

Supplementary Table 4. The pathways enriched in switched-on DNA repair genes.

GeneN - the observed number of genes belonging to a pathway in the switched-on genes.

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

Pathway ID	Pathway Name	GeneN	Ratio	p-value	q-value	Gene list
1309111.REACTOME_R-HSA-5696398	Nucleotide Excision Repair	34	29.87	1.69E-43	2.60E-40	PARP1; POLR2A; COPS6; POLE4; SUMO3; RAD23A; RFC1; POLR2H; POLR2J; ERCC2; UBE2I; UBE2V2; POLD3; COPS3; POLE; COPS8; POLR2K; CHD1L; HMGN1; SUMO2; COPS2; RPA2; YY1; TCEA1; SUMO1; POLR2F; ERCC3; RUVBL1; TFPT; RPA1; PCNA; PIAS3; CCNH; POLK
1268743.REACTOME_R-HSA-3108232	SUMO E3 ligases SUMOylate target proteins	29	27.35	1.26E-35	9.70E-33	PARP1; SUMO3; RING1; PML; PHC1; UBE2I; POM121C; TP53BP1; TPR; TDG; XRCC4; RANBP2; NUP153; CDKN2A; SCMH1; SUMO2; NUP85; PHC2; NDC1; SUMO1; NUP88; SMC1A; RAD21; SMC3; NUP62; RPA1; PCNA; PIAS3; PIAS2
1268744.REACTOME_R-HSA-3108214	SUMOylation of DNA damage response and repair proteins	26	34.73	1.59E-35	9.80E-33	PARP1; SUMO3; RING1; PML; PHC1; UBE2I; POM121C; TPR; TDG; XRCC4; RANBP2; NUP153; CDKN2A; SCMH1; SUMO2; NUP85; PHC2; NDC1; SUMO1; NUP88; SMC1A; RAD21; SMC3; NUP62; RPA1; PIAS2
1309112.REACTOME_R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	27	30.92	4.95E-35	2.54E-32	PARP1; COPS6; POLE4; SUMO3; RAD23A; RFC1; ERCC2; UBE2I; UBE2V2; POLD3; COPS3; POLE; COPS8; CHD1L; SUMO2; COPS2; RPA2; YY1; SUMO1; ERCC3; RUVBL1; TFPT; RPA1; PCNA; PIAS3; CCNH; POLK
1268738.REACTOME_R-HSA-2990846	SUMOylation	29	25.83	9.99E-35	4.40E-32	PARP1; SUMO3; RING1; PML; PHC1; UBE2I; POM121C; TP53BP1; TPR; TDG; XRCC4; RANBP2; NUP153; CDKN2A; SCMH1; SUMO2; NUP85; PHC2; NDC1; SUMO1; NUP88; SMC1A; RAD21; SMC3; NUP62; RPA1; PCNA; PIAS3; PIAS2
1309117.REACTOME_R-HSA-6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	22	26.12	1.46E-26	5.01E-24	POLR2A; COPS6; POLE4; RFC1; POLR2H; POLR2J; ERCC2; POLD3; COPS3; POLE; COPS8; POLR2K; HMGN1; COPS2; RPA2; TCEA1; POLR2F; ERCC3; RPA1; PCNA; CCNH; POLK
1269741.REACTOME_R-HSA-1640170	Cell Cycle	41	7.34	3.74E-25	1.15E-22	RUVBL2; POLE4; RFC1; MCM7; TUBA4A; MCM5; UBE2I; UBE2V2; FOXM1; POM121C; POLD3; CDC25C; POLE; TP53BP1; TPR; RANBP2; NUP153; CDKN2A; CDC45; RMI2; MCM3; NUP85; RPA2; NDC1; SUMO1; NUP88; TOPBP1; SMC1A; RAD21; RUVBL1; RHNO1; PTTG1; SMC3; NUP62; RBBP8; UIMC1; KAT5; RPA1; PCNA; CDCA5; CCNH
1309120.REACTOME_R-HSA-6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	18	26.23	6.57E-22	1.56E-19	POLR2A; POLE4; RFC1; POLR2H; POLR2J; ERCC2; POLD3; POLE; POLR2K; HMGN1; RPA2; TCEA1; POLR2F; ERCC3; RPA1; PCNA; CCNH; POLK
1309119.REACTOME_R-HSA-6782135	Dual incision in TC-NER	18	25.65	1.08E-21	2.38E-19	POLR2A; POLE4; RFC1; POLR2H; POLR2J; ERCC2; POLD3; POLE; POLR2K; HMGN1; RPA2; TCEA1; POLR2F; ERCC3; RPA1; PCNA; CCNH; POLK

