

**Table S5 Gene Ontology (GO) analysis of the genetic interactions identified with Pol  $\epsilon$  (*pol2-12*) mutation**

Gene Ontology analysis was performed using Gorilla (Eden et al. 2009), last update May 2015.

The GO term and their description are listed. The p-value, the False Discovery Rate (FDR) q-value and the enrichment (defined as follows: N is the total number of genes, B is the total number of genes associated with a specific GO term, n is the number of genes in the top of the user's input list or in the target set when appropriate, b is the number of genes in the intersection. Enrichment =  $(b/n) / (B/N)$ ) are shown for each GO term and hits with p-values of less than 0.01 were included. Results are listed beginning with GO categories with the highest enrichment.

**From negative genetic interactions:**

**Cellular processes**

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0032874	positive regulation of stress-activated MAPK cascade	6.70E-05	2.89E-03	24.49 (4334,3,177,3)	<i>HOS2 SNT1 SIF2</i>
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	6.70E-05	2.87E-03	24.49 (4334,3,177,3)	<i>HOS2 SNT1 SIF2</i>
GO:0048478	replication fork protection	6.70E-05	2.84E-03	24.49 (4334,3,177,3)	<i>CSM3 CHK1 MRC1</i>
GO:0032872	regulation of stress-activated MAPK cascade	2.60E-04	8.77E-03	18.36 (4334,4,177,3)	<i>HOS2 SNT1 SIF2</i>
GO:0070302	regulation of stress-activated protein kinase signaling cascade	2.60E-04	8.71E-03	18.36 (4334,4,177,3)	<i>HOS2 SNT1 SIF2</i>
GO:0018202	peptidyl-histidine modification	3.78E-05	1.80E-03	16.32 (4334,6,177,4)	<i>DPH5 DPH2 DPH6 JJJ3</i>
GO:0017182	peptidyl-diphthamide metabolic process	3.78E-05	1.78E-03	16.32 (4334,6,177,4)	<i>DPH5 DPH2 JJJ3 DPH6</i>
GO:0017183	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	3.78E-05	1.76E-03	16.32 (4334,6,177,4)	<i>DPH5 DPH2 DPH6 JJJ3</i>
GO:0002143	tRNA wobble position uridine thiolation	6.30E-04	1.83E-02	14.69 (4334,5,177,3)	<i>TUM1 UBA4 URM1</i>
GO:2000104	negative regulation of DNA-dependent DNA replication	6.30E-04	1.82E-02	14.69 (4334,5,177,3)	<i>CSM3 CHK1 MRC1</i>
GO:0031573	intra-S DNA damage checkpoint	1.66E-04	6.11E-03	12.24 (4334,8,177,4)	<i>RAD9 MRC1 DDC1 BRE1</i>
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	2.29E-05	1.25E-03	12.24 (4334,10,177,5)	<i>CSM3 MMS22 DPB2 CHK1 MRC1</i>
GO:0044773	mitotic DNA damage checkpoint	2.29E-05	1.24E-03	12.24 (4334,10,177,5)	<i>RAD9 MRC1 DDC1 DPB11 BRE1</i>

GO:0043486	histone exchange	4.06E-05	1.87E-03	11.13 (4334,11,177,5)	<i>SWR1 ARP6 ASF1 VPS71 SWC5</i>
GO:1902806	regulation of cell cycle G1/S phase transition	2.88E-04	9.51E-03	10.88 (4334,9,177,4)	<i>RAD9 BRE1 DCR2 XRN1</i>
GO:2000045	regulation of G1/S transition of mitotic cell cycle	2.88E-04	9.44E-03	10.88 (4334,9,177,4)	<i>RAD9 BRE1 DCR2 XRN1</i>
GO:0000077	DNA damage checkpoint	3.40E-07	3.06E-05	10.31 (4334,19,177,8)	<i>RAD9 RAD24 CHK1 MRC1 DDC1 DPB11 BRE1 RAD17</i>
GO:0000722	telomere maintenance via recombination	2.43E-05	1.28E-03	9.18 (4334,16,177,6)	<i>RAD52 IES5 RAD57 BRE1 RAD50 NHP10</i>
GO:0008156	negative regulation of DNA replication	7.08E-04	2.01E-02	8.90 (4334,11,177,4)	<i>CSM3 RAD9 CHK1 MRC1</i>
GO:0000727	double-strand break repair via break-induced replication	7.42E-05	3.11E-03	7.73 (4334,19,177,6)	<i>RAD52 PSF1 POL32 DPB11 PSF2 RAD50</i>
GO:0016575	histone deacetylation	7.42E-05	3.08E-03	7.73 (4334,19,177,6)	<i>HOS2 HDA3 SNT1 SET3 HDA1 SIF2</i>
GO:0044774	mitotic DNA integrity checkpoint	3.25E-04	1.05E-02	7.65 (4334,16,177,5)	<i>RAD9 MRC1 DDC1 DPB11 BRE1</i>
GO:0031570	DNA integrity checkpoint	1.28E-06	9.18E-05	7.60 (4334,29,177,9)	<i>CSM3 RAD9 RAD24 CHK1 MRC1 DDC1 DPB11 BRE1 RAD17</i>
GO:0006476	protein deacetylation	1.02E-04	4.10E-03	7.35 (4334,20,177,6)	<i>HOS2 HDA3 SNT1 SET3 SIF2 HDA1</i>
GO:0098732	macromolecule deacylation	1.39E-04	5.44E-03	7.00 (4334,21,177,6)	<i>HOS2 HDA3 SNT1 SET3 SIF2 HDA1</i>
GO:0035601	protein deacylation	1.39E-04	5.39E-03	7.00 (4334,21,177,6)	<i>HOS2 HDA3 SNT1 SET3 HDA1 SIF2</i>
GO:0001934	positive regulation of protein phosphorylation	5.96E-04	1.76E-02	6.80 (4334,18,177,5)	<i>RTF1 HOS2 SNT1 DPB11 SIF2</i>
GO:0042327	positive regulation of phosphorylation	7.83E-04	2.20E-02	6.44 (4334,19,177,5)	<i>RTF1 HOS2 SNT1 DPB11 SIF2</i>
GO:0006312	mitotic recombination	3.10E-04	1.01E-02	6.12 (4334,24,177,6)	<i>RAD52 IES5 RAD57 BRE1 RAD50 NHP10</i>
GO:0000725	recombinational repair	1.17E-06	8.56E-05	5.99 (4334,45,177,11)	<i>RAD52 PSF1 MMS22 CTF18 POL32 DPB11 DDC1 BRE1 PSF2 RAD50 XRS2</i>
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	1.22E-04	4.85E-03	5.91 (4334,29,177,7)	<i>RTF1 CAF40 SPN1 DST1 ASF1 GIM3 XRN1</i>
GO:0045324	late endosome to vacuole transport	3.95E-04	1.24E-02	5.88 (4334,25,177,6)	<i>VPS60 VPS30 VPS55 VPS8 VPS13 VPS21</i>
GO:0000723	telomere maintenance	5.85E-07	4.96E-05	5.76 (4334,51,177,12)	<i>RAD52 IES5 RAD57 MRC1 BRE1 RAD50 BRE2 SWD3 RRM3 NHP10 SWD1 XRS2</i>
GO:0060249	anatomical structure homeostasis	5.85E-07	4.86E-05	5.76 (4334,51,177,12)	<i>RAD52 IES5 RAD57 MRC1 BRE1 RAD50 BRE2 SWD3 RRM3 NHP10 SWD1 XRS2</i>
GO:0032200	telomere organization	7.34E-07	5.66E-05	5.65 (4334,52,177,12)	<i>RAD52 IES5 RAD57 MRC1 BRE1 RAD50 BRE2 SWD3 RRM3 NHP10 SWD1 XRS2</i>
GO:0000724	double-strand break repair via homologous recombination	6.03E-05	2.66E-03	5.60 (4334,35,177,8)	<i>RAD52 PSF1 CTF18 POL32 DPB11 BRE1 PSF2 RAD50</i>

GO:0032784	regulation of DNA-templated transcription, elongation	1.93E-04	7.05E-03	5.53 (4334,31,177,7)	<i>RTF1 CAF40 SPN1 DST1 ASF1 GIM3 XRN1</i>
GO:0006261	DNA-dependent DNA replication	6.16E-04	1.81E-02	5.44 (4334,27,177,6)	<i>PSF1 DPB2 CLB5 LGE1 DPB3 PSF2</i>
GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	6.16E-04	1.80E-02	5.44 (4334,27,177,6)	<i>RTF1 CAF40 DST1 ASF1 GIM3 XRN1</i>
GO:0016570	histone modification	3.17E-08	3.33E-06	5.22 (4334,75,177,16)	<i>ELP3 SNT1 LGE1 SET3 BRE2 RTF1 HOS2 ARP4 HDA3 SGF29 ASF1 BRE1 SIF2 HDA1 SWD3 SWD1</i>
GO:0016569	covalent chromatin modification	3.17E-08	3.26E-06	5.22 (4334,75,177,16)	<i>ELP3 SNT1 LGE1 SET3 BRE2 RTF1 HOS2 ARP4 HDA3 SGF29 ASF1 BRE1 SIF2 HDA1 SWD3 SWD1</i>
GO:0006302	double-strand break repair	2.59E-07	2.43E-05	5.19 (4334,66,177,14)	<i>RAD52 POL32 PSF2 RAD50 RAD17 MMS22 PSF1 CTF18 SRS2 DPB11 BRE1 NHP10 NUP133 XRS2</i>
GO:0000075	cell cycle checkpoint	8.16E-07	6.18E-05	5.13 (4334,62,177,13)	<i>RAD24 LTE1 BUB2 MRC1 PPH21 RAD17 CSM3 RAD9 BFA1 CHK1 DPB11 DDC1 BRE1</i>
GO:0006289	nucleotide-excision repair	9.24E-04	2.53E-02	5.07 (4334,29,177,6)	<i>RTF1 RAD9 RAD24 POL32 DPB11 SAC3</i>
GO:0032786	positive regulation of DNA-templated transcription, elongation	9.24E-04	2.51E-02	5.07 (4334,29,177,6)	<i>RTF1 CAF40 DST1 ASF1 GIM3 XRN1</i>
GO:0034728	nucleosome organization	6.41E-05	2.80E-03	4.90 (4334,45,177,9)	<i>SWR1 SPN1 ARP6 VPS71 ASF1 HIR2 HPC2 NHP10 SWC5</i>
GO:0007093	mitotic cell cycle checkpoint	7.69E-05	3.16E-03	4.79 (4334,46,177,9)	<i>BFA1 RAD9 LTE1 BUB2 MRC1 DPB11 DDC1 BRE1 PPH21</i>
GO:0006338	chromatin remodeling	1.38E-05	8.30E-04	4.73 (4334,57,177,11)	<i>ARP4 SWR1 MRN1 ELF1 ARP6 UME6 VPS71 ASF1 HTZ1 NHP10 SWC5</i>
GO:0016568	chromatin modification	5.94E-12	1.28E-08	4.51 (4334,152,177,28)	<i>LGE1 HIR2 SWR1 ELF1 ASF1 HTZ1 SWD3 SIF2 SWD1 ELP3 SNT1 RXT3 ARP6 UME6 SET3 VPS71 BRE2 SWC5 RTF1 HOS2 HDA3 ARP4 MRN1 SGF29 BRE1 HDA1 HPC2 NHP10</i>
GO:0006275	regulation of DNA replication	3.32E-04	1.06E-02	4.45 (4334,44,177,8)	<i>CSM3 RAD9 CLB5 DIA2 CHK1 MRC1 BRE1 RRM3</i>
GO:0006348	chromatin silencing at telomere	8.54E-04	2.36E-02	4.39 (4334,39,177,7)	<i>DIA2 ASF1 MRC1 BRE1 BRE2 SWD3 SWD1</i>
GO:0006325	chromatin organization	7.80E-13	3.37E-09	4.26 (4334,184,177,32)	<i>PAT1 LGE1 HIR2 SWR1 ELF1 ASF1 HTZ1 DPB3 SWD3 SIF2 SWD1 ELP3 SNT1 SPN1 RXT3 ARP6 UME6 SET3 VPS71 BRE2 SWC5 RTF1 HOS2 HDA3 ARP4 MRN1 SGF29 DPB2 BRE1 HPC2 HDA1 NHP10</i>
GO:0042325	regulation of phosphorylation	4.34E-05	1.95E-03	4.21 (4334,64,177,11)	<i>RTF1 HOS2 SNT1 CLB5 CLB2 GPB1 DPB11 LSP1 CKB2 SIF2 CKB1</i>
GO:0010948	negative regulation of cell cycle process	1.99E-05	1.11E-03	4.20 (4334,70,177,12)	<i>HOS2 BFA1 SNT1 RAD9 SET3 BUB2 LTE1 DDC1 DPB11 BRE1 PPH21 SIF2</i>

