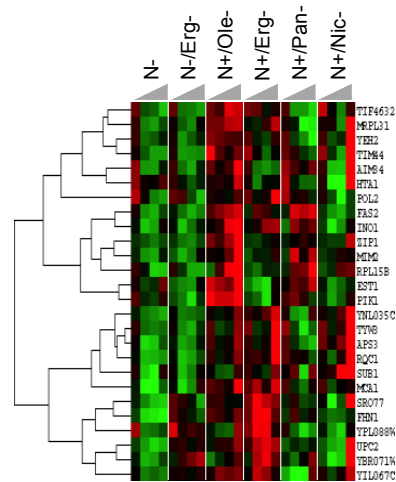


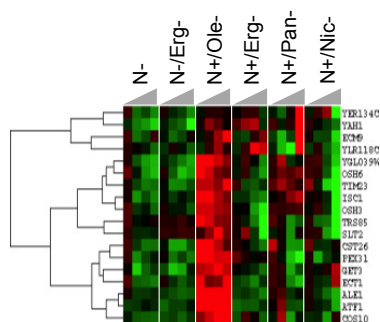
**Supplementary data 1: Impact of micronutrient starvations and nitrogen concentration on cell viability during alcoholic fermentation (from Duc et al., 2017).** (A) (green curves) Ole<sup>-</sup>: Oleic acid starvation (18 mg/L), (B) (dark blue curves) Erg<sup>-</sup>: ergosterol starvation (1.5 mg/L), (C) (light blue curves) Pan<sup>-</sup>: pantothenic acid starvation (0.02 mg/L) and (D) (yellow curves) Nic<sup>-</sup>: nicotinic acid starvation (0.08 mg/L). Open circles indicate N<sup>-</sup>: low nitrogen (71 mg/L YAN); full diamonds indicate N<sup>+</sup>: high nitrogen (425 mg/L YAN). Fermentations were performed in duplicate, error bars correspond to standard deviation.



Category	p-value	In Category from Cluster	k	f
DNA replication involved in S phase [GO:0033260]	0.00363 5	POL2	1	1
inositol biosynthetic process [GO:0006021]	0.00363 5	INO1	1	1
G-quadruplex DNA formation [GO:0071919]	0.00363 5	EST1	1	1
cellular response to hydrogen peroxide [GO:0070301]	0.00363 5	MCA1	1	1
positive regulation of transcription from RNA polymerase III promoter [GO:0045945]	0.00725 7	SUB1	1	2
cellular response to hypoxia [GO:0071456]	0.00725 7	UPC2	1	2

**Supplementary data 2: Cluster with overexpression of genes involved in lipid metabolism under oleic, ergosterol or pantothenic acid starvation conditions during alcoholic fermentation**

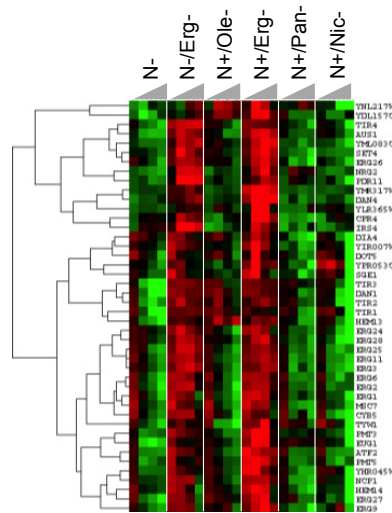
For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by (◀). Results show the mean of biological triplicates.