1339112.REACTOME_R-HSA-4570464	SUMOylation of RNA binding proteins	15	33.17	2.23E-20	4.31E-18 RING1; PHC1; UBE2I; POM121C; TPR; RANBP2; NUP153; SCMH1; SUMO2; NUP85; PHC2; NDC1; SUMO1; NUP88; NUP62
1309114.REACTOME_R-HSA-5696395	Formation of Incision Complex in GG-NER	14	29.92	2.92E-18	5.30E-16 PARP1; SUMO3; RAD23A; ERCC2; UBE2I; UBE2V2; CHD1L; SUMO2; RPA2; SUMO1; ERCC3; RPA1; PIAS3; CCNH
1339113.REACTOME_R-HSA-4615885	SUMOylation of DNA replication proteins	14	28.96	5.26E-18	9.01E-16 SUMO3; UBE2I; POM121C; TPR; RANBP2; NUP153; SUMO2; NUP85; NDC1; SUMO1; NUP88; NUP62; PCNA; PIAS3
1269058.REACTOME_R-HSA-162587	HIV Life Cycle	20	12.95	2.52E-17	4.09E-15 POLR2A; POLR2H; POLR2J; ERCC2; POM121C; POLR2K; TPR; XRCC4; RANBP2; NUP153; NUP85; NDC1; TCEA1; NUP88; POLR2F; ERCC3; SSRP1; NUP62; SUPT16H; CCNH
1269117.REACTOME_R-HSA-168325	Viral Messenger RNA Synthesis	13	29.77	5.41E-17	8.16E-15 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
1269069.REACTOME_R-HSA-162599	Late Phase of HIV Life Cycle	19	13.69	5.56E-17	8.16E-15 POLR2A; POLR2H; POLR2J; ERCC2; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; TCEA1; NUP88; POLR2F; ERCC3; SSRP1; NUP62; SUPT16H; CCNH
470351.KEGG_hsa_M00427; 890636.KEGG_M00427	Nuclear pore complex	12	34.98	7.03E-17	9.87E-15 SUMO3; UBE2I; POM121C; TPR; RANBP2; NUP153; SUMO2; NUP85; NDC1; SUMO1; NUP88; NUP62
1309101.REACTOME_R-HSA-5693607	Processing of DNA double-strand break ends	15	20.91	1.18E-16	1.58E-14 PPP4C; UBE2I; UBE2V2; TP53BP1; RMI2; SUMO2; RPA2; SUMO1; TOPBP1; RNF4; RHNO1; RBBP8; UIMC1; KAT5; RPA1
1309118.REACTOME_R-HSA-6781823	Formation of TC-NER Pre-Incision Complex	14	21.90	6.13E-16	7.56E-14 POLR2A; COPS6; POLR2H; POLR2J; ERCC2; COPS3; COPS8; POLR2K; HMGN1; COPS2; TCEA1; POLR2F; ERCC3; CCNH
1269763.REACTOME_R-HSA-69278	Cell Cycle, Mitotic	29	6.30	6.84E-16	8.11E-14 POLE4; RFC1; MCM7; TUBA4A; MCM5; FOXM1; POM121C; POLD3; CDC25C; POLE; TPR; RANBP2; NUP153; CDKN2A; CDC45; MCM3; NUP85; RPA2; NDC1; NUP88; SMC1A; RAD21; PTTG1; SMC3; NUP62; RPA1; PCNA; CDCA5; CCNH
1268701.REACTOME_R-HSA-597592	Post-translational protein modification	39	4.30	1.36E-15	1.56E-13 PARP1; SUMO3; RING1; RAD23A; PML; USP47; UBE2A; PHC1; UBE2I; TRIM25; POM121C; USP28; TP53BP1; TPR; TDG; XRCC4; RANBP2; NUP153; CDKN2A; SCMH1; BAP1; SUMO2; NUP85; PHC2; NDC1; YY1; SUMO1; NUP88; SMC1A; RAD21; RUVBL1; SMC3; NUP62; UIMC1; TFPT; RPA1; PCNA; PIAS3; PIAS2
1269723.REACTOME_R-HSA-5578749	Transcriptional regulation by small RNAs	13	23.82	1.95E-15	2.15E-13 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
1309115.REACTOME_R-HSA-5696400	Dual Incision in GG-NER	12	27.48	3.06E-15	3.25E-13 PARP1; POLE4; RFC1; ERCC2; POLD3; POLE; CHD1L; RPA2; ERCC3; RPA1; PCNA; POLK
1270374.REACTOME_R-HSA-5656169	Termination of translesion DNA synthesis	11	29.39	1.82E-14	1.88E-12 POLE4; UBE2L6; RFC1; TRIM25; POLD3; POLE; REV1; RPA2; RPA1; PCNA; POLK

1270351.REACTOME_R-HSA-73884;	Base Excision Repair; Resolution of Abasic Sites (AP sites)	10	35.62	2.37E-14	2.36E-12 PARP1; POLE4; RFC1; POLD3; POLE; TDG; PNKP; RPA2; RPA1; PCNA
1270359.REACTOME_R-HSA-73933					
452.KEGG_ko03420; 83044.KEGG_hsa03420	Nucleotide excision repair	11	27.13	5.50E-14	5.14E-12 POLE4; RAD23A; RFC1; ERCC2; POLD3; POLE; RPA2; ERCC3; RPA1; PCNA; CCNH
1269777.REACTOME_R-HSA-69242	S Phase	16	12.07	1.53E-13	1.39E-11 POLE4; RFC1; MCM7; MCM5; POLD3; POLE; CDC45; MCM3; RPA2; SMC1A; RAD21; SMC3; RPA1; PCNA; CDCA5; CCNH
1269719.REACTOME_R-HSA-211000	Gene Silencing by RNA	13	17.74	1.58E-13	1.40E-11 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
1270367.REACTOME_R-HSA-73893	DNA Damage Bypass	12	20.80	1.65E-13	1.42E-11 POLE4; UBE2L6; RFC1; TRIM25; POLD3; POLE; REV1; DTL; RPA2; RPA1; PCNA; POLK
444.KEGG_ko03030; 83039.KEGG_hsa03030	DNA replication	10	30.53	1.84E-13	1.53E-11 POLE4; RFC1; MCM7; MCM5; POLD3; POLE; MCM3; RPA2; RPA1; PCNA
1269654.REACTOME_R-HSA-3700989	Transcriptional Regulation by TP53	24	6.39	2.28E-13	1.85E-11 POLR2A; PML; POLR2H; POLR2J; ERCC2; CDC25C; POLR2K; CDKN2A; RMI2; FANCI; RPA2; TCEA1; TOPBP1; POLR2F; ERCC3; RHNO1; TTC5; SSRP1; RBBP8; SUPT16H; KAT5; RPA1; PCNA; CCNH
1270369.REACTOME_R-HSA-110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	11	24.32	2.37E-13	1.87E-11 POLE4; UBE2L6; RFC1; TRIM25; POLD3; POLE; REV1; RPA2; RPA1; PCNA; POLK
1269057.REACTOME_R-HSA-162906	HIV Infection	20	8.07	3.43E-13	2.65E-11 POLR2A; POLR2H; POLR2J; ERCC2; POM121C; POLR2K; TPR; XRCC4; RANBP2; NUP153; NUP85; NDC1; TCEA1; NUP88; POLR2F; ERCC3; SSRP1; NUP62; SUPT16H; CCNH
1269857.REACTOME_R-HSA-180786	Extension of Telomeres	9	33.95	9.05E-13	6.81E-11 RUVBL2; POLE4; RFC1; POLD3; POLE; RPA2; RUVBL1; RPA1; PCNA
1269074.REACTOME_R-HSA-167169;	HIV Transcription Elongation; Tat-mediated elongation of the HIV-1 transcript;	11	21.37	1.26E-12	9.22E-11 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH
1269076.REACTOME_R-HSA-167246;	Formation of HIV-1				
1269077.REACTOME_R-HSA-167200	elongation complex containing HIV-1 Tat				
1383075.REACTOME_R-HSA-6796648	TP53 Regulates Transcription of DNA Repair Genes	12	17.49	1.72E-12	1.20E-10 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; FANCI; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH

