Table S1 Primers used for amplification of target genes.

Primer Name	Sequence (5'-3')
PhR322F	GATCCACGTCGGTACCCGGGGGATC
PhR322R	GATCGCGATCGCAAGCTTGCAAATTAAAGCC
RAP1f	TTAAGCGGCCGCATACGCAACCGCCCTACATAA
RAP1r	TCTACATATGCGTGAATCAGTGAAATAAAGG
SOK2f	TTAAGCGGCCGCTATAACCCTGGTAAGGTCCTT
SOK2r	TCTACATATGGGCGGTAGGGTTTTGATTAA

Table S2 Target genes and primers for QRT-PCR

Gene ID	Forward primer (5'-3')	Reverse primer (5'-3')
ADH2	TTCAAGCCGCTCACATTCC	CACAAGATTGGCGCGACTT
ALD4	TTGTGGGTGAGGCCATTACA	ACCCTGTGAAGGCAACCTTTT
ARO10	AGTGTTGAATCAGCTGGCCTAAG	CATAAGCGGCGTTCAGTTCAT
ATF2	GTTCGGCCTAAACGTTTGCT	CCACGCTCATGTCCATGTTC
BAT1	CCATGTTCCGTCCGGATAAG	CAAACAAATTCTAGCGGCAG
BAT2	AATCTGTTTGCCAACGTTCGA	TGCTGGATCAGTTTCCCAATT
ERG10	CGTGCGGGTGCCAAAT	CCATCTCTTTCGACACCATCAA
ERG13	GATCGGTCCTGATGCTCCAA	CGTAGGCGTGTTCCATGTAAGA
HAT2	TGCCCGCAACCTTTCAA	GGCCGCAAGGAGGTTTG
ILV3	CGTCCCAGGCCATGCTT	CCCGACTTGAGGCTTCTTGA
RAP1	ATTGGATCCGAGTATGGTCGTT	TCCGATGGCGCTGTGACT
SOK2	TCAACCTCTGATGCCCGTATC	GCGGGTACGGCCACTGT
THI3	GGCGTGGCCGGATCTTA	GGCGGCATACCCACTATGTG
YJL218W	GGTCATCCAATTGACGTGGAA	GGTCACAGGCATGGCATATTC

Table S3   Sok2p and Rap1p activity with reference to the target genes in figure 2.

	SOK2	RAP1
ADH2	√	X
ALD4	√	√
ARO10	√	√
ATF2	√	√
BAT1	√	X
BAT2	√	√
ERG10	X	X
ERG13	X	√
HAT2	X	√
ILV3	√	X
THI3	X	X
YJL218W	X	√
RAP1	X	n/a
SOK2	n/a	√

Transcription factor activity is based on reported interaction studies by Vachova *et al.* (2004), Chua *et al.* (2006), Workman *et al*. (2006), Kasahara *et al*. (2007) and Yarragudi *et al*. (2007). Tic marks indicate evidence for regulation whereas X's are used where no evidence for regulation of the target gene by the transcription factor in question has been reported.

Table S4 Volatile alcohols and esters present in the fermentation media at day 2 of fermentation.