GO:0006260	DNA replication	9.08E-06	5.77E-04	4.19 (4334,76,177,13)	<i>LGE1 POL32 MRC1 CTF8 PSF2 RRM3 PSF1 CTF18 DPB2 CLB5 DCC1 DPB3 DPB11</i>
GO:0045930	negative regulation of mitotic cell cycle	2.42E-04	8.42E-03	4.16 (4334,53,177,9)	<i>BFA1 RAD9 BUB2 LTE1 MRC1 DPB11 DDC1 BRE1 PPH21</i>
GO:0001932	regulation of protein phosphorylation	1.48E-04	5.64E-03	4.01 (4334,61,177,10)	<i>RTF1 HOS2 SNT1 CLB5 CLB2 DPB11 LSP1 CKB2 SIF2 CKB1</i>
GO:0016197	endosomal transport	1.48E-04	5.59E-03	4.01 (4334,61,177,10)	<i>VPS30 VPS60 VPS5 VPS55 VPS29 SNX3 VPS17 VPS8 VPS13 VPS21</i>
GO:0045786	negative regulation of cell cycle	1.62E-05	9.35E-04	3.98 (4334,80,177,13)	<i>SNT1 SET3 LTE1 BUB2 MRC1 PPH21 HOS2 RAD9 BFA1 DPB11 DDC1 BRE1 SIF2</i>
GO:0030447	filamentous growth	1.02E-04	4.12E-03	3.85 (4334,70,177,11)	<i>VPS60 SOK2 NPR3 UBA4 DFG16 UME6 DIA2 GPB1 RIM8 RIM21 URM1</i>
GO:0070783	growth of unicellular organism as a thread of attached cells	2.23E-04	7.95E-03	3.83 (4334,64,177,10)	<i>SOK2 NPR3 UBA4 DFG16 UME6 DIA2 GPB1 RIM8 RIM21 URM1</i>
GO:0044182	filamentous growth of a population of unicellular organisms	2.23E-04	7.89E-03	3.83 (4334,64,177,10)	<i>SOK2 NPR3 UBA4 DFG16 UME6 DIA2 GPB1 RIM8 RIM21 URM1</i>
GO:0051784	negative regulation of nuclear division	4.87E-04	1.49E-02	3.80 (4334,58,177,9)	<i>HOS2 BFA1 SNT1 SET3 BUB2 LTE1 DDC1 PPH21 SIF2</i>
GO:0051782	negative regulation of cell division	5.54E-04	1.65E-02	3.74 (4334,59,177,9)	<i>HOS2 BFA1 SNT1 SET3 BUB2 LTE1 DDC1 SIF2 PPH21</i>
GO:0071824	protein-DNA complex subunit organization	2.41E-05	1.29E-03	3.61 (4334,95,177,14)	<i>RAD52 SPN1 NCB2 ARP6 VPS71 HIR2 SWC5 SRB2 SWR1 SRS2 ASF1 RAD57 HPC2 NHP10</i>
GO:0007346	regulation of mitotic cell cycle	3.07E-05	1.56E-03	3.53 (4334,97,177,14)	<i>LTE1 BUB2 MRC1 PPH21 DCR2 XRN1 RAD9 BFA1 CLB5 CLB2 DDC1 DPB11 BRE1 SMI1</i>
GO:0006310	DNA recombination	4.29E-06	2.77E-04	3.53 (4334,118,177,17)	<i>RAD52 IES5 RAD24 POL32 PSF2 RAD50 RAD17 CTF18 PSF1 MMS22 RAD57 DDC1 DPB11 BRE1 SOH1 NHP10 XRS2</i>
GO:1901990	regulation of mitotic cell cycle phase transition	9.07E-04	2.50E-02	3.50 (4334,63,177,9)	<i>BFA1 RAD9 BUB2 LTE1 DPB11 BRE1 DCR2 PPH21 XRN1</i>
GO:0016458	gene silencing	1.44E-04	5.54E-03	3.46 (4334,85,177,12)	<i>HDA3 DIA2 ASF1 HTZ1 MRC1 BRE1 BRE2 SWD3 HDA1 SIR1 SWD1 NUP133</i>
GO:0010564	regulation of cell cycle process	3.96E-06	2.59E-04	3.39 (4334,130,177,18)	<i>SNT1 UME6 SET3 LTE1 BUB2 MRC1 DCR2 PPH21 XRN1 HOS2 BFA1 RAD9 CLB5 CLB2 DDC1 DPB11 BRE1 SIF2</i>
GO:0006281	DNA repair	1.84E-08	2.04E-06	3.32 (4334,199,177,27)	<i>LGE1 LTE1 MRC1 TIM50 SHE4 ASF1 SIF2 ELP3 RAD52 VAM10 TRS85 CTF8 RTF1 SWF1 HDA3 MMS22 SGF29 DCC1 SHE1 RAD57 HDA1 BRE1 NHP10 SOH1 NUP133 XRS2 VPS30 BUB2 SLT2 SAC3 RAD50 RRM3 CTF18 ATG21 SSO2 SWD3 SWD1 SNT1 SPN1 IES5 ARC18 RRD2 SET3 BRE2 CSM3 HOS2 ARP4 BFA1 CLB2 VAC8</i>
GO:0040007	growth	2.25E-04	7.89E-03	3.30 (4334,89,177,12)	<i>VPS60 SOK2 NPR3 UBA4 DFG16 UME6 DIA2 GPB1 RIM8 RIM21 PPH21 URM1</i>

GO:0006974	cellular response to DNA damage stimulus	2.03E-09	3.25E-07	3.27 (4334,232,177,31)	RAD24 MRC1 CKB2 SAC3 RAD50 RRM3 CKB1 CTF18 RAD9 CHK1 DPB3 RAD52 POL32 PSF2 RAD17 CSM3 RTF1 ARP4 PSF1 MMS22 DPB2 DCC1 SRS2 RAD57 DPB11 DDC1 BRE1 SOH1 NHP10 XRS2 NUP133
GO:0018193	peptidyl-amino acid modification	8.41E-05	3.43E-03	3.23 (4334,106,177,14)	ELP3 UBA4 RRD2 DPH2 PKP1 BRE2 DPH6 ARP4 DPH5 SGF29 ASF1 SWD3 SWD1 JJJ3
GO:0051052	regulation of DNA metabolic process	5.32E-04	1.60E-02	3.21 (4334,84,177,11)	CSM3 RTF1 RAD9 CLB5 DIA2 CHK1 SRS2 MRC1 BRE1 RAD50 RRM3
GO:0051276	chromosome organization	6.39E-07	5.11E-05	3.15 (4334,179,177,23)	RAD52 IES5 MRC1 CTF8 SAC3 RAD50 RRM3 SIR1 BRE2 CSM3 CTF18 MMS22 ARP4 DCC1 SRS2 RAD57 BRE1 SWD3 SOH1 NHP10 XRS2 NUP133 SWD1
GO:0040029	regulation of gene expression, epigenetic	1.98E-04	7.19E-03	3.15 (4334,101,177,13)	MRC1 SIR1 BRE2 ELF1 DIA2 ASF1 HTZ1 BRE1 SIF2 HDA1 SWD3 NUP133 SWD1
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	5.47E-07	4.72E-05	2.99 (4334,205,177,25)	PAT1 RIM101 MRC1 HIR2 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 TIF5 RXT3 NCB2 UME6 SIR1 BRE2 RTF1 CSM3 SRB2 HDA3 DIA2 BRE1 HDA1 NUP133
GO:0010558	negative regulation of macromolecule biosynthetic process	6.00E-07	4.89E-05	2.97 (4334,206,177,25)	PAT1 RIM101 MRC1 HIR2 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 TIF5 RXT3 NCB2 UME6 SIR1 BRE2 RTF1 CSM3 SRB2 HDA3 DIA2 BRE1 HDA1 NUP133
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	6.59E-07	5.18E-05	2.96 (4334,207,177,25)	RIM101 MRC1 HIR2 RAD50 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 RXT3 NCB2 UME6 SIR1 BRE2 RTF1 CSM3 SRB2 HDA3 DIA2 SRS2 BRE1 HDA1 NUP133
GO:0051172	negative regulation of nitrogen compound metabolic process	9.51E-07	7.08E-05	2.90 (4334,211,177,25)	RIM101 MRC1 HIR2 RAD50 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 RXT3 NCB2 UME6 SIR1 BRE2 RTF1 CSM3 SRB2 HDA3 DIA2 SRS2 BRE1 HDA1 NUP133
GO:0010605	negative regulation of macromolecule metabolic process	1.48E-08	1.68E-06	2.89 (4334,280,177,33)	PAT1 RIM101 BUB2 LTE1 MRC1 PPH21 HIR2 RAD50 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 TIF5 RXT3 NCB2 UME6 BRE2 SIR1 CSM3 RTF1 SRB2 BFA1 HDA3 CLB2 DIA2 SRS2 LSP1 BRE1 HDA1 NUP133
GO:0006259	DNA metabolic process	1.80E-09	2.99E-07	2.88 (4334,315,177,37)	RAD24 LGE1 MRC1 SAC3 RAD50 RRM3 SHE4 CTF18 RAD9 CHK1 DPB3 SWD3 SWD1 RAD52 IES5 POL32 CTF8 PSF2 RAD17 BRE2 CSM3 RTF1 ARP4 PSF1 MMS22 CLB5 DPB2 DCC1 SRS2 RAD57 DPB11 DDC1 BRE1 SOH1 NHP10 XRS2 NUP133
GO:0051726	regulation of cell cycle	2.03E-05	1.12E-03	2.81 (4334,174,177,20)	CDC33 SNT1 UME6 SET3 LTE1 BUB2 MRC1 DCR2 PPH21 XRN1 HOS2 BFA1 RAD9 CLB5

					<i>CLB2 DDC1 DPB11 BRE1 SIF2 SMI1</i>
GO:0009892	negative regulation of metabolic process	7.26E-09	9.22E-07	2.79 (4334,316,177,36)	<i>PAT1 RIM101 BUB2 LTE1 MRC1 PPH21 HIR2 RAD50 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 VHS3 SWD1 TIF5 RXT3 NCB2 UME6 GPB1 BRE2 SIR1 CSM3 RTF1 SRB2 BFA1 HDA3 CLB2 DIA2 SRS2 SHE1 LSP1 BRE1 HDA1 NUP133</i>
GO:0010629	negative regulation of gene expression	1.02E-05	6.41E-04	2.76 (4334,195,177,22)	<i>PAT1 TIF5 RXT3 NCB2 RIM101 UME6 MRC1 HIR2 BRE2 SIR1 YGR122W RTF1 SRB2 HDA3 DIA2 ASF1 HTZ1 BRE1 SWD3 HDA1 SWD1 NUP133</i>
GO:0009890	negative regulation of biosynthetic process	2.69E-06	1.84E-04	2.75 (4334,223,177,25)	<i>PAT1 RIM101 MRC1 HIR2 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 TIF5 RXT3 NCB2 UME6 SIR1 BRE2 RTF1 CSM3 SRB2 HDA3 DIA2 BRE1 HDA1 NUP133</i>
GO:0031327	negative regulation of cellular biosynthetic process	2.69E-06	1.81E-04	2.75 (4334,223,177,25)	<i>PAT1 RIM101 MRC1 HIR2 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 TIF5 RXT3 NCB2 UME6 SIR1 BRE2 RTF1 CSM3 SRB2 HDA3 DIA2 BRE1 HDA1 NUP133</i>
GO:0045892	negative regulation of transcription, DNA-templated	3.08E-05	1.55E-03	2.74 (4334,179,177,20)	<i>NCB2 RXT3 RIM101 UME6 MRC1 HIR2 BRE2 SIR1 RTF1 YGR122W SRB2 HDA3 DIA2 ASF1 HTZ1 BRE1 SWD3 HDA1 NUP133 SWD1</i>
GO:0031324	negative regulation of cellular metabolic process	3.60E-08	3.62E-06	2.73 (4334,305,177,34)	<i>PAT1 RIM101 BUB2 LTE1 MRC1 PPH21 HIR2 RAD50 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SWD1 TIF5 NCB2 RXT3 UME6 GPB1 BRE2 SIR1 CSM3 RTF1 SRB2 BFA1 HDA3 CLB2 DIA2 SRS2 LSP1 BRE1 HDA1 NUP133</i>
GO:1902679	negative regulation of RNA biosynthetic process	3.35E-05	1.66E-03	2.72 (4334,180,177,20)	<i>NCB2 RXT3 RIM101 UME6 MRC1 HIR2 BRE2 SIR1 RTF1 YGR122W SRB2 HDA3 DIA2 ASF1 HTZ1 BRE1 SWD3 HDA1 NUP133 SWD1</i>
GO:1903507	negative regulation of nucleic acid-templated transcription	3.35E-05	1.64E-03	2.72 (4334,180,177,20)	<i>NCB2 RXT3 RIM101 UME6 MRC1 HIR2 BRE2 SIR1 RTF1 YGR122W SRB2 HDA3 DIA2 ASF1 HTZ1 BRE1 SWD3 HDA1 NUP133 SWD1</i>
GO:0051253	negative regulation of RNA metabolic process	3.35E-05	1.62E-03	2.72 (4334,180,177,20)	<i>NCB2 RXT3 RIM101 UME6 MRC1 HIR2 BRE2 SIR1 RTF1 YGR122W SRB2 HDA3 DIA2 ASF1 HTZ1 BRE1 SWD3 HDA1 NUP133 SWD1</i>
GO:0048519	negative regulation of biological process	1.33E-09	2.30E-07	2.58 (4334,418,177,44)	<i>PAT1 NPR3 RIM101 LTE1 BUB2 MRC1 PPH21 RAD50 HIR2 YGR122W EPS1 RAD9 CHK1 ASF1 HTZ1 SWD3 SIF2 VHS3 SWD1 SNT1 TIF5 NCB2 RXT3 UME6 SET3 GPB1 SIR1 BRE2 CSM3 RTF1 SRB2 HOS2 BFA1 HDA3 CLB2 DIA2 SHE1 SRS2 DDC1 DPB11 LSP1 BRE1 HDA1 NUP133</i>
GO:0033554	cellular response to stress	9.17E-10	1.80E-07	2.57 (4334,429,177,45)	<i>NPR3 VPS30 UBA4 TRR2 RAD24 RIM101 MRC1 SLT2 NUP188 CKB2 SAC3 RAD50 RRM3 URM1</i>