1269080.REACTOME.R-HSA-167152	Formation of HIV elongation complex in the absence of HIV Tat	11	20.75	1.83E-12	1.26E-10 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH
1269754.REACTOME.R-HSA-69473	G2/M DNA damage checkpoint	12	17.10	2.31E-12	1.55E-10 UBE2V2; CDC25C; TP53BP1; RMI2; RPA2; SUMO1; TOPBP1; RHNO1; RBBP8; UIMC1; KAT5; RPA1
198771.WikiPathways_WP466	DNA Replication	10	24.66	2.59E-12	1.70E-10 RFC1; MCM7; MCM5; POLD3; POLE; CDC45; MCM3; RPA2; RPA1; PCNA
1269753.REACTOME.R-HSA-69481	G2/M Checkpoints	16	10.06	2.96E-12	1.90E-10 MCM7; MCM5; UBE2V2; CDC25C; TP53BP1; CDC45; RMI2; MCM3; RPA2; SUMO1; TOPBP1; RHNO1; RBBP8; UIMC1; KAT5; RPA1
1269784.REACTOME.R-HSA-69190	DNA strand elongation	9	30.37	3.35E-12	2.11E-10 RFC1; MCM7; MCM5; POLD3; CDC45; MCM3; RPA2; RPA1; PCNA
1270364.REACTOME.R-HSA-110373	Resolution of AP sites via the multiple-nucleotide patch replacement pathway	8	36.64	7.84E-12	4.74E-10 PARP1; POLE4; RFC1; POLD3; POLE; RPA2; RPA1; PCNA
1269682.REACTOME.R-HSA-75955;	RNA Polymerase II Transcription Elongation;	11	17.20	1.85E-11	1.10E-09 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH
1269684.REACTOME.R-HSA-112382	Formation of RNA Pol II elongation complex				
1309116.REACTOME.R-HSA-5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	8	32.06	3.27E-11	1.87E-09 POLE4; RFC1; POLD3; POLE; RPA2; RPA1; PCNA; POLK
1269922.REACTOME.R-HSA-170822	Regulation of Glucokinase by Glucokinase Regulatory Protein	8	32.06	3.27E-11	1.87E-09 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1309098.REACTOME.R-HSA-5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	10	19.43	4.11E-11	2.31E-09 PPP5C; UBE2I; UBE2V2; TP53BP1; BAP1; SUMO1; EYA2; EYA4; UIMC1; KAT5
1269742.REACTOME.R-HSA-69620	Cell Cycle Checkpoints	16	8.48	4.35E-11	2.40E-09 MCM7; MCM5; UBE2V2; CDC25C; TP53BP1; CDC45; RMI2; MCM3; RPA2; SUMO1; TOPBP1; RHNO1; RBBP8; UIMC1; KAT5; RPA1
1269856.REACTOME.R-HSA-157579	Telomere Maintenance	9	24.05	4.44E-11	2.40E-09 RUVBL2; POLE4; RFC1; POLD3; POLE; RPA2; RUVBL1; RPA1; PCNA
1309096.REACTOME.R-HSA-5693606	DNA Double Strand Break Response	10	18.86	5.75E-11	3.06E-09 PPP5C; UBE2I; UBE2V2; TP53BP1; BAP1; SUMO1; EYA2; EYA4; UIMC1; KAT5

1268677.REACTOME.R-HSA-392499	Metabolism of proteins	42	2.91	5.85E-11	3.06E-09 PARP1; SUMO3; RING1; RAD23A; UBE2L6; PML; USP47; UBE2A; TUBA4A; PHC1; UBE2I; TRIM25; POM121C; USP28; TP53BP1; TPR; TDG; XRCC4; RANBP2; NUP153; CDKN2A; SMC1H; BAP1; SUMO2; NUP85; PHC2; NDC1; YY1; SUMO1; NUP88; SMC1A; RAD21; RUVBL1; SMC3; NUP62; UIMC1; TFPT; RPA1; PCNA; PIAS3; PIAS2; FBXO6
451.KEGG_ko03410; 83043.KEGG_hsa03410	Base excision repair	8	30.18	6.10E-11	3.14E-09 PARP1; POLE4; POLL; POLD3; POLE; NEIL3; TDG; PCNA
198917.WikiPathways_WP405	Eukaryotic Transcription Initiation	9	23.08	6.85E-11	3.46E-09 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; POLR2F; ERCC3; POLR3K; CCNH
1269650.REACTOME.R-HSA-212436	Generic Transcription Pathway	29	3.98	8.61E-11	4.29E-09 PARP1; POLR2A; PML; POLR2H; POLR2J; ERCC2; UBE2I; CDC25C; POLR2K; CDKN2A; RMI2; FANCI; RPA2; YY1; TCEA1; SUMO1; MEN1; TOPBP1; POLR2F; ERCC3; RHNO1; TTC5; SSRP1; RBBP8; SUPT16H; KAT5; RPA1; PCNA; CCNH
1269070.REACTOME.R-HSA-167172	Transcription of the HIV genome	11	15.01	9.40E-11	4.60E-09 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH
1269123.REACTOME.R-HSA-168333	NEP/NS2 Interacts with the Cellular Export Machinery	8	28.50	1.08E-10	5.07E-09 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269114.REACTOME.R-HSA-168271	Transport of Ribonucleoproteins into the Host Nucleus	8	28.50	1.08E-10	5.07E-09 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269121.REACTOME.R-HSA-168274	Export of Viral Ribonucleoproteins from Nucleus	8	28.50	1.08E-10	5.07E-09 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1309113.REACTOME.R-HSA-5696394	DNA Damage Recognition in GG-NER	9	20.61	2.23E-10	1.01E-08 PARP1; COPS6; RAD23A; COPS3; COPS8; COPS2; YY1; RUVBL1; TFPT
1270366.REACTOME.R-HSA-5651801	PCNA-Dependent Long Patch Base Excision Repair	7	34.53	3.03E-10	1.22E-08 POLE4; RFC1; POLD3; POLE; RPA2; RPA1; PCNA
1269859.REACTOME.R-HSA-174417	Telomere C-strand (Lagging Strand) Synthesis	7	34.53	3.03E-10	1.22E-08 POLE4; RFC1; POLD3; POLE; RPA2; RPA1; PCNA
1339110.REACTOME.R-HSA-3232118	SUMOylation of transcription factors	7	34.53	3.03E-10	1.22E-08 SUMO3; UBE2I; TP53BP1; CDKN2A; SUMO2; SUMO1; PIAS3
1269817.REACTOME.R-HSA-3301854	Nuclear Pore Complex (NPC) Disassembly	8	25.65	3.04E-10	1.22E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269773.REACTOME.R-HSA-68962	Activation of the pre-replicative complex	8	25.65	3.04E-10	1.22E-08 POLE4; MCM7; MCM5; POLE; CDC45; MCM3; RPA2; RPA1

