Biological Processes	PValue	Fold Enrichment	Genes
DNA repair	3.20154E-09	2.325100449	SMG1, BCCIP, MUM1, SMC3, ALKBH2, EPC2, TOPBP1, NBN, POLK, GEN1, PARP3, SUPT16H, USP3, USP45, ATRX, RECQL, SMC1A, SIRT1, UCHL5, DDB2, KIN, RRM2B, FANCD2, MORF4L2, PSME4, OTUB1, BLM, INO80E, BOD1L1, XPA, ZBTB1, PDS5B, BRCC3, PDS5A, TFPT, WRN, UBR5, RBBP8, FANCI, MBD4, POLM, ERCC6L2, MCRS1, TREX2, APEX2, CDC5L, GTF2H1, RAD50, TAOK3, TAOK1, JMY, CDK1, SPRTN, TRIP12, RAD18, ATR
transcription, DNA-templated	9.11255E-08	1.347530357	RB1, ZNF175, JMJD1C, CCAR2, IKZF5, PNN, ZMIZ2, GPBP1, ZNF845, EPC2, ZNF600, TRIM27, ZNF721, SOX7, HOXA4, TSPYL2, SMARCC1, SFMBT1, ZNF160, ZNF281, CSNK2A2, DNTTIP2, EBF4, ZNF14, THAP7, HOXB4, COMMD3-BMI1, VOPP1, SRFBP1, VPS25, CLOCK, ATF6, PRR13, ZNF277, ZNF28, URI1, ZNF273, MYCBP2, CTR9, SUPT4H1, BA22B, HIF1A, ZNF708, MIER3, DHX36, MIER1, ZSCAN12, ZNF267, ZSCAN18, ZNF140, MTERF2, NR2F1, SMARCA1, MOV10, ZZZ3, ZNF37A, TRIP6, ZNF813, ZNF702P, CREBRF, HBP1, RBAK, ZNF254, PHF3, ZNF253, ZNF131, ZNF493, ADIRF, ZNF43, ZNF808, ZMYM2, MECOM, HEY1, ZNF486, BATF2, ZNF121, PBRM1, ZNF480, COMMD3, PPHLN1, BA21A, BA21B, ZNF57, DYNLL1, SIRT1, ZFX, ZHX1, SETSIP, UCHL5, TOPORS, AES, MED22, GCFC2, ZEB1, SLTM, TFEC, WAC, ZNF117, NCOA7, SP100, ZNF350, ZNF518B, TNLNG, ARNT1L2, RXRB, BCLAF1, TCEAL6, TCEAL3, TCEAL2, ZNF107, PCGF1, ZNF347, ZNF468, APBB1, BRD7, TCEAL9, ZNF100, SUZ12, MCRS1, ATAD2, GTF2H1, LRPPRC, ZNF33A, RYBP, ZNF70, RLIM, TCEA1, PKN2, PKN1, ZNF354A, ZNF354B, ZNF451, ZNF570, ARID4B, RORA, AHR, BZW1, ZNF208, ZNF85, ZNF326, ZNF689, CIR1, KMT5B, ZNF688, ARID2, MAP3K7, ZNF320, ZNF440, ZNF99, ZBTB33, POLRMT, HIC1, ZNF91, ZNF92, ZNF93, DMTF1, TBL1XR1, MORF4L2, ZNF439, ZNF799, ZNF676, ZNF675, ZNF432, ZNF431, KMT2E, ZNF430, ZNF791, INO80E, DDX1, NPAT, ZNF876P, HNRNPDL, BPTF, ZNF782, ZNF660, CBX7, DENND4A, ZBTB11, CNOT2, TADA3, BRWD1, ZNF654, NFE2L2, ZNF512B, ZNF770, PHTF2, DDX3X, LDB1, CHD9, CHD7, CHD2, CHD1, MYSM1, PHTF1, LBH, VPS72, RB1CC1, ZNF407, ZNF525, ZNF765, ZNF644, LRRFIP1, IFT57, ZNF761, RFC1, EED, ATRX, EDF1, ZNF75A, DNAJC2, ELF2, ZNF638, ZNF517, LCOR, BDP1, ZNF510, BIRC2, HDAC5, GTF3C2, GTF3C3, PRKAA1, SMARCD2, HDAC2, USP16, ZNF195, GTF3C5, ATF6B, ZBTB45, ZBTB41, IWS1, CAND2, TFPT, TAF1B, POLR2B, TGS1, NRIP1, ERBB2, ZNF286B, POLR2E, POLR2F, POLR2G, ASCC3, POLR2J, POLR2J, E2F6, ZNF189, ZNF286A, POLR2J3, RBM39, POLR2J2, ZNF184, MACC1, CCDC59, CDC5L, TBX4, TBX2, PNRC2, POLR3B, POLR3C, ZNF616, ZNF737, ZNF615, ZNF614, ESF1, TRIM37, NAA15, ZNF732, PAXBP1, ZNF730, TRIM33
