Supplementary table S1: Transcription factors that are likely to regulate the differentially expressed genes in response to aromatic alcohols.

	CC network				GRD network				GROE network			
PheOH	name	p	d	abs	name	p	d	abs	name	p	d	abs
	CAT8	**0**	**3.6696**	**8**	RDS1	0	2.7641	8	MSN4	0	2.5023	23
	SIP4	**0.0006**	**1.9915**	**8**	YER130C	0	2.7116	9	**MSN2**	**0**	**2.0511**	**26**
	SKO1	0.0244	1.5586	5	ECM22	0.0079	2.7116	3	**MIG1**	**0**	**1.8324**	**23**
	PIP2	0.0224	1.1842	8	YER184C	0	2.6803	13	SPS18	0	1.643	17
	UME6	0.0001	1.1264	28	**RGM1**	**0**	**2.6292**	**17**	ADR1	0	1.6308	26
	MIG1	**0.0386**	**1.1264**	**7**	YPR196W	0.0003	2.519	6	**RGM1**	**0.0004**	**1.4126**	**14**
	MSN2	**0.0008**	**1.0152**	**23**	**CAT8**	**0.0121**	**2.519**	**3**	GIS1	0	1.3251	46
					WTM2	0	2.4746	12	MBP1	0	1.2682	26
					HAP3	0.0172	2.3491	3	**SIP4**	**0.0447**	**1.1651**	**6**
					YPR022C	0.002	2.3491	5	HSF1	0.0006	1.1019	20
					FLO8	0	2.2769	13	**CAT8**	**0.0105**	**1.0458**	**12**
					SRB8	0.0001	2.246	9	RSC30	0.0086	1.0301	13
					HIR1	0.0235	2.1971	3	CST6	0.0001	1.0141	30
					MBF1	0.0013	2.1971	6				
					YHP1	0.0037	2.1685	5				
					YLR278C	0.0006	2.1564	7				
					ARG80	0.0001	2.1498	9				
					CUP2	0	2.1267	10				
					GAT3	0.0017	2.1267	6				
					CSE2	0.0008	2.0975	7				
					HAL9	0.0307	2.0596	3				
					MGA2	0	2.0565	43				
					PHD1	0.0391	1.934	3				
					YFL052W	0.0391	1.934	3				
					YDR266C	0.0078	1.934	5				
					SET2	0.0078	1.934	5				
					SPT2	0.0017	1.934	7				
					CBF1	0.0002	1.8984	10				
					RPI1	0.0215	1.8466	4				
					ESC2	0.0081	1.7116	6				
					SWI4	0.0001	1.6539	14				
					SMK1	0.07	1.6121	3				
					SSN2	0.0282	1.5011	5				
					MIG1	**0.0373**	**1.398**	**5**				
					RIC1	0.0065	1.376	9				
					RPN4	0.0144	1.2902	8				
					RSC2	0.0345	1.2711	6				
					PDR1	0.0478	1.1614	6				
TrpOH	name	p	d	abs	name	p	d	abs	name	p	d	abs
	RDR1	0.0418	4.5817	1	MIG2	0.0439	4.511	1	MSN4	0	2.6226	15
	SIP4	0.0018	2.1667	6	CAF17	0.0056	3.926	2	MSN2	0	2.0876	16
	PDR3	0.0063	2.0456	5	YER130C	0.0002	2.7036	6	SPS18	0.0001	1.8774	12
	PDR1	0.0014	1.3633	13	ECM22	0.0347	2.7036	2	MIG1	0.0001	1.7463	13
	NRG1	0.0032	1.0101	18	NGG1	0.0105	2.6365	3	RAP1	0.0001	1.4552	17
					RGM1	0	2.5781	11	ADR1	0.0035	1.2523	12
					YER184C	0	2.5568	8	GAT3	0.0078	1.1751	11
					POP2	0.0449	2.511	2	HSF1	0.0082	1.1019	12
					HIR2	0.0449	2.511	2	CRZ1	0.0023	1.0983	16
					DAL82	0.0043	2.511	4	**RFX1**	**0.006**	**1.0517**	**14**
					YBR239C	0.0449	2.511	2	MET31	0.0364	1.0458	8
					CBF1	0	2.4753	10	TOS8	0.0276	1.0413	9
					RDS1	0.0067	2.341	4	MGA1	0.0037	1.0356	16
					CAD1	0.021	2.2886	3	CST6	0.0024	1.0141	18
					SSN3	0.021	2.2886	3				
					WTM2	0.0004	2.2739	7				
					SNF11	0.0039	2.189	5				
					FLO8	0.0003	2.1534	8				
					RPN4	0.0002	2.037	9				
					SWI4	0	2.0085	12				
					SRB8	0.0076	1.9749	5				
					RFX1	**0.0189**	**1.926**	**4**				
					ARG80	0.0101	1.8787	5				
					CSE2	0.0218	1.8671	4				
					SSN2	0.0283	1.7561	4				
					CUP2	0.0169	1.7036	5				
					GCR2	0.0092	1.537	7				
					RSC1	0.0055	1.5337	8				
					MGA2	0	1.4551	19				
					RIC1	0.0267	1.368	6				
					SUM1	0.0032	1.3557	11				
TyrOH	name	p	d	abs	name	p	d	abs	name	p	d	abs
	CAT8	0	3.7215	5	MIG2	0.034	4.8787	1	MSN4	0	2.4871	11
	SIP4	**0.0065**	**2.0435**	**5**	YER184C	0.0034	2.2464	5	MSN2	0	2.3065	15
	IXR1	0.0497	1.5121	4	YER130C	0.0325	2.0713	3	MIG1	0	2.0582	13
	GAL4	0.0176	1.2621	8	RGM1	0.0026	2.0713	6	**SIP4**	**0.0373**	**1.6291**	**4**
	PDR1	0.0157	1.1246	10	SRB8	0.0155	2.0207	4	TOS8	0.0021	1.5052	10
	TEC1	0.041	1.1195	7	CBF1	0.0116	1.8431	5	GIS1	0	1.4943	25
	YAP6	0.0032	1.0849	16	RPN4	0.0062	1.8198	6	RAP1	0.0003	1.4871	14
					RSC2	0.0382	1.6308	4	ADR1	0.0018	1.4387	11
					SWI4	0.0075	1.5986	7	RSC30	0.0101	1.3785	8
					RSC1	0.0187	1.4864	6	MOT3	0.0015	1.2041	15
					RIC1	0.0323	1.4727	5	XBP1	0.0003	1.2036	19
					SUM1	0.0053	1.4339	9	SPS18	0.0446	1.1894	6
					MGA2	0.0063	1.1599	12	ABF1	0.0117	1.1651	10
									MET31	0.0335	1.1651	7
									GAT4	0.0007	1.1571	18
									CST6	0.0015	1.1561	16
									MGA1	0.003	1.1549	14
									GZF3	0.0177	1.1492	9
									YOX1	0.0057	1.056	14