1269073.REACTOME.R-HSA-167160;	RNA Pol II CTD phosphorylation and interaction with CE during HIV infection; RNA Pol II CTD phosphorylation and interaction with CE	8	25.65	3.04E-10	1.22E-08 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1269681.REACTOME.R-HSA-77075					
1269094.REACTOME.R-HSA-180910	Vpr-mediated nuclear import of PICs	8	25.65	3.04E-10	1.22E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269096.REACTOME.R-HSA-180746	Nuclear import of Rev protein	8	25.65	3.04E-10	1.22E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269697.REACTOME.R-HSA-159227	Transport of the SLBP independent Mature mRNA	8	25.65	3.04E-10	1.22E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
175229.KEGG_ko03013; 177876.KEGG_hsa03013	RNA transport	14	8.98	3.54E-10	1.40E-08 SUMO3; UBE2I; UPF1; POM121C; TPR; RANBP2; NUP153; SUMO2; NUP85; NDC1; SUMO1; NUP88; TACC3; NUP62
1269676.REACTOME.R-HSA-674695	RNA Polymerase II Pre-transcription Events	11	13.06	4.71E-10	1.82E-08 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH
1269085.REACTOME.R-HSA-165054	Rev-mediated nuclear export of HIV RNA	8	24.43	4.85E-10	1.82E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269687.REACTOME.R-HSA-72086	mRNA Capping	8	24.43	4.85E-10	1.82E-08 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1269696.REACTOME.R-HSA-159230	Transport of the SLBP Dependant Mature mRNA	8	24.43	4.85E-10	1.82E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
198805.WikiPathways_WP45	G1 to S cell cycle control	10	14.57	9.53E-10	3.54E-08 MCM7; MCM5; POLE; CDKN2A; CDC45; MCM3; RPA2; RPA1; PCNA; CCNH
1269092.REACTOME.R-HSA-176033	Interactions of Vpr with host cellular proteins	8	22.30	1.14E-09	4.03E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1270368.REACTOME.R-HSA-110314	Recognition of DNA damage by PCNA-containing replication complex	8	22.30	1.14E-09	4.03E-08 POLE4; RFC1; POLD3; POLE; DTL; RPA2; RPA1; PCNA
1269131.REACTOME.R-HSA-168276	NS1 Mediated Effects on Host Pathways	8	22.30	1.14E-09	4.03E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269095.REACTOME.R-HSA-177243	Interactions of Rev with host cellular proteins	8	22.30	1.14E-09	4.03E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62

1269649.REACTOME.R-HSA-74160	Gene Expression	43	2.60	1.15E-09	4.03E-08 PARP1; POLR2A; PML; POLR2H; POLR2J; ERCC2; UBE2I; UPF1; POM121C; CDC25C; POLR2K; TPR; TDG; PRPF38A; RANBP2; NUP153; CDKN2A; UHRF1; RMI2; FANCI; NUP85; RPA2; NDC1; YY1; TCEA1; SUMO1; MEN1; NUP88; TOPBP1; POLR2F; ERCC3; RHNO1; TTC5; POLR3K; SSRP1; NUP62; RBBP8; INTS3; SUPT16H; KAT5; RPA1; PCNA; CCNH
1269853.REACTOME.R-HSA-73886	Chromosome Maintenance	9	17.49	1.16E-09	4.03E-08 RUVBL2; POLE4; RFC1; POLD3; POLE; RPA2; RUVBL1; RPA1; PCNA
920977.WikiPathways_WP2446	Retinoblastoma (RB) in Cancer	11	11.95	1.29E-09	4.42E-08 MCM7; POLD3; POLE; CDC45; MCM3; RPA2; HMGB2; SMC1A; SMC3; RPA1; PCNA
1269698.REACTOME.R-HSA-159231	Transport of Mature mRNA Derived from an Intronless Transcript	8	21.37	1.68E-09	5.71E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1270425.REACTOME.R-HSA-3371453	Regulation of HSF1-mediated heat shock response	10	13.64	1.91E-09	6.41E-08 POM121C; TPR; RANBP2; NUP153; NUP85; RPA2; NDC1; NUP88; NUP62; RPA1
1269316.REACTOME.R-HSA-1169410;	Antiviral mechanism by IFN-stimulated genes; ISG15	10	13.36	2.38E-09	7.77E-08 UBE2L6; TRIM25; POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269317.REACTOME.R-HSA-1169408	antiviral mechanism				
1269082.REACTOME.R-HSA-167243;	Tat-mediated HIV elongation arrest and recovery; Pausing	8	20.52	2.44E-09	7.77E-08 POLR2A; POLR2H; POLR2J; POLR2K; TCEA1; POLR2F; SSRP1; SUPT16H
1269083.REACTOME.R-HSA-167238	and recovery of Tat-mediated HIV elongation				
1269130.REACTOME.R-HSA-168253	Host Interactions with Influenza Factors	8	20.52	2.44E-09	7.77E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269921.REACTOME.R-HSA-70153	Glucose transport	8	20.52	2.44E-09	7.77E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269695.REACTOME.R-HSA-159234	Transport of Mature mRNAs Derived from Intronless Transcripts	8	20.52	2.44E-09	7.77E-08 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
463.KEGG_ko04110; 83054.KEGG_hsa04110	Cell cycle	12	9.62	3.05E-09	9.50E-08 MCM7; MCM5; CDC25C; CDKN2A; CDC45; MCM3; SMC1A; RAD21; PTTG1; SMC3; PCNA; CCNH

