Supplementary Figure Legends

Supplementary Figure 1. Gene expression profile changes. Expression profiles of DNA repair genes before (RTS cells, R0, or normal cells, N0) or 6, 12, or 24h after menadione treatment. The red represents up-regulated and green represents down-regulated gene expression.

Supplementary Figure 2. Sensitivity of RTS and control fibroblasts to menadione. Normal (GM0323) and primary RTS (AG5013) fibroblast cell lines were exposed to 50, 100 or 200 µM menadione (Sigma, MO, USA) for 1 hour. Cells were washed in PBS and then plated in 6-well plates at a density of 333 cells/well. Cells were allowed to grow in Amniomax-II Complete media ((Invitrogen, CA, USA) for seven days at 37 ºC at 5% CO_2. On the day of the analysis, the plates with adherent cells were incubated with CyQuant dye (Molecular Probes, OR, USA).for 30 min in the dark at 37 ºC with 5% CO_2. Fluorescence intensity, which is proportional to cell number, was measured on a Typhoon 8600 fluorescent scanner (Molecular Dynamics, CA, USA) with filters set at 480 nm excitation and 520 nm emission. Fluorescence data was analyzed and cell number estimated using ImageQuant TL (Molecular Dynamics). Significant p-values, denoted by the asterisk, between the normal and RTS cells were 0.0019, 0.0014, and 0.0255 for 50, 100 or 200 µM menadione, respectively.

Supplementary Figure 3. RECQL4 can directly interact with FEN1. 3xFlag-RECQL4 was immunoprecipitated from HeLa cells that had been transfected (+) or not (-) with pCMV23xFlag RECQL4 and purified under high salt conditions as described in the Materials and Methods section. Purified FEN1 (1 µg) was added to the beads and then the beads were washed with RIPA buffer five times. Lane 1, purified FEN1 (0.1 µg), lanes 2-3, 1/10 of each lysate, lanes 4-5, bead bound proteins. Western blot on top was probe with rabbit anti-Flag (Sigma) and the bottom was probe with rabbit and FEN1 (abCam) as described in the Materials and Methods.