Category	p-value	In Category from Cluster	k	f
phospholipid biosynthetic process [GO:0008654]	0.0001248	CST26 ECT1 ALE1	3	37
maintenance of cell polarity [GO:0030011]	0.0002499	OSH3 OSH6	2	9
sterol transport [GO:0015918]	0.0004559	OSH3 OSH6	2	12
endocytosis [GO:0006897]	0.001317	OSH3 OSH6 COS10	3	82
lipid transport [GO:0006869]	0.00143	OSH3 OSH6	2	21
peroxisome degradation [GO:0030242]	0.00143	TRS85 SLT2	2	21
fatty acid metabolic process [GO:0006631]	0.002544	YLR118C ATF1	2	28
regulation of transcription factor import into nucleus [GO:0042990]	0.002726	SLT2	1	1
protein deacylation [GO:0035601]	0.002726	YLR118C	1	1
acetate derivative biosynthetic process [GO:0030636]	0.002726	ATF1	1	1
sphingolipid catabolic process [GO:0030149]	0.002726	ISC1	1	1
sterol homeostasis [GO:0055092]	0.002726	OSH6	1	1
exocytosis [GO:0006887]	0.005149	OSH3 OSH6	2	40
cellular aromatic compound metabolic process [GO:0006725]	0.005445	YGL039W	1	2
glycerophospholipid biosynthetic process [GO:0046474]	0.005445	ALE1	1	2
positive regulation of phosphatase activity [GO:0010922]	0.005445	OSH3	1	2
cellular ketone metabolic process [GO:0042180]	0.005445	YGL039W	1	2
heme a biosynthetic process [GO:0006784]	0.008157	YAH1	1	3
cellular metal ion homeostasis [GO:0006875]	0.01086	GET3	1	4
phosphatidylethanolamine biosynthetic process [GO:0006646]	0.01086	ECT1	1	4
posttranslational protein targeting to membrane [GO:0006620]	0.01356	GET3	1	5
UFP-specific transcription factor mRNA processing involved in endoplasmic reticulum unfolded protein response [GO:0030969]	0.01356	SLT2	1	5
protein insertion into ER membrane [GO:0045048]	0.01356	GET3	1	5
protein localisation to pre-autophagosomal structure [GO:0034497]	0.01356	TRS85	1	5
response to metal ion [GO:0010038]	0.01625	GET3	1	6
ceramide biosynthetic process [GO:0046513]	0.01625	ISC1	1	6
fermentation [GO:0006113]	0.01625	ATF1	1	6
transport [GO:0006810]	0.01737	GET3 TRS85 OSH3 OSH6 TIM23 YAH1	6	815
barrier septum formation [GO:0000917]	0.01894	SLT2	1	7
response to acid [GO:0001101]	0.02428	SLT2	1	9
alcohol metabolic process [GO:0006066]	0.02428	ATF1	1	9
sterol metabolic process [GO:0016125]	0.02695	OSH6	1	10
response to arsenic-containing substance [GO:0046685]	0.0296	GET3	1	11
ubiquinone biosynthetic process [GO:0006744]	0.03225	YAH1	1	12
vesicle organisation [GO:0016050]	0.03225	TRS85	1	12
endoplasmic reticulum unfolded protein response [GO:0030968]	0.0349	SLT2	1	13
response to salt stress [GO:0009651]	0.04016	ISC1	1	15
cellular metabolic process [GO:0044237]	0.04016	YGL039W	1	15
peptidyl-tyrosine dephosphorylation [GO:0035335]	0.04278	YER134C	1	16
karyogamy involved in conjugation with cellular fusion [GO:0000742]	0.04278	OSH3	1	16
response to heat [GO:0009408]	0.0454	GET3	1	17
fungal-type cell wall organisation [GO:0031505]	0.04659	SLT2 ECM9	2	128

### Supplementary data 3: Cluster with overexpression of genes involved in lipid metabolism under oleic acid starvation conditions

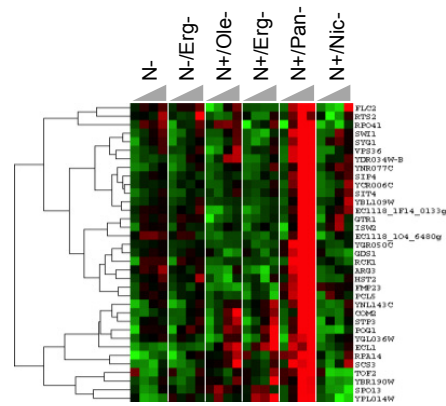
For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by ( ). Results show the mean of biological triplicates.



Category	p-value	In Category from Cluster	k	f
ergosterol biosynthetic process [GO:0006696]	<1e-14	ERG28 ERG26 ERG25 ERG1 ERG11 NCP1 ERG9 ERG3 ERG27 ERG6 ERG2 ERG24	12	23
steroid biosynthetic process [GO:0006694]	<1e-14	ERG28 ERG26 ERG25 ERG11 NCP1 ERG9 ERG3 ERG27 ERG6 ERG2 ERG24	11	25
sterol biosynthetic process [GO:0016126]	<1e-14	ERG28 ERG26 ERG25 ERG11 NCP1 ERG9 ERG3 ERG6 ERG2 CYB5 ERG24	11	29
lipid biosynthetic process [GO:0008610]	1.088e-14	ERG28 ERG26 ERG25 ERG11 NCP1 ERG9 ERG3 ERG27 ERG6 ERG2 ERG24	11	52
oxidation-reduction process [GO:0055114]	1.1e-09	HEM13 HEM14 ERG26 ERG25 ERG1 ERG11 MSC7 NCP1 ERG9 DOT5 ERG3 ERG27 ERG24 YW1	14	272
response to stress [GO:0006950]	0.000462	TIR1 TIR3 DAN1 DAN4 TIR4 TIR2	6	152
porphyrin biosynthetic process [GO:0006779]	0.001517	HEM13 HEM14	2	9
heme biosynthetic process [GO:0006783]	0.002746	HEM13 HEM14	2	12
sterol transport [GO:0015918]	0.002746	PDR11 DAN1	2	12
protein O-linked glycosylation [GO:0006493]	0.004908	PMT5 PMT3	2	16
sterol acetylation [GO:0034209]	0.006664	ATF2	1	1
steroid metabolic process [GO:0008202]	0.006664	ATF2	1	1
mitochondrial seryl-tRNA aminoacylation [GO:0070158]	0.006664	DIA4	1	1
fatty acid biosynthetic process [GO:0006633]	0.009212	ERG25 ERG3	2	22