1269075.REACTOME.R-	Formation of the HIV-1 Early Elongation Complex;	8	19.73	3.48E-09	1.06E-07 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1269683.REACTOME.R-	Formation of the Early Elongation Complex				
1269079.REACTOME.R-	HIV elongation arrest and recovery; Pausing and recovery of HIV elongation	8	19.73	3.48E-09	1.06E-07 POLR2A; POLR2H; POLR2J; POLR2K; TCEA1; POLR2F; SSRP1; SUPT16H
1269081.REACTOME.R-					
198811.WikiPathways_WP_179	Cell Cycle	11	10.85	3.81E-09	1.15E-07 MCM7; MCM5; CDC25C; CDKN2A; CDC45; MCM3; MEN1; SMC1A; PTTG1; PCNA; CCNH
1269920.REACTOME.R-	Hexose transport	8	18.32	6.75E-09	2.00E-07 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1309110.REACTOME.R-	Nonhomologous End-Joining (NHEJ)	8	17.69	9.20E-09	2.70E-07 POLL; UBE2V2; TP53BP1; XRCC4; TDP1; SUMO1; UIMC1; KAT5
1269779.REACTOME.R-	Synthesis of DNA	11	9.66	1.36E-08	3.96E-07 POLE4; RFC1; MCM7; MCM5; POLD3; POLE; CDC45; MCM3; RPA2; RPA1; PCNA
1269056.REACTOME.R-	Infectious disease	20	4.48	1.48E-08	4.26E-07 POLR2A; POLR2H; POLR2J; ERCC2; POM121C; POLR2K; TPR; XRCC4; RANBP2; NUP153; NUP85; NDC1; TCEA1; NUP88; POLR2F; ERCC3; SSRP1; NUP62; SUPT16H; CCNH
1269731.REACTOME.R-	Metabolism of non-coding RNA; snRNP Assembly	8	16.55	1.65E-08	4.71E-07 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269732.REACTOME.R-					
1270372.REACTOME.R-	Translesion synthesis by POLK	6	29.59	2.01E-08	5.70E-07 RFC1; REV1; RPA2; RPA1; PCNA; POLK
1309089.REACTOME.R-	tRNA processing in the nucleus	8	16.03	2.17E-08	6.03E-07 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
HSA-167158;					
HSA-113418					
HSA-167287;					
HSA-167290					

1269071.REACTOME.R-	HIV Transcription Initiation; RNA Polymerase II HIV	8	16.03	2.17E-08	6.03E-07 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
HSA-167161;					
1269072.REACTOME.R-	Promoter Escape; RNA Polymerase II Transcription				
HSA-167162;					
1269677.REACTOME.R-	Pre-Initiation And Promoter Opening; RNA Polymerase II				
HSA-73779;					
1269678.REACTOME.R-	Transcription Initiation And Promoter Clearance; RNA				
HSA-76042;					
1269679.REACTOME.R-	Polymerase II Transcription Initiation; RNA Polymerase II				
HSA-75953;					
1269680.REACTOME.R-	Promoter Escape				
HSA-73776					
1269115.REACTOME.R-	Influenza Viral RNA Transcription and Replication	13	7.25	2.24E-08	6.18E-07 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
HSA-168273					
1269875.REACTOME.R-	DNA Replication	11	9.16	2.43E-08	6.62E-07 POLE4; RFC1; MCM7; MCM5; POLD3; POLE; CDC45; MCM3; RPA2; RPA1; PCNA
HSA-69306					
1270421.REACTOME.R-	Cellular response to heat stress	10	10.51	2.77E-08	7.49E-07 POM121C; TPR; RANBP2; NUP153; NUP85; RPA2; NDC1; NUP88; NUP62; RPA1
HSA-3371556					
1269815.REACTOME.R-	Nuclear Envelope Breakdown	8	15.09	3.65E-08	9.78E-07 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
HSA-2980766					
1309108.REACTOME.R-	HDR through Single Strand Annealing (SSA)	7	19.52	3.81E-08	1.01E-06 RMI2; RPA2; TOPBP1; RHNO1; RBBP8; KAT5; RPA1
HSA-5685938					
309.KEGG_ko00240;	Pyrimidine metabolism	10	10.18	3.82E-08	1.01E-06 POLR2A; POLE4; POLR2H; POLR2J; POLD3; POLE; POLR2K; POLR2F; DUT; POLR3K
82946.KEGG_hsa00240					
1269109.REACTOME.R-	Influenza Life Cycle	13	6.78	5.07E-08	1.32E-06 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
HSA-168255					
1269311.REACTOME.R-	Interferon Signaling	12	7.54	5.11E-08	1.32E-06 UBE2L6; PML; TRIM25; POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; SUMO1; NUP88; NUP62
HSA-913531					
1269757.REACTOME.R-	Activation of ATR in response to replication stress	7	18.70	5.30E-08	1.35E-06 MCM7; MCM5; CDC25C; CDC45; MCM3; RPA2; RPA1
HSA-176187					
1309104.REACTOME.R-	Presynaptic phase of homologous DNA pairing and strand exchange	7	17.95	7.27E-08	1.84E-06 RMI2; RPA2; TOPBP1; RHNO1; RBBP8; KAT5; RPA1
HSA-5693616					