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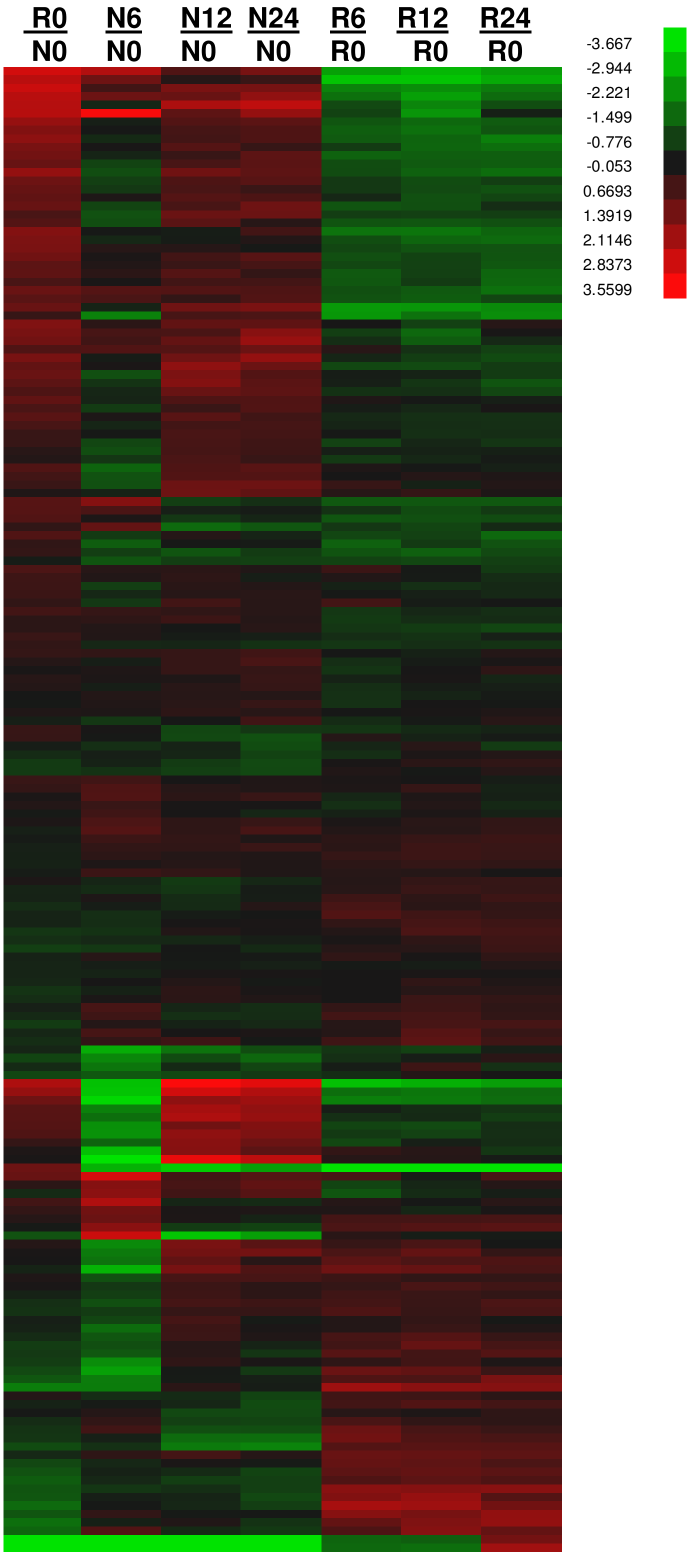
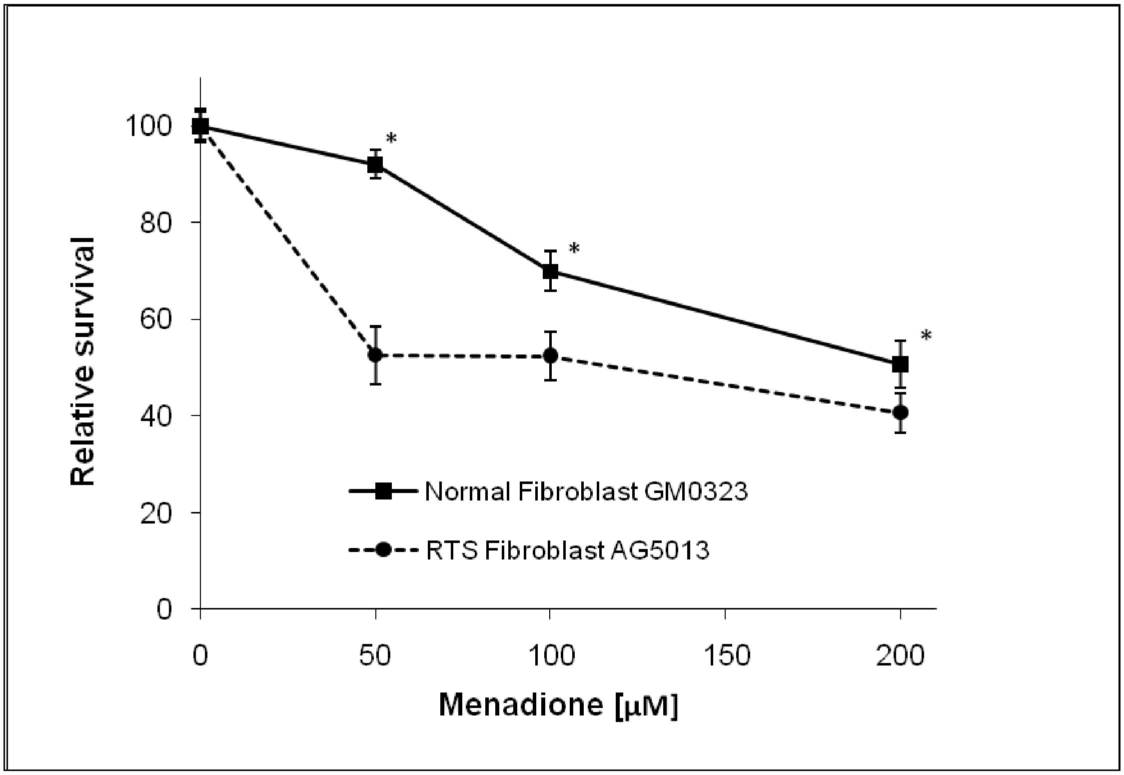


Supplementary Figure 1. Expression profile of DNA repair genes before (RTS cells, R0, or normal cells, N0) or 6, 12, or 24h after menadione treatment. The red represents up-regulated and green represents down-regulated gene expression.