DAY2	VIN13	SOK2-VIN13	BM45	RAP1-BM45	DV10
Ethyl Acetate	5.53 ± 1.40	5.70 ± 1.20	7.60 ± 0.71	6.14 ± 2.16	8.10 ± 2.13
Propanol	33.24 ± 4.38	34.25 ± 3.19	32.81 ± 1.18	27.25 ± 1.37	28.39 ± 5.21
Isobutanol	5.78 ± 0.71	**8.71 ± 0.74**	9.26 ± 0.70	8.20 ± 1.70	6.20 ± 1.62
Isoamyl Acetate	0.10 ± 0.11	**0.31 ± 0.02**	0.18 ± 0.11	0.24 ± 0.11	0.17 ± 0.17
Butanol	0.16 ± 0.2	**0.41 ± 0.12**	Bd	Bd	Bd
Isoamyl alcohol	32.58 ± 5.74	37.27 ± 3.82	37.80 ± 2.90	35.85 ± 3.30	32.78 ± 3.61
Ethyl Hexanoate	Bd	bd	Bd	Bd	0.17 ± 0.17
Hexanol	Bd	bd	Bd	Bd	Bd
Ethyl Caprylate	0.05 ± 0.04	0.09 ± 0.01	0.10 ± 0.02	0.11 ± 0.03	0.11 ± 0.03
Acetic Acid	449.5 ± 17.8	**525.2 ± 26.2**	715.3 ± 18.9	*658.8 ± 7.0*	618.4 ± 15.4
Propionic Acid	2.23 ± 0.15	2.47 ± 0.18	2.04 ± 0.19	2.15 ± 0.23	2.38 ± 0.31
Iso-Butyric Acid	0.78 ± 0.04	0.71 ± 0.02	0.79 ± 0.06	0.68 ± 0.04	0.80 ± 0.06
Butyric Acid	0.55 ± 0.04	0.52 ± 0.01	0.58 ± 0.05	0.57 ± 0.01	0.67 ± 0.02
Ethyl Caprate	0.08 ± 0.016	0.09 ± 0.02	0.12 ± 0.04	0.16 ± 0.06	0.10 ± 0.02
Iso-Valeric Acid	0.45 ± 0.03	0.37 ± 0.01	0.47 ± 0.08	*0.33 ± 0.04*	0.38 ± 0.06
Diethyl Succinate	Bd	bd	Bd	Bd	Bd
Valeric Acid	Bd	bd	Bd	Bd	Bd
2-Phenylethyl Acetate	Bd	bd	Bd	Bd	Bd
Hexanoic Acid	0.73 ± 0.03	**0.85 ± 0.07**	0.94 ± 0.13	1.05 ± 0.15	1.39 ± 0.07
2-Phenyl Ethanol	6.42 ± 0.47	7.11 ± 0.69	9.64 ± 0.35	*7.57 ± 0.78*	7.49 ± 0.50
Octanoic Acid	0.76 ± 0.15	1.14 ± 0.26	1.25 ± 0.64	1.03 ± 0.10	3.05 ± 0.92
Decanoic Acid	2.54 ± 0.19	2.34 ± 0.26	2.73 ± 0.12	2.95 ± 0.38	3.33 ± 0.09

All values are expressed in mg.L^{-1} and are the average of 4 biological repeats ± standard deviation. Metabolites present at concentrations below the detection limit are indicated by “Bd”. Values in bold indicate a statistically significant increase in concentration for a given metabolite relative to the untransformed control, whereas values in italics indicate a significant decrease in concentration.

Table S5 Volatile alcohols and esters present in the fermentation media at day 5 of fermentation.

DAY5	VIN13	SOK2-VIN13	BM45	RAP1-BM45	DV10
Ethyl Acetate	19.74 ± 2.48	22.52 ± 2.65	20.52 ± 1.13	19.38 ± 0.95	28.38 ± 1.69
Propanol	70.22 ± 2.34	**82.06 ± 4.97**	48.65 ± 3.43	44.66 ± 3.02	66.88 ± 5.64
Isobutanol	12.97 ± 1.95	**18.17 ± 1.84**	20.14 ± 1.96	17.29 ± 1.55	16.42 ± 1.81
Isoamyl Acetate	0.30 ± 0.09	**0.70 ± 0.17**	0.36 ± 0.02	0.36 ± 0.04	0.38 ± 0.09
Butanol	0.59 ± 0.09	**0.88 ± 0.04**	0.52 ± 0.03	0.58 ± 0.04	0.69 ± 0.05
Isoamyl alcohol	78.74 ± 4.54	**106.80 ± 8.47**	85.54 ± 4.69	89.53 ± 2.01	95.87 ± 7.52
Ethyl Hexanoate	0.11 ± 0.18	0.15 ± 0.01	0.16 ± 0.16	0.10 ± 0.08	0.18 ± 0.05
Hexanol	Bd	bd	Bd	bd	Bd
Ethyl Caprylate	0.11 ± 0.04	0.12 ± 0.01	0.14 ± 0.00	*0.10 ± 0.01*	0.15 ± 0.03
Acetic Acid	792.6 ± 16.4	**1047.3 ± 72.87**	1131.1 ± 44.0	1159.9 ± 113.6	1093.2 ± 81.7
Propionic Acid	4.58 ± 0.42	**6.56 ± 0.44**	2.62 ± 0.10	2.78 ± 0.28	5.05 ± 0.39
Iso-Butyric Acid	0.83 ± 0.03	0.87 ± 0.05	0.90 ± 0.05	0.81 ± 0.06	0.89 ± 0.06
Butyric Acid	0.65 ± 0.08	0.67 ± 0.05	0.68 ± 0.04	0.71 ± 0.05	0.80 ±0.08
Ethyl Caprate	0.24 ± 0.05	**0.35 ± 0.03**	0.30 ± 0.04	0.33 ± 0.07	0.46 ± 0.03
Iso-Valeric Acid	0.65 ± 0.07	0.66 ± 0.04	0.62 ± 0.09	0.50 ± 0.06	0.64 ± 0.06
Diethyl Succinate	0.03 ± 0.05	**0.14 ± 0.03**	0.10 ± 0.00	**0.15 ± 0.00**	0.11 ± 0.01
Valeric Acid	0.02 ± 0.03	0.06 ± 0.01	0.02 ± 0.02	**0.07 ± 0.00**	0.05 ± 0.00
2-Phenylethyl Acetate	0.01 ± 0.67	0.04 ± 0.00	0.03 ± 0.60	0.02 ± 0.01	0.03 ± 0.04
Hexanoic Acid	1.11 ± 0.17	1.40 ± 0.16	1.37 ± 0.28	1.56 ± 0.32	2.19 ±0.24
2-Phenyl Ethanol	10.74 ± 0.68	**14.62 ± 0.84**	12.66 ± 0.66	13.10 ± 2.10	13.52 ± 1.25
Octanoic Acid	1.38 ± 0.08	**1.65 ± 0.13**	1.34 ± 0.21	1.28 ± 0.09	2.65 ± 0.12
Decanoic Acid	2.80 ±0.17	3.28 ± 0.21	2.98 ± 0.39	3.80 ± 0.14	4.50 ± 0.29

