

Table S1. Brix of culture.

Culture days	Monoculture			Median	Mean	Standard error	Co-culture			Median	Mean	Standard error
0	18.8	18.8	18.8	18.8	18.80	0.00	18.3	18.3	18.3	18.3	18.30	0.00
1	18.8	18.8	18.8	18.8	18.80	0.00	18.3	18.3	18.3	18.3	18.30	0.00
2	18	18.1	18.1	18.1	18.07	0.03	17.6	17.7	17.6	17.6	17.63	0.03
3	16.5	16.8	16.6	16.6	16.63	0.09	16.2	16.5	16.1	16.2	16.27	0.10
4	14.6	15.2	14.9	14.9	14.90	0.17	14.4	15	14.3	14.4	14.57	0.18
5	12.2	13.7	13.2	13.2	13.03	0.44	12.1	12.9	12.3	12.3	12.50	0.20
6	10.8	12.5	12	12	11.77	0.50	10.4	11.1	10.6	10.6	10.77	0.17
7	9.8	11.6	10.9	10.9	10.77	0.52	8.9	9.6	9.6	9.6	9.60	0.20

Table S2. More than 2-fold upregulated genes of sake yeast in co-culture with the *kuratsuki Kocuria*.

Genbank ID	Gene	Product	Length (nt)	Mapped reads		RPKM		Ratio Co/Mono	References
				Monoculture	Coculture	Mono	Co		
NM_001184428.1		gag protein	1323	13	622	0.41	15.93	38.815	[23][24][25]26][27]
NM_001184429.1		gag protein	1323	29	645	0.92	16.52	18.043	[23][24][25]26][27]
NM_001184560.1		hypothetical protein	150	34	352	9.47	79.52	8.399	
NR_132263.1		SNR8	190	3328	29766	731.62	5308.49	7.256	[28]
NM_001182398.1		gag protein	1323	44	361	1.39	9.25	6.656	[23][24][25]26][27]
NM_001179028.4		gag-pol fusion protein	5269	87	699	0.69	4.50	6.518	[23][24][25]26][27]
NM_001184636.1		hypothetical protein	225	937	7299	173.94	1099.22	6.319	
NM_001184412.1		gag protein	1323	57	380	1.80	9.73	5.408	[23][24][25]26][27]
NM_001179946.1	<i>PAU5</i>	seripauperin Pau5	369	27	172	3.06	15.79	5.168	[43][44]
NM_001179407.3	<i>RGI2</i>	Rgi2	495	12	75	1.01	5.13	5.070	
NM_001184516.1	<i>SPO24</i>	Spo24	204	877	5083	179.57	844.29	4.702	[66]
NM_001179050.4		gag-pol fusion protein	5269	127	703	1.01	4.52	4.491	[23][24][25]26][27]
NM_001184417.2		gag-pol fusion protein	5269	266	1453	2.11	9.34	4.431	[23][24][25]26][27]
NM_001184632.3	<i>YDR524W-A</i>	hypothetical protein	90	10	48	4.64	18.07	3.894	
NM_001183301.1	<i>LDS2</i>	Lds2	1071	35	165	1.37	5.22	3.824	[63][64]
NM_001183307.1	<i>DDR2</i>	Ddr2	186	102	455	22.91	82.89	3.619	[34][35]