					<i>CKB1 CTF18 RAD9 CHK1 ATG21 ASF1 DPB3 RAD52 NCB2 TRS85 POL32 PSF2 DCR2 RAD17 CSM3 RTF1 MMS22 ARP4 PSF1 DPB2 DCC1 VAC8 SRS2 RAD57 DDC1 DPB11 BRE1 SOH1 NHP10 XRS2 NUP133</i>
GO:0048523	negative regulation of cellular process	1.09E-08	1.27E-06	2.52 (4334,398,177,41)	<i>PAT1 NPR3 RIM101 LTE1 BUB2 MRC1 PPH21 RAD50 HIR2 YGR122W RAD9 CHK1 ASF1 HTZ1 SWD3 SIF2 SWD1 SNT1 TIF5 NCB2 RXT3 UME6 SET3 GPB1 SIR1 BRE2 CSM3 RTF1 SRB2 HOS2 BFA1 HDA3 CLB2 DIA2 SRS2 DDC1 DPB11 LSP1 BRE1 HDA1 NUP133</i>
GO:0051716	cellular response to stimulus	6.69E-10	1.38E-07	2.48 (4334,473,177,48)	<i>NPR3 VPS30 UBA4 TRR2 RAD24 RIM101 MRC1 SLT2 NUP188 CKB2 SAC3 RAD50 RRM3 URM1 CKB1 CTF18 RAD9 CHK1 ATG21 ASF1 DPB3 RIM21 RAD52 NCB2 TRS85 POL32 PSF2 AZF1 DCR2 RAD17 CSM3 RTF1 SRB2 MMS22 ARP4 PSF1 DPB2 DCC1 VAC8 SRS2 RAD57 DDC1 DPB11 BRE1 SOH1 NHP10 XRS2 NUP133</i>
GO:0006950	response to stress	4.41E-10	9.52E-08	2.45 (4334,500,177,50)	<i>NPR3 RIM101 MRC1 CKB2 NUP188 CKB1 URM1 RAD9 CHK1 ASF1 DPB3 RAD52 TRS85 RTF1 PSF1 MMS22 DPB2 DCC1 RAD57 NHP10 SOH1 NUP133 XRS2 VPS30 UBA4 TRR2 RAD24 SLT2 SAC3 RAD50 RRM3 CTF18 ATG21 GET3 NCB2 RRD2 POL32 NST1 PSF2 DCR2 RAD17 CSM3 ARP4 TCO89 VAC8 SRS2 DPB11 DDC1 BRE1 LSP1</i>
GO:1903046	meiotic cell cycle process	1.61E-04	6.05E-03	2.44 (4334,201,177,20)	<i>RAD52 RIM9 RIM101 RAD24 LGE1 CHS5 RAD50 RAD17 CSM3 SWF1 MMS22 CLB5 RAD57 DDC1 BRE1 RIM21 VPS13 SSO2 SOH1 XRS2</i>
GO:2000112	regulation of cellular macromolecule biosynthetic process	2.95E-11	2.13E-08	2.36 (4334,613,177,59)	<i>PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SOH1 NHP10 SMI1 NUP133 SAC3 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 MRN1 CLB5 BRE1</i>
GO:0019219	regulation of nucleobase-containing compound metabolic process	2.23E-10	5.67E-08	2.35 (4334,574,177,55)	<i>LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SOH1 NHP10 SMI1 NUP133 SAC3 RAD50 RRM3 ELF1 HTZ1 SWD3 SWD1 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2</i>

					<i>ARP4 CLB5 SRS2 BRE1</i>
GO:0032268	regulation of cellular protein metabolic process	2.57E-04	8.73E-03	2.35 (4334,208,177,20)	<i>PAT1 CDC33 HCR1 SNT1 TIF5 BUB2 LTE1 CKB2 PPH21 CKB1 RTF1 HOS2 BFA1 MRN1 CLB5 CLB2 ASF1 DPB11 LSP1 SIF2</i>
GO:0010556	regulation of macromolecule biosynthetic process	3.90E-11	1.87E-08	2.34 (4334,617,177,59)	<i>PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 NHP10 SOH1 SMI1 NUP133 SAC3 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 MRN1 CLB5 BRE1</i>
GO:2001141	regulation of RNA biosynthetic process	4.28E-09	5.78E-07	2.33 (4334,516,177,49)	<i>LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 ASF1 SIF2 ELP3 CAF40 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HDA1 HPC2 SOH1 NHP10 SMI1 NUP133 SAC3 ELF1 HTZ1 SWD3 SWD1 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 HOS2 ARP4 BRE1</i>
GO:1903506	regulation of nucleic acid-templated transcription	4.28E-09	5.61E-07	2.33 (4334,516,177,49)	<i>LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 ASF1 SIF2 ELP3 CAF40 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HDA1 HPC2 SOH1 NHP10 SMI1 NUP133 SAC3 ELF1 HTZ1 SWD3 SWD1 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 HOS2 ARP4 BRE1</i>
GO:0006355	regulation of transcription, DNA-templated	4.01E-09	5.59E-07	2.33 (4334,515,177,49)	<i>LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 ASF1 SIF2 ELP3 CAF40 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HDA1 HPC2 NHP10 SOH1 SMI1 NUP133 SAC3 ELF1 HTZ1 SWD3 SWD1 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 HOS2 ARP4 BRE1</i>
GO:0051171	regulation of nitrogen compound metabolic process	4.39E-10	9.99E-08	2.31 (4334,584,177,55)	<i>LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 NHP10 SOH1 SMI1 NUP133 SAC3 RAD50 RRM3 ELF1 HTZ1 SWD3 SWD1 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 CLB5 SRS2 BRE1</i>
GO:0051252	regulation of RNA metabolic process	7.74E-09	9.29E-07	2.29 (4334,525,177,49)	<i>LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 ASF1 SIF2</i>



					<i>ELP3 CAF40 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HDA1 HPC2 SOH1 NHP10 SMI1 NUP133 SAC3 ELF1 HTZ1 SWD3 SWD1 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 HOS2 ARP4 BRE1</i>
GO:0043933	macromolecular complex subunit organization	3.75E-09	5.40E-07	2.28 (4334,548,177,51)	<i>PAT1 HCR1 TRS20 LGE1 SIW14 GIM4 NUP188 HIR2 SWR1 ASF1 DPB3 SIF2 PRE9 ELP3 RAD52 TIF5 ARP6 VPS71 GIM3 SWC5 RTF1 SRB2 HDA3 SGF29 DPB2 RAD57 HDA1 HPC2 NHP10 PPH21 ELF1 HTZ1 BUD27 SWD3 SWD1 SAD1 SNT1 SPN1 RXT3 NCB2 ARC18 RRD2 UME6 SET3 BRE2 HOS2 GCS1 ARP4 MRN1 SRS2 BRE1</i>
GO:0051246	regulation of protein metabolic process	3.99E-04	1.25E-02	2.28 (4334,215,177,20)	<i>PAT1 CDC33 HCR1 SNT1 TIF5 BUB2 LTE1 CKB2 PPH21 CKB1 RTF1 HOS2 BFA1 MRN1 CLB5 CLB2 ASF1 DPB11 LSP1 SIF2</i>
GO:0009889	regulation of biosynthetic process	1.82E-10	5.24E-08	2.26 (4334,640,177,59)	<i>PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 NHP10 SOH1 SMI1 NUP133 SAC3 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 MRN1 CLB5 BRE1</i>
GO:0031326	regulation of cellular biosynthetic process	1.82E-10	4.92E-08	2.26 (4334,640,177,59)	<i>PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SOH1 NHP10 SMI1 NUP133 SAC3 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 MRN1 CLB5 BRE1</i>
GO:0010468	regulation of gene expression	1.25E-09	2.25E-07	2.24 (4334,600,177,55)	<i>PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SOH1 NHP10 SMI1 NUP133 SAC3 PPH21 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 HOS2 ARP4 MRN1 BRE1</i>
GO:0007049	cell cycle	4.28E-05	1.95E-03	2.21 (4334,310,177,28)	<i>PAT1 NPR3 RIM101 RAD24 LTE1 BUB2 RAD50 CTF18 RAD9 CHK1 VHS3 TRS85 SAP190 SET3 CTF8 DCR2 CSM3 BFA1 PSF1 MMS22 CLB5 DPB2 CLB2 DIA2 SHE1 RAD57 DPB11 XRS2</i>

GO:0050896	response to stimulus	3.00E-09	4.47E-07	2.19 (4334,614,177,55)	<i>NPR3 RIM101 MRC1 CKB2 NUP188 CKB1 URM1 RAD9 CHK1 ASF1 DPB3 RIM21 RAD52 TRS85 RTF1 SRB2 PSF1 MMS22 DPB2 DCC1 RAD57 SOH1 NHP10 NUP133 XRS2 VPS30 UBA4 TRR2 RAD24 SLT2 SAC3 RAD50 RRM3 CTF18 ATG21 GET3 NCB2 BPH1 RRD2 POL32 NST1 PSF2 AZF1 DCR2 RAD17 CSM3 ARP4 TCO89 VAC8 SRS2 ETP1 DPB11 DDC1 BRE1 LSP1</i>
GO:1902589	single-organism organelle organization	2.35E-08	2.54E-06	2.19 (4334,560,177,50)	<i>LGE1 LTE1 MRC1 TIM50 SHE4 ASF1 SIF2 ELP3 RAD52 VAM10 TRS85 CTF8 RTF1 SWF1 HDA3 MMS22 SGF29 DCC1 SHE1 RAD57 HDA1 NHP10 SOH1 NUP133 XRS2 VPS30 BUB2 SLT2 SAC3 RAD50 RRM3 CTF18 ATG21 SSO2 SWD3 SWD1 SNT1 SPN1 IES5 ARC18 RRD2 SET3 BRE2 CSM3 HOS2 ARP4 BFA1 CLB2 VAC8 BRE1</i>
GO:0060255	regulation of macromolecule metabolic process	6.10E-11	2.03E-08	2.14 (4334,766,177,67)	<i>PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 LTE1 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SMI1 NHP10 SOH1 NUP133 BUB2 SAC3 PPH21 RAD50 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 RXT3 NCB2 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 BFA1 ARP4 MRN1 CLB5 CLB2 SRS2 DPB11 BRE1 LSP1</i>
GO:1903047	mitotic cell cycle process	3.58E-04	1.14E-02	2.14 (4334,263,177,23)	<i>RRD2 RIM101 SAP190 CHS5 BUB2 LTE1 MRC1 SLT2 SAC3 CTF8 PPH21 CSM3 BFA1 CTF18 RAD9 CLB5 CLB2 DCC1 SHE1 DPB11 DDC1 BRE1 HPC2</i>
GO:0031323	regulation of cellular metabolic process	4.28E-11	1.85E-08	2.12 (4334,797,177,69)	<i>PAT1 NPR3 HCR1 LGE1 RIM101 RRN9 CHS5 LTE1 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SOH1 SMI1 NHP10 NUP133 BUB2 SAC3 RAD50 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 NCB2 RXT3 UME6 SET3 GPB1 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 MRN1 CLB5 CLB2 SRS2 DPB11 LSP1 BRE1</i>
GO:0006351	transcription, DNA-templated	1.44E-05	8.51E-04	2.12 (4334,393,177,34)	<i>RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 UME6 SET3 DST1 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 BRE1 HPC2 HDA1 SMI1 SOH1 NHP10</i>