cell division	1.48872E-07	1.923546111	RB1, USP37, SYCP2, CLTC, KIF14, CIB1, SMC5, KIF11, SMC1A, SMC3, SMC4, CDC73, CKS1B, SMC2, BABAM1, PPP1CB, MIS18BP1, CNTRL, CDC27, KNTC1, FBXO5, SPDL1, LZTS2, LRRCC1, NSMCE2, LIG4, PRPF40A, KNL1, SMC1A, TERF1, CKAP5, CD2AP, SGO2, CDC34, CCNE2, KIF2A, BIRC6, CEP63, KIF20B, USP16, RGS14, GNAI3, NCAPG, PDS5B, BRCC3, PDS5A, HAUS7, ASUN, KATNA1, RAD21, TPR, RBBP8, EVI5, UBE2I, SPAGS, USP9X, WAPL, PPP1CA, CENPE, TPX2, STAG1, CENPF, STAG2, CDK5, FAM175B, CENPJ, CDK1, CDK10, PKN2, SPG20
regulation of transcription, DNA-templated	1.96299E-07	1.394800771	ZNF175, NUP107, JMJD1C, CCAR2, IKZF5, PNN, SOX17, ZNF728, GPBP1, ZNF845, ZNF600, ZNF721, ZNF720, HOXA4, PKNOX2, TSPYL2, SFMBT1, ZNF160, CSNK2A2, DNTTIP2, EBF4, ZNF14, CARHSP1, VOPP1, SRFBP1, VPS25, CLOCK, PRR13, ZNF277, ZNF28, ZNF273, MYCBP2, CTR9, SUPT4H1, BA22B, HIF1A, ZNF708, MIER3, ZSCAN12, ZNF146, ZNF267, ZNF141, ZRANB2, ZNF140, MTERF2, MOV10, ZZZ3, ZNF37A, GOLGB1, TRIP6, ZNF813, ZNF702P, CREBRF, HBP1, RBAK, ZNF254, ZNF253, ZNF131, AHCTF1, SETD2, ZNF493, ZNF43, RSF1, ZNF808, MECOM, HEY1, ZNF486, ZNF121, PBRM1, ZNF480, COMMD3, PPHLN1, BA21A, BA21B, ZNF57, DYNLL1, ZFX, UCHL5, PHF20L1, GCFC2, TFEC, ZNF117, TMF1, ZNF350, TXLNG, ARNT1L2, RXRB, PPP2CA, ZNF107, PCGF1, DMD, ZNF347, ZNF468, APBB1, SRSF10, ZNF100, SUZ12, BRF1, MCRS1, ATAD2, HIPK3, LRPPRC, ZNF33A, ZNF70, RLIM, PKN2, ZNF354A, ZNF354B, ZNF570, ARID4B, RORA, AHR, BZW1, ZNF208, ZNF85, ZNF689, KMT5B, ZNF688, ARID2, PDE8A, PTRF, ZNF320, ZNF440, ZNF99, HIC1, ZNF91, ZNF92, ZNF93, DMTF1, MORF4L2, ZNF439, PMS2P3, ZNF799, INO80B-WBP1, ZNF676, ZNF675, ZNF432, ZNF431, ZNF430, ZNF791, INO80E, DDX1, SBNO1, ZNF876P, HNRNPDL, BPTF, ZNF782, ZNF660, DENND4A, ZBTB11, CNOT2, ZNF654, ZNF512B, PHTF2, LDB1, CHD9, USP34, CHD7, CHD2, AFF4, PHTF1, LBH, SNAPC2, RB1CC1, ZNF407, ZNF525, LRRFIP2, ZNF765, ERC1, ZNF644, LRRFIP1, IFT57, ZNF761, ATRX, EDF1, ZNF75A, IRF3, ADORA2A, ZNF638, ZNF517, LCOR, PFDN5, ZNF510, IRF9, BIRC2, PRKAA1, ZNF195, ZBTB45, RNF6, ZBTB41, MLLT6, TFPT, TAF10, TAF1B, TAF1C, TGS1, ZNF286B, ASCC3, ZNF189, ZNF286A, RNF20, RBM39, ZNF184, TAF10, MACC1, CCDC59, TBX4, PNRC2, ZNF616, ZNF737, ZNF615, ZNF614, ESF1, ZNF732, ZNF730
cell-cell adhesion	1.23134E-06	1.980226891	TES, DDX3X, RPL34, OLA1, FNBP1L, CLINT1, BZW1, RPL7A, SLK, RAR5, KIF5B, ERC1, LRRFIP1, EIF2A, SH3GLB1, CAST, USP8, ANXA2, SWAP70, GAPVD1, CKAP5, EPN2, 5HTN1, RAB1A, NOTCH3, TXNDC9, USO1, TWF1, CAPG, IQGAP1, KIAA1524, SDCBP, SNX2, CALD1, COBLL1, MYO6, EPS8L2, HIST1H3I, CCT8, ZC3H15, HSPA5, IDH1, RDX, MPP7, RAB11B, KTN1, ANLN, RSL1D1, EIF5, FMNL2, SERBP1, CHMP2B, PKN2, DHX29, PICALM
cellular response to DNA damage stimulus	2.27992E-06	2.110914942	TOP2A, BLM, USP16, MCM8, STXBP4, FMR1, C9ORF142, BOD1L1, ZBTB1, CIB1, SMC5, SMC6, CHD2, TANK, CCAR2, NIPBL, RASSF1, WRN, CHCHD6, UBR5, TLK1, RBBP6, TOPBP1, APBB1, USP47, TIGAR, ARMT1, BAZ1B, SIRT1, WDR76, TOPORS, SETX, KIN, RAD50, APC, IRF3, TAOK3, TAOK1, PSME4, SPRTN, WAC, TRIP12, RAD18, ATR, OTUB1