NM_001184392.2		gag-pol fusion protein	5269	22	98	0.17	0.63	3.614	[23][24][25]26][27]
NM_001179315.1	<i>SSP1</i>	Ssp1	1716	10	41	0.24	0.81	3.326	[68]
NM_001178270.1	<i>PET9</i>	ADP/ATP carrier protein Pet9	957	775	3158	33.83	111.82	3.306	[98]
		tRNA-Gln	76	27	108	14.84	48.15	3.245	
	<i>15S_RRNA</i>	15S ribosomal RNA	1649	3479	13740	88.12	282.34	3.204	
NM_001181471.3	<i>IRC18</i>	Irc18	675	20	78	1.24	3.92	3.164	[63][64]
NM_001183561.3	<i>LSCI</i>	succinate-CoA ligase (GDP-forming) subunit alpha	990	4449	17253	187.71	590.52	3.146	[94]
NM_001179729.1	<i>PIR3</i>	beta-1,3-glucan linked protein	978	5095	19346	217.60	670.28	3.080	
NM_001180144.1	<i>NDE2</i>	NADH-ubiquinone reductase (H ⁺ -translocating) Nde2	1638	224	841	5.71	17.40	3.046	[97]
NM_001184424.1		gag protein	1323	53	196	1.67	5.02	3.000	[23][24][25]26][27]
NM_001181996.1	<i>AHP1</i>	thioredoxin peroxidase Ahp1	531	1796	6288	141.28	401.26	2.840	[30]
NM_001181753.1	<i>SFC1</i>	Sfc1	969	180	611	7.76	21.37	2.754	[99]
NM_001181549.1	<i>NCA3</i>	SUN family protein Nca3	1014	285	948	11.74	31.68	2.698	[96]
NM_001183868.1	<i>LEE1</i>	Lee1	906	96	317	4.43	11.86	2.679	
NR_132265.1		snoRNA SNR5	204	9020	28920	1846.85	4803.66	2.601	[28]

NM_001184127.1	<i>CSR2</i>	Csr2	3366	2040	6482	25.31	65.25	2.578	[33]
	<i>HXT12</i>		1374	25	79	0.76	1.95	2.564	
NM_001179652.1	<i>SRX1</i>	sulfiredoxin	384	74	233	8.05	20.56	2.554	[47][50]
NM_001179405.1		hypothetical protein	1884	546	1714	12.11	30.83	2.547	
NM_001181117.1	<i>HFM1</i>	Hfm1	3564	58	182	0.68	1.73	2.546	[62]
NM_001184137.1	<i>TIP41</i>	Tip41	1071	358	1118	13.96	35.37	2.533	[48][50]
		tRNA-Cys	76	11	34	6.05	15.16	2.507	
NM_001179725.1	<i>RCN1</i>	Rcn1	636	102	314	6.70	16.73	2.497	[49]
NM_001184015.1	<i>YIG1</i>	Yig1	1386	77	234	2.32	5.72	2.465	[140]
NM_001181101.1		hypothetical protein	537	27	82	2.10	5.17	2.464	
NM_001181843.1	<i>POM33</i>	nucleoporin Pom33	840	298	900	14.82	36.31	2.450	[45][46][50]
NM_001184420.1		gag protein	1323	20	60	0.63	1.54	2.434	[23][24][25]26[27]
		tRNA-Lys	74	21	62	11.85	28.39	2.395	
NM_001181372.1	<i>MPC3</i>	mitochondrial pyruvate carrier	441	680	1972	64.41	151.52	2.353	[41][42][50]
NM_001181472.1	<i>LOH1</i>	Loh1	660	18	52	1.14	2.67	2.344	[65]
NM_001179913.1	<i>AQY3</i>	Aqy3	1941	1085	3134	23.35	54.71	2.343	[141]
		tRNA-Leu	85	84	242	41.28	96.47	2.337	
NM_001183870.1	<i>LCL1</i>	Lcl1	306	23	66	3.14	7.31	2.328	
NM_001182787.1	<i>CAT8</i>	DNA-binding transcription factor Cat8	4302	870	2485	8.45	19.57	2.317	[31][32][50]
NM_001184175.1		hypothetical protein	1119	74	211	2.76	6.39	2.313	
NR_132211.1		5.8S ribosomal RNA	158	498	1414	131.65	303.25	2.303	