GO:0097659	nucleic acid-templated transcription	1.44E-05	8.39E-04	2.12 (4334,393,177,34)	RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 UME6 SET3 DST1 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 BRE1 HPC2 HDA1 SMI1 SOH1 NHP10
GO:0051128	regulation of cellular component organization	1.65E-04	6.16E-03	2.12 (4334,300,177,26)	NPR3 UBA4 LTE1 BUB2 PCP1 SLT2 PPH21 ASF1 RIM21 SIF2 SNT1 ARC18 NCB2 UME6 SET3 DST1 AZF1 XRN1 RTF1 HOS2 BFA1 CLB5 CLB2 TCO89 DDC1 HDA1
GO:0022402	cell cycle process	3.07E-06	2.04E-04	2.11 (4334,452,177,39)	RIM9 RAD24 RIM101 LGE1 CHS5 LTE1 BUB2 MRC1 SLT2 SAC3 PPH21 RAD50 RAD9 CTF18 CHK1 RIM21 SSO2 RAD52 RRD2 SAP190 CTF8 RAD17 CSM3 GCS1 BFA1 MMS22 SWF1 CLB5 CLB2 DCC1 SHE1 RAD57 DDC1 DPB11 BRE1 VPS13 HPC2 SOH1 XRS2
GO:0080090	regulation of primary metabolic process	1.59E-10	4.91E-08	2.10 (4334,782,177,67)	PAT1 HCR1 RIM101 LGE1 RRN9 CHS5 LTE1 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 HPC2 HDA1 SOH1 SMI1 NHP10 NUP133 BUB2 SAC3 RAD50 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 NCB2 RXT3 UME6 SET3 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 MRN1 CLB5 CLB2 SRS2 DPB11 LSP1 BRE1
GO:0019222	regulation of metabolic process	1.90E-11	2.73E-08	2.07 (4334,877,177,74)	PAT1 NPR3 HCR1 LGE1 RIM101 RRN9 CHS5 LTE1 MRC1 CKB2 HIR2 CKB1 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 SIF2 VHS3 ELP3 CAF40 TIF5 ARP6 GIM3 GYP1 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 DIA2 SHE1 HPC2 HDA1 SOH1 SMI1 NHP10 NUP133 BUB2 SAC3 RAD50 PPH21 RRM3 ELF1 HTZ1 SWD3 SWD1 CDC33 SNT1 SPN1 NCB2 RXT3 RRD2 UME6 SET3 GPB1 DST1 AZF1 BRE2 XRN1 CSM3 HOS2 ARP4 GCS1 BFA1 MRN1 CLB5 CLB2 SRS2 DPB11 LSP1 BRE1
GO:0006996	organelle organization	2.25E-09	3.47E-07	2.05 (4334,754,177,63)	PAT1 NPR3 RIM101 LGE1 LTE1 MRC1 NUP188 TIM50 SHE4 ASF1 SIF2 ELP3 RAD52 VAM10 TIF5 TRS85 CTF8 SIR1 RTF1 MMS22 SWF1 HDA3 SGF29 DCC1 SHE1 RAD57 ILM1 HDA1 NHP10 SOH1 VPS21 NUP133 XRS2 VPS30 BUB2 SLT2 SAC3 RAD50 RRM3 CTF18 ATG21 SWD3 SSO2 SWD1 SNT1 SPN1 ARC18 IES5 RRD2 UME6 SET3 RIM8 BRE2 XRN1 CSM3 HOS2 BFA1 ARP4 CLB2 VAC8 SRS2 DDC1 BRE1

GO:0032774	RNA biosynthetic process	3.55E-05	1.70E-03	2.03 (4334,410,177,34)	RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 UME6 SET3 DST1 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 BRE1 HPC2 HDA1 SMI1 SOH1 NHP10
GO:0034654	nucleobase-containing compound biosynthetic process	2.85E-05	1.47E-03	1.91 (4334,514,177,40)	RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 DPB3 VHS3 RAD52 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 POL32 UME6 SET3 DST1 CDC21 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 DPB2 BRE1 HPC2 HDA1 SMI1 NHP10 SOH1
GO:0090304	nucleic acid metabolic process	3.10E-11	1.91E-08	1.91 (4334,1062,177,83)	PAT1 HCR1 LGE1 RIM101 RRN9 MRC1 HIR2 URM1 SHE4 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 DPB3 NOP4 LSM1 ELP3 RAD52 CAF40 LSM7 ARP6 CTF8 SIR1 SWC5 RTF1 SRB2 MMS22 PSF1 HDA3 SGF29 DPB2 DCC1 RAD57 HPC2 HDA1 SOH1 SMI1 NHP10 XRS2 NUP133 UBA4 RAD24 SLT2 LEA1 SAC3 RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3 SWD1 TUM1 CDC33 SAD1 SPN1 IES5 NCB2 RXT3 UME6 SAP190 DEG1 POL32 SET3 DST1 PSF2 AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2 ARP4 MRN1 CLB5 SRS2 DPB11 DDC1 BRE1 IPK1
GO:0050794	regulation of cellular process	3.07E-10	7.37E-08	1.84 (4334,1107,177,83)	PAT1 NPR3 HCR1 LGE1 RIM101 RRN9 CHS5 LTE1 MRC1 PCP1 CKB2 HIR2 CKB1 YGR122W SOK2 EPS1 SWR1 RAD9 CHK1 ASF1 RIM21 SIF2 ELP3 CAF40 TIF5 ARP6 GIM3 SIR1 SWC5 RTF1 SRB2 SWF1 HDA3 SGF29 DIA2 HPC2 HDA1 VPS21 SOH1 SMI1 NHP10 NUP133 UBA4 TRR2 BUB2 SLT2 SAC3 RAD50 PPH21 RRM3 ELF1 HTZ1 SWD3 GET3 SWD1 CDC33 SNT1 SPN1 NCB2 RXT3 ARC18 UME6 SAP190 SET3 GPB1 DST1 AZF1 DCR2 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 MRN1 CLB5 CLB2 TCO89 SRS2 DPB11 DDC1 LSP1 BRE1
GO:0050789	regulation of biological process	5.33E-11	2.09E-08	1.83 (4334,1175,177,88)	PAT1 NPR3 HCR1 LGE1 RIM101 RRN9 CHS5 LTE1 MRC1 PCP1 CKB2 HIR2 CKB1 YGR122W SOK2 EPS1 SWR1 RAD9 CHK1 ASF1 RIM21 SIF2 VHS3 ELP3 CAF40 TIF5 ARP6 GIM3 GYP1 SIR1 SWC5 RTF1 SRB2 SWF1 HDA3 SGF29 DIA2 SHE1 HPC2 HDA1 VPS21 SOH1 SMI1 NHP10 NUP133 UBA4 TRR2 BUB2 SLT2 SAC3 RAD50 PPH21 RRM3 ELF1 HTZ1 SWD3 GET3 SWD1 CDC33 SNT1 SPN1 NCB2 RXT3 ARC18 RRD2

						<p>UME6 SAP190 SET3 GPB1 DST1 AZF1 DCR2 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 GCS1 MRN1 CLB5 CLB2 TCO89 SRS2 DPB11 DDC1 LSP1 BRE1</p>
GO:0015031	protein transport	8.36E-04	2.33E-02	1.81	(4334,406,177,30)	<p>SRN2 NPR3 VPS30 MRL1 CHS5 SNX3 NUP188 SAC3 TIM50 VPS29 ATG21 INP52 VPS17 VPS8 SSO2 GET3 ELP3 VPS5 VPS55 TRS85 BPH1 SHR3 VPS71 RIM8 VPS60 GCS1 VID22 VPS13 VPS21 NUP133</p>
GO:0034645	cellular macromolecule biosynthetic process	1.18E-05	7.17E-04	1.79	(4334,683,177,50)	<p>HCR1 LGE1 RIM101 RRN9 MRC1 HIR2 SOK2 SWR1 ASF1 DPB3 ELP3 RAD52 CAF40 TIF5 ARP6 CTF8 SIR1 SWC5 RTF1 SRB2 HDA3 PSF1 SGF29 DPB2 DCC1 HDA1 HPC2 SOH1 NHP10 SMI1 SAC3 RRM3 CTF18 ELF1 HTZ1 CDC33 SPN1 RXT3 NCB2 POL32 UME6 SET3 DST1 PSF2 AZF1 HOS2 ARP4 CLB5 DPB11 BRE1</p>
GO:0006464	cellular protein modification process	2.48E-04	8.59E-03	1.78	(4334,508,177,37)	<p>UBA4 LGE1 SIW14 SLT2 CKB2 PPH21 URM1 CKB1 CHK1 ATG21 ASF1 SAF1 SWD3 SIF2 JJJ3 SWD1 ELP3 SNT1 RRD2 DPH2 SET3 GPB1 PKP1 PER1 DCR2 BRE2 DPH6 RTF1 HOS2 ARP4 SWF1 HDA3 SGF29 DPH5 DIA2 BRE1 HDA1</p>
GO:0036211	protein modification process	2.48E-04	8.52E-03	1.78	(4334,508,177,37)	<p>UBA4 LGE1 SIW14 SLT2 CKB2 PPH21 URM1 CKB1 CHK1 ATG21 ASF1 SAF1 SWD3 SIF2 JJJ3 SWD1 ELP3 SNT1 RRD2 DPH2 SET3 GPB1 PKP1 PER1 DCR2 BRE2 DPH6 RTF1 HOS2 ARP4 SWF1 HDA3 SGF29 DPH5 DIA2 BRE1 HDA1</p>
GO:0065007	biological regulation	2.56E-11	2.77E-08	1.77	(4334,1330,177,96)	<p>PAT1 NPR3 HCR1 LGE1 RIM101 RRN9 CHS5 LTE1 MRC1 PCP1 CKB2 HIR2 TIM50 CKB1 YGR122W SOK2 EPS1 SWR1 RAD9 CHK1 ASF1 RIM21 SIF2 VHS3 ELP3 RAD52 VPS5 CAF40 TIF5 ARP6 GIM3 GYP1 SIR1 SWC5 RTF1 SRB2 SWF1 HDA3 SGF29 DIA2 SHE1 RAD57 VPS13 HPC2 HDA1 VPS21 NHP10 SOH1 SMI1 XRS2 NUP133 UBA4 TRR2 BUB2 SLT2 SAC3 RAD50 PPH21 RRM3 ELF1 HTZ1 SWD3 GET3 SWD1 CDC33 SNT1 SPN1 NCB2 IES5 RXT3 ARC18 RRD2 UME6 SAP190 SET3 GPB1 PER1 DST1 AZF1 DCR2 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 GCS1 MRN1 CLB5 CLB2 TCO89 SRS2 DPB11 DDC1 LSP1 BRE1</p>
GO:0016043	cellular component organization	3.36E-11	1.81E-08	1.77	(4334,1314,177,95)	<p>PAT1 NPR3 HCR1 TRS20 LGE1 RIM101 CHS5 SIW14 LTE1 MRC1 GIM4 NUP188 HIR2 TIM50 SHE4 SWR1 ASF1 DPB3 SIF2 PRE9 ELP3 RAD52 TIF5 VAM10 TRS85 ARP6 VPS71 CTF8 GIM3</p>