mRNA splicing, via spliceosome	2.46414E-06	2.065696144	SF3B5, DDX46, DHX9, CSTF3, HNRNPU, SNU13, HNRNPR, CWC27, PNN, SYNCRIP, METTL14, FIP1L1, PCF11, POLR2B, RSRC1, CWC22, DHX15, PAPOLA, POLR2E, POLR2F, POLR2G, HNRNPA1, POLR2J, SRSF10, SF3B1, POLR2J, SRSF11, SF3A3, AQR, HNRNPA3, SNRPN, CPSF3, UPF3B, CDC5L, PRPF4B, PRPF40A, PLRG1, LSM4, LSM2, HNRNPH1, HNRNPA2B1, RBM41, SRSF4, PABPC1, HNRNPH3, SLU7, SKIV2L2
protein sumoylation	4.88597E-06	2.501825117	TOP2A, TOP2B, ZNF451, BLM, SP100, NUP107, SMC5, SMC6, SMC3, SENP6, **WRN**, **RAD21**, **TPR**, NUP88, TRPM4, RANBP2, NOP58, UBE2I, XRCC4, NUP155, NSMCE2, NUP153, SMC1A, TOPORS, **SENP1**, STAG1, STAG2, MDM2, COMMD3-BMI1, **TOP1**
ubiquitin-dependent protein catabolic process	1.49348E-05	2.09081099	USP14, USP37, USP15, USP38, USP16, CUL5, PSMD14, UBA6, USP32, CUL3, CUL2, USP12, USP34, UBR3, NEDD8, RNF6, UBE3A, USP19, UBR5, USP1, ARIH1, RNF20, USP25, USP8, USP47, USP7, UBE2J, USP9X, USP3, USP45, FBXO11, TOPORS, UCHL5, COPS3, ITCH, PSMC6, TTC3, RLIM, UBE2K
DNA duplex unwinding	1.73993E-05	3.548042893	BLM, ANXA1, DDX3X, **DHX9**, DDX1, ATRX, RECQL, CHD2, CHD1, SETX, BRIP1, **WRN**, RAD50, DNA2, NBN, ASCC3
double-strand break repair	7.88521E-05	2.80886729	PARP3, XRCC4, DDX1, SMARCA5, LIG4, CIB1, ESCO2, BRCC3, BRCA2, BA21B, SETX, BABAM1, BRIP1, **WRN**, RAD50, TDP2, **RAD21**, APBB1, NBN
sister chromatid cohesion	9.06157E-05	2.368232513	AHCTF1, NUP107, SMC5, PDS5B, PDS5A, SMC3, **RAD21**, KNTC1, SPDL1, RANBP2, ESCO1, KNL1, SMC1A, CKAP5, WAPL, SGO2, CENPE, KIF18A, STAG1, CENPF, CLIP1, RPS27, STAG2, KIF2A, TAOK1
covalent chromatin modification	0.000158532	2.245000591	**RB1**, SMARCD2, CHD9, CHD7, RSF1, CHD2, CHD1, BABAM1, VPS72, TLK1, ARID2, BPTF, TSPY2, **CBX7**, SMARCC1, **PBRM1**, SFMBT1, C17ORF49, ATRX, SMARCA5, **DEK**, SMARCA1, DNAJC2, MTF2, ANP32E, COMMD3-BMI1
DNA replication	0.000201123	2.014372739	BLM, INO80E, SET, MCM8, NOL8, PTMS, ING4, POLD3, POLD4, BRIP1, **WRN**, CHTF8, RBBP8, RBBP6, TOPBP1, NBN, POLK, SUPT16H, RFC1, LIG4, NAP1L1, **SIRT1**, CCDC88A, KIN, DNAJC2, RAD50, NASP, **CDK1**, RBMS1, DNA2, **TOP1**, ATR
mitotic sister chromatid cohesion	0.000209305	5.575495974	NIPBL, CHTF8, **RAD21**, PDS5B, SMC1A, SMC3, PDS5A, WAPL
chromatin remodeling	0.000348403	2.382552059	**RB1**, HDAC5, SMARCC1, SMARCD2, **PBRM1**, HDAC2, ATRX, CHD7, ZBTB1, SUPT4H1, SMARCA5, RSF1, BAZ1A, **DEK**, SMARCA1, CHD1, MYSM1, MORF4L2, **TOP1**, INO80B-WBP1, BPTF
mitotic nuclear division	0.000397589	1.731101573	USP37, USP16, RGS14, DCTN3, CLTC, SMC5, BRCC3, SNX33, KIF11, SMC3, BABAM1, HAUS7, MIS18BP1, ASUN, KATNA1, RAD21, TPR, RBBP8, KNTC1, NUP88, FBXO5, LZTS2, LRRCC1, PBRM1, UBE2I, PPP1R12A, USP9X, NSMCE2, KNL1, TERF1, CKAP5, CD2AP, ASPM, ANLN, TPX2, STAG1, CENPF, CLIP1, STAG2, TADA3, CDK1, BIRC6, CEP63, KIF20B
