

experiment

generated with longer reads and technical replicates where not included).

Legend

Test_ID	cpar2 ID
Locus	Genomic coordinates of the transcript
Sample_1	growth in normoxia
Sample_2	growth in hypoxia
Value_1	FPKM value estimated from Sample_1
Value_2	FPKM value estimated from Sample_2
Ln.fold_change	natural log of the fold change Value_2/Value_1
test stat	value of hte test statistic used to compute significance of the observe
p_value	uncorrected p-value of the test statistic
C.a. ortholog	Candida albicans ortholog
C.a. orthologgene name	Gene name of the C. albicans ortholog
C.a. ortholog description	Description of the C. albicans ortholog from CandidaGenomeDataba

test_id	locus	sample_1	sample_2	value_1	value_2
cpar2_404850	contig006372	normoxia	hypoxia	490.003	45287.9
cpar2_203450	contig005809	normoxia	hypoxia	72.6403	3692.15
cpar2_807700	contig005807	normoxia	hypoxia	6.28353	146.629
cpar2_403510	contig006372	normoxia	hypoxia	229.08	3514.32
cpar2_102580	contig005569	normoxia	hypoxia	12.7004	186.005
cpar2_100830	contig005569	normoxia	hypoxia	221.877	3110.37
cpar2_402640	contig006372	normoxia	hypoxia	107.451	1412.8
cpar2_600270	contig005504	normoxia	hypoxia	25.8119	336.468
cpar2_603610	contig005504	normoxia	hypoxia	590.091	6928.56
cpar2_301400	contig005806	normoxia	hypoxia	220.363	2544.23
cpar2_802720	contig005807	normoxia	hypoxia	66.44	732.613
cpar2_100710	contig005569	normoxia	hypoxia	35.0517	351.144
cpar2_401300	contig006372	normoxia	hypoxia	136.912	1315.49
cpar2_802240	contig005807	normoxia	hypoxia	36.2654	347.971
cpar2_401450	contig006372	normoxia	hypoxia	29.7091	279.99
cpar2_500850	contig006139	normoxia	hypoxia	548.871	4498.3
cpar2_100100	contig005569	normoxia	hypoxia	102.127	834.376
cpar2_109010	contig005569	normoxia	hypoxia	661.039	5337.78
cpar2_804750	contig005807	normoxia	hypoxia	39.4304	307.941
cpar2_503990	contig006139	normoxia	hypoxia	1936.35	14843.3
cpar2_402940	contig006372	normoxia	hypoxia	715.993	5328.62
cpar2_602950	contig005504	normoxia	hypoxia	10150	72766
cpar2_201490	contig005809	normoxia	hypoxia	324.933	2300.7
cpar2_400770	contig006372	normoxia	hypoxia	35.3708	249.658
cpar2_108000	contig005569	normoxia	hypoxia	125.606	878.755
cpar2_105270	contig005569	normoxia	hypoxia	70.6406	489.972
cpar2_205500	contig005809	normoxia	hypoxia	51.0879	348.424
cpar2_212210	contig005809	normoxia	hypoxia	348.182	2345.66
cpar2_800230	contig005807	normoxia	hypoxia	61.3887	404.761