						SIR1 SWC5 RTF1 SRB2 SWF1 HDA3 MMS22 SGF29 DPB2 DCC1 SHE1 RAD57 VPS13 HPC2 HDA1 ILM1 VPS21 NHP10 SOH1 SMI1 XRS2 NUP133 SRN2 VPS30 BUB2 SLT2 BEM1 SAC3 RAD50 PPH21 RRM3 CTF18 ELF1 ATG21 HTZ1 BUD27 SWD3 SSO2 GET3 SWD1 SAD1 SNT1 SPN1 NCB2 IES5 RXT3 ARC18 RRD2 BPH1 UME6 SET3 RIM8 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 GCS1 MRN1 CLB2 TCO89 VAC8 SRS2 DDC1 BRE1
GO:0009059	macromolecule biosynthetic process	2.46E-05	1.28E-03	1.75 (4334,701,177,50)		HCR1 LGE1 RIM101 RRN9 MRC1 HIR2 SOK2 SWR1 ASF1 DPB3 ELP3 RAD52 CAF40 TIF5 ARP6 CTF8 SIR1 SWC5 RTF1 SRB2 HDA3 PSF1 SGF29 DPB2 DCC1 HDA1 HPC2 SOH1 NHP10 SMI1 SAC3 RRM3 CTF18 ELF1 HTZ1 CDC33 SPN1 RXT3 NCB2 POL32 UME6 SET3 DST1 PSF2 AZF1 HOS2 ARP4 CLB5 DPB11 BRE1 RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 DPB3 VHS3 RAD52 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 POL32 UME6 SET3 DST1 CDC21 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 DPB2 BRE1 HPC2 HDA1 SMI1 NHP10 SOH1
GO:0019438	aromatic compound biosynthetic process	2.17E-04	7.80E-03	1.74 (4334,562,177,40)		RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 DPB3 VHS3 RAD52 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 POL32 UME6 SET3 DST1 CDC21 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 DPB2 BRE1 HPC2 HDA1 SMI1 NHP10 SOH1
GO:0018130	heterocycle biosynthetic process	2.72E-04	9.05E-03	1.72 (4334,568,177,40)		RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 DPB3 VHS3 RAD52 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 POL32 UME6 SET3 DST1 CDC21 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 DPB2 BRE1 HPC2 HDA1 SMI1 NHP10 SOH1
GO:0006139	nucleobase-containing compound metabolic process	7.73E-09	9.54E-07	1.71 (4334,1219,177,85)		PAT1 HCR1 LGE1 RIM101 RRN9 MRC1 HIR2 URM1 SHE4 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 DPB3 NOP4 VHS3 LSM1 ELP3 RAD52 CAF40 LSM7 ARP6 CDC21 CTF8 SIR1 SWC5 RTF1 SRB2 MMS22 PSF1 HDA3 SGF29 DPB2 DCC1 RAD57 HPC2 HDA1 SOH1 SMI1 NHP10 XRS2 NUP133 UBA4 RAD24 SLT2 LEA1 SAC3 RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3 SWD1 TUM1 CDC33 SAD1 SPN1 NCB2 IES5 RXT3 UME6 SAP190 DEG1 POL32 SET3 DST1 PSF2 AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2 ARP4 MRN1 CLB5 SRS2 DPB11 DDC1 BRE1 IPK1
GO:1901362	organic cyclic compound biosynthetic process	4.61E-04	1.43E-02	1.67 (4334,602,177,41)		RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 DPB3 VHS3 RAD52 ELP3

						CAF40 SPN1 NCB2 RXT3 ARP6 POL32 UME6 SET3 DST1 CDC21 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 DPB2 ERG3 BRE1 HPC2 HDA1 SMI1 NHP10 SOH1
GO:0043412	macromolecule modification	5.07E-04	1.54E-02	1.67	(4334,585,177,40)	UBA4 LGE1 SIW14 SLT2 CKB2 PPH21 URM1 CKB1 CHK1 ATG21 ASF1 SAF1 SWD3 SIF2 JJJ3 SWD1 TUM1 ELP3 SNT1 RRD2 DEG1 SAP190 DPH2 SET3 GPB1 PKP1 PER1 DCR2 BRE2 DPH6 RTF1 HOS2 ARP4 SWF1 HDA3 DPH5 SGF29 DIA2 BRE1 HDA1
GO:0044271	cellular nitrogen compound biosynthetic process	5.07E-04	1.53E-02	1.67	(4334,585,177,40)	RIM101 LGE1 RRN9 SAC3 HIR2 SOK2 SWR1 ELF1 ASF1 HTZ1 DPB3 VHS3 RAD52 ELP3 CAF40 SPN1 NCB2 RXT3 ARP6 POL32 UME6 SET3 DST1 CDC21 AZF1 SIR1 SWC5 RTF1 SRB2 HOS2 ARP4 HDA3 SGF29 DPB2 BRE1 HPC2 HDA1 SMI1 SOH1 NHP10
GO:0071840	cellular component organization or biogenesis	1.06E-09	1.99E-07	1.66	(4334,1434,177,97)	NPR3 HCR1 RIM101 LGE1 LTE1 SIW14 MRC1 NUP188 HIR2 TIM50 SHE4 ASF1 RIM21 NOP4 SIF2 PRE9 ELP3 VAM10 CTF8 SIR1 HDA3 SGF29 DPB2 DCC1 RAD57 VPS13 ILM1 HDA1 SOH1 NHP10 VPS21 NUP133 VPS30 SAC3 RAD50 ELF1 ATG21 HTZ1 SSO2 GET3 SWD1 SNT1 SPN1 RXT3 NCB2 IES5 BPH1 RRD2 UME6 SET3 RIM8 BRE2 ARP4 CLB2 SRS2 BRE1 PAT1 TRS20 CHS5 GIM4 SWR1 DPB3 RAD52 TIF5 TRS85 ARP6 VPS71 GIM3 SWC5 RTF1 SRB2 MMS22 SWF1 SHE1 HPC2 SMI1 XRS2 SRN2 BUB2 SLT2 BEM1 PPH21 RRM3 CTF18 BUD27 SWD3 SAD1 ARC18 XRN1 CSM3 HOS2 BFA1 GCS1 MRN1 TCO89 VAC8 DDC1
GO:0016070	RNA metabolic process	4.48E-05	2.00E-03	1.64	(4334,837,177,56)	PAT1 HCR1 RIM101 LGE1 RRN9 HIR2 URM1 YGR122W SOK2 SWR1 ASF1 DPB3 NOP4 LSM1 ELP3 CAF40 LSM7 ARP6 SIR1 SWC5 RTF1 SRB2 HDA3 SGF29 HPC2 HDA1 SMI1 SOH1 NHP10 UBA4 LEA1 SLT2 SAC3 ELF1 HTZ1 TUM1 SAD1 CDC33 SPN1 NCB2 RXT3 DEG1 POL32 SAP190 UME6 SET3 DST1 AZF1 XRN1 NGL2 HOS2 ARP4 MRN1 DPB11 BRE1 IPK1
GO:0006725	cellular aromatic compound metabolic process	9.41E-08	9.24E-06	1.63	(4334,1280,177,85)	PAT1 HCR1 LGE1 RIM101 RRN9 MRC1 HIR2 URM1 SHE4 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 DPB3 NOP4 VHS3 LSM1 ELP3 RAD52 CAF40 LSM7 ARP6 CDC21 CTF8 SIR1 SWC5 RTF1 SRB2 MMS22 PSF1 HDA3 SGF29 DPB2 DCC1 RAD57 HPC2 HDA1 SOH1 SMI1 NHP10

						<p>XRS2 NUP133 UBA4 RAD24 SLT2 LEA1 SAC3  RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3 SWD1  TUM1 CDC33 SAD1 SPN1 NCB2 IES5 RXT3  UME6 SAP190 DEG1 POL32 SET3 DST1 PSF2  AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2  ARP4 MRN1 CLB5 SRS2 DPB11 DDC1 BRE1  IPK1</p>
GO:0046483	heterocycle metabolic process	1.14E-07	1.10E-05	1.62	(4334,1285,177,85)	<p>PAT1 HCR1 LGE1 RIM101 RRN9 MRC1 HIR2  URM1 SHE4 YGR122W SOK2 SWR1 RAD9 CHK1  ASF1 DPB3 NOP4 VHS3 LSM1 ELP3 RAD52  CAF40 LSM7 ARP6 CDC21 CTF8 SIR1 SWC5  RTF1 SRB2 MMS22 PSF1 HDA3 SGF29 DPB2  DCC1 RAD57 HPC2 HDA1 SOH1 SMI1 NHP10  XRS2 NUP133 UBA4 RAD24 SLT2 LEA1 SAC3  RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3 SWD1  TUM1 CDC33 SAD1 SPN1 NCB2 IES5 RXT3  UME6 SAP190 DEG1 POL32 SET3 DST1 PSF2  AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2  ARP4 MRN1 CLB5 SRS2 DPB11 DDC1 BRE1  IPK1</p>
GO:0044260	cellular macromolecule metabolic process	5.36E-11	1.93E-08	1.59	(4334,1757,177,114)	<p>HCR1 RIM101 LGE1 SIW14 MRC1 PCP1 CKB2  HIR2 URM1 SHE4 YGR122W EPS1 RAD9 ASF1  NOP4 SIF2 LSM1 PRE9 ELP3 CAF40 PKP1 CTF8  SIR1 PSF1 HDA3 SGF29 DPH5 DPB2 DIA2 DCC1  RAD57 HDA1 NHP10 SOH1 NUP133 UBA4 SAC3  RAD50 ELF1 ATG21 HTZ1 GET3 SWD1 TUM1  SNT1 SPN1 RXT3 NCB2 IES5 RRD2 SAP190  UME6 SET3 DPH2 PER1 DST1 PSF2 BRE2 ARP4  CLB5 SRS2 DPB11 BRE1 PAT1 RRN9 CHS5  GIM4 CKB1 SOK2 SWR1 CHK1 DPB3 SAF1  RAD52 TIF5 LSM7 ARP6 SHR3 GIM3 SWC5 RTF1  SRB2 SWF1 MMS22 HPC2 SMI1 XRS2 SRN2  RAD24 LEA1 SLT2 PPH21 RRM3 CTF18 SWD3  JJJ3 CDC33 SAD1 DEG1 POL32 VMS1 GPB1  AZF1 DCR2 RAD17 XRN1 NGL2 DPH6 CSM3  HOS2 MRN1 VID22 DDC1 IPK1</p>
GO:1901360	organic cyclic compound metabolic process	2.74E-07	2.51E-05	1.58	(4334,1330,177,86)	<p>PAT1 HCR1 LGE1 RIM101 RRN9 MRC1 HIR2  URM1 SHE4 YGR122W SOK2 SWR1 RAD9 CHK1  ASF1 DPB3 NOP4 VHS3 LSM1 ELP3 RAD52  CAF40 LSM7 ARP6 CDC21 CTF8 SIR1 SWC5  RTF1 SRB2 MMS22 PSF1 HDA3 SGF29 DPB2  DCC1 RAD57 ERG3 HPC2 HDA1 SOH1 SMI1  NHP10 XRS2 NUP133 UBA4 RAD24 SLT2 LEA1  SAC3 RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3</p>



						SWD1 TUM1 CDC33 SAD1 SPN1 NCB2 IES5 RXT3 UME6 SAP190 DEG1 POL32 SET3 DST1 PSF2 AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2 ARP4 MRN1 CLB5 SRS2 DPB11 DDC1 BRE1 IPK1
GO:0043170	macromolecule metabolic process	2.59E-11	2.24E-08	1.57 (4334,1837,177,118)		HCR1 DFG16 RIM101 LGE1 SIW14 MRC1 PCP1 CKB2 HIR2 URM1 SHE4 YGR122W EPS1 RAD9 ASF1 LAP2 NOP4 SIF2 LSM1 PRE9 ELP3 CAF40 PKP1 CTF8 SIR1 HDA3 PSF1 SGF29 DPH5 DPB2 DIA2 DCC1 RAD57 HDA1 NHP10 SOH1 NUP133 UBA4 SAC3 RAD50 ELF1 ATG21 HTZ1 GET3 SWD1 TUM1 SNT1 SPN1 RXT3 NCB2 IES5 RRD2 SAP190 UME6 SET3 DPH2 PER1 DST1 RIM8 PSF2 BRE2 ARP4 CLB5 SRS2 DPB11 BRE1 RIM13 PAT1 RRN9 CHS5 GIM4 CKB1 SOK2 SWR1 CHK1 DPB3 SAF1 RAD52 TIF5 LSM7 ARP6 SHR3 GIM3 SWC5 RTF1 SRB2 MMS22 SWF1 HPC2 SMI1 XRS2 SRN2 RAD24 LEA1 SLT2 PPH21 RRM3 CTF18 SWD3 JJJ3 CDC33 SAD1 POL32 DEG1 VMS1 GPB1 AZF1 DCR2 RAD17 XRN1 NGL2 DPH6 CSM3 HOS2 MRN1 VID22 DDC1 IPK1
GO:0034641	cellular nitrogen compound metabolic process	3.80E-07	3.35E-05	1.57 (4334,1339,177,86)		PAT1 HCR1 LGE1 RIM101 RRN9 PCP1 MRC1 HIR2 URM1 SHE4 YGR122W SOK2 SWR1 RAD9 CHK1 ASF1 DPB3 NOP4 VHS3 LSM1 ELP3 RAD52 CAF40 LSM7 ARP6 CDC21 CTF8 SIR1 SWC5 RTF1 SRB2 MMS22 HDA3 PSF1 SGF29 DPB2 DCC1 RAD57 HPC2 HDA1 SOH1 SMI1 NHP10 XRS2 NUP133 UBA4 RAD24 SLT2 LEA1 SAC3 RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3 SWD1 TUM1 CDC33 SAD1 SPN1 IES5 NCB2 RXT3 UME6 SAP190 DEG1 POL32 SET3 DST1 PSF2 AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2 ARP4 MRN1 CLB5 SRS2 DPB11 DDC1 BRE1 IPK1
GO:0019538	protein metabolic process	7.45E-04	2.10E-02	1.49 (4334,905,177,55)		HCR1 DFG16 LGE1 SIW14 PCP1 GIM4 CKB2 CKB1 URM1 EPS1 CHK1 ASF1 LAP2 SAF1 SIF2 PRE9 ELP3 TIF5 PKP1 SHR3 GIM3 RTF1 HDA3 SWF1 DPH5 SGF29 DIA2 HDA1 SRN2 UBA4 SLT2 PPH21 ATG21 SWD3 GET3 SWD1 JJJ3 SAD1 CDC33 SNT1 RRD2 DPH2 SET3 VMS1 GPB1 PER1 RIM8 DCR2 BRE2 DPH6 HOS2 ARP4 VID22 BRE1 RIM13
GO:0006807	nitrogen compound metabolic process	1.09E-05	6.75E-04	1.46 (4334,1462,177,87)		PAT1 HCR1 LGE1 RIM101 RRN9 CHS5 PCP1