**Supplementary data 4: Genes overexpressed in ergosterol starvation conditions**

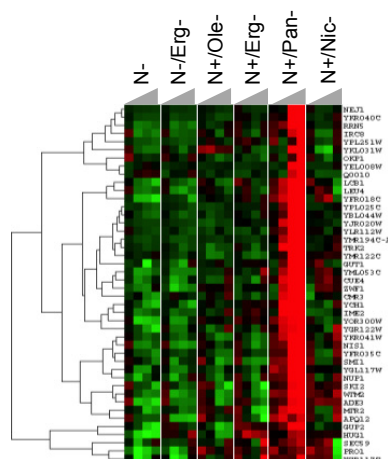
For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by (▲). Results show the mean of biological triplicates.



Category	p-value	In Category from Cluster	k	f
chromatin silencing at rDNA [GO:0000183]	0.00012 96	TOF2 ISW2 HST2	3	21
ATP-dependent chromatin remodeling [GO:0043044]	0.00451 2	ISW2 SWI1	2	21
positive regulation of sister chromatid cohesion [GO:0045876]	0.00484 6	SPO13	1	1
ornithine metabolic process [GO:0006591]	0.00967	ARG3	1	2
transcription from mitochondrial promoter [GO:0006390]	0.00967	RPO41	1	2

### Supplementary data 5: Cluster with overexpression of genes in pantothenic acid starvation conditions

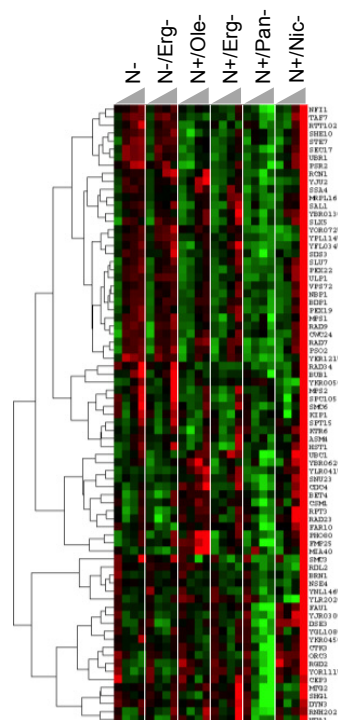
For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by (▲). Results show the mean of biological triplicates.



Category	p-value	In Category from Cluster	k	f
regulation of meiosis [GO:0040020]	0.002195	IME2 WTM2	2	11
regulation of fungal-type cell wall biogenesis [GO:0032995]	0.006512	SMI1	1	1
carbon catabolite repression of transcription [GO:0045013]	0.006512	ZWF1	1	1
poly(A)+ mRNA export from nucleus [GO:0016973]	0.008811	MTR2 NUP1	2	22
nuclear-transcribed mRNA catabolic process, non-stop decay [GO:0070481]	0.00961	YGR122W SKI2	2	23
ribosomal large subunit export from nucleus [GO:0000055]	0.00961	MTR2 NUP1	2	23

**Supplementary data 6: Cluster with overexpression of genes in pantothenic acid starvation conditions**

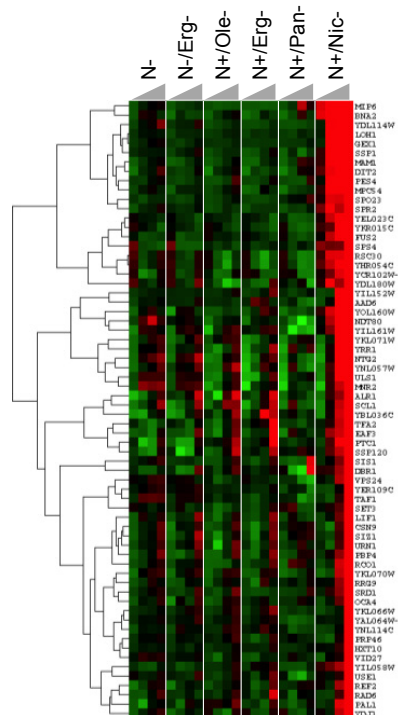
For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by (▲). Results show the mean of biological triplicates.