	CC network				GRD network				GROE network			
	name	p	d	abs	name	p	d	abs	name	p	d	abs
3OH	RDR1	0.0404	4.6295	1	WAR1	0.0358	4.8031	1	MSN4	0	2.8856	18
	CAT8	**0**	**4.1149**	**7**	HIR1	0.0045	3.0662	3	MSN2	0	2.48	21
	SIP4	0	2.7994	9	RIF2	0.0237	2.9958	2	SPS18	0	2.1994	15
	STB4	0.0423	1.5851	4	HCM1	0.0237	2.9958	2	**MIG1**	**0**	**2.0458**	**16**
	UME6	0.0005	1.205	19	RDS1	0.0003	2.9551	5	ADR1	0.0001	1.5742	15
	SKN7	0.0004	1.1453	21	YER184C	0	2.8489	8	TOS8	0.0003	1.5718	13
	PDR1	0.0235	1.0326	10	STP2	0.0309	2.8031	2	**RGM1**	**0.0033**	**1.5121**	**9**
					RTF1	0.0309	2.8031	2	GIS1	0	1.4927	31
					YLR278C	0.0001	2.8031	6	XBP1	0	1.3986	27
					YER130C	0.0007	2.7328	5	GAT4	0	1.3191	25
					PHO23	0.0388	2.6332	2	RAP1	0.0009	1.2746	15
					RGM1	**0**	**2.5808**	**9**	CRZ1	0.0003	1.2682	18
					CAD1	0.0122	2.5808	3	ABF1	0.0027	1.2317	13
					SRB8	0.0004	2.5301	6	**CAT8**	**0.0206**	**1.1978**	**8**
					YOX1	**0.0474**	**2.4812**	**2**	**GAT3**	**0.0078**	**1.1751**	**11**
					RTT107	0.0148	2.4812	3	RFX1	0.0022	1.1513	15
					YDR266C	0.0048	2.4812	4	HAP4	0.0047	1.0876	14
					GAT3	**0.0058**	**2.4108**	**4**	YHP1	0.0013	1.048	19
					YPR196W	0.0178	2.3881	3	MGA1	0.0037	1.0356	16
					WTM2	0.0009	2.3437	6	**YOX1**	**0.003**	**1.0242**	**17**
					ESC2	0.0027	2.3177	5	CST6	0.0024	1.0141	18
					FLO8	0.0005	2.2529	7	MBP1	0.0105	1.0052	13
					ARG80	0.0043	2.1709	5				
					RPN4	0.0003	2.1593	8				
					CSE2	0.011	2.1593	4				
					CHA4	0.0326	2.0662	3				
					MBF1	0.0326	2.0662	3				
					CBF1	0.0029	2.0306	6				
					CUP2	0.0074	1.9958	5				
					SPT2	0.0164	1.9958	4				
					MGA2	0	1.9588	22				
					MIG1	**0.0185**	**1.9452**	**4**				
					ISW1	0.0419	1.9287	3				
					HOG1	0.0419	1.9287	3				
					ARO80	0.047	1.8645	3				
					SRB2	0.0073	1.7734	6				
					RIC1	0.0106	1.6602	6				
					RSC2	0.045	1.5552	4				
					SWI4	0.0099	1.523	7				
					RSC1	0.0237	1.4108	6				