					<p>MRC1 HIR2 URM1 SHE4 YGR122W SOK2 SWR1  RAD9 CHK1 ASF1 DPB3 NOP4 VHS3 LSM1 ELP3  RAD52 CAF40 LSM7 ARP6 CDC21 CTF8 SIR1  SWC5 RTF1 SRB2 MMS22 PSF1 HDA3 SGF29  DPB2 DCC1 RAD57 HPC2 HDA1 NHP10 SOH1  SMI1 XRS2 NUP133 UBA4 RAD24 SLT2 LEA1  SAC3 RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3  SWD1 TUM1 CDC33 SAD1 SPN1 NCB2 IES5  RXT3 UME6 SAP190 DEG1 POL32 SET3 DST1  PSF2 AZF1 RAD17 BRE2 XRN1 NGL2 CSM3  HOS2 ARP4 MRN1 CLB5 SRS2 DPB11 DDC1  BRE1 IPK1</p>
GO:0044249	cellular biosynthetic process	6.72E-04	1.92E-02	1.45 (4334,1030,177,61)	<p>HCR1 RIM101 LGE1 RRN9 MRC1 HIR2 SOK2  SWR1 ASF1 LAP2 DPB3 VHS3 RAD52 ELP3  CAF40 TIF5 ARP6 CDC21 CTF8 SIR1 SWC5  RTF1 SRB2 HDA3 PSF1 DPH5 SGF29 DPB2  DCC1 ERG3 HPC2 HDA1 SMI1 SOH1 NHP10  VPS30 SAC3 RRM3 CTF18 ELF1 HTZ1 JJJ3  CAT5 CDC33 SPN1 NCB2 RXT3 UME6 POL32  DPH2 SET3 DST1 PER1 PSF2 AZF1 DPH6 HOS2  ARP4 CLB5 DPB11 BRE1</p>
GO:0044238	primary metabolic process	1.99E-06	1.39E-04	1.32 (4334,2327,177,125)	<p>HCR1 DFG16 RIM101 LGE1 SIW14 MRC1 PCP1  CKB2 HIR2 URM1 SHE4 YGR122W EPS1 RAD9  ASF1 LAP2 NOP4 SIF2 VHS3 LSM1 PRE9 ELP3  CAF40 PKP1 CDC21 CTF8 SIR1 HDA3 PSF1  SGF29 DPH5 DPB2 DIA2 DCC1 RAD57 HDA1  NHP10 SOH1 NUP133 VPS30 UBA4 SAC3 RAD50  ELF1 ATG21 HTZ1 GET3 SWD1 TUM1 SNT1  SPN1 RXT3 NCB2 IES5 RRD2 SAP190 UME6  SET3 DPH2 PER1 DST1 RIM8 PSF2 BRE2 ARP4  CLB5 SRS2 DPB11 BRE1 RIM13 PAT1 RRN9  CHS5 GIM4 CKB1 SOK2 SWR1 CHK1 DPB3 SAF1  RAD52 TIF5 LSM7 ARP6 SHR3 GIM3 SWC5 RTF1  SRB2 MMS22 SWF1 ERG3 HPC2 SMI1 XRS2  SRN2 RAD24 LEA1 SLT2 PPH21 RRM3 CTF18  INP52 SWD3 JJJ3 CAT5 CDC33 SAD1 POL32  DEG1 VMS1 GPB1 AZF1 DCR2 RAD17 XRN1  NGL2 DPH6 CSM3 HOS2 MRN1 TCO89 VID22  DDC1 IPK1</p>
GO:0044237	cellular metabolic process	1.51E-06	1.07E-04	1.30 (4334,2423,177,129)	<p>HCR1 RIM101 LGE1 SIW14 MRC1 PCP1 CKB2  HIR2 URM1 BET3 SHE4 YGR122W EPS1 RAD9  ASF1 LAP2 NOP4 SIF2 VHS3 LSM1 PRE9 ELP3  CAF40 PKP1 CDC21 CTF8 SIR1 HDA3 PSF1  SGF29 DPH5 DPB2 DIA2 DCC1 RAD57 HDA1</p>

						<p>NHP10 SOH1 NUP133 VPS30 UBA4 TRR2 SAC3  RAD50 ELF1 ATG21 HTZ1 GET3 SWD1 TUM1  SNT1 SPN1 RXT3 NCB2 IES5 RRD2 SAP190  UME6 SET3 DPH2 PER1 DST1 PSF2 BRE2 ARP4  CLB5 SRS2 IPP1 DPB11 BRE1 PAT1 TRS20  RRN9 CHS5 GIM4 CKB1 SOK2 SWR1 CHK1  DPB3 SAF1 RAD52 TIF5 LSM7 TRS85 ARP6  SHR3 GIM3 SWC5 RTF1 SRB2 MMS22 SWF1  ERG3 HPC2 SMI1 XRS2 SRN2 RAD24 LEA1 SLT2  PPH21 RRM3 CTF18 INP52 VIP1 SWD3 JJJ3  CAT5 CDC33 SAD1 POL32 DEG1 VMS1 GPB1  AZF1 DCR2 RAD17 XRN1 NGL2 DPH6 CSM3  HOS2 MRN1 TCO89 VID22 VAC8 DDC1 IPK1</p>
GO:0071704	organic substance metabolic process	1.71E-05	9.72E-04	1.27	(4334,2429,177,126)	<p>HCR1 DFG16 RIM101 LGE1 SIW14 MRC1 PCP1  CKB2 HIR2 URM1 SHE4 YGR122W EPS1 RAD9  ASF1 LAP2 NOP4 SIF2 VHS3 LSM1 PRE9 ELP3  CAF40 PKP1 CDC21 CTF8 SIR1 PSF1 HDA3  SGF29 DPH5 DPB2 DIA2 DCC1 RAD57 HDA1  NHP10 SOH1 NUP133 VPS30 UBA4 SAC3 RAD50  ELF1 ATG21 HTZ1 GET3 SWD1 TUM1 SNT1  SPN1 RXT3 NCB2 IES5 RRD2 SAP190 UME6  SET3 DPH2 PER1 DST1 RIM8 PSF2 BRE2 ARP4  CLB5 SRS2 DPB11 BRE1 RIM13 PAT1 RRN9  CHS5 GIM4 CKB1 SOK2 SWR1 CHK1 DPB3 SAF1  RAD52 TIF5 LSM7 ARP6 SHR3 GIM3 SWC5 RTF1  SRB2 MMS22 SWF1 ERG3 HPC2 SMI1 XRS2  SRN2 RAD24 LEA1 SLT2 PPH21 RRM3 CTF18  INP52 VIP1 SWD3 JJJ3 CAT5 CDC33 SAD1  POL32 DEG1 VMS1 GPB1 AZF1 DCR2 RAD17  XRN1 NGL2 DPH6 CSM3 HOS2 MRN1 TCO89  VID22 DDC1 IPK1</p>
GO:0008152	metabolic process	4.83E-04	1.49E-02	1.19	(4334,2723,177,132)	<p>HCR1 DFG16 RIM101 LGE1 SIW14 MRC1 PCP1  CKB2 HIR2 URM1 BET3 SHE4 YGR122W EPS1  RAD9 ASF1 LAP2 NOP4 SIF2 VHS3 LSM1 PRE9  ELP3 CAF40 PKP1 CDC21 CTF8 SIR1 HDA3  PSF1 SGF29 DPH5 DPB2 DIA2 DCC1 RAD57  HDA1 NHP10 SOH1 NUP133 VPS30 UBA4 TRR2  SAC3 RAD50 ELF1 ATG21 HTZ1 GET3 SWD1  TUM1 SNT1 SPN1 RXT3 IES5 NCB2 RRD2  SAP190 UME6 SET3 DPH2 PER1 DST1 RIM8  PSF2 BRE2 ARP4 CLB5 SRS2 IPP1 DPB11 BRE1  RIM13 PAT1 TRS20 RRN9 CHS5 GIM4 CKB1  SOK2 SWR1 CHK1 DPB3 SAF1 RAD52 TIF5  LSM7 TRS85 ARP6 SHR3 GIM3 SWC5 RTF1</p>

SRB2 MMS22 SWF1 ERG3 HPC2 SMI1 XRS2  
 SRN2 RAD24 LEA1 SLT2 PPH21 RRM3 CTF18  
 INP52 VIP1 SWD3 JJJ3 CAT5 CDC33 SAD1  
 POL32 DEG1 VMS1 GPB1 AZF1 DCR2 RAD17  
 XRN1 NGL2 DPH6 CSM3 HOS2 MRN1 TCO89  
 VID22 VAC8 DDC1 IPK1

### Cellular components

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0008622	epsilon DNA polymerase complex	2.60E-04	9.32E-03	18.36 (4334,4,177,3)	DPB2 DPB3 DPB11
GO:0030904	retromer complex	6.30E-04	1.87E-02	14.69 (4334,5,177,3)	VPS5 VPS29 VPS17
GO:0034967	Set3 complex	8.55E-05	3.87E-03	13.99 (4334,7,177,4)	HOS2 SNT1 SET3 SIF2
GO:0042575	DNA polymerase complex	1.66E-04	6.78E-03	12.24 (4334,8,177,4)	DPB2 POL32 DPB11 DPB3
GO:0097346	INO80-type complex	8.22E-07	1.01E-04	11.43 (4334,15,177,7)	SWR1 ARP4 IES5 ARP6 VPS71 NHP10 SWC5
GO:0000812	Swr1 complex	4.06E-05	2.91E-03	11.13 (4334,11,177,5)	SWR1 ARP4 ARP6 VPS71 SWC5
GO:0043596	nuclear replication fork	2.88E-04	9.19E-03	10.88 (4334,9,177,4)	CTF18 DIA2 MRC1 PSF2
GO:0005657	replication fork	5.25E-05	3.48E-03	8.16 (4334,18,177,6)	CTF18 DIA2 MRC1 DPB11 PSF2 RRM3
GO:0070210	Rpd3L-Expanded complex	5.25E-05	3.23E-03	8.16 (4334,18,177,6)	HOS2 SNT1 RXT3 UME6 SET3 SIF2
GO:0000118	histone deacetylase complex	2.33E-05	1.82E-03	6.32 (4334,31,177,8)	HOS2 HDA3 SNT1 RXT3 UME6 SET3 HDA1 SIF2
GO:0070603	SWI/SNF superfamily-type complex	4.29E-04	1.32E-02	4.90 (4334,35,177,7)	ARP4 SWR1 IES5 ARP6 VPS71 NHP10 SWC5
GO:0044440	endosomal part	6.74E-05	3.41E-03	4.02 (4334,67,177,11)	SRN2 VPS30 VPS60 MRL1 VPS5 TRS20 VPS55 SNX3 VPS8 VPS21 BET3
GO:0005768	endosome	1.88E-05	1.80E-03	3.69 (4334,93,177,14)	SRN2 MRL1 VPS30 VPS5 VPS55 SNX3 VPS60 GCS1 VPS29 ATG21 VPS17 VPS8 VPS13 VPS21 MRC1 RRM3 CTF18 SWR1 HTZ1 DPB3 SIF2 SET3 BRE1 SNT1 IES5 RXT3 ARP6 POL32 UME6 HDA1 VPS71 PSF2 RAD17 SWC5 CSM3 HOS2 ARP4 PSF1 HDA3 DPB2 DIA2 DPB11 DDC1 NHP10
GO:0044454	nuclear chromosome part	1.49E-09	4.28E-07	3.40 (4334,216,177,30)	PAT1 RAD24 MRC1 RRM3 CTF18 SWR1 RAD9 HTZ1 DPB3 SWD3 SIF2 SWD1 SNT1 IES5 RXT3 ARP6 POL32 UME6 SET3 VPS71 CTF8 PSF2
GO:0044427	chromosomal part	2.69E-12	1.16E-09	3.34 (4334,293,177,40)	