All values are expressed in mg.L^{-1} and are the average of 4 biological repeats ± standard deviation. Metabolites present at concentrations below the detection limit are indicated by “bd”. Values in bold indicate a statistically significant increase in concentration for a given metabolite relative to the untransformed control, whereas values in italics indicate a significant decrease in concentration.

Table S6 Volatile alcohols and esters present in the fermentation media at day 14 of fermentation.

DAY14	VIN13	SOK2-VIN13	BM45	RAP1-BM45	DV10
Ethyl Acetate	31.39 ± 0.66	28.09 ± 1.41	27.11 ± 2.85	23.88 ± 0.99	33.18 ± 0.43
Propanol	76.48 ± 3.09	83.37 ± 6.25	45.60 ± 1.21	41.53 ± 4.01	69.52 ± 5.30
Isobutanol	19.00 ± 1.74	**24.96 ± 0.53**	25.88 ± 2.81	22.42 ± 1.65	21.27 ± 3.07
Isoamyl Acetate	0.34 ± 0.04	**0.73 ± 0.02**	0.43 ± 0.03	0.40 ± 0.04	0.43 ± 0.11
Butanol	1.07 ± 0.07	**1.33 ± 0.04**	0.58 ± 0.06	**0.70 ± 0.05**	0.87 ± 0.06
Isoamyl alcohol	106.8 ± 9.37	**132.74 ± 7.57**	104.61 ± 3.42	108.09 ± 7.01	113.69 ± 11.49
Ethyl Hexanoate	0.22 ± 0.19	0.36 ± 0.01	0.35 ± 0.01	*0.19 ± 0.02*	0.39 ± 0.03
Hexanol	Bd	0.01 ± 0.01	Bd	**0.35 ± 0.02**	Bd
Ethyl Caprylate	0.15 ± 0.02	**0.26 ± 0.02**	0.24 ± 0.04	0.23 ± 0.05	0.29 ± 0.03
Acetic Acid	926.9 ± 50.2	**1182.9 ± 87.8**	1154.6 ± 112.7	1263.2 ± 85.9	1261.0 ± 47.1
Propionic Acid	6.05 ± 0.48	**7.93 ± 0.63**	2.81 ± 0.17	**5.07 ± 0.42**	8.01 ± 0.22
Iso-Butyric Acid	0.76 ± 0.03	**0.96 ± 0.04**	0.96 ± 0.07	0.86 ± 0.03	1.02 ± 0.10
Butyric Acid	0.49 ± 0.04	**0.59 ± 0.02**	0.61 ± 0.04	0.63 ± 0.06	0.75 ± 0.01
Ethyl Caprate	0.32 ± 0.04	**0.47 ± 0.05**	0.43 ± 0.04	0.50 ± 0.09	0.59 ± 0.04
Iso-Valeric Acid	0.84 ± 0.01	0.87 ± 0.04	0.79 ± 0.09	0.67 ± 0.07	0.91 ± 0.12
Diethyl Succinate	Bd	0.07 ± 0.03	Bd	**0.11 ± 0.04**	0.05 ± 0.05
Valeric Acid	Bd	bd	Bd	**0.22 ± 0.15**	0.01 ± 0.01
2-Phenylethyl Acetate	0.03 ± 0.02	0.06 ± 0.00	0.04 ± 0.01	0.02 ± 0.01	0.04 ± 0.01
Hexanoic Acid	1.53 ± 0.08	**2.28 ± 0.28**	2.56 ± 0.60	2.76 ± 0.30	3.28 ± 0.51
2-Phenyl Ethanol	13.68 ± 0.88	**20.43 ± 1.54**	15.16 ± 0.74	*12.93 ± 0.83*	16.07 ± 0.69
Octanoic Acid	1.15 ± 0.06	1.31 ± 0.11	1.13 ± 0.19	1.25 ± 0.29	1.93 ± 0.15
Decanoic Acid	2.18 ± 0.04	2.38 ± 0.11	1.95 ± 0.16	2.34 ± 0.21	3.45 ± 0.12

All values are expressed in mg.L^{-1} and are the average of 4 biological repeats ± standard deviation. Metabolites present at concentrations below the detection limit are indicated by “bd”. Values in bold indicate a statistically significant increase in concentration for a given metabolite relative to the untransformed control, whereas values in italics indicate a significant decrease in concentration.

