









8569	orf19.7235	orf19.7235	YMR102C	Predicted ORF from Assembly 19	NA	0.8758	0.5850	-0.0529	0.3840	NA	1.56	3.38	CACCAAGATCAACCAATCATTAAGGAGTTTGGTCAT TGATGGGAAGAAACAATGATGATTTTCATC	
5616	orf19.7517	CHT1	orf19.7517	CTS1	Chitinase, putative N-terminal catalytic domain; has secretory signal sequence.	NA	-0.1763	0.4447	0.9069	0.7941	NA	1.55	3.38	GATGACGGCTGCGCTATTGGCCGATACCTTTATGGAA CAAGCTTTGGTATGGTAAAGATGATGAGGAAAG
7773	orf19.1026	orf19.1026	orf19.1026	CSL4	Predicted ORF from Assembly 19	-0.2671	0.5331	1.2116	0.6434	0.1110	1.5850	1.55	5.31	TATTATTCTTCAACCTGCTAGAATGATTTGGGTGTG TATTTTGGCTAAACTGTGTGGCGGTGTGGGAG
7706	orf19.188	orf19.188	orf19.188	#N/A	Predicted ORF from Assembly 19	1.4060	0.1827	-0.1811	0.6978	0.8945	NA	1.55	4.34	AACAGAGATTAATGATGATGATGATGATGATGAT CGGGATTGAGTGGTGTGTTCCGAGGCTGCATACG
6025	orf19.3799	orf19.3799	orf19.3799	RTN1	Predicted ORF from Assembly 19	0.9745	0.5936	1.1846	-0.1746	-0.0380	1.2708	1.55	5.31	CAAGTTGATGCATTGTGTTGGAAGATGATGCTGTGT TTCAGGAATCAAGTTGGCAAGGTTGTGAACA
7713	orf19.3617	orf19.3617	orf19.3617	GTR1	Predicted ORF from Assembly 19	1.2066	1.0342	0.3984	0.1699	-0.0043	1.0000	1.55	4.34	TAACTATTGGGATTTTTCAGTAAACAAAGATGAT TGGCAACACTTTTATGTTTCAAGTCTTTCATGAT
8323	orf19.5399	orf19.5399	orf19.5399	YUL155C	Predicted ORF from Assembly 19	NA	0.0772	0.7355	NA	0.8679	NA	1.55	3.60	CACTACCAATGACGAGGCTGATGATATCAAC ACAAAGAAAGCTAATCATGCAATTAATGACATTCAC
5134	orf19.4801	orf19.4801	orf19.4801	MOD5	Predicted ORF from Assembly 19	1.2479	1.1947	-0.2009	0.5714	NA	0.4854	1.55	4.34	TGGCGTGGGAAGATGCCCAATTAATTTGGTGCT TGATGTGGAAGGTCACGACCAATTTGTCGATAAAGG
7340	orf19.4681	orf19.4681	orf19.4681	RAT1	Predicted ORF from Assembly 19	NA	0.8205	1.0349	-0.2498	0.3092	NA	1.55	4.34	ATATTTGTTTCAAAAGCACACACATGATGATGATG TATAGGAAGAATTCGCCAAATATAGAACGATATTTG
5630	orf19.7069	orf19.7069	orf19.7069	YBR261C	Predicted ORF from Assembly 19	-0.0939	0.5110	1.5028	0.4563	0.0272	NA	1.55	5.31	ATGAAACAGATAGTTTCAGTTACAGGAACAACAG TGGGAGGATGAGTATCAGAGATCATGGGATATAGT
5427	orf19.1457	orf19.1457	orf19.1457	SSL1	Predicted ORF from Assembly 19	1.6817	0.7155	-0.0247	0.0663	0.4351	NA	1.55	5.31	AAAGTGCAGCAACTGGGCAGTGGCTCAITTTGA ATTTCATCTCAATTTACACAGATTTCAATGCTGC
8325	orf19.2484	orf19.2484	orf19.2484	YDR415C	Predicted ORF from Assembly 19	1.4004	1.1070	0.1401	0.0412	0.5801	NA	1.55	4.34	AGAGTGAGGACAGTGGAGTGGCTTGGTGCTG TCGATTTGGTTTCACAGAGATTAACCTGATCAAA
7617	orf19.5379	ERG4	orf19.5379	ERG4	Protein described as similar to sterol C-24 reductase; flucanazole-induced, caspofungin repressed	1.1808	0.5231	0.5089	0.5450	0.4573	0.5420	1.55	1.36	AACTGTGAAAGAAAGATTGGCAAGCTGGGACG TTAGACATCAACAATTTGTTGATAGAAAGACAAT
5634	orf19.1682	orf19.1682	orf19.1682	#N/A	Predicted ORF from Assembly 19; repressed by nitric oxide	1.3265	0.5984	0.7190	0.0580	0.3774	NA	1.54	3.38	TGTTTAAACTGTTTGGGACCAAGATTAAGATG CTTGCGAGTATTGACAGATTTGATGACAGCTG
7917	orf19.5416	orf19.5416	orf19.5416	ESA1	Predicted ORF from Assembly 19	NA	1.0426	-0.3659	0.3033	0.5548	NA	1.54	5.31	CACCGAGTATGAAGATATGCGCTGATTCAAAG TGTCACAAAGCTTGATTCAGGATTTTGAAGAAG
7212	orf19.4609	orf19.4609	orf19.4609	YAL049C	Protein described as a translation initiator; downregulated in the presence of human whole blood or polymorphonuclear (PMN) cells	0.8311	0.8883	0.9978	0.7958	-0.1943	NA	1.54	3.60	GATGCTGTTTAAACCAACGGTGACCTTCAAGC
5170	orf19.6904	GCN3	orf19.6904	GCN3		0.7941	0.9396	0.3068	0.2141	0.3896	NA	1.54	2.90	GAANAATGCCGAGTTGTTTCTCAAGAGCAAAAT ATCTCGGAAGAGCTGGCGGGAATGATGATTGCC
5266	orf19.4931	orf19.4931	orf19.4931	YNL247W	Putative RNA-Cys synthetase.	0.8032	1.2957	0.7004	0.2203	0.6708	NA	1.54	3.60	TTTAAACATGAGTATGACAAATGTTGGAATAAGG AGAGATACATTTCGAAACGATATGGCGGAAGTG