DNA synthesis involved in DNA repair	0.000513139	3.345297584	POLD3, POLD4, BLM, BRIP1, **WRN**, RAD50, RBBP8, DNA2, NBN, BRCA2, PALB2, **SIRT1**
RNA processing	0.000697536	2.212954588	RBM39, SSB, RNGTT, **DHX9**, CSTF3, THOC1, DDX20, ZFC3H1, LARP7, HNRNPU, TRMT2A, LSM4, U2SURP, SETX, SYNCRIP, HNRNPDL, HNRNPH1, DHX36, RBMS1, MPHOSPH10, DHX29, HNRNPH3
positive regulation of intracellular protein transport	0.00102101	3.991548254	PCM1, ICE1, **ASPH**, RUFY3, KIF5B, **TPR**, PRR5L, KIF20B, CEP290
G2/M transition of mitotic cell cycle	0.001420001	1.922935655	CEP57, DCTN3, CCP110, HMMR, PPP1CB, PCM1, HAUS7, CEP70, CNTRL, CEP290, PLK4, HSP90AA1, PPP1R12A, CEP135, CEP152, DYNLL1, TERF1, CKAP5, TPX2, MELK, CENPJ, AKAP9, ALMS1, **CDK1**, CALM3, CEP63, TAF2
rRNA processing	0.001953008	1.686978338	LTV1, RPL30, RPL10, RPL34, RPL12, CHD7, DDX21, NOL8, SNU13, WDR43, RPL7A, EXOSC6, RPS17, EXOSC4, RPL18A, BMS1, RPL35, RPL13, RIOK2, RIOK1, NOP58, RRP7BP, UTP11, RIOK3, KRR1, DIS3, TEX10, RPS5, WDR75, DDX52, SIRT1, SENP3, RPS27, RPP21, MPHOSPH10, RPS21, SKIV2L2
I-kappaB kinase/NF-kappaB signaling	0.002490947	2.439279489	RNF31, ROCK1, CHUK, ROCK2, HACD3, TANK, TBK1, NKIRAS1, REL, TAB3, TAB2, AZI2, ZNF675, **MAP3K7**, BIRC2
strand dislocament	0.003439212	3.377463907	BLM, BRIP1, **WRN**, RAD50, RBBP8, DNA2, NBN, BRCA2, PALB2
telomere maintenance via recombination	0.003839584	3.049099361	POLD3, POLD4, **WRN**, RAD50, RFC1, NSMCE2, SMC5, DNA2, SMC6, BRCA2
DNA recombination	0.004000656	2.116001484	BLM, INO80E, XRCC4, POLM, **MCRS1**, ATRX, RECQL, APEX2, LIG4, HMGB1, RBPJ, UCHL5, SETX, KIN, TFPT, **WRN**, RAD50, **RAD21**
cell cycle	0.004518348	1.61869238	USP16, RIF1, GPS1, BCCIP, GNAI3, ARL2, TXLNG, AHR, CCAR2, CDC73, CKS1B, PCNP, RPS6KA3, RB1CC1, GPER1, TLK1, MAPK6, **BRD7**, EVI5, APP1, TSPYL2, ERBIN, LIG4, APEX2, PRPF40A, ESCO2, BLCAP, CTCFL, PPP1CA, DMTF1, NASP, CDK5, CCPG1, PIN1, PKN2, ATR
viral process	0.005463545	1.50109507	ANKRD17, RB1, NCKAP1, SP100, SET, NUP107, CUL5, COPB1, CUL2, UBE3A, IPO7, HSPD1, IPO5, SYNCRIP, PSMB4, TPR, POLR2E, NUP88, TNPO1, HNRNPA1, MPDZ, MAP3K5, RANBP2, USP7, ACOT8, RNGTT, UBE2I, NUP155, HLA-B, NUP153, CFLAR, VRK2, HLA-A, DYNLL1, SIRT1, WAPL, PSMB9, SRPK1, KIN, DLG1, RAD50, MDM2, TOP1, ABCE1, IL6ST, EIF4G3
mRNA export from nucleus	0.005778439	1.951423591	UPF2, RANBP2, **SMG1**, NUP107, NUP155, POLDIP3, CPSF3, THOC1, UPF3B, NUP153, THOC2, FIP1L1, ZC3H11A, **TPR**, HNRNPA2B1, SRSF4, NUP88, SLU7, SRSF10, SRSF11
viral entry into host cell	0.006538601	2.073387565	SCARB1, CXADR, SIVA1, CD81, **WWP1**, NUP153, IDE, DPP4, ACE2, ITCH, GRK2, DAG1, ITGAV, TNFRSF14, ITGB6, GAS6, KPNA3
protein K63-linked deubiquitination	0.006546603	3.393780158	BABAM1, USP25, USP8, ZRANB1, **PSMD14**, FAM175B, YOD1, BRCC3