					<i>RAD17 BRE2 SIR1 SWC5 CSM3 RTF1 HOS2 PSF1 HDA3 ARP4 DPB2 DIA2 DCC1 DPB11 DDC1 BRE1 HDA1 NHP10</i>
GO:0044451	nucleoplasm part	1.30E-06	1.39E-04	3.23 (4334,159,177,21)	<i>SNT1 NCB2 RXT3 UME6 SET3 PSF2 BRE2 RTF1 HOS2 SRB2 ARP4 PSF1 HDA3 SGF29 ELF1 DPB11 SWD3 SIF2 HDA1 SOH1 SWD1</i>
GO:1902494	catalytic complex	1.82E-04	7.12E-03	2.07 (4334,319,177,27)	<i>VPS30 PPH21 ATG21 DPB3 SAF1 SWD3 SIF2 VHS3 SWD1 SNT1 IES5 RXT3 RRD2 POL32 UME6 SET3 BRE2 HOS2 ARP4 HDA3 MMS22 SGF29 DPB2 DIA2 DPB11 HDA1 NHP10</i>
GO:0043234	protein complex	1.70E-13	1.46E-10	2.00 (4334,1089,177,89)	<i>PAT1 NPR3 HCR1 TRS20 RRN9 CHS5 MRC1 GIM4 CKB2 NUP188 HIR2 TIM50 CKB1 BET3 SWR1 DPB3 SAF1 SIF2 VHS3 LSM1 PRE9 ELP3 VPS5 CAF40 TRS85 ARP6 VPS71 CTF8 GIM3 SIR1 SWC5 RTF1 SRB2 MMS22 HDA3 PSF1 SGF29 DPB2 DIA2 DCC1 SHE1 RAD57 HPC2 HDA1 NHP10 SOH1 XRS2 NUP133 SRN2 VPS30 RAD24 BUB2 SAC3 RAD50 PPH21 CTF18 ELF1 VPS29 ATG21 HTZ1 VPS17 VPS8 SWD3 GET3 SWD1 CDC33 SNT1 IES5 NCB2 RXT3 ARC18 VPS55 RRD2 UME6 POL32 VMS1 SET3 PSF2 RAD17 BRE2 XRN1 CSM3 HOS2 ARP4 BFA1 TCO89 VAC8 DPB11 DDC1</i>
GO:0044428	nuclear part	2.01E-05	1.73E-03	1.68 (4334,815,177,56)	<i>RRN9 MRC1 NUP188 CKB2 CKB1 SWR1 DPB3 NOP4 SIF2 RAD52 LSM7 ARP6 VPS71 CDC21 SIR1 SWC5 RTF1 SRB2 PSF1 HDA3 SGF29 DPB2 DIA2 SHE1 RAD57 HDA1 SOH1 NHP10 NUP133 XRS2 LEA1 SAC3 RAD50 RRM3 CTF18 ELF1 HTZ1 SWD3 SWD1 SAD1 SNT1 NCB2 IES5 RXT3 POL32 UME6 SET3 PSF2 RAD17 BRE2 CSM3 HOS2 ARP4 DDC1 DPB11 BRE1</i>
GO:0032991	macromolecular complex	1.65E-09	3.55E-07	1.62 (4334,1512,177,100)	<i>NPR3 HCR1 MRC1 NUP188 CKB2 HIR2 BET3 TIM50 RAD9 NOP4 SIF2 MTC1 VHS3 LSM1 PRE9 ELP3 CAF40 VPS5 CTF8 SIR1 HDA3 PSF1 SGF29 DPB2 DIA2 DCC1 RAD57 HDA1 SOH1 NHP10 NUP133 VPS30 SAC3 RAD50 ELF1 ATG21 HTZ1 VPS8 GET3 SWD1 SNT1 RXT3 IES5 NCB2 RRD2 UME6 SET3 PSF2 BRE2 ARP4 DPB11 BRE1 PAT1 TRS20 RRN9 CHS5 GIM4 CKB1 SWR1 DPB3 SAF1 TIF5 LSM7 TRS85 ARP6 VPS71 GIM3 SWC5 RTF1 SRB2 MMS22 SHE1 HPC2 XRS2 SRN2 RAD24 BUB2 LEA1 PPH21 RRM3 CTF18 VPS29 VPS17 BUD27 SWD3 SAD1 CDC33 VPS55 ARC18 POL32 VMS1 RAD17 XRN1</i>

						CSM3 HOS2 BFA1 MRN1 TCO89 VAC8 DDC1
GO:0005634	nucleus	7.25E-05	3.46E-03	1.38	(4334,1597,177,90)	PAT1 RIM101 LGE1 MIT1 RRN9 MRC1 NUP188 HIR2 URM1 YGR122W SOK2 RAD9 SWR1 CHK1 ASF1 LAP2 DPB3 NOP4 SIF2 LSM1 PRE9 RAD52 ELP3 CAF40 LSM7 ARP6 VPS71 CDC21 CTF8 SIR1 SWC5 RTF1 SRB2 MMS22 PSF1 HDA3 SGF29 DPB2 DIA2 RAD57 HPC2 HDA1 SMI1 SOH1 NHP10 NUP133 XRS2 RAD24 LEA1 SLT2 SAC3 RAD50 PPH21 RRM3 CTF18 ELF1 HTZ1 SWD3 JJJ3 SWD1 CDC33 SAD1 SNT1 SPN1 NCB2 IES5 RXT3 POL32 DEG1 UME6 DST1 PSF2 AZF1 RAD17 BRE2 XRN1 NGL2 CSM3 HOS2 ARP4 MRN1 CLB5 CLB2 SRS2 IPP1 VID22 DPB11 DDC1 BRE1 IPK1
GO:0044446	intracellular organelle part	1.62E-04	6.97E-03	1.29	(4334,2011,177,106)	NPR3 SNX3 MRC1 PCP1 NUP188 CKB2 TIM50 BET3 EPS1 RAD9 NOP4 SIF2 MTC1 VPS5 VAM10 PKP1 CDC21 CTF8 GYP1 SIR1 VPS60 PSF1 HDA3 SGF29 DPB2 DIA2 DCC1 RAD57 HDA1 ILM1 VPS21 NHP10 SOH1 NUP133 VPS30 SAC3 RAD50 ELF1 ATG21 HTZ1 VPS8 GET3 SWD1 SNT1 RXT3 NCB2 IES5 UME6 SET3 PER1 PSF2 BRE2 ARP4 YSP1 CLB2 DPB11 BRE1 PAT1 MRL1 TRS20 RRN9 CHS5 CKB1 SWR1 DPB3 RAD52 TIF5 TRS85 LSM7 ARP6 SHR3 VPS71 PET130 SWC5 RTF1 SRB2 SWF1 SHE1 ERG3 XRS2 SRN2 RAD24 BUB2 ESBP6 LEA1 RRM3 CTF18 INP52 YSC83 SWD3 CAT5 SAD1 ARC18 VPS55 POL32 VMS1 RAD17 XRN1 CSM3 HOS2 GCS1 BFA1 TCO89 VAC8 DDC1 LSP1
GO:0044422	organelle part	2.16E-04	8.08E-03	1.28	(4334,2023,177,106)	NPR3 SNX3 MRC1 PCP1 NUP188 CKB2 TIM50 BET3 EPS1 RAD9 NOP4 SIF2 MTC1 VPS5 VAM10 PKP1 CDC21 CTF8 GYP1 SIR1 VPS60 PSF1 HDA3 SGF29 DPB2 DIA2 DCC1 RAD57 HDA1 ILM1 VPS21 NHP10 SOH1 NUP133 VPS30 SAC3 RAD50 ELF1 ATG21 HTZ1 VPS8 GET3 SWD1 SNT1 RXT3 NCB2 IES5 UME6 SET3 PER1 PSF2 BRE2 ARP4 YSP1 CLB2 DPB11 BRE1 PAT1 MRL1 TRS20 RRN9 CHS5 CKB1 SWR1 DPB3 RAD52 TIF5 TRS85 LSM7 ARP6 SHR3 VPS71 PET130 SWC5 RTF1 SRB2 SWF1 SHE1 ERG3 XRS2 SRN2 RAD24 BUB2 ESBP6 LEA1 RRM3 CTF18 INP52 YSC83 SWD3 CAT5 SAD1 ARC18 VPS55 POL32 VMS1 RAD17 XRN1 CSM3 HOS2 GCS1 BFA1 TCO89 VAC8 DDC1 LSP1

GO:0043231	intracellular membrane-bounded organelle	5.60E-05	3.21E-03	1.21 (4334,2824,177,139)	<p>NPR3 RIM101 LGE1 SNX3 PCP1 MRC1 NUP188  HIR2 URM1 BET3 TIM50 YGR122W EPS1 RAD9  ASF1 LAP2 NOP4 SIF2 MTC1 LSM1 PRE9 ELP3  VPS5 CAF40 VAM10 MID1 PKP1 CDC21 ATO2  CTF8 GYP1 SIR1 VPS60 PSF1 HDA3 SGF29  DPB2 DIA2 RAD57 VPS13 ILM1 HDA1 VPS21  NHP10 SOH1 NUP133 VPS30 TRR2 SAC3 RAD50  ELF1 ATG21 HTZ1 VPS8 SSO2 GET3 SWD1  TUM1 SNT1 SPN1 RXT3 NCB2 IES5 BPH1 UME6  PER1 DST1 PSF2 BRE2 ARP4 CLB5 YSP1 CLB2  SRS2 IPP1 DPB11 BRE1 PAT1 MRL1 TRS20  RRN9 MIT1 CHS5 SOK2 SWR1 CHK1 DPB3  RAD52 LSM7 TRS85 ARP6 SHR3 VPS71 PET130  SWC5 RTF1 SRB2 MMS22 SWF1 ERG3 HPC2  SMI1 XRS2 SRN2 RAD24 ESBP6 LEA1 SLT2  BEM1 PPH21 RRM3 CTF18 VPS29 VPS17 YSC83  SWD3 JJJ3 CAT5 CDC33 SAD1 VPS55 ARC18  POL32 DEG1 VMS1 AZF1 RAD17 XRN1 NGL2  CSM3 HOS2 GCS1 MRN1 TCO89 VID22 VAC8  DDC1 LSP1 IPK1</p>
GO:0043227	membrane-bounded organelle	5.60E-05	3.01E-03	1.21 (4334,2824,177,139)	<p>NPR3 RIM101 LGE1 SNX3 PCP1 MRC1 NUP188  HIR2 URM1 BET3 TIM50 YGR122W EPS1 RAD9  ASF1 LAP2 NOP4 SIF2 MTC1 LSM1 PRE9 ELP3  VPS5 CAF40 VAM10 MID1 PKP1 CDC21 ATO2  CTF8 GYP1 SIR1 VPS60 PSF1 HDA3 SGF29  DPB2 DIA2 RAD57 VPS13 ILM1 HDA1 VPS21  NHP10 SOH1 NUP133 VPS30 TRR2 SAC3 RAD50  ELF1 ATG21 HTZ1 VPS8 SSO2 GET3 SWD1  TUM1 SNT1 SPN1 RXT3 NCB2 IES5 BPH1 UME6  PER1 DST1 PSF2 BRE2 ARP4 CLB5 YSP1 CLB2  SRS2 IPP1 DPB11 BRE1 PAT1 MRL1 TRS20  RRN9 MIT1 CHS5 SOK2 SWR1 CHK1 DPB3  RAD52 LSM7 TRS85 ARP6 SHR3 VPS71 PET130  SWC5 RTF1 SRB2 MMS22 SWF1 ERG3 HPC2  SMI1 XRS2 SRN2 RAD24 ESBP6 LEA1 SLT2  BEM1 PPH21 RRM3 CTF18 VPS29 VPS17 YSC83  SWD3 JJJ3 CAT5 CDC33 SAD1 VPS55 ARC18  POL32 DEG1 VMS1 AZF1 RAD17 XRN1 NGL2  CSM3 HOS2 GCS1 MRN1 TCO89 VID22 VAC8  DDC1 LSP1 IPK1</p>
GO:0043226	organelle	2.79E-04	9.60E-03	1.16 (4334,3056,177,145)	<p>NPR3 RIM101 LGE1 SNX3 PCP1 MRC1 NUP188  HIR2 URM1 BET3 TIM50 YGR122W EPS1 RAD9  ASF1 LAP2 NOP4 SIF2 MTC1 LSM1 PRE9 ELP3  VPS5 CAF40 VAM10 MID1 PKP1 CDC21 ATO2</p>

