

**Table S3 Gene Ontology analysis of the genetic interactions identified with Pol  $\alpha$  (*pol1-4*) 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.

N.B. No GO terms were enriched using the positive genetic interactions as a list.

**Cellular processes**

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0031573	intra-S DNA damage checkpoint	6.05E-09	9.32E-07	29.72 (4320,8,109,6)	<i>DOT1 RAD9 MRC1 SGS1 DDC1 BRE1</i>
GO:0044783	G1 DNA damage checkpoint	6.14E-05	3.01E-03	29.72 (4320,4,109,3)	<i>DOT1 RAD9 BRE1</i>
GO:2000756	regulation of peptidyl-lysine acetylation	1.51E-04	6.50E-03	23.78 (4320,5,109,3)	<i>HIR3 ASF1 CHD1</i>
GO:2000104	negative regulation of DNA-dependent DNA replication	1.51E-04	6.43E-03	23.78 (4320,5,109,3)	<i>CSM3 MRC1 CHD1</i>
GO:1901983	regulation of protein acetylation	1.51E-04	6.37E-03	23.78 (4320,5,109,3)	<i>HIR3 ASF1 CHD1</i>
GO:0035065	regulation of histone acetylation	1.51E-04	6.31E-03	23.78 (4320,5,109,3)	<i>HIR3 ASF1 CHD1</i>
GO:0070911	global genome nucleotide-excision repair	1.51E-04	6.25E-03	23.78 (4320,5,109,3)	<i>DOT1 RTF1 ELC1</i>
GO:0044773	mitotic DNA damage checkpoint	4.35E-08	3.91E-06	23.78 (4320,10,109,6)	<i>DOT1 RAD9 MRC1 DDC1 SGS1 BRE1</i>
GO:0006336	DNA replication-independent nucleosome assembly	2.96E-04	1.16E-02	19.82 (4320,6,109,3)	<i>HIR3 ASF1 HPC2</i>
GO:0000077	DNA damage checkpoint	2.23E-10	6.00E-08	18.77 (4320,19,109,9)	<i>DOT1 BMH1 RAD9 RAD24 MRC1 DDC1 SGS1 BRE1 RAD17</i>
GO:0000722	telomere maintenance via recombination	5.09E-08	4.23E-06	17.34 (4320,16,109,7)	<i>RAD52 IES5 RAD57 SGS1 BRE1 RAD50 NHP10</i>
GO:0000729	DNA double-strand break processing	5.08E-04	1.86E-02	16.99 (4320,7,109,3)	<i>RIF1 SGS1 RAD50</i>
GO:0030472	mitotic spindle organization in nucleus	5.08E-04	1.84E-02	16.99 (4320,7,109,3)	<i>CIK1 RRD1 RRD2</i>
GO:0034724	DNA replication-independent nucleosome organization	7.98E-04	2.80E-02	14.86 (4320,8,109,3)	<i>HIR3 ASF1 HPC2</i>

GO:0044774	mitotic DNA integrity checkpoint	1.47E-06	9.58E-05	14.86 (4320,16,109,6)	<i>DOT1 RAD9 MRC1 DDC1 SGS1 BRE1</i>
GO:0008156	negative regulation of DNA replication	1.10E-04	4.91E-03	14.41 (4320,11,109,4)	<i>CSM3 RAD9 MRC1 CHD1</i>
GO:0031570	DNA integrity checkpoint	6.20E-10	1.34E-07	14.15 (4320,28,109,10)	<i>CSM3 DOT1 BMH1 RAD9 RAD24 MRC1 DDC1 SGS1 BRE1 RAD17</i>
GO:0000726	non-recombinational repair	4.53E-05	2.25E-03	11.66 (4320,17,109,5)	<i>CSM3 RAD9 TEN1 BDF2 SRS2 MRC1 SGS1 RAD50 CHD1</i>
GO:0006312	mitotic recombination	1.30E-06	8.66E-05	11.56 (4320,24,109,7)	<i>RAD52 SRS2 RSC8 RAD50 XRS2</i>
GO:0051053	negative regulation of DNA metabolic process	3.77E-08	3.46E-06	11.51 (4320,31,109,9)	<i>RAD52 IES5 RAD57 SGS1 BRE1 RAD50 NHP10</i>
GO:0031056	regulation of histone modification	3.16E-04	1.23E-02	11.32 (4320,14,109,4)	<i>RTF1 HIR3 ASF1 CHD1 ASF1 CHD1</i>
GO:0006303	double-strand break repair via nonhomologous end joining	4.22E-04	1.56E-02	10.57 (4320,15,109,4)	<i>SRS2 RSC8 RAD50 XRS2</i>
GO:0000723	telomere maintenance	1.74E-10	5.79E-08	10.10 (4320,51,109,13)	<i>RAD52 IES5 TEN1 MRC1 RAD50 RIF1 RAD57 SGS1 BRE1 SWD3 NHP10 XRS2 SWD1</i>
GO:0060249	anatomical structure homeostasis	1.74E-10	5.38E-08	10.10 (4320,51,109,13)	<i>RAD52 IES5 TEN1 MRC1 RAD50 RIF1 RAD57 SGS1 BRE1 SWD3 NHP10 XRS2 SWD1</i>
GO:0032200	telomere organization	2.28E-10	5.78E-08	9.91 (4320,52,109,13)	<i>RAD52 IES5 TEN1 MRC1 RAD50 RIF1 RAD57 SGS1 BRE1 SWD3 NHP10 XRS2 SWD1</i>
GO:0000725	recombinational repair	1.05E-07	7.96E-06	8.81 (4320,45,109,10)	<i>DOT1 RAD52 CTF18 CTF4 POL32 DDC1 SGS1 BRE1 RAD50 XRS2</i>
GO:0007064	mitotic sister chromatid cohesion	2.70E-04	1.08E-02	8.26 (4320,24,109,5)	<i>CSM3 CTF18 CTF4 MRC1 CTF8</i>
GO:0006289	nucleotide-excision repair	6.65E-05	3.23E-03	8.20 (4320,29,109,6)	<i>RTF1 DOT1 RAD9 RAD24 POL32 ELC1</i>
GO:0006368	transcription elongation from RNA polymerase II promoter	6.65E-05	3.19E-03	8.20 (4320,29,109,6)	<i>RTF1 SPT2 HIR3 RSC8 HPC2 CHD1</i>
GO:0000724	double-strand break repair via homologous recombination	2.01E-05	1.11E-03	7.93 (4320,35,109,7)	<i>RAD52 CTF18 CTF4 POL32 SGS1 BRE1 RAD50</i>
GO:0006302	double-strand break repair	4.76E-08	4.11E-06	7.32 (4320,65,109,12)	<i>RAD52 CTF18 CTF4 POL32 SRS2 SGS1 RSC8 BRE1 RAD50 RAD17 NHP10 XRS2</i>
GO:0034728	nucleosome organization	1.06E-05	6.16E-04	7.21 (4320,44,109,8)	<i>SPN1 HIR3 ASF1 RSC8 HPC2 NHP10 SWC5 CHD1</i>
GO:0006354	DNA-templated transcription, elongation	1.43E-04	6.23E-03	7.21 (4320,33,109,6)	<i>RTF1 SPT2 HIR3 RSC8 HPC2 CHD1</i>
GO:0000075	cell cycle checkpoint	2.31E-07	1.66E-05	7.15 (4320,61,109,11)	<i>CSM3 DOT1 BMH1 RAD9 RAD24 MRC1 DDC1 SGS1 BRE1 PPH21 RAD17</i>
GO:0007093	mitotic cell cycle checkpoint	1.49E-05	8.58E-04	6.89 (4320,46,109,8)	<i>DOT1 BMH1 RAD9 MRC1 DDC1 SGS1 BRE1 PPH21</i>
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	6.83E-04	2.42E-02	6.83 (4320,29,109,5)	<i>RTF1 CAF40 SPN1 ASF1 YKE2</i>