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.

Table S8 GO categorisation of differentially expressed transcripts with a fold change less than or equal to -2 (i.e. down-regulated genes).

Category	p-value	In Category from Cluster	k	f
vacuolar protein catabolic process [GO:0007039]	<1e-14	ACS1 BDH2 VID24 TPS1 NGR1 SDS24 HBT1 GYP7 NTH1 RCR2 REG1 UBC5 TPS2 KIN1 GGA1 TSA2 PEX29 GLC3 UBC8 EDC2 PIC2 GIP2 SSA4 SPI1 HSP12 RIM15 CMK1 PMC1 AMS1 ATG1 MDS3 VID30 STF2 CTT1 XKS1 SOL4 COQ6 HUA1 SOD2 GRE3 VID28 PIG2 FYV10 PFK26 GUT2 GTT1 BBC1 TPK1 PTK2 KNS1 HSP104 VPS13 TFS1 GSY2 TSL1 YPK2 PGM2 GID8 RIM11 SIP5 ALD3 ALD2 DDR48 PAI3 GAD1 TPS3 UBP15 MAM3 ATG19 DCS2 GSP2 YDC1 PIN3 GPH1 GDB1	75	129
autophagy [GO:0006914]	<1e-14	SEC17 ATG8 ATG14 ATG12 SAF1 ATG15 RPN4 ATG20 IWR1 ATG9 RRI1 GYP7 RCR2 CIS1 NRG1 UBC5 DOA4 KIN1 MFB1 RMD5 PIB1 UBX5 PEX29 UBC8 EDC2 AST2 RAD4 ATG18 PMC1 MON1 AMS1 CUP2 ATG1 VID30 NQM1 TAM41 RAD2 HSE1 ATG7 NVJ1 PIG2 FYV10 PFK26 HOS4 SNX4 TAX4 FBP26 TPK1 RAD26 IRS4 ECM4 ATG10 APC9 CLF1 PUS5 TFS1 ATG26 VPS34 NDL1 ATG17 RSF1 HFD1 GID8 PSO2 ATG16 ALD2 PAI3 RAD14 ATG4 ATG2 ATG19 PKH2 AHC1 SHE4 PEP12 GLO4 VAM3 DCS2 DGA1 ATG21 ATG29 ATG11 ATG13	83	151
cell death [GO:0008219]	5.1E-14	COR1 ATP1 ATP3 COX9 INH1 SDH4 ATP5 ATP17 QCR7 RIP1 QCR6 COX4 QCR9 QCR10 COX6 UBX6 QCR8 ATP2 ATP7 SDH1 SDH2 COX8 COX5A CYT1 PIN3 QCR2	26	29
response to temperature stimulus [GO:0009266]	2.0E-13	BDH2 HSP26 TPS1 SDS24 NTH1 UBC5 TPS2 HSP42 HSP78 SPI1 HSP12 CTT1 SOL4 SPL2 ECM4 HSP104 TFS1 TMA10 TSL1 MSC1 PGM2 ALD3	22	23
energy reserve metabolic process [GO:0006112]	3.1E-13	GIP4 GIP1 VPS15 IRA1 ICS2 LRE1 GPR1 STP4 BDF2 MRK1 MSH5 YDL180W SNF3 PRR2 RRI1 MFB1 MTH1 DOT6 RIM15 SAP155 EDC1 CPD1 MGA1 HXT4 RPI1 POG1 TAX4 GSH1 ASG7 HXT8 YJR115W HAP4 YKR017C SPO75 COX19 VPS13 GAL2 RFX1 CRR1 YLR446W FMP27 SRT1 CAT8 YNL144C ATG2 YNR034W-A AEP3 RDS2 PUF2	49	89
biological_process [GO:0008150]	5.7E-13	FUN14 FUN19 AIM2 BDH2 UIP3 YAR028W YAR029W YBL029C-A YBL029W MOH1 SEF1 YBL086C YBL095W EDS1 RFS1 YBR053C YRO2 YBR063C YBR085C-A YBR090C AIM3 OPY1 RTC2 APD1 ICS2 YBR182C-A YBR200W-A YBR204C YBR219C YBR221W-A YBR225W OM14 YBR230W-A ERT1 MTC4 AIM5 FMP21 BIT2 YBR284W YBR285W YBR287W YCL012C YCL021W-A YCL057C-A YCR007C CTR86 YCR076C HMRA2 YCR108C YDL027C STP4 BDF2 UBX3 TMA17 YDL114W SNA4 YDL133W UGX2 YDL180W RTN2 YDL206W YDL218W YDL233W YDR034W-B YDR042C RTR2 FMP16 ALT2 YDR124W YDR169C-A YDR182W-A YDR186C YDR246W-A YDR249C YDR262W BSC2 YDR282C HRQ1 YDR357C YDR366C YDR379C-A YDR381C-A YDR391C THI74 YDR444W JIP4 SPG3 PSP1 YDR506C SNA2 KRE28 HSP31 YDR541C VAB2 YEL020C UTR5 RMD6 YEL073C YEL076C PHM8 HVG1 YER039C-A SAP1 RRT13 RGI1 YER078W-A YER079W AST2 YER137C YER158C YER175W-A FMP10 YER184C YFL012W YFL034W YFL041W-A YFL042C COS4 YFL064C AIM13 YFR012W-A YFR016C YFR017C PES4 RMD8 YGL006W-A YGL007C-A YGL010W YGL081W TOS8 SNT2 RRT6 AIM14 YGL176C MTC3 SHE10 YGL235W YGL258W-A YPS5 YGR016W YGR021W NQM1 FMP48 YGR053C YGR066C YGR067C YGR079W YGR093W YGR121W-A YGR125W YGR126W YGR127W YGR130C ECL1 YGR146C-A YGR153W YGR174W-A YGR201C YGR204C-A YGR205W YGR235C SPG1 YGR237C YGR250C HUA1 YHL012W YLF2 YHL015W-A YHL018W YHL026C YHL048C-A YHR007C-A YSC83 YHR033W YHR035W YHR050W-A YHR078W YHR080C YHR097C YPT35 ANS1 YHR140W YSP1 LIN1 YHR159W AIM18 AIM46 YHR202W YIL024C YIL029C YIL055C YIL060W YIL077C AIM19 YIL089W YIL102C OM45 YIR014W YIR016W YIR018C-A PET130 IKS1 MPM1 YJL070C ICS3 YJL077W-B PRY1 IML2 AIM23 YJL132W YJL136W-A YJL147C DAS1 FMP33 YJL163C YJL181W YJL185C YJL193W YJL206C REE1 YJR005C-A YJR008W YJR039W HIT1 YJR056C YJR061W AIM24 YJR085C YJR112W-A YJR115W IML1 YJR149W DAN4 YJR151W-A YJR154W YKL018C-A YKL023W YKL050C YKL068W-A YKL070W YKL071W STB6 CUE2 YKL091C MTC2 YKL100C YKL106C-A YKL107W DGR2 RMA1 YKL133C MRP8 YKL151C YKL162C KKQ8 YKL222C YKR005C YKR011C YKR017C YKR018C FMP46 YKR051W YKR096W UBP11 YLL056C YLL066W-B YLR001C YLR030W YLR031W YLR046C YLR049C YLR053C YLR125W YLR149C PCD1 YLR152C RRT15 YLR164W YLR173W YLR177W SKG3 IRC20 YLR257W BOP2 YLR283W YLR297W YLR312C TMA10 STP3 ART10 YLR422W YLR445W YLR446W FMP27 YLR466C-B YML002W YML003W YML007C-A YML020W AIM31 YML037C PRM6 AIM32 TCB3 AIM33 YML100W-	447	1237