5455	orf19.2167	orf19.2167	orf19.2167	RRP14	Predicted ORF from Assembly 19	0.7233	0.6517	0.7790	-0.0604	0.6717	0.9568	1.54	2.38	AGGAGATGATGATATGAAGTGAAGGCGGATGAC AATGATGACGTCCGGTGAATCAGACGATGATGAT
7536	orf19.7290	orf19.7290	orf19.7290	LSM1	Predicted ORF from Assembly 19	0.9635	0.1493	0.6987	0.4027	0.1454	1.3505	1.54	4.34	CTTTGGGAGTATTGCGGCAAGATTTGCGGCTGCT TTGTCGGGTGATTGACGCCCAAAATTTTGCTC
5289	orf19.6973	orf19.6973	orf19.6973	PIM1	Predicted ORF from Assembly 19; regulated by Gcn2p and Gcn4p	0.7127	0.8294	0.7459	0.2228	0.6708	NA	1.53	0.99	T

6300	orf19.337	orf19.337	orf19.337	VT11	Predicted ORF from Assembly 19	-1.3004	-0.7394	-1.0058	-0.0336	-0.1681	-0.5458	-1.55	3.38	GAATGGGGAGAGAGTAACTGCTCAATAAAATTATTA CTTATGGTATTATTGCGGTTGGATTCTTTGGTTG
6340	orf19.2737	orf19.2737	orf19.2737	YDR109C	Predicted ORF from Assembly 19	-0.8237	-0.5713	-1.2793	-0.3921	-0.0939	-0.6349	-1.55	2.38	AAAGCTCAACTGAGATTGGATGGCAATTGCTATT TGTTTAAGCGTTGTTTAGTGGAATCTGGCGTT
6371	orf19.7597	PGA12	orf19.7597	PMU1	Putative GPI-anchored protein of unknown function. Predicted carnitine acetyl transferase; similar to <i>S. cerevisiae</i> Yat1p; transcriptionally induced in macrophage.	-1.1329	0.1953	0.0144	-0.5395	-1.2176	-1.1234	-1.55	5.31	TGTTATCCCTTGGGTGATTTGAATCAACAAGACAATT TAATGACCCCTGATGTTGATGATGATGATGATGAT
8100	orf19.4551	CTN1	orf19.4551	YAT1	Predicted ORF from Assembly 19; macrophage/pseudohyphal-repressed	-1.2311	-0.5395	-0.0425	-0.3310	-0.4016	-1.2653	-1.55	3.38	CTGATTTCCTTGGGTGATTTGAATCAACAAGACAATT ATGATTTACTAAACCAAAATGAATGCAACAT
6237	orf19.3675	GAL7	orf19.3675	GAL7	Protein similar to <i>A. niger</i> predicted peroxisomal copper amino oxidase; induced upon biofilm formation	-0.6506	-0.7760	-1.1140	-0.3585	-0.7809	-0.1329	-1.55	1.62	OCCTTAATCAATCATCTCCCGATTCAATGGGCAAT TCACCAAGAGCGCGTGGAGTGCCTGCATGATG
7220	orf19.3152	AMO2	orf19.3152	#N/A	Predicted ORF from Assembly 19	-0.6873	-0.3548	-0.6827	0.0936	-0.5374	-1.6529	-1.56	4.34	TACCAAGAGTTTGGCGTTATGATGGTTGGTGTTCA TATGACCCCAAGCAAGTCTCTGATGATGATGATGAT
6112	orf19.478	orf19.478	orf19.478	#N/A	Predicted ORF from Assembly 19	-0.9490	-0.5756	-0.8997	-0.2636	-0.5437	-0.8160	-1.56	1.23	TTTCAACGTGATGATGATGATGATGATGATGATGAT GATGCCCAATTGTCGTCAAGCAATTCATGATAT
5966	orf19.5926	ARG11	orf19.5926	ORT1	Protein induced during the mating process	-0.1894	-0.6416	-0.3997	-0.2706	-0.5002	-1.8365	-1.56	5.31	CTTTTCATGTTTCCGCAATTGATCATCTGCAAGTCCAA TATCAAAACCGATGATATATCTTTGTCGCAACA
8349	orf19.5735	orf19.5735	orf19.5735	CDC50	Predicted ORF from Assembly 19	-0.7084	-0.2671	-0.5799	-0.4403	-0.4093	-1.4540	-1.56	2.38	AGGTTATCATCTGCTCGCTGTTGCTCTGCTGCTGCT AGGTTATCGGGTCTCTGCTGCTGCTGCTGCTGCTG
6626	orf19.7118	orf19.7118	orf19.7118	ADK2	Predicted ORF from Assembly 19 Protein described as ubiquinol-cytochrome-c reductase; antigenic in human; transcriptionally induced by interaction with macrophage.	-1.5023	-0.9024	-0.9462	0.0990	-0.0454	-0.5756	-1.56	4.34	TAGGGTATGAGAAGTTTGTGTGGGAAGAACTAGT GACATATATCTCTCAAGTTGAAAGTTGGTA
6795	orf19.2644	OCR2	orf19.2644	OCR2	Predicted ORF from Assembly 19	-1.2828	-0.7370	-1.3771	0.0635	0.1137	-0.6552	-1.56	5.31	CTGCTTGCAAGGATTTTAATTCATGCGCGCTTTGGT ATTTCGATTTTGGCTGATCTGTTATGCGAGTT
6323	orf19.3084	orf19.3084	orf19.3084	#N/A	Predicted ORF from Assembly 19	-1.4228	-0.3147	-1.1172	-0.0247	-0.3058	-0.7060	-1.57	3.60	ATGCTTAAGCTTGTAATAATGGCCATCTATCCGAC GTGTTATTGGGCAACTCTACAACGCACTGTTT
8419	orf19.1881	orf19.1881	orf19.1881	YOR175C	Predicted ORF from Assembly 19	-1.1714	0.1467	0.0745	-1.0000	-1.1520	-0.8211	-1.57	4.34	TTTCTATACAGATTGAAGTATCTGATCATCT
6194	orf19.4947	orf19.4947	orf19.4947	YPR098C	Predicted ORF from Assembly 19	-0.8810	-0.9269	-1.5146	0.1030	0.1966	-0.9187	-1.58	5.31	ACTTGCTATTTTGTCATGGGCTGTGTCAGGATGGA CTGTAGGCAAAAGGTTGACTTGTATGCAATAT