GO:0032784	regulation of DNA-templated transcription, elongation	9.39E-04	3.21E-02	6.39 (4320,31,109,5)	<i>RTF1 CAF40 SPN1 ASF1 YKE2</i>
GO:0006348	chromatin silencing at telomere	3.21E-04	1.24E-02	6.26 (4320,38,109,6)	<i>DOT1 ASF1 MRC1 BRE1 SWD3 SWD1</i>
GO:0006310	DNA recombination	4.11E-10	9.32E-08	6.05 (4320,118,109,18)	<i>DOT1 UPF3 RAD52 IES5 RAD24 POL32 CTF4 RAD50 RAD17 CTF18 RAD57 NMD2 DDC1 MMS4 SGS1 BRE1 NHP10 XRS2</i>
GO:0045930	negative regulation of mitotic cell cycle	4.38E-05	2.20E-03	5.98 (4320,53,109,8)	<i>DOT1 BMH1 RAD9 MRC1 DDC1 SGS1 BRE1 PPH21</i>
GO:0051052	regulation of DNA metabolic process	1.16E-06	7.82E-05	5.53 (4320,86,109,12)	<i>CSM3 RTF1 RAD9 TEN1 SRS2 BDF2 MRC1 SGS1 MMS4 BRE1 RAD50 CHD1</i>
GO:0071824	protein-DNA complex subunit organization	3.06E-06	1.86E-04	5.06 (4320,94,109,12)	<i>RAD52 SPN1 NCB2 HIR3 SRS2 ASF1 RAD57 RSC8 HPC2 NHP10 SWC5 CHD1</i>
GO:0007346	regulation of mitotic cell cycle	4.29E-06	2.57E-04	4.90 (4320,97,109,12)	<i>DOT1 BMH1 RAD9 CIK1 CLA4 MRC1 DDC1 SGS1 SIS2 BRE1 PPH21 SMI1</i>
GO:0006281	DNA repair	4.58E-11	1.98E-08	4.83 (4320,197,109,24)	<i>DOT1 RAD52 RAD24 POL32 CTF4 MRC1 RSC8 RAD50 RAD17 CSM3 RTF1 CTF18 RAD9 RRD1 SRS2 BDF2 RAD57 MMS4 SGS1 DDC1 BRE1 ELC1 NHP10 XRS2</i>
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	7.43E-10	1.53E-07	4.43 (4320,206,109,23)	<i>DOT1 BMH1 HIR3 NCB2 TEN1 MRC1 RAD50 CSM3 RTF1 SPT2 RAD9 HDA3 ASF1 BDF2 SRS2 RIF1 HTZ1 SGS1 SKO1 BRE1 SWD3 SWD1 CHD1</i>
GO:0051276	chromosome organization	1.12E-08	1.42E-06	4.43 (4320,179,109,20)	<i>RAD52 CIK1 IES5 CTF4 TEN1 MRC1 CTF8 RAD50 CSM3 CTF18 RIF1 SRS2 RAD57 MMS4 SGS1 BRE1 SWD3 NHP10 XRS2 SWD1</i>
GO:0051172	negative regulation of nitrogen compound metabolic process	1.10E-09	2.15E-07	4.34 (4320,210,109,23)	<i>DOT1 BMH1 HIR3 NCB2 TEN1 MRC1 RAD50 CSM3 RTF1 SPT2 RAD9 HDA3 ASF1 SRS2 BDF2 RIF1 HTZ1 SGS1 SKO1 BRE1 SWD3 SWD1 CHD1</i>
GO:0006974	cellular response to DNA damage stimulus	2.10E-10	6.05E-08	4.31 (4320,230,109,25)	<i>DOT1 BMH1 RAD24 MRC1 RSC8 RAD50 RAD9 CTF18 SGS1 MMS4 ELC1 RAD52 CTF4 POL32 RAD17 RTF1 CSM3 RRD1 SRS2 BDF2 RAD57 DDC1 BRE1 NHP10 XRS2</i>
GO:0016458	gene silencing	2.26E-04	9.18E-03	4.25 (4320,84,109,9)	<i>DOT1 HDA3 ASF1 RIF1 HTZ1 MRC1 BRE1 SWD3 SWD1</i>
GO:0016570	histone modification	5.26E-04	1.89E-02	4.23 (4320,75,109,8)	<i>DOT1 RTF1 HDA3 ASF1 BRE1 SWD3 CHD1 SWD1</i>
GO:0016569	covalent chromatin modification	5.26E-04	1.87E-02	4.23 (4320,75,109,8)	<i>DOT1 RTF1 HDA3 ASF1 BRE1 SWD3 SWD1 CHD1</i>
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	1.84E-08	2.09E-06	4.10 (4320,203,109,21)	<i>DOT1 PAT1 BMH1 TIF5 NCB2 HIR3 MRC1 EAP1 CSM3 RTF1 SPT2 RAD9 HDA3 ASF1 RIF1 HTZ1 SKO1 BRE1 SWD3 SWD1 CHD1</i>