cpar2_209460	contig005809 normoxia hypoxia	1989.03	12926
cpar2_301300	contig005806 normoxia hypoxia	95.6978	596.247
cpar2_405010	contig006372 normoxia hypoxia	1595.1	9927.91
cpar2_405780	contig006372 normoxia hypoxia	270.246	1669.26
cpar2_503040	contig006139 normoxia hypoxia	135.827	826.585
cpar2_403180	contig006372 normoxia hypoxia	1747.64	10608.7
cpar2_404310	contig006372 normoxia hypoxia	548.238	3293.24
cpar2_108280	contig005569 normoxia hypoxia	777.556	4517.09
cpar2_701390	contig006110 normoxia hypoxia	217.858	1262.2
cpar2_807600	contig005807 normoxia hypoxia	33.2561	190.852
cpar2_503690	contig006139 normoxia hypoxia	238.058	1361.79
cpar2_704060	contig006110 normoxia hypoxia	104.868	597.662
cpar2_301390	contig005806 normoxia hypoxia	33.5799	188.508
cpar2_808410	contig005807 normoxia hypoxia	32.0137	170.261
cpar2_400570	contig006372 normoxia hypoxia	288.037	1524.68
cpar2_109500	contig005569 normoxia hypoxia	99.8157	523.037
cpar2_405900	contig006372 normoxia hypoxia	332.864	1719.52
cpar2_807040	contig005807 normoxia hypoxia	149.559	770.558
cpar2_101870	contig005569 normoxia hypoxia	233.468	1197.48
cpar2_304060	contig005806 normoxia hypoxia	873.921	4469.18
cpar2_405810	contig006372 normoxia hypoxia	683.813	3471.25
cpar2_211810	contig005809 normoxia hypoxia	9476.58	47541.8
cpar2_302890	contig005806 normoxia hypoxia	137.265	687.477
cpar2_800020	contig005807 normoxia hypoxia	157.771	789.253
cpar2_807230	contig005807 normoxia hypoxia	24.9205	124.378
cpar2_702400	contig006110 normoxia hypoxia	5033.14	25059.6
cpar2_102550	contig005569 normoxia hypoxia	85.7988	425.242
cpar2_700380	contig006110 normoxia hypoxia	2270.37	11026.2
cpar2_701130	contig006110 normoxia hypoxia	63.11	305.205
cpar2_804260	contig005807 normoxia hypoxia	229.65	1109.42
cpar2_401110	contig006372 normoxia hypoxia	38.4445	184.479
cpar2_106140	contig005569 normoxia hypoxia	1439.61	6835.67
cpar2_601230	contig005504 normoxia hypoxia	232.44	1094.25
cpar2_100770	contig005569 normoxia hypoxia	992.811	4640.17
cpar2_106950	contig005569 normoxia hypoxia	680.066	3165.45
cpar2_303740	contig005806 normoxia hypoxia	1687.47	7822.38
cpar2_103400	contig005569 normoxia hypoxia	258.183	1193.25
cpar2_500880	contig006139 normoxia hypoxia	71.0884	328.253
cpar2_401550	contig006372 normoxia hypoxia	112.863	519.018
cpar2_806400	contig005807 normoxia hypoxia	89.296	406.3
cpar2_703370	contig006110 normoxia hypoxia	111.15	502.229
cpar2_804060	contig005807 normoxia hypoxia	3027.36	13465.2
cpar2_103450	contig005569 normoxia hypoxia	5820.15	25732.2
cpar2_201370	contig005809 normoxia hypoxia	804.113	3530.22
cpar2_807620	contig005807 normoxia hypoxia	193.983	848.022
cpar2_805790	contig005807 normoxia hypoxia	159.397	691.952