NM_001181931.1	<i>PDC1</i>	indolepyruvate decarboxylase 1	1692	32021	90465	790.48	1811.69	2.292	[103]
NM_001182181.1	<i>GSP1</i>	Ran GTPase Gsp1	660	730	2047	46.20	105.09	2.275	[72]
NM_001184631.1		hypothetical protein	201	3624	10137	753.09	1708.90	2.269	
NM_001182838.1	<i>PAU19</i>	seripauperin Pau19	375	25	69	2.78	6.23	2.239	[43]
NM_001183409.1	<i>HXT11</i>	hexose transporter Hxt11	1704	66	182	1.62	3.62	2.237	[89]
NM_001181342.1	<i>RTA1</i>	Rta1	954	15	41	0.66	1.46	2.217	[142]
NM_001182026.1	<i>SLS1</i>	Sls1	1932	74	201	1.60	3.53	2.204	[100]
NM_001179454.1	<i>MOB1</i>	Mob1	945	849	2282	37.53	81.83	2.181	[39][40][50]
NM_001178185.1	<i>CLN3</i>	cyclin Cln3	1743	170	455	4.07	8.85	2.171	[71][75][76]
NM_001178718.1	<i>CIT2</i>	citrate (Si)- synthase Cit2	1383	8469	22252	255.78	545.19	2.132	[93]
NM_001181592.1	<i>HSP150</i>	heat shock protein Hsp150	1242	7217	18840	242.71	514.00	2.118	[37][38]
NM_001181736.3	<i>BNA2</i>	dioxygenase Bna2	1362	482	1258	14.78	31.30	2.117	
NM_001180555.1	<i>VHS1</i>	putative serine/threonine protein kinase Vhs1	1386	762	1986	22.96	48.55	2.114	[73]
NM_001181080.1	<i>CLG1</i>	Clg1	1359	5439	14119	167.17	352.04	2.106	[69][70]
NM_001178711.1	<i>GEX1</i>	glutathione exchanger	1848	25	64	0.57	1.17	2.077	[36]
NM_001183040.1	<i>SPS19</i>	Sps19	879	200	511	9.50	19.70	2.073	[67]

NM_001182899.3	<i>NOP2</i>	rRNA (cytosine- C5-)- methyltransferase	1857	1001	2545	22.52	46.44	2.063	[29]
NM_001179865.1		Nop2 hypothetical protein	924	572	1435	25.86	52.62	2.035	
NM_001182327.1	<i>MRPL4</i>	mitochondrial 54S ribosomal protein YmL4	960	64	160	2.78	5.65	2.028	[95]

Table S3. Less than 0.5-fold downregulated genes of sake yeast in co-culture with the *kuratsuki Kocuria*.

Genbank ID	Gene	Product	Length (nt)	Mapped reads		RPKM		Ratio Co/Mono	References
				Monoculture	Coculture	Mono	Co		
NM_001179350.3		hypothetical protein	1875	150	13	3.34	0.23	0.070	
NM_001182870.1	<i>HHT2</i>	histone H3	411	36894	4354	3749.46	358.96	0.096	
NM_001184393.1		gag protein	1323	168	25	5.30	0.64	0.121	[23][24][25]26][27]
NM_001178994.3	<i>SSA4</i>	Hsp70 family chaperone Ssa4	1929	14393	2257	311.65	39.65	0.127	[57][60]
NM_001184395.1		gag protein	1323	146	23	4.61	0.59	0.128	[23][24][25]26][27]
NM_001179244.1	<i>BZZ1</i>	Bzz1	1902	922	151	20.25	2.69	0.133	[143]
NM_001178706.1	<i>CHAI</i>	L-serine/L-threonine ammonia-lyase Chal	1083	5808	1196	224.00	37.42	0.167	[78]
NM_001181321.3	<i>TDH3</i>	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) Tdh3	999	4822	1273	201.61	43.18	0.214	[86][87]
NM_001183303.1	<i>GSH2</i>	glutathione synthase	1476	2088	556	59.09	12.76	0.216	[56][57]
NM_001184399.1		gag protein	1323	448	137	14.14	3.51	0.248	[23][24][25]26][27]
NM_001181666.1	<i>TDH2</i>	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) Tdh2	999	17009	5428	711.16	184.11	0.259	[86][87]