GO:0010558	negative regulation of macromolecule biosynthetic process	2.01E-08	2.23E-06	4.08 (4320,204,109,21)	<i>DOT1 PAT1 BMH1 TIF5 NCB2 HIR3 MRC1 EAP1 CSM3 RTF1 SPT2 RAD9 HDA3 ASF1 RIF1 HTZ1 SKO1 BRE1 SWD3 SWD1 CHD1</i>
GO:0006259	DNA metabolic process	2.86E-12	2.47E-09	3.98 (4320,319,109,32)	<i>DOT1 RAD24 MRC1 RSC8 RAD50 CTF18 RAD9 RIF1 NMD2 SGS1 MMS4 SWD3 ELC1 SWD1 UPF3 RAD52 IES5 POL32 CTF4 TEN1 CTF8 RAD17 CSM3 RTF1 RRD1 SRS2 BDF2 RAD57 DDC1 BRE1 NHP10 XRS2</i>
GO:0010605	negative regulation of macromolecule metabolic process	9.29E-11	3.34E-08	3.98 (4320,279,109,28)	<i>PAT1 DOT1 BMH1 HIR3 MRC1 PPH21 RAD50 SPT2 RAD9 RIF1 ASF1 CLA4 HTZ1 SGS1 SKO1 SWD3 CHD1 SWD1 TIF5 NCB2 TEN1 EAP1 CSM3 RTF1 HDA3 SRS2 BDF2 BRE1</i>
GO:0045786	negative regulation of cell cycle	8.14E-04	2.83E-02	3.96 (4320,80,109,8)	<i>DOT1 BMH1 RAD9 MRC1 DDC1 SGS1 BRE1 PPH21</i>
GO:0010629	negative regulation of gene expression	2.16E-07	1.58E-05	3.90 (4320,193,109,19)	<i>DOT1 PAT1 BMH1 TIF5 NCB2 HIR3 MRC1 EAP1 RTF1 SPT2 HDA3 ASF1 RIF1 CLA4 HTZ1 SKO1 BRE1 SWD3 SWD1</i>
GO:0006342	chromatin silencing	9.60E-04	3.26E-02	3.87 (4320,82,109,8)	<i>DOT1 ASF1 RIF1 HTZ1 MRC1 BRE1 SWD3 SWD1</i>
GO:0045814	negative regulation of gene expression, epigenetic	9.60E-04	3.23E-02	3.87 (4320,82,109,8)	<i>DOT1 ASF1 RIF1 HTZ1 MRC1 BRE1 SWD3 SWD1</i>
GO:0009890	negative regulation of biosynthetic process	8.32E-08	6.65E-06	3.77 (4320,221,109,21)	<i>DOT1 PAT1 BMH1 TIF5 NCB2 HIR3 MRC1 EAP1 CSM3 RTF1 SPT2 RAD9 HDA3 ASF1 RIF1 HTZ1 SKO1 BRE1 SWD3 SWD1 CHD1</i>
GO:0031327	negative regulation of cellular biosynthetic process	8.32E-08	6.53E-06	3.77 (4320,221,109,21)	<i>DOT1 PAT1 BMH1 TIF5 NCB2 HIR3 MRC1 EAP1 CSM3 RTF1 SPT2 RAD9 HDA3 ASF1 RIF1 HTZ1 SKO1 BRE1 SWD3 SWD1 CHD1</i>
GO:0006325	chromatin organization	2.14E-06	1.32E-04	3.70 (4320,182,109,17)	<i>DOT1 PAT1 SPN1 HIR3 RSC8 SWC5 SPT2 RTF1 HDA3 ASF1 HTZ1 BRE1 SWD3 HPC2 NHP10 CHD1 SWD1</i>
GO:0009892	negative regulation of metabolic process	3.29E-10	7.88E-08	3.65 (4320,315,109,29)	<i>PAT1 DOT1 BMH1 HIR3 MRC1 SIS2 PPH21 RAD50 SPT2 RAD9 RIF1 ASF1 CLA4 HTZ1 SGS1 SKO1 SWD3 CHD1 SWD1 TIF5 NCB2 TEN1 EAP1 CSM3 RTF1 HDA3 SRS2 BDF2 BRE1</i>
GO:0031324	negative regulation of cellular metabolic process	3.50E-09	6.56E-07	3.52 (4320,304,109,27)	<i>PAT1 DOT1 BMH1 HIR3 MRC1 RAD50 PPH21 SPT2 RAD9 RIF1 ASF1 HTZ1 SGS1 SKO1 SWD3 CHD1 SWD1 TIF5 NCB2 TEN1 EAP1 CSM3 RTF1 HDA3 BDF2 SRS2 BRE1</i>
GO:0016568	chromatin modification	8.32E-05	3.74E-03	3.43 (4320,150,109,13)	<i>DOT1 RSC8 SWC5 RTF1 HDA3 ASF1 HTZ1 BRE1 HPC2 SWD3 NHP10 SWD1 CHD1</i>
GO:0045892	negative regulation of transcription, DNA-templated	2.95E-05	1.57E-03	3.36 (4320,177,109,15)	<i>DOT1 BMH1 HIR3 NCB2 MRC1 SPT2 RTF1 HDA3 ASF1 RIF1 HTZ1 BRE1 SKO1 SWD3</i>

					SWD1
GO:0010564	regulation of cell cycle process	3.73E-04	1.40E-02	3.35 (4320,130,109,11)	<i>DOT1 BMH1 RAD9 CIK1 CLA4 MRC1 DDC1 SGS1 MMS4 BRE1 PPH21</i>
GO:1902679	negative regulation of RNA biosynthetic process	3.15E-05	1.66E-03	3.34 (4320,178,109,15)	<i>DOT1 BMH1 HIR3 NCB2 MRC1 SPT2 RTF1 HDA3 ASF1 RIF1 HTZ1 BRE1 SKO1 SWD3 SWD1</i>
GO:1903507	negative regulation of nucleic acid-templated transcription	3.15E-05	1.64E-03	3.34 (4320,178,109,15)	<i>DOT1 BMH1 HIR3 NCB2 MRC1 SPT2 RTF1 HDA3 ASF1 RIF1 HTZ1 BRE1 SKO1 SWD3 SWD1</i>
GO:0051253	negative regulation of RNA metabolic process	3.15E-05	1.62E-03	3.34 (4320,178,109,15)	<i>DOT1 BMH1 HIR3 NCB2 MRC1 SPT2 RTF1 HDA3 ASF1 RIF1 HTZ1 BRE1 SKO1 SWD3 SWD1 SWD3 SWD1</i>
GO:0051726	regulation of cell cycle	3.72E-04	1.41E-02	2.96 (4320,174,109,13)	<i>DOT1 BMH1 CIK1 MRC1 SIS2 PPH21 RAD9 CLA4 MMS4 SGS1 DDC1 BRE1 SMI1</i>
GO:0048519	negative regulation of biological process	1.37E-08	1.68E-06	2.95 (4320,416,109,31)	<i>PAT1 DOT1 BMH1 HIR3 MRC1 SIS2 PPH21 RAD50 SPT2 RAD9 RIF1 ASF1 CLA4 HTZ1 SGS1 SKO1 SWD3 SWD1 CHD1 TIF5 NCB2 TEN1 EAP1 GPB2 RTF1 CSM3 HDA3 BDF2 SRS2 DDC1 BRE1</i>
GO:0048523	negative regulation of cellular process	6.85E-08	5.57E-06	2.90 (4320,396,109,29)	<i>PAT1 DOT1 BMH1 HIR3 MRC1 PPH21 RAD50 SPT2 RAD9 RIF1 ASF1 HTZ1 SGS1 SKO1 SWD3 CHD1 SWD1 TIF5 NCB2 TEN1 EAP1 GPB2 CSM3 RTF1 HDA3 BDF2 SRS2 DDC1 BRE1</i>
GO:0033554	cellular response to stress	2.42E-08	2.61E-06	2.88 (4320,426,109,31)	<i>DOT1 BMH1 UBA4 RAD24 MRC1 RSC8 RAD50 YKL069W RAD9 CTF18 ASF1 SGS1 MMS4 SKO1 ELC1 RAD52 NCB2 POL32 CTF4 RAD17 RTF1 CSM3 RRD1 BDF2 SRS2 RAD57 YPD1 DDC1 BRE1 NHP10 XRS2</i>
GO:0006950	response to stress	5.11E-09	8.17E-07	2.79 (4320,497,109,35)	<i>DOT1 BMH1 UBA4 RAD24 MRC1 RSC8 SIS2 RAD50 YKL069W RAD9 CTF18 ASF1 MMS4 SGS1 SKO1 ELC1 RAD52 NCB2 RRD2 POL32 CTF4 NST1 RAD17 RTF1 CSM3 RRD1 TCO89 BDF2 SRS2 RAD57 YPD1 DDC1 BRE1 NHP10 XRS2</i>
GO:1903046	meiotic cell cycle process	4.07E-04	1.52E-02	2.79 (4320,199,109,14)	<i>DOT1 BMH1 RAD52 RAD24 RAD50 RAD17 GPB2 CSM3 RAD57 SGS1 DDC1 MMS4 BRE1 XRS2</i>
GO:1903047	mitotic cell cycle process	8.03E-05	3.69E-03	2.71 (4320,263,109,18)	<i>DOT1 BMH1 CIK1 HIR3 RRD2 CTF4 MRC1 RSC8 CTF8 PPH21 CSM3 CTF18 RAD9 RRD1 SGS1 DDC1 BRE1 HPC2</i>
GO:0019219	regulation of nucleobase-containing compound metabolic process	4.31E-09	7.16E-07	2.64 (4320,571,109,38)	<i>DOT1 BMH1 HIR3 MRC1 RSC8 RAD50 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1</i>