cpar2_807980	contig005807 normoxia hypoxia	10055.7	43410.8
cpar2_807720	contig005807 normoxia hypoxia	131.835	563.312
cpar2_101620	contig005569 normoxia hypoxia	1414.32	6008.59
cpar2_207210	contig005809 normoxia hypoxia	19327.4	81923.2
cpar2_703940	contig006110 normoxia hypoxia	457.762	1939.29
cpar2_701420	contig006110 normoxia hypoxia	51.3913	215.344
cpar2_109780	contig005569 normoxia hypoxia	254.712	1052.71
cpar2_300740	contig005806 normoxia hypoxia	94.7451	391.244
cpar2_402710	contig006372 normoxia hypoxia	76.0894	313.868
cpar2_804310	contig005807 normoxia hypoxia	243.395	1002.39
cpar2_702980	contig006110 normoxia hypoxia	55.0152	225.639
cpar2_300730	contig005806 normoxia hypoxia	37.965	155.132
cpar2_602940	contig005504 normoxia hypoxia	99.4443	405.328
cpar2_104530	contig005569 normoxia hypoxia	55.23	224.185
cpar2_200280	contig005809 normoxia hypoxia	2894.19	11723.4
cpar2_407170	contig006372 normoxia hypoxia	1122.69	4522.34
cpar2_304120	contig005806 normoxia hypoxia	124.975	499.7
cpar2_401230	contig006372 normoxia hypoxia	16726	66339.8
cpar2_101860	contig005569 normoxia hypoxia	49.505	195.112
cpar2_211260	contig005809 normoxia hypoxia	53.6371	205.708
cpar2_601530	contig005504 normoxia hypoxia	350.598	1343.47
cpar2_209240	contig005809 normoxia hypoxia	5086.82	19472.2
cpar2_106260	contig005569 normoxia hypoxia	315.67	1206.72
cpar2_800220	contig005807 normoxia hypoxia	1239.69	4728.51
cpar2_211400	contig005809 normoxia hypoxia	259.315	986.33
cpar2_211270	contig005809 normoxia hypoxia	183.872	698.262
cpar2_105550	contig005569 normoxia hypoxia	742.481	2800.76
cpar2_106960	contig005569 normoxia hypoxia	3230.3	12174.2
cpar2_808670	contig005807 normoxia hypoxia	42676	159891
cpar2_207780	contig005809 normoxia hypoxia	356.61	1331.89
cpar2_403820	contig006372 normoxia hypoxia	28.242	104.77
cpar2_802000	contig005807 normoxia hypoxia	80.8028	297.149
cpar2_201200	contig005809 normoxia hypoxia	149.441	545.133
cpar2_204880	contig005809 normoxia hypoxia	2871.05	10436.9
cpar2_101480	contig005569 normoxia hypoxia	670.466	2435.84
cpar2_804740	contig005807 normoxia hypoxia	5602.62	20315.3
cpar2_808380	contig005807 normoxia hypoxia	106.967	386.784
cpar2_209770	contig005809 normoxia hypoxia	245.774	884.91
cpar2_802070	contig005807 normoxia hypoxia	33.284	114.158
cpar2_400970	contig006372 normoxia hypoxia	2561.45	8773.56
cpar2_204260	contig005809 normoxia hypoxia	1437.44	4872.49
cpar2_210880	contig005809 normoxia hypoxia	119.268	399.667
cpar2_700580	contig006110 normoxia hypoxia	340.359	1139.61
cpar2_808820	contig005807 normoxia hypoxia	358.93	1196.46
cpar2_100870	contig005569 normoxia hypoxia	66.6701	220.743
cpar2_206020	contig005809 normoxia hypoxia	10229.3	33840.9

cpar2_105690	contig005569 normoxia	hypoxia	85.1455	281.096
cpar2_101670	contig005569 normoxia	hypoxia	3189.24	10443.1
cpar2_704260	contig006110 normoxia	hypoxia	408.351	1333.57
cpar2_101230	contig005569 normoxia	hypoxia	811.234	2639.27
cpar2_206900	contig005809 normoxia	hypoxia	4268.91	13881.8
cpar2_301310	contig005806 normoxia	hypoxia	79.7245	258.36
cpar2_502980	contig006139 normoxia	hypoxia	405.415	1308.98
cpar2_808510	contig005807 normoxia	hypoxia	149.829	482.627
cpar2_201730	contig005809 normoxia	hypoxia	106.867	342.476
cpar2_102080	contig005569 normoxia	hypoxia	398.569	1274.62
cpar2_211700	contig005809 normoxia	hypoxia	614.16	1957.12
cpar2_803890	contig005807 normoxia	hypoxia	305.565	973.694
cpar2_404780	contig006372 normoxia	hypoxia	39.6992	125.979
cpar2_503420	contig006139 normoxia	hypoxia	237.135	751.81
cpar2_407270	contig006372 normoxia	hypoxia	52.0313	164.562
cpar2_501170	contig006139 normoxia	hypoxia	1222.61	3854.89
cpar2_502580	contig006139 normoxia	hypoxia	29190.4	91138.3
cpar2_210480	contig005809 normoxia	hypoxia	1563.06	4867.44
cpar2_808070	contig005807 normoxia	hypoxia	36.072	112.186
cpar2_807400	contig005807 normoxia	hypoxia	3006.67	9304.12
cpar2_302650	contig005806 normoxia	hypoxia	2862.07	8848.21
cpar2_803600	contig005807 normoxia	hypoxia	160.724	494.465
cpar2_600530	contig005504 normoxia	hypoxia	362.414	1114.72
cpar2_101070	contig005569 normoxia	hypoxia	2255.28	6866.8
cpar2_502810	contig006139 normoxia	hypoxia	2622.92	7951.8
cpar2_108370	contig005569 normoxia	hypoxia	408.349	1235.72
cpar2_104660	contig005569 normoxia	hypoxia	49.3679	149.13
cpar2_601670	contig005504 normoxia	hypoxia	999.744	3012.45
cpar2_203520	contig005809 normoxia	hypoxia	5901.09	17763.4
cpar2_802660	contig005807 normoxia	hypoxia	90.9252	273.378
cpar2_405360	contig006372 normoxia	hypoxia	170.555	512.634
cpar2_601780	contig005504 normoxia	hypoxia	107.251	320.879
cpar2_300190	contig005806 normoxia	hypoxia	126.663	378.773
cpar2_202420	contig005809 normoxia	hypoxia	100.656	299.734
cpar2_602260	contig005504 normoxia	hypoxia	2089.89	6217.83
cpar2_701650	contig006110 normoxia	hypoxia	86.3528	256.881
cpar2_400130	contig006372 normoxia	hypoxia	388.209	1150.96
cpar2_802250	contig005807 normoxia	hypoxia	1185.89	3513.81
cpar2_106080	contig005569 normoxia	hypoxia	1187.2	3514.42
cpar2_402140	contig006372 normoxia	hypoxia	94.1716	278.215
cpar2_400960	contig006372 normoxia	hypoxia	224.312	661.418
cpar2_212810	contig005809 normoxia	hypoxia	1807.09	5314.98
cpar2_808660	contig005807 normoxia	hypoxia	743.701	2176.22
cpar2_603150	contig005504 normoxia	hypoxia	558.842	1634.8
cpar2_100530	contig005569 normoxia	hypoxia	1001.07	2923.22
cpar2_208800	contig005809 normoxia	hypoxia	1339.34	3907.31