NM_001184291.1	<i>OPT2</i>	Opt2	2634	1913	726	30.34	9.34	0.308	[91]
NM_001184408.2		gag-pol fusion protein	5269	683	261	5.41	1.68	0.310	[23][24][25]26][27]
NM_001182279.3	<i>ECM19</i>	Ecm19	339	232	95	28.59	9.50	0.332	
NM_001182486.1	<i>PHO84</i>	phosphate transporter Pho84	1764	194	80	4.59	1.54	0.335	[92]
NM_001184433.1		gag protein	1323	633	268	19.98	6.86	0.343	[23][24][25]26][27]
NM_001182001.1	<i>AVL9</i>	Avl9	2295	4285	1834	77.99	27.08	0.347	[144]
NM_001178757.1		hypothetical protein	384	504	225	54.82	19.85	0.362	
NM_001180959.1	<i>PAN2</i>	poly(A)-specific ribonuclease	3348	7651	3512	95.45	35.54	0.372	
NM_001182742.1	<i>RNAI</i>	GTPase-activating protein Rna1	1224	2262	1045	77.19	28.93	0.375	
NM_001181854.1	<i>RIX7</i>	putative AAA family ATPase Rix7	2514	1830	848	30.40	11.43	0.376	
NM_001180096.1	<i>BSC1</i>	Bsc1	987	45	21	1.90	0.72	0.379	
NM_001180854.3	<i>SOM1</i>	Som1	225	107	51	19.86	7.68	0.387	[101]
NM_001182472.1	<i>COQ5</i>	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase	924	3075	1473	139.00	54.02	0.389	[79]
NM_001348877.1		hypothetical protein	336	52	25	6.46	2.52	0.390	
NM_001184586.1		hypothetical protein	195	521	251	111.60	43.62	0.391	

NM_001182770.1	<i>SAP30</i>	Sap30	606	467	230	32.19	12.86	0.400	[53]
NM_001179305.1	<i>ENO2</i>	phosphopyruvate hydratase Eno2	1314	22862	11406	726.73	294.13	0.405	[82]
NM_001178735.1	<i>HSP30</i>	Hsp30	999	2622	1332	109.63	45.18	0.412	[58][59]
NM_001181844.1	<i>SSA2</i>	Hsp70 family chaperone Ssa2	1920	33734	17185	733.87	303.29	0.413	[57][60]
NM_001348822.1		hypothetical protein	408	99	51	10.14	4.24	0.418	
NM_001179539.3	<i>MET28</i>	Met28	564	2863	1499	212.03	90.06	0.425	[85]
NM_001182754.1	<i>FAA4</i>	long-chain fatty acid-CoA ligase Faa4	2085	30530	15998	611.61	259.99	0.425	[83]
NM_001182301.1	<i>INA1</i>	Ina1	2028	1868	979	38.47	16.36	0.425	
NM_001183408.1	<i>HPF1</i>	mannoprotein	2904	557	298	8.01	3.48	0.434	
NM_001181273.1	<i>THI4</i>	thiamine thiazole synthase	981	8158	4499	347.35	155.40	0.447	[88]
NM_001182423.1	<i>TEM1</i>	Ras family GTPase Tem1	738	335	185	18.96	8.49	0.448	[74]
NM_001346794.1		hypothetical protein	309	27	15	3.65	1.64	0.451	
NM_001182299.3	<i>CTR3</i>	high-affinity Cu transporter Ctr3	726	665	373	38.26	17.41	0.455	[90]
NM_001270754.1		hypothetical protein	354	235	132	27.73	12.63	0.456	
NM_001181629.1	<i>ELO1</i>	fatty acid elongase Elo1	933	5804	3330	259.84	120.94	0.465	[81]