					<i>MMS4 SGS1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 NCB2 TEN1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 SRS2 BRE1 HPC2 NHP10 SMI1</i>
GO:0051716	cellular response to stimulus	2.41E-07	1.70E-05	2.61 (4320,470,109,31)	<i>DOT1 BMH1 UBA4 RAD24 MRC1 RSC8 RAD50 YKL069W RAD9 CTF18 ASF1 SGS1 MMS4 SKO1 ELC1 RAD52 NCB2 POL32 CTF4 RAD17 RTF1 CSM3 RRD1 BDF2 SRS2 RAD57 YPD1 DDC1 BRE1 NHP10 XRS2</i>
GO:0010468	regulation of gene expression	4.21E-09	7.57E-07	2.59 (4320,597,109,39)	<i>DOT1 BMH1 HIR3 MRC1 RSC8 RAD50 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 MMS4 SGS1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 NCB2 TEN1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 SRS2 BRE1 HPC2 NHP10 SMI1</i>
GO:0051171	regulation of nitrogen compound metabolic process	7.10E-09	1.06E-06	2.59 (4320,581,109,38)	<i>PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 CLA4 RIF1 ASF1 HTZ1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 EAP1 SWC5 GPB2 RTF1 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0033043	regulation of organelle organization	9.73E-04	3.25E-02	2.56 (4320,217,109,14)	<i>DOT1 BMH1 CIK1 HIR3 TEN1 PPH21 RTF1 ASF1 BDF2 CLA4 SGS1 DDC1 MMS4 CHD1 PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 EAP1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:2000112	regulation of cellular macromolecule biosynthetic process	7.91E-09	1.14E-06	2.53 (4320,610,109,39)	<i>PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 EAP1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0010556	regulation of macromolecule biosynthetic process	9.56E-09	1.25E-06	2.52 (4320,614,109,39)	<i>PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 EAP1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0090304	nucleic acid metabolic process	6.12E-16	2.64E-12	2.47 (4320,1060,109,66)	<i>PAT1 RPS0B HIR3 MRC1 RSC8 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 IES5 NCB2 POL32 CTF4 TEN1 EAP1 RAD17 CSM3</i>

					<i>RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1</i>
GO:0009889	regulation of biosynthetic process	2.75E-08	2.83E-06	2.43 (4320,637,109,39)	<i>PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 EAP1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0031326	regulation of cellular biosynthetic process	2.75E-08	2.76E-06	2.43 (4320,637,109,39)	<i>PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 EAP1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0051252	regulation of RNA metabolic process	7.52E-07	5.15E-05	2.43 (4320,521,109,32)	<i>DOT1 BMH1 HIR3 MRC1 RSC8 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 CHD1 SWD1 RPB7 CAF40 SPN1 NCB2 SWC5 GPB2 RTF1 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0034645	cellular macromolecule biosynthetic process	1.37E-08	1.65E-06	2.40 (4320,677,109,41)	<i>SUI2 RPS1B RPS0B DOT1 RPS9B BMH1 RPL14A HIR3 RPL31B MRC1 RSC8 SPT2 SOK2 CTF18 ELP6 ASF1 HTZ1 SGS1 SKO1 FRS2 CHD1 RAD52 CAF40 RPB7 RPC11 SPN1 TIF5 NCB2 POL32 CTF4 TEN1 CTF8 SWC5 RTF1 HDA3 RPS20 BDF2 BRE1 HPC2 SMI1 NHP10</i>
GO:0050896	response to stimulus	9.57E-08	7.37E-06	2.40 (4320,610,109,37)	<i>DOT1 BMH1 UBA4 RAD24 MRC1 RSC8 SIS2 RAD50 YKL069W RAD9 CTF18 YKL075C CLA4 ASF1 MMS4 SGS1 SKO1 ELC1 RAD52 NCB2 RRD2 POL32 CTF4 NST1 RAD17 RTF1 CSM3 RRD1 TCO89 BDF2 SRS2 RAD57 YPD1 DDC1 BRE1 NHP10 XRS2</i>
GO:2001141	regulation of RNA biosynthetic process	1.64E-06	1.04E-04	2.40 (4320,512,109,31)	<i>DOT1 BMH1 HIR3 MRC1 RSC8 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 CHD1 SWD1 CAF40 SPN1 NCB2 SWC5 GPB2 RTF1 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:1903506	regulation of nucleic acid-templated transcription	1.64E-06	1.02E-04	2.40 (4320,512,109,31)	<i>DOT1 BMH1 HIR3 MRC1 RSC8 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1 SWD3 CHD1 SWD1 CAF40 SPN1 NCB2 SWC5 GPB2 RTF1 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1</i>
GO:0006355	regulation of transcription, DNA-templated	1.57E-06	1.01E-04	2.40 (4320,511,109,31)	<i>DOT1 BMH1 HIR3 MRC1 RSC8 YKE2 SPT2 SOK2 RAD9 ELP6 RIF1 ASF1 HTZ1 SKO1</i>

