

Supplementary Table 5. The pathways enriched in switched-off DNA repair genes.

GeneN - the observed number of genes belonging to a pathway in the switched-off genes.
Ratio - the ratio of observed to expected numbers of genes belonging to a pathway in the switched-off genes.

Pathway ID	Pathway Name	GeneN	Ratio	p-value	q-value	Gene list
1270350__REACTOME__R- HSA-73894	DNA Repair	24	14.55	4.26E-22	4.38E-19	REV3L; NSD2; MRE11; FANCG; MUS81; RAD50; RAD9A; RNF8; BRCA2; AQR; RNF168; POLM; FEN1; RAD17; FAAP24; APBB1; CDK7; CHEK1; NBN; USP43; GTF2H4; PALB2; RAD18; CHEK2
1269741__REACTOME__R- HSA-1640170	Cell Cycle	28	8.11	8.53E-19	6.58E-16	GIN54; NUP35; NSD2; MRE11; NUP210; REC8; GINS2; AURKB; RAD50; MCPH1; RAD9A; RNF8; BRCA2; PDS5A; MLH3; CEP164; RNF168; FEN1; RAD17; NUP50; NCAPD3; CDK7; CHEK1; SEH1L; NUP188; NBN; FZR1; CHEK2
1309095__REACTOME__R- HSA-5693532	DNA Double-Strand Break Repair	16	19.29	6.71E-17	3.45E-14	NSD2; MRE11; MUS81; RAD50; RAD9A; RNF8; BRCA2; POLM; RNF168; FEN1; RAD17; APBB1; CHEK1; NBN; CHEK2; PALB2
1309099__REACTOME__R- HSA-5693538	Homology Directed Repair	13	20.43	3.12E-14	1.37E-11	RNF168; FEN1; RAD17; NSD2; MRE11; MUS81; RAD50; CHEK1; RAD9A; RNF8; BRCA2; NBN; PALB2
1309100__REACTOME__R- HSA-5693567	HDR through Homologous Recombination (HR) or Single Strand Annealing (SSA)	12	19.44	6.11E-13	2.36E-10	RNF168; RAD17; NSD2; MRE11; MUS81; RAD50; CHEK1; RAD9A; BRCA2; RNF8; NBN; PALB2
1268743__REACTOME__R- HSA-3108232	SUMO E3 ligases SUMOylate target proteins	12	18.30	1.31E-12	4.51E-10	RNF168; NUP35; TOP2B; NUP50; NUP210; AURKB; NSMCE1; CBX8; MTA1; NUP188; SEH1L; NSMCE3
1268738__REACTOME__R- HSA-2990846	SUMOylation	12	17.28	2.69E-12	8.30E-10	RNF168; NUP35; TOP2B; NUP50; NUP210; AURKB; NSMCE1; CBX8; MTA1; NUP188; SEH1L; NSMCE3
1269754__REACTOME__R- HSA-69473	G2/M DNA damage checkpoint	10	23.05	9.54E-12	2.68E-09	RNF168; RAD17; NSD2; MRE11; CHEK1; RAD50; RAD9A; RNF8; NBN; CHEK2
1309103__REACTOME__R- HSA-5693579	Homologous DNA Pairing and Strand Exchange	8	31.91	7.13E-11	1.83E-08	RAD50; CHEK1; RAD9A; RAD17; BRCA2; NBN; MRE11; PALB2
1309102__REACTOME__R- HSA-5685942	HDR through Homologous Recombination (HRR)	9	21.71	1.98E-10	4.70E-08	RAD17; MRE11; MUS81; CHEK1; RAD50; RAD9A; BRCA2; NBN; PALB2
1309101__REACTOME__R- HSA-5693607	Processing of DNA double-strand break ends	9	20.29	3.78E-10	7.77E-08	RNF168; RAD17; NSD2; MRE11; CHEK1; RAD50; RAD9A; RNF8; NBN
1268744__REACTOME__R- HSA-3108214	SUMOylation of DNA damage response and repair proteins	9	19.44	5.66E-10	1.09E-07	RNF168; NUP35; NUP50; NUP210; NSMCE1; CBX8; NUP188; SEH1L; NSMCE3