1383076.REACTOME.R-HSA-5633007	Regulation of TP53 Activity	12	7.26	7.90E-08	1.98E-06 PML; CDKN2A; RMI2; RPA2; TOPBP1; RHNO1; TTC5; SSRP1; RBBP8; SUPT16H; KAT5; RPA1
1309103.REACTOME.R-HSA-5693579	Homologous DNA Pairing and Strand Exchange	7	17.26	9.82E-08	2.43E-06 RMI2; RPA2; TOPBP1; RHNO1; RBBP8; KAT5; RPA1
1269108.REACTOME.R-HSA-168254	Influenza Infection	13	6.41	9.85E-08	2.43E-06 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
377128.KEGG_ko03460; 377262.KEGG_hsa03460	Fanconi anemia pathway	7	16.62	1.31E-07	3.18E-06 REV1; RMI2; FANCI; RPA2; FAAP100; RPA1; POLK
1269788.REACTOME.R-HSA-69186	Lagging Strand Synthesis	5	32.06	2.02E-07	4.88E-06 RFC1; POLD3; RPA2; RPA1; PCNA
1269688.REACTOME.R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	14	5.51	2.11E-07	5.04E-06 POLR2A; POLR2H; POLR2J; POM121C; POLR2K; TPR; PRPF38A; RANBP2; NUP153; NUP85; NDC1; NUP88; POLR2F; NUP62
1339139.REACTOME.R-HSA-5619507;	Activation of HOX genes during differentiation;	8	12.21	2.13E-07	5.07E-06 POLR2A; POLR2H; POLR2J; POLR2K; PAGR1; YY1; POLR2F; PIAS2
1339140.REACTOME.R-HSA-5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis				
1269793.REACTOME.R-HSA-2468052	Establishment of Sister Chromatid Cohesion	4	51.30	2.79E-07	6.58E-06 SMC1A; RAD21; SMC3; CDCA5
442.KEGG_ko03020; 83037.KEGG_hsa03020	RNA polymerase	6	20.25	2.95E-07	6.89E-06 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F; POLR3K
1383080.REACTOME.R-HSA-6804756	Regulation of TP53 Activity through Phosphorylation	9	9.62	3.13E-07	7.25E-06 RMI2; RPA2; TOPBP1; RHNO1; SSRP1; RBBP8; SUPT16H; KAT5; RPA1
1269675.REACTOME.R-HSA-73857	RNA Polymerase II Transcription	11	7.12	3.42E-07	7.88E-06 POLR2A; POLR2H; POLR2J; ERCC2; POLR2K; TCEA1; POLR2F; ERCC3; SSRP1; SUPT16H; CCNH
453.KEGG_ko03430; 83045.KEGG_hsa03430	Mismatch repair	5	29.15	3.66E-07	8.31E-06 RFC1; POLD3; RPA2; RPA1; PCNA
413415.KEGG_hsa_M00180; 890456.KEGG_M00180	RNA polymerase II, eukaryotes	5	29.15	3.66E-07	8.31E-06 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
1269694.REACTOME.R-HSA-159236	Transport of Mature mRNA derived from an Intron-Containing Transcript	8	11.40	3.75E-07	8.44E-06 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62

1269764.REACTOME.R-HSA-453279	Mitotic G1-G1/S phases	11	7.05	3.79E-07	8.48E-06 POLE4; MCM7; MCM5; POLE; CDKN2A; CDC45; MCM3; RPA2; RPA1; PCNA; CCNH
1270373.REACTOME.R-HSA-5656121	Translesion synthesis by POLI	5	26.72	6.20E-07	1.37E-05 RFC1; REV1; RPA2; RPA1; PCNA
1270370.REACTOME.R-HSA-110312	Translesion synthesis by REV1	5	26.72	6.20E-07	1.37E-05 RFC1; REV1; RPA2; RPA1; PCNA
1269768.REACTOME.R-HSA-69206	G1/S Transition	10	7.54	7.00E-07	1.53E-05 POLE4; MCM7; MCM5; POLE; CDC45; MCM3; RPA2; RPA1; PCNA; CCNH
1269865.REACTOME.R-HSA-1500620	Meiosis	7	13.20	7.24E-07	1.57E-05 UBE2I; RPA2; SMC1A; RAD21; SMC3; RBBP8; RPA1
1269661.REACTOME.R-HSA-73772	RNA Polymerase I Promoter Escape	6	17.49	7.80E-07	1.67E-05 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1269663.REACTOME.R-HSA-73863	RNA Polymerase I Transcription Termination	6	17.49	7.80E-07	1.67E-05 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1270412.REACTOME.R-HSA-5358565	Mismatch repair (MMR) directed by MSH2:MSH6 (MutSalpha)	4	42.75	8.27E-07	1.75E-05 POLD3; RPA2; RPA1; PCNA
1268742.REACTOME.R-HSA-3065678	SUMO is transferred from E1 to E2 (UBE2I, UBC9)	4	42.75	8.27E-07	1.75E-05 SUMO3; UBE2I; SUMO2; SUMO1
1269693.REACTOME.R-HSA-72202	Transport of Mature Transcript to Cytoplasm	8	10.06	1.02E-06	2.15E-05 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1383045.REACTOME.R-HSA-8851708	Signaling by FGFR2 IIIa TM	5	22.90	1.53E-06	3.15E-05 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
1269724.REACTOME.R-HSA-5601884	PIWI-interacting RNA (piRNA) biogenesis	5	22.90	1.53E-06	3.15E-05 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
1270413.REACTOME.R-HSA-5358606	Mismatch repair (MMR) directed by MSH2:MSH3 (MutSbeta)	4	36.64	1.91E-06	3.82E-05 POLD3; RPA2; RPA1; PCNA
1269863.REACTOME.R-HSA-174437	Removal of the Flap Intermediate from the C-strand	4	36.64	1.91E-06	3.82E-05 POLD3; RPA2; RPA1; PCNA
1270411.REACTOME.R-HSA-5358508	Mismatch Repair	4	36.64	1.91E-06	3.82E-05 POLD3; RPA2; RPA1; PCNA
1269862.REACTOME.R-HSA-174414	Processive synthesis on the C-strand of the telomere	4	36.64	1.91E-06	3.82E-05 POLD3; RPA2; RPA1; PCNA