Supplementary Figure 2



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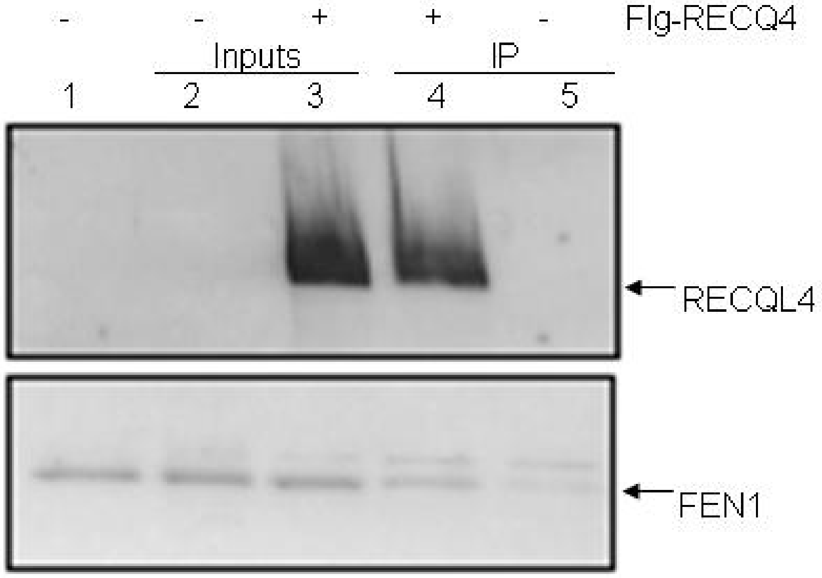
Supplementary Figure 3



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Supplementary Table 1

All annotated DNA repair and related genes in the gene ontology group DNA Repair from the Broad Institute at MIT.

This table lists the Z-ratios at each time point for each gene.

The genes in bold are those we grouped into the long and short patch BER pathways.

SYMBOL	DEFINITION	Z ratio R0-N0	Z ratio N6-N0	Z ratio N12-N0	Z ratio N24-N0	Z ratio R6-R0	Z ratio R12-R0	Z ratio R24-R0
ADA	adenosine deaminase (ADA)	1.232	0.899	0.879	0.816	-1.044	-1.213	-1.636
ALKBH2	alkB, alkylation repair homolog 2 (E. coli) (ALKBH2)	1.561	-0.328	-0.125	0.123	-1.001	-1.453	-1.517
ALKBH3	alkB, alkylation repair homolog 3 (E. coli) (ALKBH3)	0.343	-0.330	-0.291	-0.515	-0.594	-0.449	-0.520
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1 (APEX1), transcript variant 3	**0.989**	**0.747**	**0.372**	**0.859**	**-1.100**	**-1.277**	**-0.881**
APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2 (APEX2), nuclear gene encoding mitochondrial protein	1.470	-0.036	0.910	0.436	-0.692	-1.449	-1.584
APTX	aprataxin (APTX), transcript variant 5	0.439	-0.026	-0.889	-0.607	-0.574	-0.365	-0.261
ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A)	-0.135	-1.136	-0.731	-0.776	-0.819	-0.903	-0.751
ATM	ataxia telangiectasia mutated (ATM), transcript variant 1	-0.536	0.611	-1.037	-1.029	1.277	0.706	0.482
ATR	ataxia telangiectasia and Rad3 related (ATR)	-0.088	0.103	0.224	0.435	-0.502	-0.051	-0.079
ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX), transcript variant 1	-0.313	0.681	-0.035	0.027	0.154	0.956	0.432
BCCIP	BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant B	1.126	-0.974	0.715	0.866	-0.695	-1.167	-0.639
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1)	0.079	0.047	0.281	0.209	-0.063	-0.011	0.074
BLM	Bloom syndrome (BLM)	-0.015	-0.638	0.516	0.252	0.391	0.733	0.588
BRCA1	breast cancer 1, early onset (BRCA1), transcript variant BRCA1-delta14-17	-0.215	-2.435	1.725	0.888	1.081	1.098	0.317
BRIP1	BRCA1 interacting protein C-terminal helicase 1 (BRIP1)	-0.069	0.134	0.185	0.165	-0.487	-0.253	-0.123
CCNH	cyclin H (CCNH)	1.643	-0.085	-0.151	0.620	-1.693	-1.720	-1.410
CDC2	cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 1	2.390	-1.911	2.705	2.605	-2.082	-1.881	-2.269
CHAF1A	chromatin assembly factor 1, subunit A (p150) (CHAF1A)	-0.012	-1.833	1.399	1.407	0.753	1.141	0.381
CHAF1B	chromatin assembly factor 1, subunit B (p60) (CHAF1B)	0.055	-3.058	1.704	1.012	0.365	0.199	-0.588
CHEK1	CHK1 checkpoint homolog (S. pombe) (CHEK1)	0.884	-1.012	0.994	0.192	-1.125	-1.170	-1.058
CLSPN	claspin homolog (Xenopus laevis) (CLSPN)	0.071	-0.240	1.307	1.098	0.197	0.391	0.055