Category	p-value	In Category from Cluster	k	f
sister chromatid biorientation [GO:0031134]	5.161e-05	MPS1 SPC105 BUB1	3	7
mitotic cell cycle spindle assembly checkpoint [GO:0007094]	0.0001066	MPS1 SPC105 BUB1 CEP3	4	22
response to DNA damage stimulus [GO:0006974]	0.000435	SLX5 NSE4 RAD9 RAD34 RAD23 RAD7 SMC6 CTK3 PSO2	9	197
spindle pole body duplication in nuclear envelope [GO:0007103]	0.0006273	MPS1 MPS2 NBP1	3	15
DNA repair [GO:0006281]	0.001227	SLX5 NSE4 RAD9 RAD34 RAD23 RAD7 SMC6 PSO2	8	183
protein ubiquitination involved in ubiquitin-dependent protein catabolic process [GO:0042787]	0.001292	UBC1 CDC4 RAD7	3	19
RNA polymerase III transcriptional preinitiation complex assembly [GO:0070898]	0.001953	SPT15 BDP1	2	6
nucleotide-excision repair, DNA damage recognition [GO:0000715]	0.001953	RAD23 RAD7	2	6
chromosome condensation [GO:0030261]	0.002714	BRN1 NFI1	2	7
histone deacetylation [GO:0016575]	0.003647	SDS3 HDA1 HST1	3	27
protein localization to kinetochore [GO:0034501]	0.004583	SPC105 BUB1	2	9
protein sumoylation [GO:0016925]	0.005685	SLX5 NFI1	2	10
transcription from RNA polymerase III promoter [GO:0006383]	0.008214	SPT15 BDP1	2	12
nucleotide-excision repair [GO:0006289]	0.008259	RAD9 RAD34 RAD23	3	36

**Supplementary data 7: Cluster with lower expression of genes in pantothenic acid starvation conditions**

For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by (▲). Results show the mean of biological triplicates.



Category	p-value	In Category from Cluster	k	f
sporulation resulting in formation of a cellular spore [GO:0030435]	5.486e-05	SPO23 DIT2 RAD6 SSP1 LOH1 MPC54 SPS4	7	103
meiosis [GO:0007126]	0.0002872	SPO23 MAM1 NDT80 SSP1 SET3 MPC54 SPS4	7	134
negative regulation of antisense RNA transcription [GO:0060195]	0.000548	RCO1 EAF3	2	4
chromatin modification [GO:0016568]	0.0007704	RAD6 TAF1 RSC30 SET3 RCO1 EAF3	6	114
histone deacetylation [GO:0016575]	0.002152	SET3 RCO1 EAF3	3	27
regulation of transcription, DNA-dependent [GO:0006355]	0.003028	SRD1 FLO8 RAD6 TAF1 RSC30 NDT80 SET3 TFA2 RCO1 YRR1 ULS1 EAF3	12	507
transcription, DNA-dependent [GO:0006351]	0.005059	SRD1 FLO8 RAD6 TAF1 RSC30 NDT80 SET3 TFA2 RCO1 YRR1 ULS1 EAF3	12	540
regulation of DNA-dependent DNA replication initiation [GO:0030174]	0.005734	RCO1 EAF3	2	12
metal ion transport [GO:0030001]	0.007808	MNR2 ALR1	2	14
meiotic sister chromatid cohesion involved in meiosis I [GO:0010789]	0.009693	MAM1	1	1
cellular magnesium ion homeostasis [GO:0010961]	0.009693	MNR2	1	1
transposition, RNA-mediated [GO:0032197]	0.009693	DBR1	1	1
ascospore wall assembly [GO:0030476]	0.0098	DIT2 SSP1 MPC54	3	46

**Supplementary data 8: Cluster with overexpression of genes in nicotinic acid starvation conditions**

For: N-: low nitrogen, 71 mg/L YAN; N-/Erg-: low nitrogen/low ergosterol, 71 mg/L YAN, 1.5 mg/L ergosterol; N+/Ole-: high nitrogen/low oleic acid, 425 mg/L YAN, 18 mg/L oleic acid; N+/Erg-: high nitrogen/low ergosterol, 425 mg/L YAN, 1.5 mg/L ergosterol; N+/Pan-: high nitrogen/low pantothenic acid, 425 mg/L YAN, 0.02 mg/L pantothenic acid and N+/Nic-: high nitrogen/low nicotinic acid, 425 mg/L YAN, 0.08 mg/L nicotinic acid; transcriptomic assays were performed at four time-points during alcoholic fermentation (T1, 20 10<sup>6</sup> cells/mL; T2, 12 g CO<sub>2</sub> produced; T3, 40 g CO<sub>2</sub> produced; T4, 75 g CO<sub>2</sub> produced) indicated by (▲). Results show the mean of biological triplicates.