						SWD3 CHD1 SWD1 CAF40 SPN1 NCB2 SWC5 GPB2 RTF1 HDA3 RRD1 IMP2' BDF2 BRE1 HPC2 NHP10 SMI1
GO:0009059	macromolecule biosynthetic process	3.00E-08	2.88E-06	2.34	(4320,695,109,41)	PAT1 DOT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 PPH21 RAD50 YKE2 SPT2 SOK2 RAD9 ELP6 CLA4 RIF1 ASF1 HTZ1 MMS4 SGS1 SKO1 SWD3 SWD1 CHD1 CAF40 RPB7 SPN1 TIF5 NCB2 TEN1 EAP1 SWC5 GPB2 RTF1 CSM3 HDA3 RRD1 IMP2' BDF2 SRS2 BRE1 HPC2 NHP10 SMI1
GO:0006351	transcription, DNA-templated	7.39E-05	3.46E-03	2.34	(4320,389,109,23)	SUI2 RPS1B RPS0B DOT1 RPS9B BMH1 RPL14A HIR3 RPL31B MRC1 RSC8 SPT2 SOK2 CTF18 ELP6 ASF1 HTZ1 SGS1 SKO1 FRS2 CHD1 RAD52 CAF40 RPB7 RPC11 SPN1 TIF5 NCB2 POL32 CTF4 TEN1 CTF8 SWC5 RTF1 HDA3 RPS20 BDF2 BRE1 HPC2 SMI1 NHP10
GO:0097659	nucleic acid-templated transcription	7.39E-05	3.43E-03	2.34	(4320,389,109,23)	DOT1 CAF40 RPB7 RPC11 SPN1 HIR3 NCB2 RSC8 SWC5 SPT2 RTF1 SOK2 HDA3 ELP6 BDF2 ASF1 HTZ1 SKO1 BRE1 HPC2 SMI1 NHP10 CHD1
GO:0060255	regulation of macromolecule metabolic process	4.27E-09	7.37E-07	2.33	(4320,764,109,45)	DOT1 CAF40 RPB7 RPC11 SPN1 HIR3 NCB2 RSC8 SWC5 SPT2 RTF1 SOK2 HDA3 ELP6 BDF2 ASF1 HTZ1 SKO1 BRE1 HPC2 SMI1 NHP10 CHD1
GO:0006357	regulation of transcription from RNA polymerase II promoter	3.71E-04	1.42E-02	2.33	(4320,323,109,19)	BMH1 CAF40 SPN1 NCB2 HIR3 YKE2 GPB2 RTF1 SPT2 HDA3 RAD9 RRD1 IMP2' ELP6 ASF1 HTZ1 SKO1 HPC2 CHD1
GO:0022402	cell cycle process	3.21E-05	1.63E-03	2.30	(4320,449,109,26)	DOT1 BMH1 GIK1 HIR3 RAD24 MRC1 RSC8 RAD50 PPH21 CTF18 RAD9 SGS1 MMS4 RAD52 RRD2 CTF4 CTF8 RAD17 GPB2 CSM3 RRD1 RAD57 DDC1 BRE1 HPC2 XRS2
GO:0032774	RNA biosynthetic process	1.38E-04	6.06E-03	2.25	(4320,405,109,23)	DOT1 CAF40 RPB7 RPC11 SPN1 HIR3 NCB2 RSC8 SWC5 SPT2 RTF1 SOK2 HDA3 ELP6 BDF2 ASF1 HTZ1 SKO1 BRE1 HPC2 SMI1 NHP10 CHD1
GO:0080090	regulation of primary metabolic process	2.80E-08	2.74E-06	2.24	(4320,780,109,44)	DOT1 PAT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 RAD50 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 ASF1 RIF1 HTZ1 MMS4 SGS1 SKO1 SWD3 CHD1 SWD1 RPB7 CAF40 TIF5 SPN1 NCB2 TEN1 EAP1 SWC5 GPB2 CSM3 RTF1 HDA3 RRD1 IMP2' BDF2 SRS2 BRE1 HPC2 SMI1 NHP10



GO:0065008	regulation of biological quality	9.91E-04	3.29E-02	2.22 (4320,322,109,18)	RPS9B RAD52 SPN1 IES5 RPL31B TEN1 MRC1 RAD50 TIM50 RIF1 RAD57 SGS1 BRE1 SWD3 NHP10 XRS2 CHD1 SWD1 SWD1
GO:0031323	regulation of cellular metabolic process	5.07E-08	4.29E-06	2.19 (4320,795,109,44)	DOT1 PAT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 RAD50 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 ASF1 RIF1 HTZ1 MMS4 SGS1 SKO1 SWD3 CHD1 SWD1 RPB7 CAF40 TIF5 SPN1 NCB2 TEN1 EAP1 SWC5 GPB2 CSM3 RTF1 HDA3 RRD1 IMP2' BDF2 SRS2 BRE1 HPC2 SMI1 NHP10
GO:0043933	macromolecular complex subunit organization	1.81E-05	1.02E-03	2.18 (4320,545,109,30)	PAT1 RPS0B HIR3 MRC1 RSC8 SIS2 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 NCB2 IES5 POL32 CTF4 TEN1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1
GO:0006139	nucleobase-containing compound metabolic process	2.17E-13	3.12E-10	2.18 (4320,1217,109,67)	RPS0B PAT1 DOT1 SUI2 CIK1 HIR3 RSC8 GIM4 PPH21 YKE2 SPT2 ASF1 HTZ1 SWD3 CHD1 SWD1 RAD52 SPN1 TIF5 NCB2 RRD2 SWC5 RTF1 HDA3 RRD1 SRS2 RAD57 BRE1 HPC2 NHP10
GO:0019222	regulation of metabolic process	3.42E-08	3.20E-06	2.13 (4320,875,109,47)	DOT1 PAT1 RPS9B BMH1 HIR3 RPL31B MRC1 RSC8 SIS2 RAD50 PPH21 YKE2 SPT2 SOK2 RAD9 ELP6 ASF1 RIF1 CLA4 HTZ1 MMS4 SGS1 SKO1 SWD3 CHD1 SWD1 RPB7 CAF40 TIF5 SPN1 NCB2 RRD2 TEN1 EAP1 SWC5 GPB2 CSM3 RTF1 HDA3 RRD1 IMP2' BDF2 SRS2 BRE1 HPC2 NHP10 SMI1
GO:1902589	single-organism organelle organization	2.78E-05	1.50E-03	2.13 (4320,557,109,30)	DOT1 CIK1 MRC1 RSC8 RAD50 TIM50 ATG3 CTF18 RIF1 ASF1 SGS1 SWD3 SWD1 CHD1 RAD52 SPN1 IES5 RRD2 CTF4 TEN1 CTF8 TIM10 RTF1 CSM3 HDA3 RRD1 RAD57 BRE1 NHP10 XRS2
GO:0006725	cellular aromatic compound metabolic process	2.89E-12	2.08E-09	2.08 (4320,1279,109,67)	PAT1 RPS0B HIR3 MRC1 RSC8 SIS2 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2

					CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 IES5 NCB2 POL32 CTF4 TEN1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1
GO:0046483	heterocycle metabolic process	3.53E-12	2.18E-09	2.07 (4320,1284,109,67)	PAT1 RPS0B HIR3 MRC1 RSC8 SIS2 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 NCB2 IES5 POL32 CTF4 TEN1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1
GO:0016070	RNA metabolic process	5.41E-07	3.76E-05	2.06 (4320,829,109,43)	DOT1 RPS0B RPS1B PAT1 RPS9B UBA4 TRM11 HIR3 LEA1 RSC8 TPT1 SPT2 SOK2 ELP6 ASF1 HTZ1 NMD2 SKO1 FRS2 CHD1 UPF3 RPB7 RPC11 CAF40 SPN1 NCB2 LSM7 NHP2 POL32 LSM6 EAP1 SWC5 RTF1 HDA3 BUD21 RPS20 RTT10 BDF2 PUS7 BRE1 HPC2 SMI1 NHP10
GO:0034654	nucleobase-containing compound biosynthetic process	2.68E-04	1.08E-02	2.02 (4320,509,109,26)	DOT1 HIR3 RSC8 SIS2 SPT2 SOK2 ELP6 ASF1 HTZ1 SKO1 CHD1 RAD52 RPC11 RPB7 CAF40 SPN1 NCB2 POL32 SWC5 RTF1 HDA3 BDF2 BRE1 HPC2 NHP10 SMI1
GO:0034641	cellular nitrogen compound metabolic process	7.55E-12	4.07E-09	2.01 (4320,1338,109,68)	PAT1 RPS0B HIR3 MRC1 RSC8 SIS2 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 NCB2 IES5 POL32 CTF4 TEN1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1 SPE1
GO:1901360	organic cyclic compound metabolic process	1.97E-11	9.42E-09	2.00 (4320,1328,109,67)	PAT1 RPS0B HIR3 MRC1 RSC8 SIS2 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 NCB2 IES5 POL32 CTF4 TEN1 EAP1 RAD17 CSM3

					<i>RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1</i>
GO:0050794	regulation of cellular process	1.43E-08	1.67E-06	1.97 (4320,1104,109,55)	<i>PAT1 HIR3 MRC1 RSC8 SIS2 YKE2 SOK2 RAD9 CLA4 RIF1 ASF1 MMS4 SKO1 CAF40 TIF5 SWC5 RTF1 HDA3 RRD1 IMP2' SOK1 HPC2 SMI1 NHP10 DOT1 RPS9B BMH1 CIK1 UBA4 RPL31B YPT6 RAD50 PPH21 SPT2 ELP6 HTZ1 SGS1 SWD3 TPK3 SWD1 CHD1 RPB7 SPN1 NCB2 TEN1 EAP1 GPB2 CSM3 MF(ALPHA)1 TCO89 SRS2 BDF2 DDC1 YPD1 BRE1</i>
GO:0006996	organelle organization	1.82E-05	1.02E-03	1.95 (4320,752,109,37)	<i>PAT1 DOT1 CIK1 MRC1 RSC8 RAD50 TIM50 ATG3 CTF18 CLA4 RIF1 ASF1 MMS4 SGS1 SWD3 TPK3 SWD1 CHD1 RAD52 SPN1 TIF5 IES5 RRD2 CTF4 TEN1 CTF8 TIM10 RTF1 CSM3 HDA3 RRD1 SRS2 RAD57 DDC1 BRE1 NHP10 XRS2</i>
GO:0006807	nitrogen compound metabolic process	5.14E-11	2.01E-08	1.90 (4320,1461,109,70)	<i>PAT1 RPS0B HIR3 MRC1 RSC8 SIS2 TPT1 SOK2 RAD9 ASF1 RIF1 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS1B RPS9B BMH1 UBA4 TRM11 RAD24 LEA1 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 ALT1 CHD1 SWD1 UPF3 RPB7 RPC11 SPN1 IES5 NCB2 POL32 CTF4 TEN1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1 SPE1</i>
GO:0050789	regulation of biological process	4.61E-08	4.06E-06	1.89 (4320,1172,109,56)	<i>PAT1 HIR3 MRC1 RSC8 SIS2 YKE2 SOK2 RAD9 CLA4 RIF1 ASF1 MMS4 SKO1 CAF40 TIF5 SWC5 RTF1 HDA3 RRD1 IMP2' SOK1 HPC2 SMI1 NHP10 DOT1 RPS9B BMH1 UBA4 CIK1 RPL31B YPT6 RAD50 PPH21 SPT2 ELP6 HTZ1 SGS1 SWD3 TPK3 SWD1 CHD1 RPB7 SPN1 NCB2 RRD2 TEN1 EAP1 GPB2 CSM3 MF(ALPHA)1 TCO89 SRS2 BDF2 DDC1 YPD1 BRE1</i>
GO:0044260	cellular macromolecule metabolic process	1.10E-13	2.38E-10	1.85 (4320,1754,109,82)	<i>SUI2 PAT1 RPS0B HIR3 STI1 MRC1 GIM4 RSC8 YKE2 TPT1 SOK2 RAD9 ASF1 RIF1 CLA4 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 TIF5 LSM7 PBY1 NHP2 LSM6 SHR3 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 RPS1B DOT1 RPS9B BMH1 RPL14A UBA4 TRM11 RAD24 RPL31B LEA1 RAD50 PPH21 SPT2</i>

						ATG3 CTF18 ELP6 HTZ1 SGS1 TPK3 SWD3 FRS2 CHD1 SWD1 UPF3 RPC11 RPB7 SPN1 NCB2 IES5 RRD2 POL32 CTF4 TEN1 VMS1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1
GO:0044271	cellular nitrogen compound biosynthetic process	9.15E-04	3.16E-02	1.84	(4320,581,109,27)	DOT1 HIR3 RSC8 SIS2 SPT2 SOK2 ELP6 ASF1 HTZ1 SKO1 CHD1 RAD52 RPC11 RPB7 CAF40 SPN1 NCB2 POL32 SWC5 RTF1 HDA3 BDF2 BRE1 HPC2 NHP10 SMI1 SPE1
GO:0065007	biological regulation	2.73E-08	2.87E-06	1.82	(4320,1327,109,61)	PAT1 HIR3 MRC1 RSC8 SIS2 YKE2 TIM50 SOK2 RAD9 CLA4 ASF1 RIF1 MMS4 SKO1 RAD52 CAF40 TIF5 SWC5 RTF1 HDA3 RRD1 IMP2' SOK1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS9B BMH1 UBA4 CIK1 RPL31B YPT6 RAD50 PPH21 SPT2 ELP6 HTZ1 SGS1 SWD3 TPK3 CHD1 SWD1 RPB7 SPN1 IES5 NCB2 RRD2 TEN1 EAP1 GPB2 CSM3 MF(ALPHA)1 TCO89 SRS2 BDF2 DDC1 YPD1 BRE1
GO:0043170	macromolecule metabolic process	2.02E-12	2.17E-09	1.77	(4320,1834,109,82)	SUI2 PAT1 RPS0B HIR3 STI1 MRC1 GIM4 RSC8 YKE2 TPT1 SOK2 RAD9 ASF1 RIF1 CLA4 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 TIF5 LSM7 PBY1 NHP2 LSM6 SHR3 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 RPS1B DOT1 RPS9B BMH1 RPL14A UBA4 TRM11 RAD24 RPL31B LEA1 RAD50 PPH21 SPT2 ATG3 CTF18 ELP6 HTZ1 SGS1 TPK3 SWD3 FRS2 CHD1 SWD1 UPF3 RPC11 RPB7 SPN1 NCB2 IES5 RRD2 POL32 CTF4 TEN1 VMS1 EAP1 RAD17 CSM3 RPS20 RTT10 SRS2 BDF2 DDC1 PUS7 BRE1
GO:0044249	cellular biosynthetic process	6.91E-05	3.27E-03	1.70	(4320,1025,109,44)	DOT1 RPS0B RPS1B SUI2 RPS9B BMH1 RPL14A HIR3 RPL31B MRC1 RSC8 SIS2 SPT2 SOK2 CTF18 ELP6 ASF1 HTZ1 SGS1 SKO1 FRS2 ALT1 CHD1 RAD52 RPB7 RPC11 CAF40 TIF5 SPN1 NCB2 CTF4 POL32 TEN1 CTF8 SWC5 RTF1 HDA3 RPS20 BDF2 BRE1 HPC2 SMI1 SPE1 NHP10
GO:1901576	organic substance biosynthetic process	1.64E-04	6.74E-03	1.64	(4320,1061,109,44)	DOT1 RPS0B RPS1B SUI2 RPS9B BMH1 RPL14A HIR3 RPL31B MRC1 RSC8 SIS2 SPT2 SOK2 CTF18 ELP6 ASF1 HTZ1 SGS1 SKO1 FRS2 ALT1 CHD1 RAD52 RPB7 RPC11 CAF40 TIF5 SPN1 NCB2 CTF4 POL32 TEN1