1309098__REACTOME__R- HSA-5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	8	25.14	6.00E-10	1.09E-07	RNF168; NSD2; MRE11; APBB1; RAD50; RNF8; NBN; CHEK2
1309096__REACTOME__R- HSA-5693606	DNA Double Strand Break Response	8	24.40	7.79E-10	1.34E-07	RNF168; NSD2; MRE11; APBB1; RAD50; RNF8; NBN; CHEK2
1458202__WikiPathways__ WP3878	ATM Signaling Network in Development and Disease	8	23.70	1.00E-09	1.63E-07	RNF168; MRE11; AURKB; CHEK1; RAD50; RNF8; NBN; CHEK2
1309104__REACTOME__R- HSA-5693616	Presynaptic phase of homologous DNA pairing and strand exchange	7	29.04	2.49E-09	3.84E-07	RAD50; CHEK1; RAD9A; RAD17; BRCA2; NBN; MRE11
454__KEGG__ko03440; 83046__KEGG__hsa03440	Homologous recombination	7	27.92	3.38E-09	4.97E-07	RAD50; BRCA2; RAD54L; NBN; MRE11; MUS81; PALB2
377128__KEGG__ko03460; 377262__KEGG__hsa03460	Fanconi anemia pathway	7	26.89	4.53E-09	6.35E-07	WDR48; REV3L; BRCA2; FAAP24; FANCG; MUS81; PALB2
920969__WikiPathways__ WP2516	ATM Signaling Pathway	7	25.03	7.84E-09	1.01E-06	RAD50; CHEK1; RAD9A; NBN; MRE11; CHEK2; GADD45A
1309110__REACTOME__R- HSA-5693571	Nonhomologous End-Joining (NHEJ)	7	25.03	7.84E-09	1.01E-06	RNF168; POLM; RAD50; RNF8; NSD2; NBN; MRE11
198788__WikiPathways__ WP707	DNA Damage Response	8	18.44	8.49E-09	1.05E-06	RAD17; MRE11; GADD45A; CHEK1; RAD50; RAD9A; NBN; CHEK2
1309105__REACTOME__R- HSA-5693537	Resolution of D-Loop Structures	6	34.57	1.13E-08	1.29E-06	RAD50; BRCA2; NBN; MRE11; MUS81; PALB2
1309106__REACTOME__R- HSA-5693568	Resolution of D-loop Structures through Holliday Junction Intermediates	6	34.57	1.13E-08	1.29E-06	RAD50; BRCA2; NBN; MRE11; MUS81; PALB2
1339113__REACTOME__R- HSA-4615885	SUMOylation of DNA replication proteins	7	23.42	1.30E-08	1.43E-06	SEH1L; NUP188; NUP35; TOP2B; NUP50; NUP210; AURKB
920989__WikiPathways__ WP1530	miRNA Regulation of DNA Damage Response	8	17.28	1.45E-08	1.55E-06	RAD17; MRE11; GADD45A; CHEK1; RAD50; RAD9A; NBN; CHEK2
219801__WikiPathways__ WP1984	Integrated Breast Cancer Pathway	10	10.69	2.51E-08	2.59E-06	PTEN; SIRT1; RAD54L; MRE11; CDK7; GADD45A; CHEK1; RAD50; BRCA2; CHEK2
1269753__REACTOME__R- HSA-69481	G2/M Checkpoints	10	10.17	4.10E-08	3.95E-06	RNF168; RAD17; NSD2; MRE11; CHEK1; RAD50; RAD9A; RNF8; NBN; CHEK2
1383080__REACTOME__R- HSA-6804756	Regulation of TP53 Activity through Phosphorylation	8	13.83	8.97E-08	8.39E-06	RAD17; MRE11; AURKB; CHEK1; RAD50; RAD9A; NBN; CHEK2