cpar2_109870	contig005569 normoxia hypoxia	506.784	1470.71
cpar2_204420	contig005809 normoxia hypoxia	162.613	471.402
cpar2_301770	contig005806 normoxia hypoxia	828.586	2382.45
cpar2_703570	contig006110 normoxia hypoxia	102.561	291.447
cpar2_808750	contig005807 normoxia hypoxia	2214.5	6289.25
cpar2_106620	contig005569 normoxia hypoxia	150.363	426.192
cpar2_105770	contig005569 normoxia hypoxia	264.258	747.995
cpar2_701400	contig006110 normoxia hypoxia	1258.61	3561.05
cpar2_703970	contig006110 normoxia hypoxia	1154.21	3255.23
cpar2_213720	contig005809 normoxia hypoxia	438.338	1233.78
cpar2_603730	contig005504 normoxia hypoxia	306.936	856.359
cpar2_800050	contig005807 normoxia hypoxia	64.9692	180.845
cpar2_102970	contig005569 normoxia hypoxia	219.104	606.941
cpar2_208010	contig005809 normoxia hypoxia	440.633	1218.52
cpar2_406710	contig006372 normoxia hypoxia	336.59	930.174
cpar2_807710	contig005807 normoxia hypoxia	107.263	295.661
cpar2_502820	contig006139 normoxia hypoxia	223.04	614.355
cpar2_401470	contig006372 normoxia hypoxia	161.175	443.888
cpar2_301610	contig005806 normoxia hypoxia	582.669	1583.62
cpar2_703030	contig006110 normoxia hypoxia	2033.9	5506.84
cpar2_100920	contig005569 normoxia hypoxia	388.435	1049.9
cpar2_103000	contig005569 normoxia hypoxia	648.176	1744.1
cpar2_500390	contig006139 normoxia hypoxia	2282.92	6131.8
cpar2_808490	contig005807 normoxia hypoxia	1403.41	3748.13
cpar2_210410	contig005809 normoxia hypoxia	244.535	651.06
cpar2_703580	contig006110 normoxia hypoxia	69.6394	185.383
cpar2_800630	contig005807 normoxia hypoxia	177.79	473.275
cpar2_406760	contig006372 normoxia hypoxia	1105.09	2939.94
cpar2_407080	contig006372 normoxia hypoxia	129.369	343.864
cpar2_109770	contig005569 normoxia hypoxia	172.055	455.636
cpar2_301660	contig005806 normoxia hypoxia	227.067	601.175
cpar2_100090	contig005569 normoxia hypoxia	404.725	1071.01
cpar2_603350	contig005504 normoxia hypoxia	677.383	1786.59
cpar2_701830	contig006110 normoxia hypoxia	421.324	1107.32
cpar2_203580	contig005809 normoxia hypoxia	136.754	357.721
cpar2_110070	contig005569 normoxia hypoxia	293.73	766.701
cpar2_200170	contig005809 normoxia hypoxia	247.28	644.729
cpar2_404240	contig006372 normoxia hypoxia	3947.91	10284.9
cpar2_205820	contig005809 normoxia hypoxia	129.491	336.423
cpar2_109160	contig005569 normoxia hypoxia	160.898	415.848
cpar2_201500	contig005809 normoxia hypoxia	55.6263	143.724
cpar2_105130	contig005569 normoxia hypoxia	318.208	819.674
cpar2_602050	contig005504 normoxia hypoxia	215.919	554.998
cpar2_104190	contig005569 normoxia hypoxia	813.871	2086.04
cpar2_211650	contig005809 normoxia hypoxia	34.6462	88.732
cpar2_703710	contig006110 normoxia hypoxia	581.741	1482.31