6404	orf19.3616	ERG9	orf19.3616	ERG9	Putative farnesyl-diphosphate farnesyl transferase (squalene synthase) involved in the sterol biosynthesis pathway.	-0.7418	-0.9434	-1.0058	-0.1844	-0.3771	-0.6920	-1.58	1.36	AAACATTAAACAAAGCTCGTTTGTAGGTTTATTG TGTTATGTTAGGCCATTATTTCATTACATATA
6700	orf19.673	orf19.673	orf19.673	OYE3	Predicted ORF from Assembly 19	-0.9379	-1.1649	-0.3884	-0.8034	-0.2828	NA	-1.58	1.62	TACGTCATGATGAATGATGGTGTCAATCAATTGAGT CAGAAGTGCACAGATCTCTGATGATGATGATGAT
5952	orf19.4449	orf19.4449	orf19.4449	CCS1	Predicted ORF from Assembly 19	-0.9546	-1.3474	-0.2863	-0.6016	-0.6326	-0.1910	-1.59	2.38	AATGAGATTAATGATGATGATGATGATGATGATGAT TATGATCAAGTGAAGTGAAGAAGTCTTCTTGT
8751	orf19.5253	orf19.5253	orf19.5253	YAK1	Predicted ORF from Assembly 19	-1.5995	-0.6552	-0.7539	-0.1125	-0.1536	-0.7466	-1.59	3.38	GTGGGAAGTTTGTGCTCAAGTGTGCTAAAGACATT TGTCAATCTCTGCAAGCGTCAATGTTTGGGA
7408	orf19.1728	orf19.1728	orf19.1728	#N/A	Predicted ORF from Assembly 19	-1.2076	-1.0831	-1.3076	-0.2863	-0.0725	-0.0725	-1.59	3.60	TGCTATCTGGCAATTATCAACATCATCTTCCATA TCGTATCTGGCAATGCTGATGATGATGATGATGAT
5974	orf19.5335	SGS1	orf19.5335	#N/A	Protein described as a DNA helicase; upregulated upon treatment of biofilm with farnesol	-0.7686	-0.2210	-0.6461	-0.3548	-0.4501	-1.5907	-1.59	2.90	TTGATGATGGGGCACTTATGATGAGCCCTTCA TTCCAAACTCACTCTGCTGCTGAGTTTCTCC

7808	orf19.3176	RIM21	orf19.3176	RIM21	Protein involved in the pH response pathway; required for activation of the transcription factor RimD1p.	-1.7909	-0.2109	-0.6506	-0.7013	-0.2328	-0.8417	-1.67	2.90	GTCTATCACTCACTGAGGGCTCTTCGGTACAGT GTGGTCTATCATTCAGTATGCTTACGCTACGG
8399	orf19.4372	orf19.4372	orf19.4372	#N/A	Predicted ORF from Assembly 19	-1.3076	0.1776	-0.4344	-0.6920	-0.9051	-1.2969	-1.67	2.90	AAGTACATCAGCAGTGAATGCAACCTGTGGTTAT TTTAATTATTTACAGCAGCAAAATGGAAAT
6150	orf19.7325	orf19.7325	orf19.7325	SCO1	Predicted ORF from Assembly 19	-0.9771	-0.5437	-1.2447	-0.0233	-0.0499	-1.6349	-1.68	3.60	CAGAGGCGTATATCCCAAAGCAGAGAGAAGAAGC AAAGACAAAGAGATGTTTGGATGCTTTATAAAC
8184	orf19.3051	orf19.3051	orf19.3051	YJR116W	Predicted ORF from Assembly 19; shows colony morphology-related gene regulation by Snf6p	-1.6349	-0.7784	-0.3401	-0.3328	0.2041	-1.6126	-1.68	5.31	TTTGTGATGCTTTGGTGTGTTTAAACAGATGGTTA TCGGTATGATTTGGTTCGTAATTTATGATTCGCGA
8199	orf19.3422	FMP27	orf19.3422	YLR454W	Predicted ORF from Assembly 19; fungal-specific (no human or murine homolog)	-1.5606	-0.0816	-0.3940	-0.3040	-1.1266	-1.0321	-1.68	2.90	TTAAATGTGAAGCGTGAAGTATCAAGAAAGAT TTGTGTGATGATGTGAAAGTGTGTCTTATACAGTT
8519	orf19.4688	DAG7	orf19.4688	#N/A	sigma factor induced	-1.8783	-0.1628	-1.0893	-0.1795	-0.2042	-0.9743	-1.68	3.60	CGGACACTTTTGGTTTGAATTTCTGCGATTTGAT ACATCGATCAAGAAATGATTTTGACTGTTCTGCTG
7413	orf19.4997	KIS2	orf19.4997	SIP2	Scaffold protein of Snf1p complex; similar to S. cerevisiae Gal83p and Sip2p; interacts with Snf4p.	-1.5312	-1.2619	-1.3771	1.1801	-0.2923	-1.4344	-1.69	4.34	ATATACAGTATCTGGGTAAGTTTGTCACACA
7566	orf19.4616	POL30	orf19.4616	POL30	Protein described as proliferating cell nuclear antigen (PCNA); RNA abundance regulated by tyrosol and cell density.	-0.7202	-0.6506	-1.5907	0.0649	-0.1795	-1.4322	-1.69	3.60	AGACTCTCGCTTGTGTTGAGTTTAAATTTGATGTG TGAGTATGATGATGATCTTCTGCGACATCAAAA
6778	orf19.2517	orf19.2517	orf19.2517	HOL1	Predicted ORF from Assembly 19	-1.1456	-1.0679	-1.0233	0.1596	-0.1109	-1.3328	-1.69	3.38	TTGATGATGATGATGATGATGATGATGATGATGAT TTTGTGCAATTTGGTGGTGTGTAATGAAGTGAAT