					CTF8 SWC5 RTF1 HDA3 RPS20 BDF2 BRE1 HPC2 SMI1 SPE1 NHP10
GO:0009058	biosynthetic process	2.89E-04	1.14E-02	1.61 (4320,1086,109,44)	DOT1 RPS0B RPS1B SUI2 RPS9B BMH1 RPL14A HIR3 RPL31B MRC1 RSC8 SIS2 SPT2 SOK2 CTF18 ELP6 ASF1 HTZ1 SGS1 SKO1 FRS2 ALT1 CHD1 RAD52 RPB7 RPC11 CAF40 TIF5 SPN1 NCB2 CTF4 POL32 TEN1 CTF8 SWC5 RTF1 HDA3 RPS20 BDF2 BRE1 HPC2 SMI1 SPE1 NHP10
GO:0071840	cellular component organization or biogenesis	2.05E-05	1.12E-03	1.58 (4320,1427,109,57)	PAT1 RPS0B SUI2 HIR3 MRC1 GIM4 RSC8 YKE2 TIM50 RE1 CLA4 ASF1 RIF1 MMS4 RAD52 TIF5 NHP2 CTF8 SWC5 APQ12 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS9B BMH1 CIK1 RAD50 PPH21 ATG3 SPT2 CTF18 HTZ1 SGS1 SWD3 TPK3 SWD1 CHD1 SPN1 IES5 NCB2 RRD2 CTF4 TEN1 TIM10 CSM3 TCO89 SRS2 DDC1 BRE1 PUS7
GO:0016043	cellular component organization	8.31E-05	3.77E-03	1.57 (4320,1309,109,52)	SUI2 PAT1 RPS0B HIR3 MRC1 RSC8 GIM4 YKE2 TIM50 CLA4 ASF1 RIF1 MMS4 RAD52 TIF5 CTF8 APQ12 SWC5 RTF1 HDA3 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 BMH1 CIK1 RAD50 PPH21 ATG3 SPT2 CTF18 HTZ1 SGS1 SWD3 TPK3 SWD1 CHD1 SPN1 NCB2 IES5 RRD2 CTF4 TEN1 TIM10 CSM3 TCO89 SRS2 DDC1 BRE1
GO:0044238	primary metabolic process	8.69E-09	1.21E-06	1.48 (4320,2322,109,87)	SUI2 PAT1 RPS0B HIR3 STI1 MRC1 SIS2 GIM4 RSC8 YKE2 TPT1 SOK2 RAD9 ASF1 RIF1 CLA4 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 TIF5 LSM7 PBY1 NHP2 LSM6 SHR3 CTF8 APQ12 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 SMI1 NHP10 XRS2 RPS1B DOT1 RPS9B BMH1 RPL14A UBA4 TRM11 RAD24 RPL31B LEA1 RAD50 PPH21 SPT2 ATG3 CTF18 ELP6 HTZ1 SGS1 TPK3 SWD3 FRS2 ALT1 CHD1 SWD1 UPF3 RPC11 RPB7 SPN1 NCB2 IES5 RRD2 POL32 CTF4 TEN1 VMS1 EAP1 RAD17 CSM3 RPS20 RTT10 TCO89 SRS2 BDF2 DDC1 PUS7 BRE1 SPE1
GO:0044237	cellular metabolic process	9.48E-09	1.28E-06	1.46 (4320,2418,109,89)	SUI2 PAT1 RPS0B HIR3 STI1 MRC1 SIS2 GIM4 RSC8 YKE2 TPT1 SOK2 RAD9 ASF1 RIF1 CLA4 NMD2 MMS4 SKO1 ELC1 RAD52 CAF40 TIF5 LSM7 PBY1 NHP2 LSM6 SHR3

					<p>CTF8 APQ12 SWC5 RTF1 HDA3 BUD21  RRD1 RAD57 HPC2 SMI1 NHP10 XRS2  RPS1B DOT1 RPS9B BMH1 RPL14A UBA4  TRM11 RAD24 RPL31B LEA1 RAD50 PPH21  SPT2 ATG3 CTF18 ELP6 HTZ1 SGS1 TPK3  SWD3 FRS2 ALT1 CHD1 SWD1 UPF3 RPB7  RPC11 SPN1 IES5 NCB2 RRD2 POL32 CTF4  TEN1 VMS1 EAP1 PET20 RAD17 CSM3  RPS20 RTT10 TCO89 SRS2 IPP1 BDF2 DDC1  PUS7 BRE1 SPE1</p>
GO:0071704	organic substance metabolic process	1.28E-07	9.51E-06	1.42 (4320,2424,109,87)	<p>SUI2 PAT1 RPS0B HIR3 STI1 MRC1 SIS2  GIM4 RSC8 YKE2 TPT1 SOK2 RAD9 ASF1  RIF1 CLA4 NMD2 MMS4 SKO1 ELC1 RAD52  CAF40 TIF5 LSM7 PB1 NHP2 LSM6 SHR3  CTF8 APQ12 SWC5 RTF1 HDA3 BUD21  RRD1 RAD57 HPC2 SMI1 NHP10 XRS2  RPS1B DOT1 RPS9B BMH1 RPL14A UBA4  TRM11 RAD24 RPL31B LEA1 RAD50 PPH21  SPT2 ATG3 CTF18 ELP6 HTZ1 SGS1 TPK3  SWD3 FRS2 ALT1 CHD1 SWD1 UPF3 RPC11  RPB7 SPN1 NCB2 IES5 RRD2 POL32 CTF4  TEN1 VMS1 EAP1 RAD17 CSM3 RPS20  RTT10 TCO89 SRS2 BDF2 DDC1 PUS7 BRE1  SPE1</p>
GO:0008152	metabolic process	4.75E-06	2.81E-04	1.31 (4320,2717,109,90)	<p>SUI2 PAT1 RPS0B HIR3 STI1 MRC1 SIS2  GIM4 RSC8 YKL069W YKE2 TPT1 SOK2  RAD9 ASF1 RIF1 CLA4 NMD2 MMS4 SKO1  ELC1 RAD52 CAF40 TIF5 LSM7 PB1 NHP2  LSM6 SHR3 CTF8 APQ12 SWC5 RTF1 HDA3  BUD21 RRD1 RAD57 HPC2 SMI1 NHP10  XRS2 RPS1B DOT1 RPS9B BMH1 RPL14A  UBA4 TRM11 RAD24 RPL31B LEA1 RAD50  PPH21 SPT2 ATG3 CTF18 ELP6 HTZ1 SGS1  TPK3 SWD3 FRS2 ALT1 CHD1 SWD1 UPF3  RPB7 RPC11 SPN1 NCB2 IES5 RRD2 POL32  CTF4 TEN1 VMS1 EAP1 PET20 RAD17 CSM3  RPS20 RTT10 TCO89 SRS2 IPP1 BDF2 DDC1  PUS7 BRE1 SPE1</p>