Table S1 Transcription factors that are likely to regulate the genes differentially expressed after various treatments (rows) according to each of the three networks (columns). Only transcription factors where $d_f > 1$ and where $p < 0.05$ are included (see **Materials and Methods** for details). Transcription factors that regulate the expression of the differentially expressed genes in a treatment according to more than one network are highlighted in **bold**. PheOH: phenylethanol treatment, TrpOH: tryptophol treatment, TyrOH: tyrosol treatment, 3OH: treatment with a combination of all three aromatic alcohols. The three transcriptional networks CC, GRD and GROE were obtained using three different methods (see **Materials and Methods**).

Supplementary Figure S2: Overlap between genes that are differentially expressed upon treatment with four different aromatic alcohols.

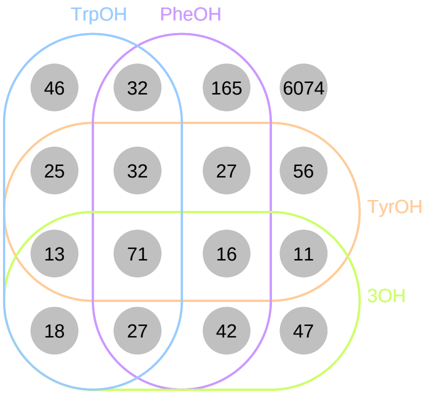

Fig. S2 Overlap between the genes differentially expressed after the addition of different aromatic alcohols. Of a total of 6702 *S. cerevisiae* genes, 628 are differentially regulated in response to at least one of the treatments. 264 genes are differentially regulated in response to tryptophol (TrpOH), 412 in response to phenylethanol (PheOH), 251 in response to tyrosol (TyrOH), and 246 in response to a combination of all three aromatic alcohols (3OH). 71 genes are differentially expressed in response to all four treatments.