						CTF8 GYP1 SIR1 VPS60 HDA3 PSF1 SGF29 DDC1 DPB2 DIA2 RAD57 VPS13 ILM1 HDA1 IPK1 VPS21 SOH1 NHP10 NUP133 VPS30 TRR2 SAC3 RAD50 ELF1 ATG21 HTZ1 VPS8 SSO2 GET3 SWD1 LSP1 TUM1 SNT1 SPN1 RXT3 IES5 NCB2 BPH1 UME6 DST1 PER1 PSF2 BRE2 ARP4 CLB5 YSP1 CLB2 SRS2 IPP1 DPB11 BRE1 PAT1 MRL1 TRS20 RRN9 MIT1 CHS5 SOK2 SWR1 CHK1 DPB3 RAD52 LSM7 TRS85 ARP6 SHR3 VPS71 PET130 SWC5 RTF1 SRB2 MMS22 SWF1 SHE1 ERG3 HPC2 SMI1 XRS2 SRN2 RAD24 BUB2 ESBP6 LEA1 SLT2 BEM1 PPH21 RRM3 CTF18 VPS29 INP52 VIP1 VPS17 BUD27 YSC83 SWD3 JJJ3 CAT5 CDC33 SAD1 VPS55 ARC18 POL32 DEG1 VMS1 AZF1 RAD17 XRN1 NGL2 CSM3 HOS2 BFA1 GCS1 MRN1 TCO89 VAC8 VID22
GO:0043229	intracellular organelle	2.79E-04	9.23E-03	1.16 (4334,3056,177,145)		NPR3 RIM101 LGE1 SNX3 PCP1 MRC1 NUP188 HIR2 URM1 BET3 TIM50 YGR122W EPS1 RAD9 ASF1 LAP2 NOP4 SIF2 MTC1 LSM1 PRE9 ELP3 VPS5 CAF40 VAM10 MID1 PKP1 CDC21 ATO2 CTF8 GYP1 SIR1 VPS60 HDA3 PSF1 SGF29 IPK1 DPB2 DIA2 RAD57 VPS13 ILM1 HDA1 VPS21 SOH1 NHP10 NUP133 VPS30 TRR2 SAC3 RAD50 ELF1 ATG21 HTZ1 VPS8 SSO2 GET3 SWD1 TUM1 SNT1 SPN1 RXT3 NCB2 IES5 BPH1 UME6 DST1 PER1 PSF2 BRE2 ARP4 CLB5 YSP1 CLB2 SRS2 IPP1 DPB11 BRE1 PAT1 MRL1 TRS20 RRN9 MIT1 CHS5 SOK2 SWR1 CHK1 DPB3 LSP1 RAD52 LSM7 TRS85 ARP6 SHR3 VPS71 PET130 SWC5 RTF1 SRB2 MMS22 SWF1 SHE1 ERG3 HPC2 SMI1 XRS2 SRN2 RAD24 BUB2 ESBP6 LEA1 SLT2 BEM1 PPH21 RRM3 CTF18 VPS29 INP52 VIP1 VPS17 BUD27 YSC83 SWD3 JJJ3 CAT5 CDC33 SAD1 VPS55 ARC18 POL32 DEG1 VMS1 AZF1 RAD17 XRN1 NGL2 CSM3 HOS2 BFA1 GCS1 MRN1 TCO89 VAC8 VID22 DDC1
GO:0044424	intracellular part	3.05E-07	4.38E-05	1.14 (4334,3683,177,171)		NPR3 HCR1 LGE1 RIM101 SIW14 SNX3 LTE1 MRC1 PCP1 NUP188 CKB2 HIR2 TIM50 URM1 BET3 SHE4 YGR122W EPS1 RAD9 ASF1 LAP2 NOP4 SIF2 MTC1 VHS3 LSM1 PRE9 ELP3 CAF40 VPS5 VAM10 MID1 PKP1 CDC21 CTF8 ATO2 GYP1 SIR1 VPS60 HDA3 PSF1 SGF29 DPH5 DPB2 DIA2 DCC1 RAD57 VPS13 HDA1 ILM1 VPS21 NHP10 SOH1 NUP133 VPS30 UBA4 TRR2



					<p>SAC3 RAD50 ELF1 ATG21 HTZ1 VPS8 SSO2  GET3 SWD1 TUM1 SNT1 SPN1 IES5 NCB2 RXT3  RRD2 BPH1 UME6 SAP190 DPH2 SET3 PER1  DST1 PSF2 BRE2 ARP4 YSP1 CLB5 CLB2 IPP1  SRS2 DPB11 BRE1 PAT1 MRL1 TRS20 MTC4  MIT1 RRN9 CHS5 GIM4 CKB1 SOK2 SWR1 CHK1  DPB3 SAF1 RAD52 TIF5 LSM7 TRS85 ARP6  YGR237C VPS71 SHR3 GIM3 PET130 SWC5  RTF1 SRB2 SWF1 MMS22 SHE1 ERG3 HPC2  SMI1 XRS2 SRN2 RAD24 BUB2 ESBP6 SLT2  LEA1 BEM1 PPH21 RRM3 AIM4 CTF18 VPS29  INP52 VIP1 VPS17 YSC83 BUD27 SWD3 JJJ3  CAT5 CDC33 SAD1 ARC18 VPS55 DEG1 POL32  VMS1 GPB1 NST1 AZF1 DCR2 RAD17 XRN1  NGL2 DPH6 CSM3 HOS2 GCS1 BFA1 MRN1  TCO89 VAC8 VID22 ETP1 DDC1 LSP1 IPK1</p>
					<p>NPR3 HCR1 DFG16 LGE1 RIM101 SIW14 SNX3  LTE1 MRC1 PCP1 NUP188 CKB2 HIR2 TIM50  URM1 BET3 SHE4 YGR122W EPS1 RAD9 ASF1  LAP2 NOP4 RIM21 SIF2 VHS3 MTC1 LSM1 PRE9  ELP3 CAF40 VPS5 VAM10 MID1 PKP1 CDC21  CTF8 ATO2 GYP1 SIR1 VPS60 HDA3 PSF1  SGF29 DPH5 DPB2 DIA2 DCC1 RAD57 VPS13  HDA1 ILM1 VPS21 NHP10 SOH1 NUP133 VPS30  UBA4 TRR2 SAC3 RAD50 ELF1 ATG21 HTZ1  VPS8 SSO2 GET3 SWD1 TUM1 SNT1 SPN1 IES5  NCB2 RXT3 RRD2 BPH1 UME6 SAP190 DPH2  SET3 PER1 DST1 RIM8 PSF2 BRE2 ARP4 YSP1  CLB5 CLB2 IPP1 SRS2 DPB11 BRE1 RIM13 PAT1  MRL1 TRS20 MTC4 MIT1 RRN9 CHS5 GIM4  CKB1 SOK2 SWR1 YDR090C CHK1 DPB3 SAF1  RAD52 TIF5 LSM7 TRS85 ARP6 YGR237C VPS71  SHR3 GIM3 PET130 SWC5 RTF1 SRB2 SWF1  MMS22 SHE1 ERG3 HPC2 SMI1 XRS2 SRN2  RIM9 RAD24 BUB2 ESBP6 SLT2 LEA1 BEM1  PPH21 RRM3 AIM4 CTF18 VPS29 INP52 VIP1  VPS17 YSC83 BUD27 SWD3 JJJ3 CAT5 CDC33  SAD1 ARC18 VPS55 DEG1 POL32 VMS1 GPB1  NST1 AZF1 DCR2 RAD17 XRN1 NGL2 DPH6  CSM3 HOS2 GCS1 BFA1 MRN1 TCO89 VAC8  VID22 ETP1 DDC1 LSP1 IPK1</p>
GO:0044464	cell part	9.82E-09	1.69E-06	1.11 (4334,3914,177,177)	

From positive genetic interactions:

Cellular processes

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0002181	cytoplasmic translation	8.42E-04	6.07E-01	3.56 (4331,92,119,9)	<i>RPL29 RPL13A RPP1B RPL16A RPL9A RPS17B RPS10A RPL24B RPL37B</i>
GO:0006511	ubiquitin-dependent protein catabolic process	3.46E-04	7.50E-01	3.16 (4331,138,119,12)	<i>HUL5 VID30 UBP3 RPN6 RPN12 RPN14 YDR161W RPT3 APC4 RPN7 YRB1 PRE2</i>
GO:0019941	modification-dependent protein catabolic process	3.46E-04	5.00E-01	3.16 (4331,138,119,12)	<i>HUL5 VID30 UBP3 RPN6 RPN12 RPN14 YDR161W RPT3 APC4 RPN7 YRB1 PRE2</i>
GO:0051603	proteolysis involved in cellular protein catabolic process	6.19E-04	5.35E-01	2.97 (4331,147,119,12)	<i>HUL5 VID30 UBP3 RPN6 RPN12 RPN14 YDR161W RPT3 APC4 RPN7 YRB1 PRE2</i>
GO:0043632	modification-dependent macromolecule catabolic process	9.39E-04	5.80E-01	2.84 (4331,154,119,12)	<i>HUL5 VID30 UBP3 RPN6 RPN12 RPN14 YDR161W RPT3 APC4 RPN7 YRB1 PRE2</i>
GO:0019538	protein metabolic process	1.64E-04	7.12E-01	1.69 (4331,905,119,42)	<i>RPL29 HUL5 SGF73 RPP1B GPI15 SDS3 YDR161W RPL9A RPS10A TIF6 RPL37B RCK1 MMS2 RPN6 PPT1 RPL16A ALG7 RPN14 RPS17B PRE2 TAF12 HEM3 UBP3 RKM2 VID30 RPL13A BTN2 ALG6 RPT3 NOP1 APC4 FLC2 ARV1 ICP55 TFB4 RPN12 ATG16 YRB1 RPN7 DBF2 SUP45 RPL24B</i>
GO:0044260	cellular macromolecule metabolic process	5.79E-04	6.26E-01	1.37 (4331,1753,119,66)	<i>TFA2 RPL29 HUL5 PRP11 GPI15 PCF11 IRC5 RPL9A NOP56 RPL37B SWI4 RCK1 RAD10 RPA43 SSF1 PPT1 RPL16A RPN14 ALG7 PRE2 HEM3 UBP3 VID30 ULS1 BTN2 RGR1 NOP1 APC4 RPC17 TFB4 MAF1 RPN12 SNM1 YRB1 RPL24B RPP1B SGF73 RPC19 SDS3 YDR161W DBP3 RPS10A TIF6 MMS2 CIA1 RPN6 RTG2 TPA1 RPS17B MRT4 TAF12 RKM2 RPL13A PRP38 ALG6 SLX9 RPT3 PML1 FLC2 MCM3 ARV1 ATG16 RPN7 DBF2 TPP1 SUP45</i>
GO:0002181	cytoplasmic translation	8.42E-04	6.07E-01	3.56 (4331,92,119,9)	<i>RPL29 RPL13A RPP1B RPL16A RPL9A RPS17B RPS10A RPL24B RPL37B</i>

## Cellular components

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0046695	SLIK (SAGA-like) complex	3.81E-04	5.48E-02	18.20 (4331,6,119,3)	<i>SGF73 RTG2 TAF12</i>
GO:0000502	proteasome complex	3.52E-05	3.04E-02	7.28 (4331,35,119,7)	<i>HUL5 RPN6 RPN12 RPN14 RPT3 RPN7 PRE2</i>
GO:0022625	cytosolic large ribosomal subunit	5.35E-04	6.60E-02	4.81 (4331,53,119,7)	<i>RPL29 RPL13A RPP1B RPL16A RPL9A RPL24B RPL37B</i>
GO:0015934	large ribosomal subunit	2.51E-04	5.41E-02	4.70 (4331,62,119,8)	<i>RPL29 RPL13A RPP1B RPL16A RPL9A PUF6 RPL24B RPL37B</i>
GO:0044445	cytosolic part	4.28E-05	1.85E-02	3.44 (4331,148,119,14)	<i>RPL29 RPL13A RPP1B RPL9A RPS10A RPL37B GCN1 CIA1 RPN6 RPN12 RPL16A RPS17B PRE2 RPL24B</i>
GO:0044391	ribosomal subunit	8.94E-04	9.64E-02	3.25 (4331,112,119,10)	<i>RPL29 RPP1B RPL13A RPL16A RPL9A RPS17B RPS10A PUF6 RPL24B RPL37B</i>
GO:0030529	ribonucleoprotein complex	3.68E-04	6.36E-02	2.03 (4331,448,119,25)	<i>RPL29 PRP11 RPP1B DBP3 RPL9A YGR283C PUF6 RPS10A TIF6 NOP56 RPL37B SSF1 BRX1 RPL16A RPS17B MRT4 AIM14 RPL13A PRP38 SLX9 NOP1 GCN1 SNM1 RPL24B SUP45</i>
GO:0032991	macromolecular complex	7.17E-05	2.06E-02	1.49 (4331,1512,119,62)	<i>HUL5 RPL29 TFA2 PRP11 GPI15 PCF11 SEC20 RPL9A YGR283C PUF6 RPL37B NOP56 SWI4 SPO20 RAD10 RPA43 SSF1 BRX1 RPL16A ALG7 RPN14 PRE2 AIM14 VID30 RGR1 NOP1 APC4 TOM22 RPC17 TFB4 GUT2 RPN12 SNM1 RPL24B FIN1 SGF73 VT11 RPP1B ORM1 RPC19 SDS3 DBP3 RPS10A TIF6 MMS2 CIA1 RPN6 RTG2 RPS17B MRT4 TAF12 RPL13A PRP38 PDX1 SLX9 RPT3 PML1 MCM3 GCN1 ATG16 RPN7 SUP45</i>