## Cellular components

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0030870	Mre11 complex	6.31E-04	6.03E-02	39.63 (4320,2,109,2)	<i>RAD50 XRS2</i>
GO:0030896	checkpoint clamp complex	6.31E-04	5.43E-02	39.63 (4320,2,109,2)	<i>DDC1 RAD17</i>
GO:0022627	cytosolic small ribosomal subunit	3.21E-04	3.46E-02	6.26 (4320,38,109,6)	<i>RPS1B PAT1 RPS0B RPS9B TIF5 RPS20</i>
GO:0044427	chromosomal part	2.80E-08	8.02E-06	3.42 (4320,290,109,25)	<i>PAT1 RAD24 MRC1 RAD9 CTF18 RIF1 HTZ1 SGS1 SWD3 CHD1 SWD1 IES5 CTF4 POL32 TEN1 CTF8 RAD17 SWC5 RTF1 CSM3 HDA3 RRD1 DDC1 BRE1 NHP10</i>
GO:0044454	nuclear chromosome part	1.82E-05	3.13E-03	3.16 (4320,213,109,17)	<i>IES5 POL32 CTF4 TEN1 MRC1 RAD17 SWC5 CSM3 CTF18 HDA3 RRD1 RIF1 HTZ1 DDC1 BRE1 NHP10 CHD1</i>
GO:0044428	nuclear part	3.94E-05	5.65E-03	1.86 (4320,809,109,38)	<i>RPS9B MRC1 LEA1 RSC8 RAD50 CTF18 RIF1 HTZ1 SGS1 SWD3 ELC1 CHD1 SWD1 UPF3 RAD52 RPB7 RPC11 IES5 NCB2 LSM7 NHP2 POL32 CTF4 LSM6 TEN1 RAD17 SWC5 APQ12 CSM3 RTF1 HDA3 BUD21 RRD1 RAD57 DDC1 BRE1 NHP10 XRS2</i>
GO:0032991	macromolecular complex	2.47E-10	2.12E-07	1.84 (4320,1506,109,70)	<i>PAT1 RPS0B SUI2 HIR3 MRC1 GIM4 RSC8 SIS2 YKE2 TIM50 REI1 RAD9 RIF1 NMD2 MMS4 ELC1 MTC1 CAF40 TIF5 LSM7 PBY1 NHP2 LSM6 CTF8 SWC5 RTF1 HDA3 BUD21 RRD1 RAD57 HPC2 NHP10 XRS2 RPS1B RPS9B RPL14A CIK1 TRM11 RAD24 RPL31B LEA1 RAD50 PPH21 CTF18 ELP6 HTZ1 SGS1 SWD3 FRS2 TPK3 CHD1 SWD1 UPF3 RPB7 RPC11 NCB2 IES5 RRD2 POL32 CTF4 TEN1 VMS1 EAP1 RAD17 TIM10 CSM3 RPS20 TCO89 DDC1 BRE1</i>
GO:0043234	protein complex	9.88E-06	2.12E-03	1.75 (4320,1084,109,48)	<i>PAT1 SUI2 CIK1 TRM11 HIR3 RAD24 MRC1 GIM4 RSC8 SIS2 RAD50 PPH21 YKE2 TIM50 CTF18 ELP6 HTZ1 MMS4 SGS1 SWD3 ELC1 FRS2 TPK3 CHD1 SWD1 RPB7 RPC11 CAF40 IES5 NCB2 RRD2 CTF4 POL32 VMS1 EAP1 CTF8 RAD17 SWC5 TIM10 CSM3 RTF1 HDA3 TCO89 RAD57 DDC1 HPC2 NHP10 XRS2</i>
GO:0005634	nucleus	1.13E-08	4.84E-06	1.72 (4320,1588,109,69)	<i>PAT1 HIR3 MRC1 SIS2 RSC8 YKL069W YKE2 TPT1 SOK2 RAD9 ASF1 RIF1 CLA4</i>

						MMS4 SKO1 ELC1 RAD52 CAF40 LSM7 NHP2 LSM6 CTF8 APQ12 SWC5 RTF1 HDA3 BUD21 RRD1 SOK1 RAD57 HPC2 SMI1 NHP10 XRS2 DOT1 RPS9B BMH1 CIK1 RAD24 LEA1 PPH21 RAD50 SPT2 CTF18 ELP6 HTZ1 SGS1 TPK3 SWD3 SWD1 CHD1 UPF3 RPC11 RPB7 SPN1 IES5 NCB2 POL32 CTF4 TEN1 RAD17 CSM3 SRS2 BDF2 IPP1 YPD1 DDC1 PUS7 BRE1
GO:0044424	intracellular part	1.13E-04	1.39E-02	1.13	(4320,3670,109,105)	HIR3 STI1 MRC1 RSC8 SIS2 YKE2 TIM50 RAD9 ASF1 CLA4 MMS4 ELC1 MTC1 CAF40 PBY1 CTF8 APQ12 HDA3 BUD21 SOK1 AIM29 RAD57 NHP10 DOT1 RPS1B RPL14A UBA4 CIK1 YPT6 RAD50 ATG3 HTZ1 SGS1 TPK3 SWD1 RPB7 SPN1 IES5 NCB2 RRD2 CTF4 TEN1 EAP1 PET20 GPB2 SRS2 IPP1 BDF2 BRE1 PUS7 SPE1 RPS0B PAT1 SUI2 MTC4 GIM4 YKL069W TPT1 REI1 SOK2 YKL075C RIF1 NMD2 SKO1 RAD52 TIF5 LSM7 NHP2 LSM6 SHR3 YMD8 SWC5 RTF1 RRD1 IMP2' HPC2 SMI1 XRS2 BMH1 RPS9B TRM11 RAD24 RPL31B LEA1 PPH21 SPT2 CTF18 ELP6 SWD3 FRS2 ALT1 CHD1 UPF3 RPC11 POL32 VMS1 NST1 RAD17 TIM10 CSM3 RPS20 RTT10 TCO89 YPD1 DDC1