1269763__REACTOME__R- HSA-69278	Cell Cycle, Mitotic	15	5.27	1.08E-07	9.76E-06	GIN54; FEN1; NUP35; NUP50; NCAPD3; NUP210; CDK7; GINS2; AURKB; SEH1L; MCPH1; NUP188; FZR1; PDS5A; CEP164
1309109__REACTOME__R- HSA-5685939	HDR through MMEJ (alt-NHEJ)	4	69.14	1.19E-07	1.05E-05	RAD50; FEN1; NBN; MRE11
1309107__REACTOME__R- HSA-5693554	Resolution of D-loop Structures through Synthesis- Dependent Strand Annealing (SDSA)	5	34.57	2.05E-07	1.75E-05	RAD50; BRCA2; NBN; MRE11; PALB2
1269742__REACTOME__R- HSA-69620	Cell Cycle Checkpoints	10	8.57	2.10E-07	1.75E-05	RNF168; RAD17; NSD2; MRE11; CHEK1; RAD50; RAD9A; RNF8; NBN; CHEK2
1339112__REACTOME__R- HSA-4570464	SUMOylation of RNA binding proteins	6	21.46	2.65E-07	2.15E-05	CBX8; SEH1L; NUP188; NUP35; NUP50; NUP210
1269922__REACTOME__R- HSA-170822	Regulation of Glucokinase by Glucokinase Regulatory Protein	5	32.41	2.96E-07	2.34E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269654__REACTOME__R- HSA-3700989	Transcriptional Regulation by TP53	13	5.59	4.28E-07	3.22E-05	PTEN; RAD17; MRE11; CDK7; AURKB; GADD45A; RAD50; CHEK1; RAD9A; NBN; GTF2H4; TNKS1BP1; CHEK2
1269123__REACTOME__R- HSA-168333	NEP/NS2 Interacts with the Cellular Export Machinery	5	28.81	5.72E-07	3.92E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269866__REACTOME__R- HSA-912446	Meiotic recombination	5	28.81	5.72E-07	3.92E-05	RAD50; BRCA2; NBN; MRE11; MLH3
1269114__REACTOME__R- HSA-168271	Transport of Ribonucleoproteins into the Host Nucleus	5	28.81	5.72E-07	3.92E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269121__REACTOME__R- HSA-168274	Export of Viral Ribonucleoproteins from Nucleus	5	28.81	5.72E-07	3.92E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269865__REACTOME__R- HSA-1500620	Meiosis	6	18.30	7.23E-07	4.80E-05	RAD50; BRCA2; NBN; MRE11; REC8; MLH3
413426__KEGG__hsa_M00 291;	MRN complex	3	103.70	8.64E-07	5.56E-05	RAD50; NBN; MRE11
890552__KEGG__M00291						
1269817__REACTOME__R- HSA-3301854	Nuclear Pore Complex (NPC) Disassembly	5	25.93	1.02E-06	6.05E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269094__REACTOME__R- HSA-180910	Vpr-mediated nuclear import of PICs	5	25.93	1.02E-06	6.05E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269096__REACTOME__R- HSA-180746	Nuclear import of Rev protein	5	25.93	1.02E-06	6.05E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269697__REACTOME__R- HSA-159227	Transport of the SLBP independent Mature mRNA	5	25.93	1.02E-06	6.05E-05	SEH1L; NUP188; NUP35; NUP50; NUP210

1269085__REACTOME__R- HSA-165054	Rev-mediated nuclear export of HIV RNA	5	24.69	1.33E-06	7.45E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269696__REACTOME__R- HSA-159230	Transport of the SLBP Dependant Mature mRNA	5	24.69	1.33E-06	7.45E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
470351__KEGG__hsa_M00427; 890636__KEGG__M00427	Nuclear pore complex	5	23.57	1.70E-06	9.39E-05	SEH1L; NUP188; NUP35; NUP50; NUP210
1269092__REACTOME__R- HSA-176033	Interactions of Vpr with host cellular proteins	5	22.54	2.16E-06	1.11E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269131__REACTOME__R- HSA-168276	NS1 Mediated Effects on Host Pathways	5	22.54	2.16E-06	1.11E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1309108__REACTOME__R- HSA-5685938	HDR through Single Strand Annealing (SSA)	5	22.54	2.16E-06	1.11E-04	RAD50; RAD9A; RAD17; NBN; MRE11
1269095__REACTOME__R- HSA-177243	Interactions of Rev with host cellular proteins	5	22.54	2.16E-06	1.11E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
198890__WikiPathways__ WP186	Homologous recombination	4	37.71	2.52E-06	1.27E-04	RAD50; BRCA2; NBN; MRE11
1269811__REACTOME__R- HSA-68875	Mitotic Prophase	7	11.17	2.65E-06	1.32E-04	SEH1L; MCPH1; NUP188; NUP35; NUP50; NCAPD3; NUP210
1269698__REACTOME__R- HSA-159231	Transport of Mature mRNA Derived from an Intronless Transcript	5	21.60	2.71E-06	1.33E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269130__REACTOME__R- HSA-168253	Host Interactions with Influenza Factors	5	20.74	3.36E-06	1.57E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269921__REACTOME__R- HSA-70153	Glucose transport	5	20.74	3.36E-06	1.57E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269695__REACTOME__R- HSA-159234	Transport of Mature mRNAs Derived from Intronless Transcripts	5	20.74	3.36E-06	1.57E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
455__KEGG__ko03450; 83047__KEGG__hsa03450	Non-homologous end-joining	4	34.57	3.75E-06	1.73E-04	POLM; RAD50; FEN1; MRE11
1269058__REACTOME__R- HSA-162587	HIV Life Cycle	8	8.38	4.43E-06	1.98E-04	SEH1L; NUP188; FEN1; NUP35; NUP50; GTF2H4; NUP210; CDK7
672450__WikiPathways__ WP1971	Integrated Cancer Pathway	5	19.20	5.03E-06	2.22E-04	PTEN; RAD50; CHEK1; MRE11; CHEK2
1270425__REACTOME__R- HSA-3371453	Regulation of HSF1-mediated heat shock response	6	13.24	5.22E-06	2.27E-04	SIRT1; SEH1L; NUP188; NUP35; NUP50; NUP210