cpar2_101330	contig005569 normoxia	hypoxia	304.63	774.399
cpar2_102630	contig005569 normoxia	hypoxia	97.2581	246.622
cpar2_406820	contig006372 normoxia	hypoxia	137.659	348.88
cpar2_807310	contig005807 normoxia	hypoxia	689.666	1744.52
cpar2_212140	contig005809 normoxia	hypoxia	157.979	398.427
cpar2_209600	contig005809 normoxia	hypoxia	313.882	788.083
cpar2_804730	contig005807 normoxia	hypoxia	151.126	377.929
cpar2_106650	contig005569 normoxia	hypoxia	295.905	733.838
cpar2_212780	contig005809 normoxia	hypoxia	292.692	725.092
cpar2_205560	contig005809 normoxia	hypoxia	152.127	376.84
cpar2_700920	contig006110 normoxia	hypoxia	48.5827	120.086
cpar2_801560	contig005807 normoxia	hypoxia	336.395	831.353
cpar2_405150	contig006372 normoxia	hypoxia	414.261	1021.32
cpar2_202120	contig005809 normoxia	hypoxia	152.44	374.635
cpar2_405830	contig006372 normoxia	hypoxia	386.192	948.345
cpar2_207280	contig005809 normoxia	hypoxia	467.544	1148.09
cpar2_703300	contig006110 normoxia	hypoxia	3915.13	9568.33
cpar2_209840	contig005809 normoxia	hypoxia	151.916	370.362
cpar2_213920	contig005809 normoxia	hypoxia	103.174	250.158
cpar2_109530	contig005569 normoxia	hypoxia	1062.44	2550.49
cpar2_109030	contig005569 normoxia	hypoxia	167.091	401.03
cpar2_804900	contig005807 normoxia	hypoxia	941.204	2251.85
cpar2_210470	contig005809 normoxia	hypoxia	251.442	601.17
cpar2_201540	contig005809 normoxia	hypoxia	127.985	305.808
cpar2_703040	contig006110 normoxia	hypoxia	124.844	296.84
cpar2_402160	contig006372 normoxia	hypoxia	387.381	916.021
cpar2_301800	contig005806 normoxia	hypoxia	287.268	677.247
cpar2_106210	contig005569 normoxia	hypoxia	450.984	1060.23
cpar2_101880	contig005569 normoxia	hypoxia	220.427	517.82
cpar2_401990	contig006372 normoxia	hypoxia	88.8206	208.317
cpar2_502100	contig006139 normoxia	hypoxia	257.053	602.147
cpar2_803840	contig005807 normoxia	hypoxia	2157.04	5052.4
cpar2_206270	contig005809 normoxia	hypoxia	694.174	1623.41
cpar2_602960	contig005504 normoxia	hypoxia	1176.82	2737.43
cpar2_105460	contig005569 normoxia	hypoxia	171.135	397.837
cpar2_407410	contig006372 normoxia	hypoxia	1872.47	4350.97
cpar2_200120	contig005809 normoxia	hypoxia	2077.52	4802.35
cpar2_208240	contig005809 normoxia	hypoxia	65.9288	152.336
cpar2_201240	contig005809 normoxia	hypoxia	196.169	453.197
cpar2_302800	contig005806 normoxia	hypoxia	1180.94	2726.92
cpar2_200790	contig005809 normoxia	hypoxia	91.2239	210.523
cpar2_101910	contig005569 normoxia	hypoxia	50.2485	115.905
cpar2_805890	contig005807 normoxia	hypoxia	145.384	334.838
cpar2_102830	contig005569 normoxia	hypoxia	3038.48	6992.56
cpar2_200640	contig005809 normoxia	hypoxia	890.909	2047.56
cpar2_301020	contig005806 normoxia	hypoxia	165.436	380.054