ER-associated ubiquitin-dependent protein catabolic proc	0.006834964	2.276660856	EDEM3, **HSPA5**, WFS1, CCDC47, YOD1, USP19, HSP90B1, DNAJB2, ERLEC1, PSMC6, KIAA0368, DNAJC10, MAN1B1, UBXN4
nucleic acid phosphodiester bond hydrolysis	0.008303827	2.081518497	GEN1, DDX1, TREX2, APEX2, ZC3H12C, **WRN**, RAD50, XRN1, TDP2, RBBP8, REV3L, PMS2, DXO, DNA2, N4BP2, DNASE1L1
telomere maintenance	0.008871759	2.710310543	POLD3, POLD4, SP100, PARP3, **SMG1**, **WRN**, RAD50, DNA2, NBN, TERF1
proteasome-mediated ubiquitin-dependent protein catab	0.008978345	1.586132475	PSMD12, UBXN2B, **PSMD14**, CUL3, KIF14, RNF6, ARRB2, PCNP, RMND5B, PSMD8, PSMB4, CDC27, PSMD1, EDEM3, **WWP1**, **SIRT1**, TOPORS, PSMB9, CD2AP, ABTB1, PSMC6, CDC34, APC, TBL1XR1, PSME4, **CDK1**, RLIM, PLAA, SPOPL, UBE2K, CLOCK, BIRC2, **NFE2L2**
antigen processing and presentation of exogenous peptid	0.010387506	2.168244834	HLA-H, PSMD12, **PSMD14**, HLA-B, HLA-A, HLA-F, PSMB9, HLA-E, PSMD8, PSMB4, PSMC6, PSME4, PSMD1, ITGAV
negative regulation of protein kinase B signaling	0.01068251	2.637058907	DLG1, BANK1, GPER1, PRKCDBP, DAG1, CIB1, ARRB2, **SIRT1**, LEMD2, MTM1
cell aging	0.010705764	3.122277745	**WRN**, PDCD4, **CDK1**, PRELP, **MIF**, BRCA2, **SIRT1**, **TBX2**
small GTPase mediated signal transduction	0.011080108	1.507197082	RASL12, RAB1A, RAB1B, DOCK7, RASEF, RAP1GDS1, ITSN1, ARL2, HACD3, PLD2, DOCK10, DOCK11, RAP1A, RRAS, ARL13B, NKIRAS1, RAC2, HRAS, RABBB, RALGPS2, SH2D3C, ARL2-SNX15, RAB27A, RHOC, RSG1, RAB11B, ARL4A, RAB18, RABL3, IFT27, RAPGEF2, KRAS, RAPGEF6, RGL2, RABSA, SOS2, RHOQ, ARF5
transcription elongation from RNA polymerase II promote	0.013096924	1.928732619	SETD2, SUPT16H, TAF10, SUPT4H1, GTF2H1, RTF1, CDC73, POLR2B, **LEO1**, POLR2E, TCEA1, TCEB2, POLR2F, POLR2G, POLR2I, POLR2J, TAF2
striated muscle cell differentiation	0.013881646	4.878558977	SPAG9, **RB1**, CHUK, BNIP2, KRAS
endoplasmic reticulum unfolded protein response	0.013973605	2.385073278	ERO1A, EDEM3, ATF6B, **HSPA5**, WFS1, EIF2AK3, YOD1, UGGT2, UGGT1, ATF6, **NFE2L2**
regulation of transcription from RNA polymerase II promo	0.013982833	1.349624025	RB1, ZNF770, ZNF131, ARID4A, ARID4B, NUCKS1, AHR, HMGB1, CHD2, CHD1, ZMYM2, EPC2, CIR1, LRRFIP1, SOX7, PKNOX2, BATF2, SMARCC1, WDR75, MED4, MED22, ZEB1, ELF2, DMTF1, SLTM, LCORL, ATF6, CLOCK, BLZF1, URI1, SMARCD2, USP16, ATF6B, ZNF518B, SUPT4H1, NEDD8, ARNTL2, BRIP1, TCEAL6, TCEAL3, TCEAL2, TTC21B, RAD21, NRIP1, RBBP8, BRD7, ZSCAN18, TCEAL9, ABCA2, ZNF143, SMARCA5, CDC5L, DEK, CNOT2, TADA3, JMY, TCEA1, PKN1, ZNF354A, BRWD1, BRWD3
maturation of LSU-rRNA	0.013994865	3.902847182	RPL7A, **RSL1D1**, MRPL1, TEX10, MAK16, SNU13