1269117__REACTOME__R- HSA-168325	Viral Messenger RNA Synthesis	5	18.52	6.08E-06	2.54E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269920__REACTOME__R- HSA-189200	Hexose transport	5	18.52	6.08E-06	2.54E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1383076__REACTOME__R- HSA-5633007	Regulation of TP53 Activity	8	7.83	7.40E-06	3.04E-04	RAD17; MRE11; AURKB; CHEK1; RAD50; RAD9A; NBN; CHEK2
1269731__REACTOME__R- HSA-194441;	Metabolism of non-coding RNA; snRNP Assembly	5	16.73	1.03E-05	4.12E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269732__REACTOME__R- HSA-191859						
1309089__REACTOME__R- HSA-6784531	tRNA processing in the nucleus	5	16.20	1.21E-05	4.78E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
711360__WikiPathways__ WP2377	Integrated Pancreatic Cancer Pathway	8	7.09	1.54E-05	6.00E-04	PTEN; SIRT1; MRE11; GADD45A; CHEK1; RAD50; BRCA2; CHEK2
1269815__REACTOME__R- HSA-2980766	Nuclear Envelope Breakdown	5	15.25	1.65E-05	6.35E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1309097__REACTOME__R- HSA-5693548	Sensing of DNA Double Strand Breaks	3	51.85	1.69E-05	6.37E-04	RAD50; NBN; MRE11
1458264__WikiPathways__ WP2942	DDX1 as a regulatory component of the Drosha microprocessor	3	51.85	1.69E-05	6.37E-04	RAD50; NBN; MRE11
1269723__REACTOME__R- HSA-5578749	Transcriptional regulation by small RNAs	5	14.81	1.91E-05	7.00E-04	SEH1L; NUP188; NUP35; NUP50; NUP210
1269069__REACTOME__R- HSA-162599	Late Phase of HIV Life Cycle	7	8.16	2.18E-05	7.90E-04	SEH1L; NUP188; NUP35; NUP50; GTF2H4; NUP210; CDK7
1270421__REACTOME__R- HSA-3371556	Cellular response to heat stress	6	10.20	2.43E-05	8.71E-04	SIRT1; SEH1L; NUP188; NUP35; NUP50; NUP210
1269810__REACTOME__R- HSA-68886	M Phase	9	5.43	3.78E-05	1.34E-03	NUP35; NUP50; NCAPD3; NUP210; AURKB; NUP188; MCPH1; SEH1L; PDS5A
1270414__REACTOME__R- HSA-2262752	Cellular responses to stress	11	4.35	3.86E-05	1.35E-03	SIRT1; NUP35; NUP50; MRE11; NUP210; CBX8; RAD50; SEH1L; NUP188; NBN; FZR1
137959__Pathway Interaction Database__bard1pathway	BARD1 signaling events	4	19.75	4.24E-05	1.47E-03	RAD50; NBN; MRE11; FANCG

