Table S7 GO categorisation of differentially expressed transcripts with a fold change greater than or equal to 2 (i.e. up-regulated genes).

Category	p-value	In Category from Cluster	k	f
ribosome biogenesis [GO:0042254]	<1e-14	RPS9B ENP1 SPB1 PWP2 NOP1 NOP14 NHP2 RLI1 UTP4 UTP5 SNU13 TMA20 NSA2 SPB4 LOC1 CGR1 DBP3 ROK1 SLX9 UTP8 CIC1 RRP3 GAR1 IMP3 RIX1 UTP18 UTP10 ALB1 MRT4 URB1 EBP2 RPL40B SOF1 RLP24 SDO1 DIP2 CBF5 EMG1 NOP56 UTP13 DBP9 UTP21 ERB1 UTP15 RRB1 HAS1 NOP2 DBP2 NOG2 ESF2 NOP12 BRX1 NOC2 PUS7 YTM1 RRS1 NOP58 RRP12 RPS9A NOG1 NIP7 RRP9	62	184
regulation of translation [GO:0006417]	<1e-14	RBG1 URA7 ILS1 RPS11B RPG1 GRS1 RPS9B ARO4 SRO9 THR4 RPL13A SSB1 RPL4B RPS11A RLI1 RPL12A RPS8B YGR054W VAS1 TIF4631 ADE3 RPS0A MES1 RPL14B IMD2 RPS24B THS1 URA2 RPL17B SUI2 TEF4 EAP1 GCN3 DPS1 FRS1 SAM1 PWP1 IMD3 RPS1A RPL6B IMD4 RPL6A NIP1 DBP2 SSB2 RPL18B WRS1 PRT1 RPS9A CDC60 NEW1 TIF5 TKL1	53	172
cellular amino acid and derivative metabolic process [GO:0006519]	3.5E-14	ILS1 ADH5 HIS7 ARO4 ILV6 LYS21 GGC1 KRS1 TRP4 HOM3 HIS1 ILV1 TRP2 TRP5 ARO2 ARO8 ASN2 LYS1 ACO2 TRP3 SAM1 ATR1 ARG7 ADE4 ARG1 LEU9 ORT1 HIS3 SAM4 YMC1 ASN1	31	71
cellular amino acid biosynthetic process [GO:0008652]	1.7E-13	LYS2 HIS7 ARO4 ILV6 THR4 LYS21 LYS4 TRP4 PRO3 HOM3 HIS1 SER3 ILV1 TRP2 IRC7 TRP5 ARO2 ASN2 ADE3 SER2 THR1 LYS12 LYS1 ARG3 MDE1 TRP3 ILV5 YML096W ARG7 LYS9 ARG1 LEU9 ORT1 HIS3 PRO2 SAM4 ARO7 ASN1	38	107
nitrogen compound metabolic process [GO:0006807]	3.2E-13	ILS1 ADH5 HIS7 ARO4 ILV6 LYS21 GGC1 KRS1 TRP4 HOM3 HIS1 ILV1 TRP2 TRP5 ARO2 ARO8 ASN2 ADE3 NIT1 LYS1 URA2 ACO2 TRP3 SHM2 SAM1 ATR1 ARG7 ADE4 ARG1 LEU9 ORT1 HIS3 SAM4 YMC1 ASN1	35	94
cellular aromatic compound metabolic process [GO:0006725]	6.3E-13	ADH5 HIS7 ARO4 ILV6 LYS21 GGC1 KRS1 TRP4 HOM3 HIS1 ILV1 TRP2 TRP5 YGL039W ARO2 ARO8 ASN2 LYS1 ACO2 TRP3 ATR1 ARG7 ARG1 LEU9 ORT1 HIS3 SAM4 YMC1 ASN1	29	68
organic acid metabolic process [GO:0006082]	2.0E-11	ADH5 HIS7 ARO4 ILV6 LYS21 GGC1 KRS1 TRP4 HOM3 HIS1 ILV1 TRP2 TRP5 ARO2 ARO8 ASN2 LYS1 ACO2 MAE1 TRP3 SAM1 ATR1 ARG7 ARG1 LEU9 ORT1 HIS3 SAM4 YMC1 ASN1	30	81
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) [GO:0000462]	4.3E-10	RPS11B RPS9B PWP2 NOP1 NOP14 RPS11A UTP4 UTP5 SNU13 RPS8B PRP43 SLX9 UTP8 EFG1 RRP3 RPS24B UTP25 UTP10 SOF1 DIP2 NOP56 UTP13 TSR2 RPS1A UTP15 RRP12 RPS9A	27	75
tRNA aminoacylation for protein translation [GO:0006418]	6.3E-09	ILS1 GRS1 SES1 KRS1 FRS2 ARC1 VAS1 TYS1 MES1 DED81 YHR020W THS1 DPS1 YNL247W WRS1 GLN4 CDC60	17	36
metabolic process [GO:0008152]	2.7E-08	BNA4 LYS2 ADH5 HIS7 ARO4 MAL32 ILV6 THR4 SLC1 QRI1 LYS21 PHO13 LYS4 EXG2 TRP4 URH1 URA3 UTR2 HPA3 PRO3 SAH1 HOM3 SER3 ILV1 TRP5 SCW11 YGL039W ARI1 CRH1 ADE3 SER2 ARD1 PAN5 IMD2 RHR2 SUC2 LYS1 RPE1 URA2 ACO2 BNA1 PGU1 YKL027W MAE1 MCD4 TRP3 URA1 ACS2 DPH5 ILV5 DUS3 YLR426W IMD3 ERG6 IMD4 ERG13 PLB2 ERG12 ADE4 SCW10 NRK1 SPS19 LYS9 DSE4 GPD2 LEU9 PRO2 ERG10 ALD6 TKL1	70	377
sterol biosynthetic process [GO:0016126]	1.4E-06	ERG25 ERG11 ERG3 ERG6 HMG1 ERG13 ERG5 ERG2 ERG12 CYB5 MVD1 HES1 IDI1	13	30
steroid biosynthetic process [GO:0006694]	1.5E-06	ERG25 ERG11 ERG3 ERG6 HMG1 ERG13 ERG5 ERG2 ERG12 MVD1 HES1 IDI1	12	26
peptidyl-amino acid modification [GO:0018193]	2.4E-06	NCL1 PRS4 HMT1 ARO4 DUT1 FEN1 DTD1 PHO13 RLI1 UTP5 UTR2 MAK10 ARD1 PHO90 HAM1 LIA1 SUR4 OST6 APT1 URA5 GAS3 SEC63 ALG5	23	84
alcohol metabolic process [GO:0006066]	3.7E-06	YAT1 ERG25 ATF2 ERG11 YEH1 ERG3 ACS2 ERG6 HMG1 ERG13 ERG5 ERG2 ERG12 CYB5 MVD1 ERG10 IDI1	17	52
endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA	1.0E-05	ENP1 PWP2 NOP14 LOC1 RPS0A NOP9 UTP18 UTP10 DIP2 EMG1 UTP13 RPS18B ESF2 RRS1 NOP58	15	45

transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) [GO:0000447]				
translational elongation [GO:0006414]	2.7E-05	BNA4 AAC3 ADH5 CTP1 ILV6 APA1 BSC1 PRM7 RPP1B GGC1 PAD1 GLY1 HPA3 DLD3 HOM3 PTC2 TRP2 WWM1 IRC7 MF(ALPHA)2 SCS3 SUT1 MIG2 BUD9 PTI1 INM1 TIM44 POR2 PAN6 LYS1 PRY3 ARG3 ESS1 SFK1 TEF4 HOT13 EAP1 SSA2 NEJ1 DIC1 HXT2 SSO2 DSK2 RNH201 DSE4 ARG1 GPD2 HPF1 NRT1 HIS3 FIT2 ALD6 DIP5 DPM1	54	322
RNA modification [GO:0009451]	4.0E-05	MAK16 HMT1 ENP1 SPB1 RSA4 RPC53 TRM82 DBP3 YVH1 ALB1 CBF5 DUS3 TSR2 GCD10 TRM11 PUS7 RRS1 PUS1	18	67
pyrimidine nucleotide biosynthetic process [GO:0006221]	4.5E-05	URA7 URA3 DCD1 URA2 URA8 URA1 URA4 URA5	8	16
glutamine metabolic process [GO:0006541]	5.4E-05	URA7 HIS7 ASN2 URA2 URA8 TRP3 YML096W GUA1 ADE4 ASN1	10	25
lipid biosynthetic process [GO:0008610]	9.1E-05	FEN1 ERG25 ERG11 SFK1 ERG3 SUR4 ERG6 HMG1 ERG13 ERG5 ERG2 ERG12 MVD1 HES1 IDI1	15	53
ergosterol biosynthetic process [GO:0006696]	2.3E-04	ERG25 ERG11 ERG3 ERG6 HMG1 ERG13 ERG5 ERG2 ERG12 ERG10	10	29
GMP biosynthetic process [GO:0006177]	3.9E-04	IMD2 IMD3 IMD4 GUA1	4	5
lysine biosynthetic process [GO:0009085]	4.3E-04	LYS2 LYS21 LYS4 LYS12 LYS1 LYS9	6	12
cellular amino acid metabolic process [GO:0006520]	4.3E-04	THR4 ASP1 GLY1 ILV1 IRC7 ARG3 URA2 MAE1 AAT1 ASP3-1	10	31
translation [GO:0006412]	4.4E-04	MAK16 FUN12 ILS1 RPS11B RPG1 GRS1 RPS9B SRO9 RPL13A RPP1B RPL41A DTD1 SSB1 RPL4B SES1 RPS11A KRS1 RLI1 RPS17B RPL12A TMA20 RPL34A RPS8B RPS26B FRS2 RPL22B RPL9A YGR054W VAS1 RPL24B TIF4631 TYS1 RPS0A MES1 RPL14B DED81 YHR020W RPS24B THS1 RPL17B RPS22A SUI2 RPL43B TEF4 GCN3 RPL40B DPS1 RLP24 FRS1 RPL31B RPS1A RPL6B RPS18B RPL6A TIF34 RPL36A RPS10B NIP1 SSB2 YNL247W RPL18B WRS1 RPL18A RPS19A RPS28A GLN4 RPS10A PRT1 RPS9A CDC60 TIF5 TIF3	72	511
aromatic amino acid family biosynthetic process [GO:0009073]	3.5E-03	ARO4 TRP4 TRP2 TRP5 ARO2 TRP3 ARO7	7	22
lysine biosynthetic process via aminoadipic acid [GO:0019878]	3.6E-03	LYS2 LYS21 LYS4 LYS1 LYS9	5	12
de novo NAD biosynthetic process from tryptophan [GO:0034354]	7.6E-03	BNA4 BNA1 BNA2	3	5

k refers to the number of differentially expressed genes annotated with the GO term.
f refers to the total number of genes present in the yeast genome annotated with the GO term.