		A NAB6 NGL3 YML131W YMR018W YMR031C YMR034C YET2 YMR084W YMR085W YMR090W YMR105W-A SPG4 YMR114C YMR118C YMR124W YMR155W YMR158C-A YMR160W SIP18 YMR175W-A YMR178W YMR181C YMR182W-A YMR185W SPG5 ICY1 YMR196W YMR206W YMR252C YMR253C YMR258C YMR262W YMR265C PGM3 YMR295C SNO4 ERR3 YNL011C YNL033W YNL040W YNL042W-B APJ1 YNL092W AIM37 YNL115C YNL144C YNL146C-A YNL155W YNL165W YNL176C YNL193W YNL195C SLZ1 YNL200C VID27 YNL234W YTP1 RTC4 YNL260C BSC4 YNL277W-A YNL295W YNL305C SWM2 YNR034W-A YNR068C BSC5 IRC10 YOL024W YOL036W RRT8 AIM39 YOL073C PHM7 YOL087C RTC1 ZPS1 YOL159C YOR011W-A YOR032W-A YOR034C-A IRC23 YOR052C RTS2 TCB1 YOR097C YOR152C PNS1 YOR161C-C YOR186W YOR192C-C YOR214C AIM41 RCN2 YOR223W YOR228C RDL1 YOR289W YOR292C YOR293C-A YOR316C-A MNE1 YOR365C YOR376W-A YOR381W-A FRE5 YOR389W PAU21 YPL038W-A YPL039W LEE1 CWC27 YTA6 YPL077C YPL107W YPL109C YPL119C-A PRM4 YPL162C SET6 YPL168W UIP4 FMP40 GRE1 YPL236C YPL247C YPL257W YPL260W YPL277C YPL278C YPR022C JID1 ASA1 YPR091C YPR098C YPR109W YPR117W YPR127W URN1 CUR1 YPR159C-A		
phosphorus metabolic process [GO:0006793]	3.6E-12	COR1 ATP1 PKC1 ATP3 ATP16 MPS1 STE7 INH1 SDH4 ATP5 ATP17 QCR7 RIP1 COX13 QCR9 QCR10 COX6 KIC1 PBS2 QCR8 ATP2 ATP7 MDH1 SDH3 SDH1 SDH2 COX12 RIM11 COX7 FPK1 CYT1 ATP4 ATP20 QCR2	34	48
mitochondrion degradation [GO:0000422]	2.8E-10	ATG8 ATG12 PTC6 ATG20 ATG9 CIS1 ATG1 ATG7 ATG32 SNX4 FCJ1 ATG10 ATG33 ATG17 ATG16 ATG4 ATG2 YOR019W ATG21 ATG29 ICY2 ATG11 ATG13	23	29
nucleotide metabolic process [GO:0009117]	1.2E-09	PET9 COR1 ATP1 ATP3 ATP16 COX9 INH1 SDH4 RAV2 ATP5 ATP17 URC2 QCR7 APA2 RIP1 PRS2 QCR6 PMC1 COX4 COX13 QCR9 QCR10 COX6 QCR8 RAV1 ATP2 ATP7 MDH1 SDH3 SDH1 SDH2 COX12 ATP14 COX8 ATP18 STV1 COX7 COX5A CYT1 ATP4 ATP15 ATP20 QCR2	43	78
cofactor metabolic process [GO:0051186]	1.8E-09	COR1 ATP3 COX9 INH1 SDH4 ATP5 ATP17 QCR7 COX4 BIO2 QCR8 ATP7 MDH1 SDH2 CIT1 ISU1 QCR2	17	19