5803	orf19.820	SDS22	orf19.820	SDS22	Predicted ORF from Assembly 19; macrophage/pseudohyphal-repressed	-1.4739	-0.4344	-0.8651	-0.4383	-0.6990	-0.6104	-1.69	1.36	CGATTCGATCATTTGATCATCGGGATATTTGCTACTA TGTATGATGATGATGATGATGATGATGATGATGAT
7157	orf19.3663	PHO91	orf19.3663	PHO91	Putative low-affinity phosphate transporter; fungal-specific (no human or murine homolog)	-1.1681	-1.1617	-1.8059	-0.0365	0.0454	-0.4074	-1.69	4.34	ACCTTTATTCGCCCTTAAAGTTTCCGCCCAATGGAAT CGTCAAAAATAGGATATGCAAGTGGCTATACAT
8110	orf19.894	orf19.894	orf19.894	#N/A	Predicted ORF from Assembly 19	-0.2619	-0.1440	0.1137	-0.8810	-1.4150	NA	-1.69	5.31	ATCGTTTGGTATCGCCGCTTCTTGATTTCTTCGGTT TTCTTCAGCGCAAGCAAAAGGATTTTACATGTT
6677	orf19.6976	orf19.6976	orf19.6976	YJL163C	Predicted ORF from Assembly 19	-1.0469	-0.2898	-0.4711	-0.9885	-0.8186	-0.9856	-1.69	0.00	TTAATTTGATGATGATGATGATGATGATGATGATGAT GCAATCTGCTGTGTGATGATGATGATGATGATGAT
6146	orf19.2892	orf19.2892	orf19.2892	SBE2	Predicted ORF from Assembly 19	-1.4383	-0.2379	-0.7170	-0.2481	0.0922	-1.9434	-1.69	5.31	CGAATCTGCTGTGTGATGATGATGATGATGATGAT TTTAAAGGGTGTGTCTTCTTCCTCTTCTTGAAGAT
5990	orf19.6211	orf19.6211	orf19.6211	#N/A	Predicted ORF from Assembly 19	-1.0862	-0.7226	-0.3940	0.0398	-0.3603	-0.2033	-1.69	4.34	CTTGGATCGTGGGCTTGTGATGATGATGATGATGAT GATTTATGATCATTAATTTCTATCTATAATGCAACTG
8248	orf19.5751	orf19.5751	orf19.5751	ORM1	Predicted ORF from Assembly 19	-2.1779	-0.8314	-0.1234	-0.2916	-0.2193	-0.9105	-1.69	5.31	TTTATTTGAAAGTGTGATGTTGTTGTTGTTGTTGTT ATGCAAGGAGACTTTGATGATGATGATGATGATGAT
7149	orf19.5769	orf19.5769	orf19.5769	SNF4	Predicted ORF from Assembly 19	-1.4941	-0.8009	-1.2969	0.0594	-0.0908	-0.9434	-1.69	3.38	GATTTCTAAACATATAATTTTGTGGAGAGAC TTGAATTTGAAATTTGATTAATGATTCACCAATTTAA
6312	orf19.3235	orf19.3235	orf19.3235	CAP1	Predicted ORF from Assembly 19	-1.3733	-1.5064	-1.3328	-0.2059	-0.0755	-0.0862	-1.70	3.60	TCAACAATCATTCAGAAATTTGAGAAGATGT TTATGATAGGCGCAACTGATATGCCATTCAGTGTAC
7546	orf19.3655	orf19.3655	orf19.3655	#N/A	Predicted ORF from Assembly 19; possibly spurious ORF (Annotation Working Group prediction)	-1.4941	-0.3997	-1.5064	0.0314	-0.3165	NA	-1.70	3.38	CGTTTTCGAGGGAAATACATGCAAGCTCTCTTT ATGTTGATGATGATGATGATGATGATGATGATGAT
6963	orf19.2308	orf19.2308	orf19.2308	PFK26	Predicted ORF from Assembly 19	-0.1078	-1.1779	-1.2515	-0.3846	-0.5270	-1.1520	-1.70	2.37	ATGAGCAAAAGTGTGGAGGAAAAGGATGGAGC ATATTAGTCACGATGGAAGCTTTGTGGCGTT

7936	orf19.6476	orf19.6476	orf19.6476	YLR114C	Predicted ORF from Assembly 19; filament induced	-1.6394	0.2534	-0.2243	-0.5864	-1.4739	-1.4820	-1.81	3.60	TTGTTGGACCAATTGTTCGCAAAATTTGAATGATTCAGT TTAAAGCTTGCGTAATGAGCAATCCAGCTGGT
8934	orf19.355	orf19.355	orf19.355	JLP1	Predicted ORF from Assembly 19	-1.9658	-1.0087	-0.3511	-0.0755	-0.5228	-1.2413	-1.82	2.90	GGGATGATACCCCTATATTCGCAAGAACGATCAGAT CCGCTAAATTTGTTGACGAAGCTTTTGGCAATTA
6682	orf19.2101	orf19.2101	orf19.2101	GET1	Predicted ORF from Assembly 19	-1.6712	-0.6326	-0.5084	-0.9214	-0.0970	-1.3437	-1.82	2.37	TAAAGCTTTGGATGTTTGGCTGTGAATTATGCTTCTGA GTGATTTAACTCTTATGTTTCTTCTGCGCATTT
8133	orf19.3835	orf19.3835	orf19.3835	TFC3	Putative DNA-binding transcription factor	-0.7984	-0.3456	0.0029	-0.7539	-1.9658	-1.3255	-1.82	2.90	TAAATCTCTATGACAGCAATTTTGGATGATGATTA CAATTTGAGTCAAAATATCAATCAATCTTTCCG
6633	orf19.101	orf19.101	orf19.101	RIM9	Predicted ORF from Assembly 19	-0.9187	0.1309	-0.0130	-0.9856	-1.4383	-1.9771	-1.82	3.60	AAAGAGGAACAGATTTTGGAGCCCTTATTTGAATATA TTCTTAATCTCTACTATATTTTTCGCTGTAAAC
6400	orf19.1723	orf19.1723	orf19.1723	YJL055W	Predicted ORF from Assembly 19	-2.0233	-1.4422	-1.3696	-0.1094	0.1097	-0.3752	-1.83	4.34	AAGTCTTACTGGCTATGGAGATTAATCGGATCTCTGT AGGGAGCAATCACTAAAGCTGGAGAGAGCACTG
7275	orf19.2788	orf19.2788	orf19.2788	RIB2	Predicted ORF from Assembly 19	-0.5143	-0.7394	-0.6552	-0.4364	-0.9997	-0.8678	-1.83	0.00	TTCCAGCAAGACGTTTGGCTTCAATTTGATGACGGCT TTGAGACTGAGTTTCCACCTTGGGCAAAATTT