NM_001181485.3	<i>TDHI</i>	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) Tdh1 transcription initiation factor	999	232778	134242	9732.65	4553.31	0.468	[86][87]
NM_001183613.1	<i>TOAI</i>	IIA large subunit	861	1458	846	70.73	33.29	0.471	
NM_001181363.1	<i>YHBI</i>	flavo-hemoglobin	1200	4260	2476	148.28	69.92	0.472	[61]
NM_001180491.3	<i>PLP1</i>	Plp1	693	270	158	16.27	7.73	0.475	[145]
NM_001181110.1	<i>RTF1</i>	Rtf1	1677	1390	815	34.62	16.47	0.476	[52]
NM_001179554.1	<i>DAL3</i>	ureidoglycolate hydrolase protein	588	1168	692	82.97	39.88	0.481	[80]
NM_001183877.1	<i>TIM50</i>	translocase subunit Tim50	1431	942	561	27.50	13.28	0.483	[102]
NM_001184257.1	<i>GPH1</i>	glycogen phosphorylase	2709	25020	14950	385.77	187.00	0.485	[84]
NM_001184242.1	<i>ASN1</i>	asparagine synthase (glutamine-hydrolyzing) 1	1719	16038	9586	389.70	188.96	0.485	[77]
NM_001179432.1	<i>SDS3</i>	Sds3	984	1997	1194	84.77	41.12	0.485	[54]
NM_001178954.1	<i>THO1</i>	Tho1	657	1037	623	65.93	32.13	0.487	[146]
NM_001182905.1	<i>RPL9B</i>	ribosomal 60S subunit protein L9B	576	1758	1057	127.48	62.18	0.488	
NM_001182949.3	<i>CYB5</i>	Cyb5	363	1635	987	188.13	92.13	0.490	[147]

NM_001184190.1	<i>ASR1</i>	ubiquitin-protein ligase Asr1	867	478	289	23.03	11.29	0.490	[55]
NM_001179122.1		hypothetical protein carbonyl reductase (NADPH- dependent)	453	2315	1407	213.46	105.24	0.493	
NM_001180904.1		peptidylprolyl isomerase Cpr6	1116	6246	3814	233.77	115.80	0.495	
NM_001184662.3		hypothetical protein	258	31	19	5.02	2.50	0.497	
NM_001179829.3	<i>GAP1</i>	amino acid permease Gap1	1809	9237	5673	213.28	106.26	0.498	

References

- [140] Granath, K.; Modig, T.; Forsmark, A.; Adler, L.; Lidén, G. The *YIG1* (*YPL201c*) encoded protein is involved in regulating anaerobic glycerol metabolism in *Saccharomyces cerevisiae*. *Yeast* **2005**, *22*, 1257-1268.
- [141] Salas-Navarrete, P.C.; Rosas-Santiago, P.; Suárez-Rodríguez, R.; Martínez, A.; Caspeta, L. Adaptive responses of yeast strains tolerant to acidic pH, acetate, and supraoptimal temperature. *Appl. Microbiol. Biotechnol.* **2023**, *107*, 4051-4068.
- [142] Soustre, I.; Letourneux, Y.; Karst, F. Characterization of the *Saccharomyces cerevisiae* *RTA1* gene involved in 7-amincholesterol resistance. *Curr. Genet.* **1996**, *30*, 121-125.
- [143] Soulard, A.; Lechler, T.; Spiridonov, V.; Shevchenko, A.; Shevchenko, A.; Li, R.; Winsor, B. *Saccharomyces cerevisiae* Bzz1p is implicated with type I myosins in actin patch polarization and is able to recruit actin-polymerizing machinery *in vitro*. *Mol. Cell. Biol.* **2002**, *22*, 7889-7906.
- [144] Harsay, E.; Schekman, R. Avl9p, a member of a novel protein superfamily, functions in the late secretory pathway. *Mol. Biol. Cell* **2007**, *18*, 1203-1219.
- [145] Flanary, P.L.; DiBello, P.R.; Estrada, P.; Dohlman, H.G. Functional analysis of Plp1 and Plp2, two homologues of phosducin in yeast. *J. Biol. Chem.* **2000**, *275*, 18462-18469.
- [146] Jimeno, S.; Luna, R.; García-Rubio, M.; Aguilera, A. Tho1, a novel hnRNP, and Sub2 provide alternative pathways for mRNP biogenesis in yeast THO mutants. *Mol. Cell. Biol.* **2006**, *26*, 4387-4398.
- [147] Truan, G.; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D. Cloning and characterization of a yeast cytochrome b5-encoding gene which suppresses ketoconazole hypersensitivity in a NADPH-P-450 reductase-deficient strain. *Gene* **1994**, *142*, 123-127.