CRB2	crumbs homolog 2 (Drosophila) (CRB2)	0.025	0.845	0.250	0.465	-0.309	0.073	-0.207
CRY1	cryptochrome 1 (photolyase-like) (CRY1)	-0.753	-0.623	-0.062	-0.359	0.179	0.211	0.515
CRY2	cryptochrome 2 (photolyase-like) (CRY2)	-0.247	0.198	-0.079	-0.090	0.338	-0.021	0.320
CSNK1D	casein kinase 1, delta (CSNK1D), transcript variant 1	-1.252	-1.379	-0.555	-1.348	1.278	1.681	0.553
CSNK1E	casein kinase 1, epsilon (CSNK1E), transcript variant 1	0.359	-0.665	0.537	0.373	-0.244	-0.236	-0.876
CUL4A	cullin 4A (CUL4A), transcript ariant 2	-1.092	-0.217	-0.381	-0.822	1.029	1.138	1.002
DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A)	-0.192	-0.861	0.673	-0.119	0.134	0.368	-0.077
DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae) (DCLRE1B)	-0.232	-0.742	0.541	0.277	0.570	0.476	0.367
DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae) (DCLRE1C), transcript variant c	-0.393	-1.166	0.502	0.088	0.678	0.908	0.426
DDB1	PREDICTED: damage-specific DNA binding protein 1, 127kDa (DDB1)	-0.012	0.496	-0.646	-0.567	-0.336	-0.091	-0.487
DDB2	damage-specific DNA binding protein 2, 48kDa (DDB2)	2.508	1.314	0.179	0.472	-3.123	-3.127	-2.662
EAF1	ELL associated factor 1 (EAF1)	-0.297	-2.723	-1.702	-0.990	-0.571	-0.788	-0.184
EEF1E1	eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1)	1.387	0.590	1.147	1.986	-0.433	-1.279	-0.353
EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe) (EME1)	0.205	-1.002	0.669	0.535	-0.184	-0.240	-0.212
EPC2	enhancer of polycomb homolog 2 (Drosophila) (EPC2)	-0.212	0.265	0.152	0.097	0.406	0.527	0.446
ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) (ERCC1), transcript variant 2	0.995	0.609	0.425	0.589	-1.296	-1.331	-1.184
ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D) (ERCC2)	-1.124	-0.593	-0.451	-0.757	1.746	1.663	1.733
ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3)	0.035	-0.300	-0.665	-0.337	0.160	0.390	0.413
ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) (ERCC5)	-0.582	-0.202	-1.531	-1.580	1.381	0.833	0.712
ERCC6	excision repair cross-complementing rodent repair	0.375	0.809	0.192	0.092	0.049	0.415	-0.239