mitotic G2 DNA damage checkpoint	0.013994865	3.902847182	FANCI, BLM, TAOK3, **CDK1**, TOPBP1, NBN
regulation of signal transduction by p53 class mediator	0.014388618	1.731101573	BLM, PRKAA1, HDAC2, SUPT16H, TAF10, CSNK2A2, TPX2, BRIP1, **WRN**, RAD50, CDK5, JMY, MDM2, TRIM24, RBBP8, PIN1, TOPBP1, DNA2, NBN, **BRD7**, TAF2, ATR
peptidyl-serine phosphorylation	0.015676946	1.71725276	**SMG1**, DMPK, DYRK1A, EIF2AK3, TTK, VRK2, VRK3, HIPK3, TBK1, GRK2, CDK5, PRKD3, C8ORF44-SGK3, **CDK1**, STK38L, PRKD2, RICTOR, PKN2, SGK3, PKN1, GAS6, ATR
positive regulation of interferon-beta production	0.016507624	2.890997912	MAVS, TBK1, DDX3X, POLR3B, **IRF3**, POLR3C, POLR3F, HMGB1
regulation of mRNA stability	0.016547904	1.79985671	PSMD12, SET, **PSMD14**, DIS3, FMR1, TNFSF13, PSMB9, PSMD8, EXOSC6, CARHSP1, PSMB4, PSMC6, EXOSC4, XRN1, SERBP1, PSME4, PSMD1, PABPC1, TNPO1
positive regulation of mitotic metaphase/anaphase transi	0.01691419	6.504745303	**RB1**, CUL3, NSMCE2, DLGAP5
endodermal cell fate commitment	0.01691419	6.504745303	CTR9, **LEO1**, RTF1, CDC73
double-strand break repair via homologous recombinatio	0.016976345	1.97779418	GEN1, BLM, **PSMD14**, MCM8, NSMCE2, RECQL, XRCC1, SMC5, NUCKS1, SMC6, BRCA2, PALB2, RAD50, RBBP8, NBN
chromosome segregation	0.019313466	2.008818402	TOP2A, UBE2I, DDX3X, RGS14, SPAG5, RIOK3, USP9X, ESCO2, KIF11, SRPK1, CENPE, CENPF, FAM175B, **TOP1**
cellular protein modification process	0.019883526	1.765573725	UBLA4, ERO1A, USP25, ATG3, UBE2I, YES1, UBA7, UBA6, **MCRS1**, ARPC4-TTLL3, NEDD8, PLOD2, FBXO11, TTLL7, UEVLD, CDC34, PPP4R2, TTLL3, TTLL11
histone monoubiquitination	0.020071296	4.435053616	RNF20, CTR9, **LEO1**, WAC, CDC73
mRNA polyadenylation	0.020114614	2.787747987	CPSF4, PCF11, CSTF3, CPSF3, **LEO1**, PAPOLA, PABPC1, CDC73
positive regulation of gene expression, epigenetic	0.02195342	2.045847313	SMARCA5, DDX21, **DEK**, BAZ1B, TAF1D, MYO1C, TAF1B, TAF1C, POLR2E, POLR2F, HIST1H3I, HIST1H4C, SF3B1
positive regulation of I-kappaB kinase/NF-kappaB signalin	0.022795669	1.575683645	ANKRD17, RNF31, GPR89A, ATP2C1, GPR89B, MALT1, MTDH, TBK1, MIER1, ECT2, **MAP3K7**, TMED4, UBE2I, CHUK, CFLAR, RHOC, ZDHHC17, BST2, PPM1A, MAVS, **IRF3**, REL, S100A4, TAB2, CCDC22, BIRC2
protein deubiquitination	0.022836153	1.774021446	USP25, USP14, USP8, USP7, USP15, USP37, USP38, USP53, USP9X, USP32, USP3, USP12, USP34, USP45, UCHL5, USP19, USP1, OTUB1
double-strand break repair via nonhomologous end joinir	0.024674812	2.013373546	**PSMD14**, RIF1, XRCC4, POLM, C9ORF142, NSMCE2, LIG4, SMC5, BRCC3, BABAM1, RAD50, NBN, HIST1H4C
cellular senescence	0.0250669	2.969557638	C2ORF40, OPA1, NSMCE2, SMC5, SMC6, **HRAS**, **TBX2**