454_KEGG_ko03440;	Homologous recombination	6	14.80	2.29E-06	4.55E-05 POLD3; RPA2; TOPBP1; RBBP8; UIMC1; RPA1
83046_KEGG_hsa03440					
1269810.REACTOME_R-HSA-68886	M Phase	13	4.85	2.52E-06	4.98E-05 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; SMC1A; RAD21; PTTG1; SMC3; NUP62; CDCA5
1270414.REACTOME_R-HSA-2262752	Cellular responses to stress	16	3.92	2.82E-06	5.54E-05 RING1; PHC1; POM121C; TPR; RANBP2; NUP153; CDKN2A; SCMH1; NUP85; PHC2; RPA2; NDC1; NUP88; NUP62; KAT5; RPA1
1269662.REACTOME_R-HSA-73777	RNA Polymerase I Chain Elongation	6	14.25	2.90E-06	5.67E-05 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1309088.REACTOME_R-HSA-72306	tRNA processing	8	8.69	3.21E-06	6.23E-05 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1269734.REACTOME_R-HSA-212165	Epigenetic regulation of gene expression	8	8.55	3.66E-06	7.05E-05 POLR2H; ERCC2; POLR2K; TDG; UHRF1; POLR2F; ERCC3; CCNH
198875_WikiPathways_WP531	Mismatch repair	3	64.12	3.71E-06	7.09E-05 RFC1; RPA1; PCNA
1269790.REACTOME_R-HSA-69166	Removal of the Flap Intermediate	4	32.06	3.77E-06	7.09E-05 POLD3; RPA2; RPA1; PCNA
1268739.REACTOME_R-HSA-3215018	Processing and activation of SUMO	4	32.06	3.77E-06	7.09E-05 SUMO3; UBE2I; SUMO2; SUMO1
1269789.REACTOME_R-HSA-69183	Processive synthesis on the lagging strand	4	32.06	3.77E-06	7.09E-05 POLD3; RPA2; RPA1; PCNA
1269720.REACTOME_R-HSA-203927	MicroRNA (miRNA) biogenesis	5	18.86	4.55E-06	8.51E-05 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
1269831.REACTOME_R-HSA-68874;	M/G1 Transition; DNA Replication Pre-Initiation	8	8.02	6.00E-06	1.12E-04 POLE4; MCM7; MCM5; POLE; CDC45; MCM3; RPA2; RPA1
1269832.REACTOME_R-HSA-69002					
138029_Pathway Interaction Database_ranbp2pathway	Sumoylation by RanBP2 regulates transcriptional repression	4	28.50	6.70E-06	1.23E-04 UBE2I; RANBP2; SUMO1; PIAS2
1269785.REACTOME_R-HSA-176974	Unwinding of DNA	4	28.50	6.70E-06	1.23E-04 MCM7; MCM5; CDC45; MCM3
1269811.REACTOME_R-HSA-68875	Mitotic Prophase	8	7.89	6.76E-06	1.23E-04 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
1268870.REACTOME_R-HSA-1839126	FGFR2 mutant receptor activation	5	16.87	8.34E-06	1.51E-04 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F

1269078.REACTOME.R-HSA-167242	Abortive elongation of HIV-1 transcript in the absence of Tat	5	16.87	8.34E-06	1.51E-04 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
1309121.REACTOME.R-HSA-6783310	Fanconi Anemia Pathway	5	16.03	1.10E-05	1.94E-04 FANCI; RPA2; FAAP20; FAAP100; RPA1
1383022.REACTOME.R-HSA-6803529	FGFR2 alternative splicing	5	16.03	1.10E-05	1.94E-04 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
413416.KEGG.hsa_M00181; 890457.KEGG.M00181	RNA polymerase III, eukaryotes	4	25.65	1.10E-05	1.94E-04 POLR2H; POLR2K; POLR2F; POLR3K
1269660.REACTOME.R-HSA-73762	RNA Polymerase I Transcription Initiation	6	11.32	1.21E-05	2.10E-04 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1458202.WikiPathways.W-P3878	ATM Signaling Network in Development and Disease	6	10.99	1.44E-05	2.49E-04 PPP5C; TP53BP1; HMGN1; SMC1A; RBBP8; KAT5
1269739.REACTOME.R-HSA-427413	NoRC negatively regulates rRNA expression	6	10.69	1.70E-05	2.93E-04 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
1269670.REACTOME.R-HSA-73780	RNA Polymerase III Chain Elongation	4	23.32	1.71E-05	2.94E-04 POLR2H; POLR2K; POLR2F; POLR3K
1269737.REACTOME.R-HSA-5250941	Negative epigenetic regulation of rRNA expression	6	10.12	2.35E-05	4.01E-04 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
307.KEGG.ko00230; 82944.KEGG.hsa00230	Purine metabolism	9	5.77	2.38E-05	4.03E-04 POLR2A; POLE4; POLR2H; POLR2J; POLD3; POLE; POLR2K; POLR2F; POLR3K
1268869.REACTOME.R-HSA-5655253	Signaling by FGFR2 in disease	5	12.82	3.53E-05	5.93E-04 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
1270371.REACTOME.R-HSA-110320	Translesion Synthesis by POLH	4	19.73	3.62E-05	5.95E-04 RFC1; RPA2; RPA1; PCNA
1269671.REACTOME.R-HSA-73980	RNA Polymerase III Transcription Termination	4	19.73	3.62E-05	5.95E-04 POLR2H; POLR2K; POLR2F; POLR3K
1268741.REACTOME.R-HSA-3065676	SUMO is conjugated to E1 (UBA2:SAE1)	3	38.47	3.62E-05	5.95E-04 SUMO3; SUMO2; SUMO1
1268740.REACTOME.R-HSA-3065679	SUMO is proteolytically processed	3	38.47	3.62E-05	5.95E-04 SUMO3; SUMO2; SUMO1
1269658.REACTOME.R-HSA-73854	RNA Polymerase I Promoter Clearance	6	9.38	3.69E-05	6.02E-04 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH

1269656.REACTOME.R-	RNA Polymerase I, RNA Polymerase III, and Mitochondrial Transcription	7	7.48	3.71E-05	6.03E-04 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; POLR3K; CCNH
HSA-504046					
1383088.REACTOME.R-	RNA polymerase II transcribes snRNA genes	6	9.16	4.25E-05	6.86E-04 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F; INTS3
HSA-6807505					
1270346.REACTOME.R-	Transcriptional regulation of pluripotent stem cells	5	12.33	4.32E-05	6.95E-04 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
HSA-452723					
1269657.REACTOME.R-	RNA Polymerase I Transcription	6	8.95	4.87E-05	7.79E-04 POLR2H; ERCC2; POLR2K; POLR2F; ERCC3; CCNH
HSA-73864					
466.KEGG_ko04120;	Ubiquitin mediated proteolysis	8	5.90	5.87E-05	9.34E-04 UBE2L6; PML; TRIP12; UBE2A; UBE2I; UBR5; PIAS3; PIAS2
83056.KEGG_hsa04120					
1268854.REACTOME.R-	Disease	21	2.54	6.61E-05	1.04E-03 POLR2A; POLR2H; POLR2J; ERCC2; POM121C; CDC25C; POLR2K; TPR; XRCC4; RANBP2; NUP153; NUP85; NDC1; TCEA1; NUP88; POLR2F; ERCC3; SSRP1; NUP62; SUPT16H; CCNH
HSA-1643685					
1269907.REACTOME.R-	SLC-mediated transmembrane transport	9	5.06	6.75E-05	1.06E-03 POM121C; TPR; RANBP2; NUP153; SLC25A10; NUP85; NDC1; NUP88; NUP62
HSA-425407					
413421.KEGG_hsa_M00285	MCM complex	3	32.06	7.16E-05	1.11E-03 MCM7; MCM5; MCM3
5; 890547.KEGG_M00285					
1269830.REACTOME.R-	Cohesin Loading onto Chromatin	3	32.06	7.16E-05	1.11E-03 SMC1A; RAD21; SMC3
HSA-2470946					
1269667.REACTOME.R-	RNA Polymerase III Transcription Initiation From Type 1 Promoter	4	16.03	8.89E-05	1.36E-03 POLR2H; POLR2K; POLR2F; POLR3K
HSA-76061					
1269669.REACTOME.R-	RNA Polymerase III Transcription Initiation From Type 3 Promoter	4	16.03	8.89E-05	1.36E-03 POLR2H; POLR2K; POLR2F; POLR3K
HSA-76071					
1269668.REACTOME.R-	RNA Polymerase III Transcription Initiation From Type 2 Promoter	4	16.03	8.89E-05	1.36E-03 POLR2H; POLR2K; POLR2F; POLR3K
HSA-76066					
920989.WikiPathways_WP1530	miRNA Regulation of DNA Damage Response	6	8.02	9.20E-05	1.40E-03 RFC1; PML; MCM7; CDC25C; RPA2; SMC1A
1269091.REACTOME.R-	Host Interactions of HIV factors	8	5.52	9.46E-05	1.43E-03 POM121C; TPR; RANBP2; NUP153; NUP85; NDC1; NUP88; NUP62
HSA-162909					

1269786.REACTOME.R-	Leading Strand Synthesis; Polymerase switching;	3	27.48	1.24E-04	1.86E-03 RFC1; POLD3; PCNA
HSA-69109;					
1269787.REACTOME.R-	Polymerase switching on the C-strand of the telomere				
HSA-69091;					
1269861.REACTOME.R-					
HSA-174411					
413425.KEGG.hsa_M0029	Holo-TFIIH complex	3	27.48	1.24E-04	1.86E-03 ERCC2; ERCC3; CCNH
0; 890551.KEGG.M00290					
1268863.REACTOME.R-	Signaling by FGFR in disease	5	9.16	1.91E-04	2.84E-03 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
HSA-1226099					
1269821.REACTOME.R-	Resolution of Sister Chromatid Cohesion	6	6.87	2.20E-04	3.25E-03 RANBP2; NUP85; SMC1A; RAD21; SMC3; CDCA5
HSA-2500257					
1269666.REACTOME.R-	RNA Polymerase III Transcription Initiation	4	12.82	2.26E-04	3.31E-03 POLR2H; POLR2K; POLR2F; POLR3K
HSA-76046					
413423.KEGG.hsa_M0028	RPA complex	2	64.12	2.41E-04	3.53E-03 RPA2; RPA1
8; 468376.KEGG.M00288					
1269867.REACTOME.R-	Meiotic synapsis	4	12.21	2.75E-04	4.01E-03 UBE2I; SMC1A; RAD21; SMC3
HSA-1221632					
413479.KEGG.hsa_M0018	RNA polymerase I, eukaryotes	3	21.37	2.91E-04	4.19E-03 POLR2H; POLR2K; POLR2F
2; 890458.KEGG.M00182					
1269829.REACTOME.R-	Mitotic Telophase/Cytokinesis	3	21.37	2.91E-04	4.19E-03 SMC1A; RAD21; SMC3
HSA-68884					
1269664.REACTOME.R-	RNA Polymerase III Transcription; RNA	4	11.66	3.32E-04	4.77E-03 POLR2H; POLR2K; POLR2F; POLR3K
HSA-74158;					
1269665.REACTOME.R-	Polymerase III Abortive And Retractive Initiation				
HSA-749476					
1269691.REACTOME.R-	mRNA Splicing - Minor Pathway	5	7.82	4.08E-04	5.83E-03 POLR2A; POLR2H; POLR2J; POLR2K; POLR2F
HSA-72165					
1269820.REACTOME.R-	Mitotic Prometaphase	6	6.11	4.21E-04	5.98E-03 RANBP2; NUP85; SMC1A; RAD21; SMC3; CDCA5
HSA-68877					
198806.WikiPathways_WP	Androgen receptor signaling pathway	6	5.92	4.99E-04	7.03E-03 UBE2I; SUMO1; RNF4; KAT5; PIAS3; PIAS2
138					