	deficiency, complementation group 6 (ERCC6)							
EXO1	exonuclease 1 (EXO1), transcript variant 1	-0.798	-4.259	0.199	0.088	0.453	0.470	0.643
FANCA	Fanconi anemia, complementation group A (FANCA), transcript variant 1	-0.218	0.043	0.172	0.088	0.276	0.402	0.329
FANCB	Fanconi anemia, complementation group B (FANCB), transcript variant 1	1.277	-0.537	1.222	1.387	-0.802	-0.798	-0.561
FANCC	Fanconi anemia, complementation group C (FANCC)	-0.442	0.369	0.552	-0.084	0.561	1.033	0.571
FANCD2	Fanconi anemia, complementation group D2 (FANCD2), transcript variant 2	1.340	-2.374	2.315	2.539	-0.287	-1.011	-0.936
FANCG	Fanconi anemia, complementation group G (FANCG)	1.038	-0.537	1.662	1.002	-0.193	-0.584	-1.136
FANCI	Fanconi anemia, complementation group I (FANCI)	-0.264	-2.843	1.459	0.808	1.317	1.178	0.708
FANCL	Fanconi anemia, complementation group L (FANCL)	1.127	0.004	1.839	1.267	-0.892	-0.946	-0.678
FBXO18	F-box protein, helicase, 18 (FBXO18), transcript variant 2	-1.167	-0.181	-0.282	-0.923	1.624	1.948	0.883
FEN1	flap structure-specific endonuclease 1 (FEN1)	**0.954**	**-1.918**	**2.181**	**1.866**	**-0.167**	**-0.393**	**-0.557**
GADD45A	growth arrest and DNA-damage-inducible, alpha (GADD45A)	1.293	-2.805	-3.242	-2.471	-4.930	-3.994	-4.435
GIYD2	GIY-YIG domain containing 2 (GIYD2), transcript variant 1	0.134	-0.590	0.747	0.443	-0.646	-0.328	-0.108
GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa (GTF2H1)	-0.969	-0.490	-1.825	-1.977	0.886	0.954	0.936
GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa (GTF2H2)	1.389	-0.278	0.467	1.030	-1.384	-1.317	-1.308
GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa (GTF2H3)	0.845	-0.668	0.168	-0.279	-0.882	-0.798	-1.478
GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa (GTF2H4)	-0.383	-1.717	-0.371	-0.868	-0.154	0.543	-0.494
GTF2H5	general transcription factor IIH, polypeptide 5 (GTF2H5)	2.461	3.476	1.054	1.938	-0.819	-2.295	-0.207
HAT1	histone acetyltransferase 1 (HAT1), transcript variant 1	2.203	-0.966	1.265	2.335	-2.087	-2.575	-2.330
HSPA1A	heat shock 70kDa protein 1A (HSPA1A)	-6.431	-11.836	-7.363	-5.109	-1.459	-1.313	1.413
HSPA1B	heat shock 70kDa protein 1B (HSPA1B)	-7.066	-11.240	-9.150	-5.519	-1.487	-1.588	2.121
HUS1	HUS1 checkpoint homolog (S. pombe) (HUS1)	-0.438	0.009	0.260	0.101	-0.051	0.502	0.359
IGHMBP2	immunoglobulin mu binding protein 2 (IGHMBP2)	-0.179	-0.607	-0.065	0.593	-0.404	-0.099	0.207
INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa (INPP5E)	1.356	0.014	0.626	0.945	-1.050	-0.813	-1.126
KCTD13	potassium channel tetramerisation domain containing 13 (KCTD13)	0.475	0.117	-0.125	-0.191	-0.429	-0.525	-0.201

KIN	KIN, antigenic determinant of recA protein homolog (mouse) (KIN)	-0.278	-0.170	-0.112	-0.197	-0.090	-0.144	0.136
LIG1	ligase I, DNA, ATP-dependent (LIG1)	**1.924**	**-1.014**	**1.354**	**1.049**	**-0.969**	**-1.365**	**-1.568**
LIG3	ligase III, DNA, ATP-dependent (LIG3), nuclear gene encoding mitochondrial protein, transcript variant alpha	**-0.045**	**-0.197**	**0.525**	**0.263**	**0.449**	**0.419**	**0.339**
LIG4	ligase IV, DNA, ATP-dependent (LIG4), transcript variant 2	-0.354	-0.281	-0.059	-0.018	-0.062	0.208	0.123
LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) (LRP1)	1.199	2.923	0.606	0.891	0.695	-0.126	0.707
MBD4	methyl-CpG binding domain protein 4 (MBD4)	-0.886	-1.183	-0.920	-0.648	-0.411	0.144	-0.041
MCL1	myeloid cell leukemia sequence 1 (BCL2-related) (MCL1), transcript variant 2	0.102	0.294	0.245	0.109	-0.181	0.063	-0.331
MDC1	mediator of DNA damage checkpoint 1 (MDC1)	1.307	-0.751	0.787	0.949	-0.629	-0.995	-0.733
MGMT	O-6-methylguanine-DNA methyltransferase (MGMT)	0.362	1.355	0.014	0.067	0.074	-0.320	0.005
MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1)	-0.232	-1.563	0.517	0.002	0.122	0.465	0.085
MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) (MLL)	-0.241	-0.119	-0.310	-0.976	0.616	0.860	0.631
MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis) (MNAT1)	1.625	-0.059	0.671	0.812	-1.316	-1.651	-1.151
MPG	N-methylpurine-DNA glycosylase (MPG), transcript variant 2	-0.144	0.358	0.242	-0.154	0.304	0.585	0.438
MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 1	0.821	-0.001	0.193	-0.040	-0.783	-0.346	-0.349
MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2)	0.453	-0.881	0.705	0.556	-0.804	-0.320	-0.584
MSH3	mutS homolog 3 (E. coli) (MSH3)	0.178	1.252	0.031	-0.254	0.647	0.657	0.703
MSH6	mutS homolog 6 (E. coli) (MSH6)	-1.870	-1.860	0.237	-0.144	2.076	1.747	1.680
MSI1	musashi homolog 1 (Drosophila) (MSI1)	0.256	0.132	-0.056	0.216	-0.599	-0.682	-0.889
MUS81	MUS81 endonuclease homolog (S. cerevisiae) (MUS81)	1.609	0.259	1.115	1.085	-0.040	-0.798	0.198
MUTYH	mutY homolog (E. coli) (MUTYH), transcript variant gamma2	1.802	-0.370	0.614	0.813	-1.229	-1.421	-1.896
NBN	nibrin (NBN), transcript variant 1	-0.645	-1.199	0.214	-0.582	0.931	0.626	0.885
NCOA6	nuclear receptor coactivator 6 (NCOA6)	-0.422	0.345	-0.769	-0.848	0.738	0.339	0.282
NEIL1	nei endonuclease VIII-like 1 (E. coli) (NEIL1)	**0.131**	**0.454**	**-0.012**	**-0.029**	**-0.464**	**0.134**	**-0.356**
NEIL2	nei like 2 (E. coli) (NEIL2)	0.139	-0.424	-0.375	-0.828	0.585	0.559	0.257
NEIL3	nei endonuclease VIII-like 3 (E. coli) (NEIL3)	0.392	-1.413	1.736	1.265	-0.895	-0.195	-0.424