Wnt signaling pathway	0.025941667	1.513135939	PRKAA1, DDX3X, LDB1, NXN, CUL3, USP34, CTR9, VPS26A, RTF1, CCAR2, CDC73, TNKS2, **LEO1**, RSPO3, LRRFIP2, LZTS2, BRD7, ZRANB1, DST, CSNK2A2, WNT7A, ZBTB33, WNT9A, HIC1, AES, PPM1A, APC, HBP1, STRN
protein localization to cytoplasmic stress granule	0.027367543	5.575495974	SSB, DDX3X, **DHX9**, DDX1
atrioventricular canal development	0.027367543	5.575495974	CHD7, PTPN11, RBPJ, **TBX2**
type I interferon signaling pathway	0.027635258	1.981914585	HLA-H, SP100, IFITM2, HLA-B, IFI6, HLA-A, IFI35, HLA-F, HLA-E, BST2, IFI27, **IRF3**, IRF9
positive regulation of interferon-alpha production	0.027711767	4.065465814	MAVS, TBK1, **IRF3**, HMGB1, HSPD1
circadian regulation of gene expression	0.028119962	2.054130096	PPP1CB, HDAC2, GFPT1, NRIP1, PRKCDBP, HNRNPU, RORA, AHR, **TOP1**, **SIRT1**, CLOCK, PPP1CA
intrinsic apoptotic signaling pathway	0.028901998	2.601898121	DDX3X, CUL5, SIVA1, BAD, CUL3, CUL2, NBN, **HRAS**
regulation of Rap protein signal transduction	0.029313131	9.757117955	RDX, **TIMP2**, KIF14
regulation of release of sequestered calcium ion into cyto	0.030844574	3.252372652	**ASPH**, CHD7, FKBP1B, CALM3, DMD, CLIC2
protein dephosphorylation	0.031468977	1.626186326	MTMR2, PPP1R12A, PPP2R3B, PTPRK, PPP4R3B, CTDSPL2, PTPN12, PTPN13, STYXL1, MTMR6, MTM1, PPP1CA, PPP2CA, PPP1CB, PPM1A, DLG1, **PPM1B**, UBLCP1, PHPT1, DLGAP5, LHPP
protein import into nucleus	0.031602703	2.01871406	PDIA3, NUP107, NUP155, CSE1L, CFL1, **TPR**, NUP153, NUP88, KPNA2, IPO7, KPNA3, KPNA1
negative regulation of ERK1 and ERK2 cascade	0.031602703	2.01871406	**RPS6KA6**, DLG1, RGS14, GPER1, GSTP1, CNKSR3, RANBP9, PIN1, TIMP3, DMD, VRK3, EIF3A
intracellular transport of virus	0.032009884	2.104476422	RANBP2, NUP107, NUP155, **TPR**, KPNA4, NUP153, NUP88, KPNA2, KPNA3, VPS28, KPNA1
gene silencing by RNA	0.033017506	1.670137308	RANBP2, TSNAX, NUP107, NUP155, FMR1, NUP153, TARBP2, POLR2B, CNOT2, **TPR**, POLR2E, POLR2F, POLR2G, NUP88, HIST1H3I, PABPC1, HIST1H4C, POLR2I, POLR2J
nuclear-transcribed mRNA catabolic process, nonsense-m	0.033533729	1.639851757	UPF2, **SMG1**, RPL30, RPL10, RPS5, RPL34, RPL12, UPF3B, SMG9, GSPT1, PNRC2, PPP2CA, RPL7A, RPS17, RPS27, RPL18A, RPL35, RPL13, PABPC1, RPS21
protein phosphorylation	0.03559331	1.28383131	MAML1, FASTKD2, GMFG, CCNC, RPS6KA3, RPS6KA6, COL4A3BP, RSRC1, TLK1, RIOK2, RIOK1, ROS1, SCYL2, EIF2A, MAP3K5, CHUK, CSNK2A2, DYRK1A, CASK, PRPF4B, IRAK3, VRK2, PIK3CA, PRKD3, PRKD2, PIK3C3, BIRC6, SGK3, GAS6, PRKAA1, ROCK1, ROCK2, DGUOK, ERBB2, STK38L, MAP4K5, MAPK6, CDK17, PLK4, MAP3K2, DMPK, RIOK3, TNK1, EIF2AK3, PHKB, CDC42BPA, HIPK3, SRPK1, CDK8, FER, TEC, TAOK3, C8ORF44-SGK3, STK17B, TAOK1, WNK3, CDK10, PKN2, PKN1, FRK
regulation of embryonic development	0.036857262	3.752737675	NIPBL, SOX17, LAMA2, **CDK1**, **NFE2L2**