8452	orf19.4700	orf19.4700	orf19.4700	#N/A	Predicted ORF from Assembly 19	-1.2379	-0.8546	-1.1584	-0.0262	-0.3094	-1.6259	-1.83	2.37	CAATTGTTTGGACTAGGTTGCTATTGAGGTTTGCAT TTAGATGATCTATAACTATGCTATGAAGCGCT
6178	orf19.6488	orf19.6488	orf19.6488	#N/A	Predicted ORF from Assembly 19	-1.4189	-0.4580	-0.3566	-0.8034	-0.3696	NA	-1.83	2.37	TTTGTGGGCACTAACCTTGGCATATGCTGATGTGCTG ATCTCTGATGACAGATCTGCTCAATTTGATGATGCT
7053	orf19.4376	orf19.4376	orf19.4376	#N/A	Predicted ORF from Assembly 19	-1.1811	-0.2758	-0.3456	-0.9799	-0.7490	-1.6897	-1.83	1.62	ACATTTGAATTGGGTTCAACCAATCATTTTTCGTT CAGCGGTTATTAACGAATCTTATCTTCTCTCG
8299	orf19.1595	orf19.1595	orf19.1595	UBX3	Predicted ORF from Assembly 19	-1.5692	-0.5002	0.3010	-0.7588	-1.1811	-1.5146	-1.83	2.90	CAAGACTAACCTGCTATTTTCCCAAAATCTTCAAAG TTGAGTAAATATTCACATTTTGTGGTAAGCTTGT
7803	orf19.3707	YHB1	orf19.3707	YHB1	Nitric oxide dioxygenase; acts in nitric oxide scavenging/detoxification	-0.2026	-0.7809	-1.6804	-0.5864	-0.7484	-1.2042	-1.83	1.36	TTGAAGGCTTTTATGCAAGTGTCTTCAACCCATT CCAGTTCTGGGTCGAAGCAATTTATGATGTAAT
5877	orf19.194	orf19.194	orf19.194	#N/A	Predicted ORF from Assembly 19; possibly spurious ORF (Annotation Working Group prediction)	-1.6574	-1.6171	-0.9406	-0.2723	-0.4788	-1.2243	-1.84	3.60	AGAAATTTCTTCCCAACCAATGTAGACCTTGST TAAAGACTTGGAAGCTTTTTCATTAATGACGACCT
8526	orf19.1050	orf19.1050	orf19.1050	#N/A	Predicted ORF from Assembly 19; possibly spurious ORF (Annotation Working Group prediction)	-1.1361	-1.3437	-1.5922	0.0186	-0.5353	-0.7394	-1.84	1.62	TAAGACTGATCGATTTTTCATTAATGAACGACCAT ACAGTAATTTGGAAGTTTGATGATTTGATTAAT
8906	orf19.5022	orf19.5022	orf19.5022	SMF2	Predicted ORF from Assembly 19	-1.0923	0.4761	-0.4208	-1.4739	-0.6215	-2.1714	-1.85	4.34	TAACTATTCGACAGAGTTTTCATTAATGATGATGAT CAAGTATAGGCTTTGATTTTCCATATATTT
6336	orf19.728	orf19.728	orf19.728	TSC11	Predicted ORF from Assembly 19	-1.2243	0.2892	-0.8186	0.0827	-1.8160	NA	-1.85	4.34	GCCTTTTATTTGGATTTAGGATTTCTCTAGTACTGAT TTGGACTCAAGTATCTATCTCTGAGCAAGATC
6678	orf19.278	orf19.278	orf19.278	#N/A	Predicted ORF from Assembly 19	-1.5564	-0.2740	-0.1376	-1.3255	-0.5187	-1.5395	-1.86	2.38	GCCTTGGAGTTTATTTCTAGTGGCCGGTTTGTAT GCTACTGTTTCAAAGTTATTAATGATGCTTATGA
7925	orf19.3951	orf19.3951	orf19.3951	YIP1	Predicted ORF from Assembly 19	-1.9051	-0.3474	-0.4189	-0.6758	-0.5819	-1.4035	-1.86	2.37	TCAGCTATGATGCTTATGATGATGCTTATGATGAT GCCAATGATGAGCCCTTTGATTCGATGATCAAT
8892	XP_457517.1	#N/A	#N/A	#N/A	"D. hansenii" - hypothetical protein.	-1.4860	-0.4131	-0.1001	-0.6711	-0.7859	-1.9885	-1.86	2.90	AATCTTCAACAACACTGACGACTTTCTGTGGGACGC TTGCTGTTGACCTCGCTCCGGATTAACATCTT
7767	orf19.7387	orf19.7387	orf19.7387	ELP3	Predicted ORF from Assembly 19	-1.2210	0.2833	-0.2550	-0.7155	-1.7418	-1.7466	-1.87	3.38	GTGCTATGATTGATTATGCTCAATTTTGGGCTGT TTGTTCTCCATGAGCTGACTGATCTCTGTTGAT
6823	orf19.4898	orf19.4898	orf19.4898	YER004										



7278	orf19.5156	orf19.5156	orf19.5156	PHS1	Predicted ORF from Assembly 19; has six putative membrane-spanning regions, similar to <i>S. cerevisiae</i> Yli09p.	-1.5522	-0.5270	0.0257	-0.7686	-0.9885	-2.2723	-2.38	2.38	ATATGCACATTGTGTTGAGTGTGGTCCATACTGA	
6140	orf19.7604	orf19.7604	orf19.7604	TRS120	Predicted ORF from Assembly 19	-0.7515	-0.3603	-0.5564	-1.5995	-0.5479	-2.2934	-2.03	2.37	ATATGAGGAATAACTAATCAATCACTGTAACGT	
7072	orf19.5121	OPT5	orf19.5121	OPT2	Putative oligopeptide transporter; fungal-specific (no human or murine homology)	-0.7710	0.0990	-0.7442	-1.0710	-1.2550	-2.4344	-2.04	2.38	CGACACTTTGACGCCATTATGCTTGTCGCAAGGT	