Supplementary Figure S3: Difference in different histone modifications between those genes that are differentially expressed upon the addition of phenylethanol or tryptophol and those that are not.

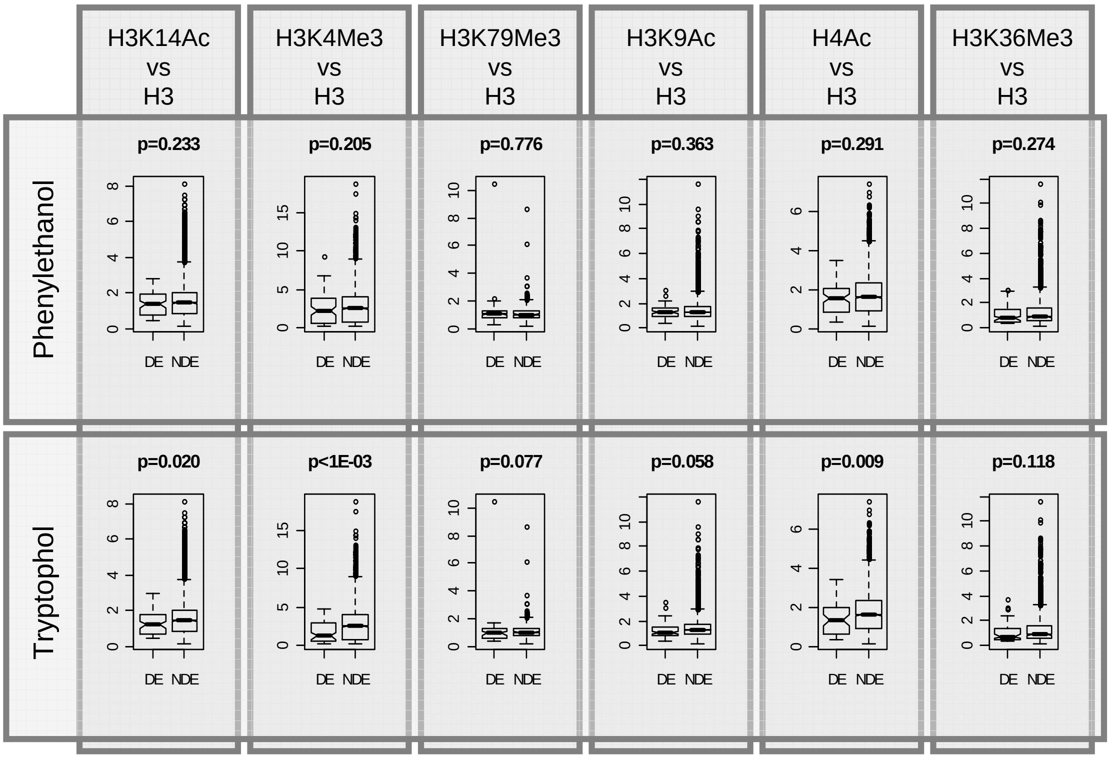

Fig. S3 Six different histone modifications in genes that are differentially expressed upon the addition of the aromatic alcohols phenylethanol and tryptophol (DE) and those that are not (NDE). As before, genes that are differentially expressed upon entry into stationary phase have been subtracted. The *p*-values between the two sets were computed using a Wilcoxon signed-rank test. Only the histone modifications H3K4Me (Methylation of Lysine 4 on histone H3) and H4Ac (Acetylation of histone H4) are significantly ($p <$ 0.01) less prevalent in genes that are differentially expressed upon the addition of tryptophol. No histone modifications have a significantly different prevalence in genes that are differentially expressed upon the addition of phenylethanol.