413428__KEGG_hsa_M00295;	BRCA1-associated genome surveillance complex (BASC)	3	38.89	4.67E-05	1.60E-03	RAD50; NBN; MRE11
890555__KEGG_M00295						
1269694__REACTOME_R-HSA-159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	5	11.52	6.65E-05	2.23E-03	SEH1L; NUP188; NUP35; NUP50; NUP210
1269719__REACTOME_R-HSA-211000	Gene Silencing by RNA	5	11.03	8.22E-05	2.73E-03	SEH1L; NUP188; NUP35; NUP50; NUP210
1269316__REACTOME_R-HSA-1169410;	Antiviral mechanism by IFN-stimulated genes; ISG15 antiviral mechanism	5	10.80	9.11E-05	2.98E-03	SEH1L; NUP188; NUP35; NUP50; NUP210
1269317__REACTOME_R-HSA-1169408						
413422__KEGG_hsa_M00286;	GIN5 complex	2	103.70	9.19E-05	2.98E-03	GIN54; GIN52
890548__KEGG_M00286						
1269649__REACTOME_R-HSA-74160	Gene Expression	23	2.25	1.13E-04	3.61E-03	NUP35; MRE11; NUP210; AURKB; GADD45A; RAD50; RAD9A; AQR; PTEN; SIRT1; NCOA6; RAD17; NUP50; CDK7; CHEK1; SEH1L; NUP188; MTA1; SUV39H1; NBN; GTF2H4; TNKS1BP1; CHEK2
1269693__REACTOME_R-HSA-72202	Transport of Mature Transcript to Cytoplasm	5	10.17	1.22E-04	3.85E-03	SEH1L; NUP188; NUP35; NUP50; NUP210
1269650__REACTOME_R-HSA-212436	Generic Transcription Pathway	14	3.11	1.30E-04	4.05E-03	PTEN; NCOA6; RAD17; MRE11; CDK7; AURKB; GADD45A; RAD50; CHEK1; RAD9A; NBN; GTF2H4; TNKS1BP1; CHEK2
1269057__REACTOME_R-HSA-162906	HIV Infection	8	5.22	1.38E-04	4.25E-03	SEH1L; NUP188; FEN1; NUP35; NUP50; GTF2H4; NUP210; CDK7
1269777__REACTOME_R-HSA-69242	S Phase	6	7.32	1.59E-04	4.86E-03	GIN54; FEN1; FZR1; PDS5A; CDK7; GIN52
1309088__REACTOME_R-HSA-72306	tRNA processing	5	8.79	2.45E-04	7.42E-03	SEH1L; NUP188; NUP35; NUP50; NUP210
1269734__REACTOME_R-HSA-212165	Epigenetic regulation of gene expression	5	8.64	2.65E-04	7.95E-03	SIRT1; MTA1; SUV39H1; GTF2H4; CDK7
1268701__REACTOME_R-HSA-597592	Post-translational protein modification	15	2.68	3.75E-04	1.11E-02	PTEN; RNF168; WDR48; NUP35; TOP2B; NUP50; NUP210; AURKB; NSMCE1; CBX8; SEH1L; MTA1; NUP188; NSMCE3; UCHL5
1269737__REACTOME_R-HSA-5250941	Negative epigenetic regulation of rRNA expression	4	10.92	4.62E-04	1.36E-02	SIRT1; SUV39H1; GTF2H4; CDK7

413476__KEGG_hsa_M00413; 890628__KEGG_M00413	FA core complex	2	51.85	5.44E-04	1.58E-02	FAAP24; FANCG
1269784__REACTOME_R- HSA-69190	DNA strand elongation	3	16.37	7.49E-04	2.16E-02	GIN54; FEN1; GINS2
1309121__REACTOME_R- HSA-6783310	Fanconi Anemia Pathway	3	15.56	8.75E-04	2.50E-02	FAAP24; FANCG; MUS81
465__KEGG_ko04115; 83055__KEGG_hsa04115	p53 signaling pathway	4	9.22	8.85E-04	2.51E-02	PTEN; CHEK1; CHEK2; GADD45A
1084767__KEGG_hsa_M00691; 1108230__KEGG_M00691	DNA damage-induced cell cycle checkpoints	2	41.48	9.01E-04	2.53E-02	CHEK1; CHEK2
463__KEGG_ko04110; 83054__KEGG_hsa04110	Cell cycle	5	6.48	1.01E-03	2.80E-02	CHEK1; FZR1; CDK7; CHEK2; GADD45A
137987__Pathway Interaction Database__telomerasepathway	Regulation of Telomerase	4	8.83	1.05E-03	2.88E-02	RAD50; RAD9A; NBN; MRE11
137935__Pathway Interaction Database__foxm1pathway	FOX M1 transcription factor network	3	13.53	1.33E-03	3.64E-02	BRCA2; CHEK2; AURKB
1270429__REACTOME_R- HSA-2559586	DNA Damage/Telomere Stress Induced Senescence	3	12.96	1.51E-03	4.05E-02	RAD50; NBN; MRE11
1269757__REACTOME_R- HSA-176187	Activation of ATR in response to replication stress	3	12.96	1.51E-03	4.05E-02	CHEK1; RAD9A; RAD17
137925__Pathway Interaction Database__aurora_a_pathway	Aurora A signaling	3	12.44	1.71E-03	4.54E-02	FZR1; AURKB; GADD45A
413425__KEGG_hsa_M00290; 890551__KEGG_M00290	Holo-TFIIH complex	2	29.63	1.87E-03	4.85E-02	GTF2H4; CDK7

198895__WikiPathways__	Non-homologous end joining	2	29.63	1.87E-03	4.85E-02	RAD50; MRE11
WP438						
1458190__WikiPathways__	ATR Signaling	2	29.63	1.87E-03	4.85E-02	CHEK1; RAD9A
WP3875						