5810	orf19.2455	orf19.2455	orf19.2455	YBR281C	Predicted ORF from Assembly 19	-0.0985	-1.3733	-0.1763	-1.6758	NA	NA	-2.05	2.37	TAACATCAATGAATGTGACGTGGAACAAACCCCTCAT	
6902	orf19.2149	orf19.2149	orf19.2149	YPR003C	Predicted ORF from Assembly 19	-1.9105	-1.1520	-1.3696	-0.3622	-0.0619	-1.4150	-2.06	1.62	TTAGTGAATGTTTGAAGATGATGTAGAGAT	
6372	orf19.3446	orf19.3446	orf19.3446	MOG1	Predicted ORF from Assembly 19	-1.6666	-1.4189	-1.5023	-0.0291	-0.4699	-1.1976	-2.07	1.36	TCGTATGTCACCAAGTGTGTTGATGCTG	
5294	orf19.3356	orf19.3356	orf19.3356	ESP1	Predicted ORF from Assembly 19	-1.2345	0.3584	-0.4759	NA	-1.4266	-2.4501	-2.08	3.38	TTGATATTCACGATGTGCAAGTGTGATGCTG	
8566	orf19.5388	orf19.5388	orf19.5388	SWD1	Predicted ORF from Assembly 19	-1.7959	-1.1078	-1.3511	-0.4901	-0.0695	-1.5312	-2.08	1.36	TTTCACGGAATGATTTGAAATGTGCTGCTC	
8885	XP_451524.1	#N/A	#N/A	#N/A	"K. lactis" - some similarities with <i>slpP53054</i> <i>Saccharomyces cerevisiae</i> YGL262w singleton, hypothetical start	-1.7418	-1.1877	-2.1078	0.0566	-0.2987	NA	-2.38	2.38	GAGAGGTATATCTCAATCAATGATGGTGATCGATG	
7150	orf19.7629	orf19.7629	orf19.7629	YOL138C	Predicted ORF from Assembly 19	-1.0029	-1.0923	-0.2210	-0.9296	-0.2671	-2.8783	-2.09	3.38	ATATTTATGCTGAACGATGATGCTGATGCTG	
8621	orf19.1943	orf19.1943	orf19.1943	#N/A	Predicted ORF from Assembly 19	-1.1424	0.2618	-0.5084	-1.3622	-1.1552	-2.4901	-2.09	2.90	TTATGATGATGCTGTTGCTGAGTCAACCGC	
8742	orf19.5097	CAT8	orf19.5097	CAT8	Predicted zinc-cluster protein; homozygous null mutant shows a defect in transcription of <i>JEN1</i> lactate permease gene.	-1.2502	0.0072	-0.7984	-0.8688	-0.6689	-1.9602	-2.09	2.38	AAATTTGATGCTGATGACGATCAATGCTGATG	
6018	orf19.7331	orf19.731	orf19.731	EMP47	Predicted ORF from Assembly 19	-1.4074	-0.9714	-1.5312	-0.6758	-0.5886	-1.2311	-2.10	0.00	1.36	TCAGGATGATGATGATGATGATGATGATGATG
7858	orf19.433	orf19.433	orf19.433	KRE11	Predicted ORF from Assembly 19	-0.8943	-1.5479	-1.5864	-0.8520	-0.4880	-1.0954	-2.11	0.00	1.36	TTAGTGTGATGATGATGATGATGATGATGATG
5983	orf19.2940	orf19.2940	orf19.2940	BOS1	Predicted ORF from Assembly 19	-1.3659	-0.4800	-1.3997	-0.3566	-0.5084	-2.3585	-2.11	2.37	ATGATGATGATGATGATGATGATGATGATG	
8208	orf19.550	PDX3	orf19.550	PDX3	Transcription is regulated upon yeast-hyphal switch; regulated by Nrg1p, Mig1p, and Tup1p; caspofungin repressed	-1.4035	-1.2142	-1.9546	-0.1376	-0.2688	-1.5395	-2.12	1.62	5.31	ATGATGATGATGATGATGATGATGATGATG
5340	orf19.4760	orf19.4760	orf19.4760	YIL110W	Predicted ORF from Assembly 19	-0.8443	-0.1779	0.0949	-0.6282	-1.8836	-3.1203	-2.13	5.31	1.36	TTAGTGTGATGATGATGATGATGATGATGATG
6910	orf19.5559	STE23	orf19.5559	RAV2	Protein similar to <i>S. cerevisiae</i> Ste23p, is involved in maturation of pheromone; transposon mutation affects filamentous growth	-2.5312	-0.2260	-0.2706	-0.5886	-1.0469	-1.8997	-2.13	2.90	1.36	TTAGTGTGATGATGATGATGATGATGATGATG
7388	orf19.2173	MAF1	orf19.2173	MAF1	Protein described as affecting nucleocytoplasmic transport and synthesis of RNA Polymerase III	-1.5395	-1.0740	-0.3147	-0.6620	-0.7394	-2.2447	-2.14	1.36	1.36	TTAGTGTGATGATGATGATGATGATGATGATG
7115	orf19.4526	HSP30	orf19.4526	HSP30	Protein described as similar to heat shock protein; fluconazole-downregulated; amphotericin B induced	-0.2987	-1.6620	-1.8365	-0.4521	-0.9942	-1.3548	-2.14	1.23	1.36	TTAGTGTGATGATGATGATGATGATGATGATG
6471	orf19.6134	0	orf19.6134	SEC39	Predicted ORF from Assembly 19	-0.6712	0.4709	-0.0923	-2.5564	-1.3997	-2.3808	-2.15	5.31	1.36	TTAGTGTGATGATGATGATGATGATGATGATG
7550	orf19.6638	PTC4	orf19.6638	PTC4	Protein described as a serine/threonine phosphatase, type PP2C; decreased expression in hyphae compared to yeast-form cells	-1.8783	-1.2898	-1.7084	-0.0755	-0.4383	-1.2688	-2.16	1.36	1.36	TTATGTTGCTTTACATCTGTTAAAGTGTACAGC