cpar2_407750	contig006372 normoxia hypoxia	441.666	1012.61
cpar2_105300	contig005569 normoxia hypoxia	1453.5	3329.63
cpar2_808260	contig005807 normoxia hypoxia	1926.65	4400.81
cpar2_106000	contig005569 normoxia hypoxia	81.0655	184.772
cpar2_105760	contig005569 normoxia hypoxia	52.2923	118.896
cpar2_702060	contig006110 normoxia hypoxia	68.0816	154.6
cpar2_806500	contig005807 normoxia hypoxia	247.083	560.705
cpar2_702390	contig006110 normoxia hypoxia	1064.34	2410.58
cpar2_807240	contig005807 normoxia hypoxia	42.2706	95.0904
cpar2_110330	contig005569 normoxia hypoxia	727.957	1636.31
cpar2_207460	contig005809 normoxia hypoxia	204.836	459.421
cpar2_203540	contig005809 normoxia hypoxia	65.4024	146.61
cpar2_101350	contig005569 normoxia hypoxia	1420.76	3184.52
cpar2_403550	contig006372 normoxia hypoxia	151.189	338.54
cpar2_402830	contig006372 normoxia hypoxia	689.686	1544.04
cpar2_205350	contig005809 normoxia hypoxia	90.7252	202.756
cpar2_203720	contig005809 normoxia hypoxia	94.1678	210.448
cpar2_202280	contig005809 normoxia hypoxia	379.191	845.362
cpar2_212450	contig005809 normoxia hypoxia	180.705	402.545
cpar2_805040	contig005807 normoxia hypoxia	1010.23	2247.42
cpar2_403640	contig006372 normoxia hypoxia	77.0575	171.123
cpar2_801030	contig005807 normoxia hypoxia	266.557	590.666
cpar2_703660	contig006110 normoxia hypoxia	350.316	775.071
cpar2_407910	contig006372 normoxia hypoxia	224.347	494.487
cpar2_805300	contig005807 normoxia hypoxia	425.651	935.876
cpar2_204970	contig005809 normoxia hypoxia	206.256	453.417
cpar2_202130	contig005809 normoxia hypoxia	398.569	875.525
cpar2_700310	contig006110 normoxia hypoxia	281.566	617.305
cpar2_800970	contig005807 normoxia hypoxia	2130.88	4666.21
cpar2_806490	contig005807 normoxia hypoxia	1447.34	3166.51
cpar2_212180	contig005809 normoxia hypoxia	150.965	329.645
cpar2_406510	contig006372 normoxia hypoxia	87.052	189.968
cpar2_808740	contig005807 normoxia hypoxia	167.602	364.119
cpar2_501020	contig006139 normoxia hypoxia	25153.2	54456.7
cpar2_301150	contig005806 normoxia hypoxia	696.743	1503.21
cpar2_603420	contig005504 normoxia hypoxia	475.255	1022.49
cpar2_211790	contig005809 normoxia hypoxia	140.057	300.476
cpar2_803760	contig005807 normoxia hypoxia	317.566	680.93
cpar2_803110	contig005807 normoxia hypoxia	234.634	502.601
cpar2_304210	contig005806 normoxia hypoxia	472.974	1007.91
cpar2_213670	contig005809 normoxia hypoxia	445.816	947.934
cpar2_800860	contig005807 normoxia hypoxia	1140.78	2418.42
cpar2_500820	contig006139 normoxia hypoxia	49.0079	103.819
cpar2_602730	contig005504 normoxia hypoxia	677.242	1434.44
cpar2_211730	contig005809 normoxia hypoxia	552.776	1170.4
cpar2_302990	contig005806 normoxia hypoxia	11148.6	23579.9