NHEJ1	nonhomologous end-joining factor 1 (NHEJ1)	-0.197	0.907	0.309	0.698	0.135	0.195	0.361
NONO	non-POU domain containing, octamer-binding (NONO)	0.626	0.419	0.331	0.205	-0.617	-0.328	-0.449
NSMCE1	non-SMC element 1 homolog (S. cerevisiae) (NSMCE1)	0.462	0.595	-0.046	0.086	0.011	-0.049	-0.145
NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae) (NSMCE2)	0.860	0.026	-0.615	-0.296	-1.143	-1.037	-0.977
NTHL1	nth endonuclease III-like 1 (E. coli) (NTHL1)	**0.540**	**0.113**	**0.291**	**-0.163**	**0.108**	**-0.122**	**-0.412**
NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1), transcript variant 3A	0.618	-1.093	0.856	0.879	-0.042	0.158	0.062
OGG1	8-oxoguanine DNA glycosylase (OGG1), nuclear gene encoding mitochondrial protein, transcript variant 1a	**1.026**	**0.120**	**0.483**	**0.681**	**-0.898**	**-0.796**	**-1.190**
PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) (PAN3)	0.920	0.751	-0.202	-0.125	-0.526	-0.974	-0.665
PARP1	poly (ADP-ribose) polymerase family, member 1 (PARP1)	-1.142	0.357	-0.096	-0.079	1.717	1.458	1.892
PARP2	poly (ADP-ribose) polymerase family, member 2 (PARP2), transcript variant 2	0.520	-0.745	0.228	0.150	-0.227	-0.469	-0.356
PCNA	proliferating cell nuclear antigen (PCNA), transcript variant 2	0.906	-0.103	1.367	1.522	-1.338	-1.015	-0.975
PMS2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae) (PMS2), transcript variant 2, transcribed RNA.	2.493	1.282	1.224	1.871	-1.645	-2.478	-1.533
PNKP	polynucleotide kinase 3'-phosphatase (PNKP)	-0.252	-0.445	-0.134	-0.062	0.862	0.566	0.383
POLB	polymerase (DNA directed), beta (POLB)	**0.431**	**-0.089**	**-0.924**	**-1.059**	**0.155**	**-0.234**	**-0.120**
POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa (POLD1)	**1.244**	**-1.036**	**1.553**	**0.877**	**-0.145**	**-0.257**	**-0.683**
POLE	polymerase (DNA directed), epsilon (POLE)	0.163	-2.098	1.486	0.979	0.431	0.731	-0.070
POLE3	polymerase (DNA directed), epsilon 3 (p17 subunit) (POLE3)	-0.726	-2.139	0.322	0.007	0.301	0.602	0.056
POLG2	polymerase (DNA directed), gamma 2, accessory subunit (POLG2)	0.379	-0.732	-1.131	-0.677	-1.120	-1.350	-0.943
POLH	polymerase (DNA directed), eta (POLH)	-0.356	0.553	-0.476	-0.427	0.612	0.668	0.348
POLI	polymerase (DNA directed) iota (POLI)	-0.669	-0.530	-0.750	-0.910	0.098	-0.074	0.178
POLL	polymerase (DNA directed), lambda (POLL)	-0.090	0.577	-0.036	-0.316	-0.227	0.031	-0.218
POLQ	polymerase (DNA directed), theta (POLQ)	-0.051	-1.696	1.110	0.211	1.022	0.778	0.796
PRKDC	protein kinase, DNA-activated, catalytic polypeptide (PRKDC),	-1.529	-0.077	-0.312	-0.737	2.225	2.080	1.375