sporulation resulting in formation of a cellular spore [GO:0030435]	6.9E-09	OAF1 SEF1 GIP1 REG2 MUM2 SPO23 UBX7 SNT1 BDF2 FMP45 ADY3 NTH1 REG1 DOA4 SPO71 SAC6 RMD5 DON1 ZIP1 XRS2 DIT1 RMD6 GPA2 MEI4 GIP2 SHC1 SPR6 DMC1 PES4 RMD8 RIM8 ATG1 IME4 HOS2 MDS3 SEC9 GSC2 SPR3 AMA1 SPO11 SPS100 SSP1 PIG2 SPO22 SGA1 SLM1 HOS4 ATG32 BBC1 LOH1 UBX6 GSM1 YAK1 TPK1 CDC16 SPO14 TGL4 SPO75 KNS1 OSW2 CRR1 GSY2 CDC25 BDF1 SMA2 MSC1 SPO20 RIM11 FKS3 SPS18 SHE4 MPC54 GAC1 SPR1 SMA1 LGE1 CSM4 CSR2	78	185
piecemeal microautophagy of nucleus [GO:0034727]	4.1E-07	ATG8 ATG14 ATG12 ATG15 ATG9 CIS1 ATG18 ATG1 VAM7 ATG7 SNX4 ATG10 ATG17 ATG16 ATG4 ATG2 VAM3 ATG21 ATG29 ATG11 ATG13	21	32
ion transport [GO:0006811]	4.5E-06	PET9 COR1 ATP1 ATP3 YRO2 FTH1 YBR241C PCA1 HSP30 ATP16 MCH1 COX9 INH1 YDL206W ENA5 SDH4 ATP5 TIM11 ATP17 YDR506C QCR7 FIT1 RIP1 FET5 QCR6 PMC1 PMR1 COX4 COX13 QCR9 DUR3 ARN1 QCR10 COX6 CTR2 TOK1 KHA1 TRK1 QCR8 ATP2 ATP7 MDH1 SDH3 SDH1 ZRT3 SDH2 FRE6 COX12 FRE8 NHA1 ATP14 COX8 ATP18 STV1 COX7 COX5A ATO2 MAM3 ATP19 CYT1 FRE3 FIT3 FRE5 PMA2 YPL060W ATP4 ATP15 ATP20 QCR2	69	181
electron transport chain [GO:0022900]	1.5E-05	COR1 GRX1 TRX3 SDH4 ARH1 GRX2 QCR7 RIP1 QCR6 OLE1 QCR9 QCR10 YJL045W QCR8 SDH3 SDH1 SDH2 FRE6 FRE8 YLR164W ERO1 YMR118C CYT1 FRE3 FRE5 QCR2	26	51
ATP biosynthetic process [GO:0006754]	3.3E-05	ATP1 ATP3 PCA1 ATP16 ENA5 ATP5 TIM11 ATP17 PMC1 PMR1 ATP2 ATP7 ATP14 ATP18 ATP19 PMA2 ATP15 ATP20	18	31
CVT pathway [GO:0032258]	7.2E-05	ATG8 ATG14 ATG12 ATG20 ATG9 ATG18 ATG1 ATG7 SNX4 TAX4 IRS4 ATG10 ATG16 ATG4 ATG2 ATG19 ATG21 ATG11 ATG13	19	35
regulation of transcription, DNA-dependent [GO:0006355]	4.2E-04	OAF1 HAP3 SEF1 EDS1 ERT1 THI2 MAL33 SRD1 HMRA2 MBP1 ARO80 CAD1 URC2 SWI4 YER184C GAT1 RIM15 PDR1 HSF1 TOS8 CUP2 HOS2 HAP2 MGA1 STB5 SKN7 CST6 XBP1 MET28 YAP5 GSM1 YJL206C RGT1 HAP4 YKL222C GAT3 RFX1 HAP1 YAP1 ARG81 MAC1 GAT2 CAT8 MET4 HAL9 CIN5 AZF1 SFL1 YRR1 YRM1 SAS5 PIP2 RDR1 ECM23 RDS2 SPP1 HAA1 SUA7	58	166
energy reserve metabolic process [GO:0006112]	5.0E-04	TPS1 NTH1 REG1 GLC3 GIP2 PCL10 PIG2 PCL7 YAK1 TPK1 GLG1 GSY2 PGM2 GAC1 GPH1	15	28
negative regulation of gluconeogenesis [GO:0045721]	8.6E-04	VID24 RMD5 UBC8 VID30 VID28 FYV10 GID8	7	9