5460	orf19.6071	orf19.6071	orf19.6071	MDM20	Predicted ORF from Assembly 19	-0.2881	-0.2533	-0.6282	-2.1203	-1.3401	NA	-2.17	2.37	5.31	AACTTGTTGAAATTCAGCCGCAATTAACGTGAT
6809	orf19.5129	orf19.5129	orf19.5129	#N/A	Predicted ORF from Assembly 19	-1.7131	-0.4364	-0.9296	-0.4189	-1.0831	-2.1910	-2.19	1.36	1.36	GAATGTGGGATTTGGTATGATTTATGATATAG
8496	orf19.3332	orf19.3332	orf19.3332	#N/A	Predicted ORF from Assembly 19	-1.3301	0.0895	-0.0380	-1.4189	-1.7563	-2.3437	-2.20	2.90	1.36	TTGTTGTTTATGCTTGGCAGCATTAACAAATCT
5465	orf19.4157	orf19.4157	orf19.4157	SPS19	Predicted ORF from Assembly 19	-2.0529	0.0129	-1.3004	-0.8599	-1.1779	-1.4501	-2.20	1.23	1.36	AGAGAGAGATTCCTATTGACGATATAGGACCACT
7346	orf19.100	orf19.100	orf19.100	YJR107W	Predicted ORF from Assembly 19	-1.4580	-0.2126	-0.0695	-1.5228	-1.7226	-1.8468	-2.20	1.62	1.36	CTCTTTTATTTGCTATGACAGACGAGACTTATCT
6808	orf19.1976	orf19.1976	orf19.1976	#N/A	Predicted ORF from Assembly 19	-1.5146	0.2916	-0.2934	-0.4699	-1.8262	-3.0233	-2.20	4.34	1.36	AGGTCGATGATCAACATCTTAGAAGATGGGG
7503	orf19.409	orf19.409	orf19.409	YNR018W	Predicted membrane protein; similar to <i>S. cerevisiae</i> Ynr018wp	-1.0559	-1.6126	-1.4035	-0.8757	-0.9971	-1.9379	-2.21	0.00	1.36	GTCTTAATTAAGAATAGGAGCTGAAATCTTTGCT
5619	orf19.4048	DES1	orf19.4048	#N/A	Putative delta-4-sphingolipid desaturase	-1.1877	-1.0923	0.0144	-1.3076	-0.6735	-2.6220	-2.22	2.37	1.36	TTTTCATTTGGATGATCTTCGATAGAATGAGGG
8108	orf19.5515	orf19.5515	orf19.5515	CBP3	Predicted ORF from Assembly 19	-1.4228	0.0607	-0.7060	-0.4860	-1.9714	-2.4344	-2.22	2.38	1.36	CTTGCAAACTATGCGGAATCTTCGGTGGTCTGGT
5106	orf19.5307	orf19.5307	orf19.5307	JEN1	Predicted ORF from Assembly 19	-0.6574	0.4125	-0.3846	-2.0174	-2.0710	-2.2653	-2.24	3.38	1.36	CAATCTCTGGTATCTTCTGATGATGCTG
7304	orf19.4631	ERG251	orf19.4631	ERG25	Predicted ORF from Assembly 19; ketoconazole-induced; amphotericin B, caspofungin repressed	-2.2176	-0.8314	-1.6804	-0.2481	-0.5995	-1.4112	-2.24	1.36	1.36	CTTGCACTGAATGTGGCAAACTGACCAAGAACT
8695	orf19.406	ERG1	orf19.406	ERG1	Squalene epoxidase, catalyzes epoxidation of squalene to 2,3-oxidosqualene in the ergosterol biosynthetic pathway.	-1.6758	-0.6371	-1.2969	-0.6394	-1.2243	-1.5187	-2.24	0.00	1.36	ATGGGAAGCATTTAGGAATGTGTTTACGTGCTATGTT
6642	orf19.6687	orf19.6687	orf19.6687	#N/A	Predicted ORF from Assembly 19	-1.7959	-0.3603	-0.3219	-0.7418	-0.6082	-3.2379	-2.26	3.38	1.36	TGSGTITGTTTATGTCACATGATGATGATGATGCTG
8736	orf19.5000	CYB2	orf19.5000	CYB2	Protein described as precursor protein of cytochrome b2; transcriptionally regulated by iron; expression greater in high iron	-1.9942	-1.3959	-1.1681	-0.3111	-0.7322	-1.6897	-2.32	0.00	1.36	CTTCAGAAGATAAATTTTGTAGAAGTTTCTTCAAC
8275	orf19.5212	orf19.5212	orf19.5212	#N/A	Predicted ORF from Assembly 19	-1.4461	-0.0321	-0.7108	-1.0469	-1.6990	-2.4035	-2.33	1.36	1.36	CCATCTCGAGCCCGCAATGTTCAAGCTTGAATTT
5236	orf19.5759	SNQ2	orf19.5759	SNQ2	Protein similar to <i>S. cerevisiae</i> Snq2p transporter; member of the PDR subfamily of ABC family	-2.1520	-1.7037	0.9949	-1.4580	-1.0233	-2.0058	-2.34	3.38	1.36	CTGCTGGGTTTGTGAGTTTATGTACAGATGTGCA
7671	orf19.6816	orf19.6816	orf19.6816	YJR096W	Predicted ORF from Assembly 19	-1.2379	-1.0058	-2.0233	-0.7486	-1.0233	-1.4150	-2.36	0.00	1.36	CCATCAGAAGAAATGGTCTAGTGTATGATCAACCTG
6984	orf19.6602	orf19.6602	orf19.6602	COQ9	Predicted ORF from Assembly 19	-2.0078	-1.7760	-2.2653	0.1270	-0.1520	-1.3884	-2.37	2.38	1.36	TTGATGATGAGCAACTGTGGGATGTACCAA
6078	orf19.6044	orf19.6044	orf19.6044	MOB2	Predicted ORF from Assembly 19	-2.1976	-1.0893	-0.4840	-1.6259	-0.3529	-1.8262	-2.42	1.23	1.36	TTGAACGCGATGATGATGATGATGATGATGATG