	transcript variant 2							
PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae) (PRPF19)	0.723	-0.293	0.616	0.664	-0.280	-0.445	-0.475
PTTG1	pituitary tumor-transforming 1 (PTTG1)	2.439	-0.313	2.299	2.607	-0.942	-2.007	-1.000
RAD1	RAD1 homolog (S. pombe) (RAD1), transcript variant 3	-0.238	0.047	-0.401	-0.144	0.542	0.287	0.539
RAD17	RAD17 homolog (S. pombe) (RAD17), transcript variant 6	0.080	0.217	0.466	0.520	-0.446	0.184	-0.517
RAD18	RAD18 homolog (S. cerevisiae) (RAD18)	-0.601	-0.524	0.116	-0.014	0.131	0.762	0.636
RAD21	RAD21 homolog (S. pombe) (RAD21)	0.718	-0.011	0.608	0.633	-1.192	-0.677	-1.469
RAD23A	RAD23 homolog A (S. cerevisiae) (RAD23A)	1.096	-0.271	0.804	0.837	0.075	-0.078	-0.180
RAD23B	RAD23 homolog B (S. cerevisiae) (RAD23B)	-0.899	-0.336	0.003	-0.112	1.155	1.058	0.763
RAD50	RAD50 homolog (S. cerevisiae) (RAD50), transcript variant 2	-0.200	0.706	-0.297	-0.442	0.361	0.538	0.297
RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae) (RAD51), transcript variant 1	0.942	-1.596	2.335	1.947	-0.471	-0.373	-0.716
RAD51AP1	RAD51 associated protein 1 (RAD51AP1)	1.313	-3.483	1.821	2.054	-1.899	-1.780	-1.555
RAD51C	RAD51 homolog C (S. cerevisiae) (RAD51C), transcript variant 2	3.108	0.131	1.794	2.332	-2.175	-2.741	-2.488
RAD51L1	RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1	0.026	0.776	0.302	0.453	0.020	0.223	0.349
RAD51L3	RAD51-like 3 (S. cerevisiae) (RAD51L3), transcript variant 4	1.199	-0.822	0.717	1.008	-0.985	-1.237	-1.290
RAD52	RAD52 homolog (S. cerevisiae) (RAD52)	-0.125	0.506	0.368	0.075	0.186	0.156	-0.028
RAD54B	RAD54 homolog B (S. cerevisiae) (RAD54B)	0.160	-0.166	0.421	0.730	-0.447	-0.133	0.009
RAD54L	RAD54-like (S. cerevisiae) (RAD54L)	0.485	-1.054	1.289	1.306	0.443	-0.214	0.127
RBX1	ring-box 1 (RBX1)	1.483	0.693	0.735	1.733	-0.742	-1.479	-0.024
RECQL	RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1	-1.002	-1.475	-0.592	-1.706	1.134	1.113	0.734
RECQL5	RecQ protein-like 5 (RECQL5), transcript variant 1	0.822	1.408	0.704	0.109	-0.669	-0.355	-0.454
REV1	REV1 homolog (S. cerevisiae) (REV1), transcript variant 1	-1.265	-0.327	-0.737	-0.757	0.812	1.037	0.805
REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L)	-1.092	2.784	-3.165	-2.465	0.227	-0.150	-0.117
RFC1	replication factor C (activator 1) 1, 145kDa (RFC1)	-0.261	-0.406	-0.602	-0.137	0.185	0.472	0.405
RFC5	replication factor C (activator 1) 5, 36.5kDa (RFC5), transcript variant 1	0.832	-2.234	1.842	1.573	-0.657	-0.806	-0.454
RPA1	replication protein A1, 70kDa	0.802	-0.316	1.216	1.050	-0.507	-0.471	-0.878