protein folding in endoplasmic reticulum	0.036857262	3.752737675	ERO1A, PDIA3, **HSPA5**, DNAJC10, HSP90B1
positive regulation of protein export from nucleus	0.038431819	3.081195144	PPM1A, **TPR**, MDM2, CTDSPL2, ANP32B, GAS6
mitotic cell cycle checkpoint	0.039967463	2.439279489	**RB1**, DLG1, KNTC1, TTK, NBN, WNT9A, SMC1A, **HRAS**
embryonic cleavage	0.0405052	4.878558977	TOP2A, CUL3, PIK3C3, **TOP1**
protein desumoylation	0.0405052	4.878558977	SENP6, USPL1, SENP3, **SENP1**
histone H2B ubiquitination	0.0405052	4.878558977	RNF20, CTR9, **LEO1**, CDC73
cellular response to antibiotic	0.0405052	4.878558977	**HSPA5**, MDM2, PLA2G4A, CRIP1
positive regulation of transcription elongation from RNA p	0.047530494	3.484684984	SUPT16H, CTR9, **LEO1**, RTF1, CDC73
RNA export from nucleus	0.050634556	1.951423591	NUP155, POLDIP3, ZC3H11A, **TPR**, THOC1, UPF3B, SRSF4, THOC2, HNRNPA1, SLU7, SRSF11
DNA topological change	0.056230102	4.336496869	TOP2A, TOP2B, HMGB1, TOP1
ATF6-mediated unfolded protein response	0.056230102	4.336496869	ATF6B, HSPA5, ATF6, HSP90B1
protein polyubiquitination	0.056691667	1.431751004	RNF31, PSMD12, LRSAM1, **PSMD14**, CUL3, PSMD8, PSMB4, TNKS2, RNF19A, RNF217, UBR5, PSMD1, RBBP6, ARIH1, RNF20, ANKIB1, TOPORS, PSMB9, **DDB2**, RNF167, PSMC6, CDC34, PSME4, RLIM, TPP2, TRIP12, BIRC2
translation	0.060553974	1.349798927	HBS1L, RPL30, RPL10, MRPS11, RPL34, RPL12, RMND1, TARS, SNU13, MRPL37, MRPL34, MRPL10, MRPL11, MRPL3, RPL7A, RPS17, MRPL1, RPL18A, ZNF525, RPL35, RPL13, SLC25A24, DARS, EFL1, RPS5, DHPS, MRPS18B, MRPS18A, MRPL43, MRPL21, MRPLS2, **RSL1D1**, RPS27, GUF1, RPS21
cellular response to hydrogen peroxide	0.06220398	1.882952588	SETX, PRKAA1, HDAC2, ANXA1, MDM2, **CDK1**, ECT2, **SIRT1**, MAP3K5, ZNF277, **NFE2L2**
viral transcription	0.063691329	1.568108243	RANBP2, RPL30, NUP107, RPL10, NUP155, RPS5, RPL34, RPL12, NUP153, RPL7A, RPS17, RPS27, RPL18A, **TPR**, RPL35, RPL13, NUP88, RPS21
protein ubiquitination involved in ubiquitin-dependent pr	0.064229105	1.466756294	ANKIB1, CUL5, UBA6, CUL3, CUL2, **WWP1**, RCHY1, FBXL14, RMND5B, ABTB1, ITCH, HECTD1, RNF19A, CDC27, RNF217, UBR5, KLHL8, MDM2, **CDK1**, SPOPL, TRIP12, RBBP6, ARIH1
stem cell population maintenance	0.065173659	1.951423591	METTL14, NIPBL, RIF1, MTF2, CTR9, **LEO1**, RTF1, SMC1A, SMC3, CDC73
negative regulation of proteasomal ubiquitin-dependent	0.067478827	2.661032169	SDCBP, SMARCC1, WAC, CCAR2, **SENP1**, MTM1
negative regulation of GTPase activity	0.067741682	2.042187479	ARFGEF1, GPS1, RDX, ARL2, ARRB2, IQGAP1, IQGAP2, **HRAS**, IPO5
positive regulation of type I interferon production	0.072280182	1.913160383	TBK1, POLR3B, **IRF3**, **DHX9**, POLR3C, DHX36, POLR2E, POLR3F, POLR2F, LRRFIP1
Notch receptor processing	0.074299959	3.034099361