8359	orf19.7065	orf19.7065	orf19.7065	PSF3	Predicted ORF from Assembly 19	-1.1617	-0.2076	-0.8443	-1.3997	-1.2413	-2.7563	-2.41	1.36	1.36	ACAATGATGACCAATATCTTCAAACTATG
7337	orf19.4789	orf19.4789	orf19.4789	#N/A	Predicted ORF from Assembly 19	-1.8573	1.3730	-0.7760	-1.3921	-2.4422	-2.5479	-2.42	5.31	1.36	ATGACCCGCGATCACTTGATTTGCTGCTTGCCAA
7945	orf19.1070	orf19.1070	orf19.1070	YMR010W	Predicted ORF from Assembly 19	-1.1329	0.1916	-0.5458	-1.3585	-2.0410	-1.9885	-2.48	2.38	1.36	TGTTGAAGTTGGAGTTTCTTCAAACTGGGTATTAAP
5708	orf19.6360	orf19.6360	orf19.6360	RCK2	Predicted ORF from Assembly 19	-1.2550	-0.9771	-0.6016	-3.2653	-0.4170	-1.3622	-2.48	2.37	1.36	CMAGATGATGAGATATGCTGTTTCTTATGATG
8024	orf19.6294	orf19.6294	orf19.6294	MYO1	Predicted ORF from Assembly 19	-1.7466	0.1164	-0.9828	-1.8059	-0.7834	-2.8059	-2.52	1.62	1.36	AATGCAACTTTACTGATGATGATGATGATGATG
5122	orf19.5377	HOS2	orf19.5377	HOS2	Histone deacetylase; similar to <i>S. cerevisiae</i> Hos2p; has conserved deacetylation motif.	0.3242	-0.1552	-0.1313	-2.3292	-3.0954	NA	-2.62	4.34	1.36	TTTCAATGATGATGATGATGATGATGATGATG
6982	orf19.1496	orf19.1496	orf19.1496	#N/A	Putative transcription factor with zinc finger DNA-binding motif; possibly spurious ORF (Annotation Working Group prediction)	-1.0499	-0.5649	-1.9051	-1.6126	-1.3959	-2.0350	-2.69	0.00	1.36	ATTTGCTCCACCACTCATCAAGAACTGTGATGAT
8810	orf19.6621	orf19.6621	orf19.6621	MHP1	Predicted ORF from Assembly 19	-2.3219	-1.7037	-2.1910	-0.7179	-0.8288	-1.1584	-2.80	0.00	1.36	ATCTCTCAAAGATCCAGCTGATGACGACAGATGTT
8329	orf19.5664	HOF1	orf19.5664	#N/A	Protein not essential for viability; similar to <i>S. cerevisiae</i> Hof1p, which is a protein localized to the bud neck	-1.1844	0.6220	-0.3529	-1.7959	-3.4020	-3.1844	-2.93	3.38	1.36	TCCTGCGATGATAAATCAATGATTTCAATATGTAT
6376	orf19.2366	orf19.2366	orf19.2366	#N/A	Predicted ORF from Assembly 19	-2.6712	0.6060	-0.9132	-2.3884	-1.7179	-3.0293	-3.21	2.37	1.36	TAACATCACTACCTTTGTTGTTTGATGCTAGAT
8217	orf19.5877	orf19.5877	orf19.5877	#N/A	Predicted ORF from Assembly 19; caspofungin repressed	-1.5146	-0.7859	0.6267	-1.8365	-4.1128	-2.4901	-3.22	2.90	1.36	TTTGAACGATTTTATGACGATGATGATGATG
6886	orf19.7514	PKC1	orf19.7514	PKC1	Phosphoenolpyruvate carboxykinase; role in gluconeogenesis	-0.9828	-1.2277	-2.7959	-1.4505	-1.7322	-2.3219	-3.36	0.00	1.36	GTGTTAGTGGGAAGTCGCGCCTCTGACGTGGG
7026	orf19.6173	orf19.6173	orf19.6173	MTH1	Predicted ORF from Assembly 19	-3.0954	-1.6484	-1.8730	-1.4344	-1.8836	-2.0291	-3.38	0.00	1.36	CAAAAGAAATTAATGATCTGTTGGAAGAAGTCAA
6368	orf19.2659	orf19.2659	orf19.2659	YIL057C	Predicted ORF from Assembly 19; downregulation correlates with clinical development of fluconazole resistance.	-2.2243	-2.6820	-2.3004	-1.2277	-1.4620	-2.7661	-4.31	0.00	1.36	GAGAAATTAATGATGATGATGATGATGATG

\* The oligonucleotide probes were designed to target open reading frames putatively identified from orthologs in *S. albicans* (assembly 19) and other species. The orf19 name is given for *S. albicans* orthologs, and the GenBank accession number for other sequences.

\* The names of the orthologs from *S. albicans* assembly 19 from the Candida Genome Database ([www.candidagenome.org](http://www.candidagenome.org)) are shown.

\* The names of the orthologs from *Saccharomyces cerevisiae* from the Saccharomyces Genome Database ([www.yeastgenome.org](http://www.yeastgenome.org)) are shown.

\* Putative gene descriptions are taken from the Candida Genome Database where possible, or from GenBank (indicated with an asterisk)

\* False Discovery rate from Significance Analysis of Microarrays.

Sequence of the oligonucleotide probes.