	(RPA1)							
RPA2	replication protein A2, 32kDa (RPA2)	1.951	-0.194	0.879	1.023	-1.151	-1.484	-1.247
RPAIN	RPA interacting protein (RPAIN)	2.900	2.389	0.828	1.454	-2.487	-2.890	-2.417
RPLP0	ribosomal protein, large, P0 (RPLP0), transcript variant 2	2.083	1.764	1.553	2.222	-2.184	-2.583	-2.195
RPS3	ribosomal protein S3 (RPS3)	0.250	1.681	0.697	1.091	-0.851	-0.314	0.160
RRM2B	ribonucleotide reductase M2 B (TP53 inducible) (RRM2B)	0.335	1.141	-1.517	-1.161	-0.616	-0.871	-0.358
RUVBL2	RuvB-like 2 (E. coli) (RUVBL2)	0.838	-1.418	0.810	0.966	0.063	-0.078	-0.200
SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) (SFPQ)	-1.158	-1.860	-0.112	-0.193	0.830	0.775	1.510
SHPRH	SNF2 histone linker PHD RING helicase (SHPRH), transcript variant 2	-0.661	-0.232	-0.688	-0.936	-0.014	0.240	0.342
SMC3	structural maintenance of chromosomes 3 (SMC3)	0.979	0.038	0.971	0.582	-0.341	-0.478	-0.484
SMC5	structural maintenance of chromosomes 5 (SMC5)	-0.306	-0.053	0.151	-0.103	-0.043	0.340	0.080
SMC6	structural maintenance of chromosomes 6 (SMC6)	0.732	-1.086	1.256	1.275	-0.726	-0.771	-0.745
SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1 (SMUG1)	0.516	-0.321	0.199	0.220	-0.082	-0.202	-0.340
SSB	Sjogren syndrome antigen B (autoantigen La) (SSB)	0.395	0.349	0.412	0.594	-0.068	-0.223	0.143
SSRP1	structure specific recognition protein 1 (SSRP1)	1.470	-0.126	1.326	1.926	-0.295	-0.715	-0.958
SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae) (SUPT16H)	-0.255	-0.441	-0.024	-0.005	0.357	0.671	0.542
TDG	thymine-DNA glycosylase (TDG)	-0.196	-0.283	-0.586	-0.828	0.164	1.261	0.645
TDP1	tyrosyl-DNA phosphodiesterase 1 (TDP1), transcript variant 1	-0.342	0.296	0.658	0.175	1.218	1.157	1.054
TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial) (TNFAIP1)	-0.090	1.769	-0.689	-0.818	0.770	0.893	0.975
TOPBP1	topoisomerase (DNA) II binding protein 1 (TOPBP1)	-0.926	-2.490	-0.095	-0.647	1.251	1.107	0.500
TPP1	tripeptidyl peptidase I (TPP1)	0.622	2.346	-0.300	-0.378	0.160	-0.064	0.224
TREX1	three prime repair exonuclease 1 (TREX1), transcript variant 2	-0.262	0.151	0.143	0.590	-0.155	0.350	0.458
TYMS	thymidylate synthetase (TYMS)	2.320	-3.072	3.886	3.169	-3.057	-2.768	-2.440
UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)	-0.688	0.148	-0.241	-0.351	0.171	0.693	0.676
UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast) (UBE2N)	-0.475	-1.039	0.663	0.544	0.638	0.460	0.762
UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1), transcript variant 1	-0.015	-4.041	3.284	2.577	0.172	0.166	-0.111
UNG	uracil-DNA glycosylase (UNG), transcript variant 2	**1.010**	**0.035**	**0.876**	**1.207**	**-1.061**	**-0.453**	**-0.099**
UVRAG	UV radiation resistance associated gene (UVRAG)	-0.087	0.162	-0.911	-0.935	0.195	0.052	0.298

WRNIP1	Werner helicase interacting protein 1 (WRNIP1), transcript variant 1	0.082	0.193	0.341	0.116	-0.335	-0.237	-0.837
XAB2	XPA binding protein 2 (XAB2)	1.522	0.199	0.180	-0.085	-0.878	-1.097	-1.104
XPA	xeroderma pigmentosum, complementation group A (XPA)	0.146	-0.166	0.209	0.422	-0.448	-0.148	-0.183
XPC	xeroderma pigmentosum, complementation group C (XPC)	0.937	1.673	-0.741	-0.465	-1.194	-1.176	-1.207
XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1)	**1.179**	**-0.634**	**0.728**	**0.473**	**-0.633**	**-0.953**	**-1.080**
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2)	-0.204	0.356	0.341	0.492	0.233	0.520	0.470
XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), transcript variant 3	0.747	-0.693	0.471	0.863	-0.152	-0.322	-0.018
XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2	-0.474	-0.341	-0.337	-0.169	-0.003	0.305	0.558
XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa) (XRCC5)	-1.609	-0.211	0.101	-0.520	1.142	1.594	1.900
XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa) (XRCC6)	-0.700	-1.015	0.195	-0.260	0.596	1.191	0.661
XRN2	5'-3' exoribonuclease 2 (XRN2)	-0.157	-0.467	-0.264	-0.996	-0.293	0.201	-0.679