aerobic respiration [GO:0009060]	1.1E-03	PET9 COR1 ETR1 DLD1 PET100 COX20 QCR7 RIP1 RPO41 QCR6 COX4 COX13 SHY1 QCR9 QCR10 QCR8 CBP1 MDH1 MBR1 PET10 HAP1 RSF1 AAC1 ISF1 PAH1 NCA2 QCR2	27	66
fatty acid metabolic process [GO:0006631]	1.4E-03	OAF1 AGP2 FAA2 YAT2 POX1 POT1 MGA2 SPT23 FOX2 ECI1 CAT2 IZH2 CRC1 DCI1 FAA1 PIP2	16	33
ubiquitin-dependent endocytosis [GO:0070086]	1.7E-03	RSP5 ROG3 RIM8 ART5 ALY2 ALY1 LDB19 CSR2	8	12
response to toxin [GO:0009636]	2.0E-03	PRX1 AAD3 AAD4 HSP31 GTO1 AAD10 CYT2 ECM4 SUL2 GTO3 AAD14 IZH2 GRE2 PDR10 FRE3	15	31
cristae formation [GO:0042407]	3.3E-03	TIM11 FCJ1 UPS2 ATP14 ATP20	5	6
signal transduction [GO:0007165]	4.6E-03	PSK1 GPB2 PKC1 IRA1 COS111 ERT1 GPR1 SNF3 MTH1 SAC7 GPA2 STE2 CMK1 GPG1 SIP2 GPA1 PKP1 CYR1 TOR1 TUS1 PSK2 IRA2 RTS1 BAG7 GSP2 GPB1 RDS2 MKK2 PLC1 TIP41	30	82
autophagic vacuole assembly [GO:0000045]	5.0E-03	ATG8 ATG12 ATG9 ATG1 ATG17 ATG4 ATG2	7	11
macroautophagy [GO:0016236]	6.0E-03	VPS15 ATG14 ATG12 PTC6 ATG20 ATG18 ATG7 ATG10 ATG16 ATG21 ATG29 ATG13	12	25
DNA metabolic process [GO:0006259]	6.6E-03	MMS4 DMC1 SPO11 CST6 TOP3 MEC3 TOP2 RAD1	8	14
cellular ion homeostasis [GO:0006873]	6.6E-03	FYV5 CRD1 MDM31 PTK2 GIS4 SKY1 MDM32 HRK1	8	14
lipid metabolic process [GO:0006629]	7.0E-03	ATG15 YDL109C YDR444W FAA2 YAT2 OLE1 POX1 POT1 TAX4 FOX2 IRS4 TGL4 ECI1 CAT2 TGL3 IZH2 DCI1 DGA1 FAA1 GDE1 PGC1 PLC1	22	57
negative regulation of Ras protein signal transduction [GO:0046580]	9.4E-03	GPB2 IRA1 AVO1 IRA2 GPB1	5	7

