gene (MGC4659),
IL11RA	NM_147162	-1.73	interleukin 11 receptor, alpha, transcript variant 2
XM_290732	XM_290732	-2.43	KIAA1917 protein (KIAA1917),
PLXND1	NM_015103	-1.465	plexin D1 (PLXND1),
A_24_P357933	A_24_P357933	-1.36	Unknown
ENST00000333397	ENST00000333397	-1.57	Unknown
A_24_P323805	A_24_P323805	-1.4	Unknown
AK097672	AK097672	-7.275	cDNA FLJ40353 fis,
AK128746	AK128746	-1.53	cDNA FLJ44672 fis, clone BRACE3006553
THC1858543	THC1858543	-4.285	Unknown
ST5	NM_005418	-1.5	Unknown
NM_178507	NM_178507	-1.9	NS5ATP13TP2 protein
CNN1	NM_001299	-2.59	calponin 1, basic, smooth muscle (CNN1),
A_24_P50666	A_24_P50666	-2.175	Unknown
AK074565	AK074565	-2.39	cDNA FLJ90084 fis,
EFEMP1	NM_004105	-4.14	fibulin-like extracellular matrix protein 1
ADFP	NM_001122	-1.655	adipose differentiation-related protein (ADFP),
THC1941864	THC1941864	-2.7	Unknown
D90278	D90278	-2.385	CGM1b for CD66d, complete cds
THC1914497	THC1914497	-1.93	Unknown
ACTG2	NM_001615	-4.575	actin, gamma 2, smooth muscle, enteric
AK022020	AK022020	-1.615	cDNA FLJ11958 fis, clone HEMBB1000996
PSG1	NM_006905	-3.63	pregnancy specific beta-1-glycoprotein 1
ENST00000330895	ENST00000330895	-2.99	Unknown
AK000900	AK000900	-1.48	cDNA FLJ10038 fis, clone HEMBA1000971
NM_173638	NM_173638	-1.695	hypothetical protein MGC8902
PCOLCE	NM_002593	-3.195	procollagen C-endopeptidase enhancer
BC032042	BC032042	-1.575	polyadenylation specific factor 6,
BAMBI	NM_012342	-2.31	BMP membrane-bound inhibitor homolog
SMPDL3A	NM_006714	-3.255	sphingomyelin phosphodiesterase, acid-like 3A
THC1857957	THC1857957	-2.505	Unknown
PSG2	NM_031246	-2.53	pregnancy specific beta-1-glycoprotein 2
ENST00000243927	ENST00000243927	-1.595	similar to X-linked ribosomal protein 4
ENST00000322312	ENST00000322312	-2.675	Unknown
A_24_P144163	A_24_P144163	-1.5	Unknown
A_24_P341006	A_24_P341006	-1.37	Unknown
A_23_P370707	A_23_P370707	-2.235	Unknown
ENST00000330704	ENST00000330704	-1.705	Unknown
ENST00000325265	ENST00000325265	-1.355	Unknown
NM_024600	NM_024600	-1.73	hypothetical protein FLJ20898 (FLJ20898),
ACTA2	NM_001613	-2.185	actin, alpha 2, smooth muscle, aorta (ACTA2)
THC1805416	THC1805416	-3.435	Unknown
THC1891770	THC1891770	-1.93	Unknown

Gene ontology group			
Sequence Name	**Accession #**	**Fold Change**	**Sequence Description**
AY040873	AY040873	-1.88	C21orf57 isoform A protein
BC062438	BC062438	-2.63	cDNA clone IMAGE:6494968
AL137500	AL137500	-1.985	cDNA DKFZp761F171
CEACAM7	NM_006890	-2.895	carcinoembryonic antigen-related molecule 7
FBLN1	NM_001996	-3.245	fibulin 1 (FBLN1), transcript variant C,
MAGED4	NM_030801	-2.84	melanoma antigen, family D,
COL4A2	NM_001846	-3.06	collagen, type IV, alpha 2 (COL4A2),
NM_020190	NM_020190	-2.03	olfactomedin-like 3 (OLFML3),
A_23_P125109	A_23_P125109	-1.985	Unknown
A_23_P211468	A_23_P211468	-1.67	Unknown
LTB4DH	NM_012212	-1.87	leukotriene B4 12-hydroxydehydrogenase
A_24_P195510	A_24_P195510	-1.635	Unknown
ENST00000293569	ENST00000293569	-2.47	DJ377H14
A_24_P366768	A_24_P366768	-1.38	Unknown
ACTN1	NM_001102	-1.72	actinin, alpha 1 (ACTN1),
THC1957039	THC1957039	-1.635	Unknown
BC035647	BC035647	-2.485	Homo sapiens, clone IMAGE:5575764,
AL137734	AL137734	-2.5	cDNA DKFZp586C0721
NM_022480	NM_022480	-1.535	hypothetical protein FLJ12587
THC1822857	THC1822857	-2.79	Unknown
PSG4	NM_002780	-2.42	Unknown
ENST00000308589	ENST00000308589	-1.63	Unknown
AK090500	AK090500	-1.645	similar to HLA classI histocompatibilty antigene
MARCKS	NM_002356	-1.725	myristoylated alanine-rich protein kinase C substr

The expression of these genes was altered on all arrays. The fold expression changes represent the mean value of the arrays, the deviation is < +/-0.4. The + and – marks show up- and down-regulated genes, respectively.