Table S9 Fold changes of genes involved in fermentation and amino acid catabolism for the SOK2 overexpressing strain versus control.

Systematic name	Gene name	Functional Description	SOK vs Control
YJR155w	AAD10	Putative aryl-alcohol dehydrogenase	-4.17
YNL331c	AAD14	Putative aryl-alcohol dehydrogenase	-2.33
YCR107w	AAD3	Putative aryl-alcohol dehydrogenase	-1.57
YDL243c	AAD4	Putative aryl-alcohol dehydrogenase	-1.60
YGL256w	ADH4	alcohol dehydrogenase IV	3.10
YBR145w	ADH5	alcohol dehydrogenase V	1.57
YMR170c	ALD2	aldehyde dehydrogenase 2 (NAD+)	-1.82
YMR169c	ALD3	stress inducible aldehyde dehydrogenase	-11.49
YPL061w	ALD6	aldehyde dehydrogenase, cytosolic	1.69
YGL148w	ARO2	chorismate synthase	2.31
YBR249c	ARO4	2-dehydro-3-deoxyphosphoheptonate aldolase, catalyzes the first step in aromatic amino acid biosynthesis	3.35
YGL202w	ARO8	Aromatic aminotransferase, expression is regulated by general control of amino acid biosynthesis	2.18
YHR137w	ARO9	Aromatic aminotransferase, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism	-2.05
YDR380w	ARO10	Phenylpyruvate decarboxylase, catalyzes the first specific step in the Ehrlich pathway	-3.02
YGR177C	ATF2	Alcohol acetyltransferase, forms volatile esters during fermentation	4.38
YCL064c	CHA1	L-serine/L-threonine deaminase, catalyzes the degradation of both L-serine and L-threonine	3.33
YDL174c	DLD1	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate	-2.52
YEL071w	DLD3	D-lactate dehydrogenase	3.06
YEL066W	HPA3	D-Amino acid N-acetyltransferase, catalyzes N-acetylation of D-amino acids	2.29
YER086w	ILV1	Threonine deaminase, catalyzes the first step in isoleucine biosynthesis	1.97
YMR108w	ILV2	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis	1.50
YLR355c	ILV5	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis	1.58
YCL009c	ILV6	Regulatory subunit of acetolactate synthase	1.62
YOR108w	LEU9	2-Isopropylmalate synthase, catalyzes the first step in the leucine biosynthesis pathway	2.32
YDR081c	PDC2	pyruvate decarboxylase regulatory protein	-1.51

YLR134w	PDC5	pyruvate decarboxylase, isozyme 2	-2.21
YGR087c	PDC6	pyruvate decarboxylase 3	-5.09
YPR026w	ATH1	acid trehalase, vacuolar	-3.40
YDR001c	NTH1	neutral trehalase (alpha,alpha-trehalase)	-2.20
YBR001c	NTH2	alpha,alpha-trehalase	-3.92
YKL127w	PGM1	phosphoglucomutase, minor isoform	3.03
YMR105c	PGM2	phosphoglucomutase, major isoform	-1.85
YBR126c	TPS1	alpha,alpha-trehalose-phosphate synthase, 56 KD subunit	-1.80
YDR074w	TPS2	alpha,alpha-trehalose-phosphate synthase, 102 KD subunit	-2.45
YMR261c	TPS3	alpha,alpha-trehalose-phosphate synthase, 115 KD subunit	-1.52
YML100w	TSL1	alpha,alpha-trehalose-phosphate synthase, 123 KD subunit	-2.77
YAL054c	ACS1	acetyl-CoA synthetase	-2.20
YLR153c	ACS2	acetyl-coenzyme A synthetase	2.17
YPL028W	ERG10	Acetyl-CoA C-acetyltransferase; involved in the first step in mevalonate biosynthesis	1.77
YML126C	ERG13	3-hydroxy-3-methylglutaryl-CoA synthase, involved in the second step in mevalonate biosynthesis	2.09
YIL160C	POT1	3-ketoacyl-CoA thiolase involved in beta-oxidation of fatty acids	-4.82