cpar2_203590	contig005809 normoxia hypoxia	110.751	233.649
cpar2_600610	contig005504 normoxia hypoxia	324.389	684.208
cpar2_107310	contig005569 normoxia hypoxia	181.337	381.924
cpar2_805400	contig005807 normoxia hypoxia	50.0619	105.382
cpar2_800610	contig005807 normoxia hypoxia	184.405	388.017
cpar2_406050	contig006372 normoxia hypoxia	970.114	2038.84
cpar2_801500	contig005807 normoxia hypoxia	57.3608	120.412
cpar2_205030	contig005809 normoxia hypoxia	762.73	1599.61
cpar2_108720	contig005569 normoxia hypoxia	677.7	1421.21
cpar2_202450	contig005809 normoxia hypoxia	106.901	223.815
cpar2_806350	contig005807 normoxia hypoxia	177.129	370.429
cpar2_601770	contig005504 normoxia hypoxia	1098.72	2295.25
cpar2_103490	contig005569 normoxia hypoxia	266.401	556.349
cpar2_103480	contig005569 normoxia hypoxia	191.946	400.795
cpar2_104460	contig005569 normoxia hypoxia	442.143	922.305
cpar2_807180	contig005807 normoxia hypoxia	134.552	280.498
cpar2_700390	contig006110 normoxia hypoxia	57.7453	119.862
cpar2_500680	contig006139 normoxia hypoxia	200.953	417.032
cpar2_601480	contig005504 normoxia hypoxia	247.556	511.226
cpar2_200980	contig005809 normoxia hypoxia	42.4994	87.7444
cpar2_205570	contig005809 normoxia hypoxia	196.348	405.311
cpar2_211130	contig005809 normoxia hypoxia	164.055	338.034
cpar2_805590	contig005807 normoxia hypoxia	1702.2	3504.62
cpar2_700910	contig006110 normoxia hypoxia	526.776	1082.37
cpar2_202600	contig005809 normoxia hypoxia	5036.71	10329.8
cpar2_801070	contig005807 normoxia hypoxia	97.4518	199.443
cpar2_803870	contig005807 normoxia hypoxia	104.894	214.508
cpar2_600870	contig005504 normoxia hypoxia	126.171	257.81
cpar2_101160	contig005569 normoxia hypoxia	1179.26	2408.71
cpar2_702150	contig006110 normoxia hypoxia	556.769	1135.58
cpar2_100780	contig005569 normoxia hypoxia	2546.65	5163.19
cpar2_204160	contig005809 normoxia hypoxia	1881.93	3814.91
cpar2_108910	contig005569 normoxia hypoxia	157.172	318.389
cpar2_212900	contig005809 normoxia hypoxia	799.523	1618.75
cpar2_102250	contig005569 normoxia hypoxia	130.869	263.378
cpar2_800690	contig005807 normoxia hypoxia	85.2185	171.377
cpar2_200460	contig005809 normoxia hypoxia	112.858	226.7
cpar2_203890	contig005809 normoxia hypoxia	48.6734	97.642
cpar2_214160	contig005809 normoxia hypoxia	244.405	490.09
cpar2_406140	contig006372 normoxia hypoxia	111.21	222.707
cpar2_402200	contig006372 normoxia hypoxia	1796.86	3593.46
cpar2_208360	contig005809 normoxia hypoxia	1913.35	3815.88
cpar2_304320	contig005806 normoxia hypoxia	449.253	225.254
cpar2_801670	contig005807 normoxia hypoxia	213.965	107.259
cpar2_107090	contig005569 normoxia hypoxia	9132.37	4576.5
cpar2_100740	contig005569 normoxia hypoxia	107.459	53.7475

cpar2_504170	contig006139 normoxia hypoxia	16851.7	8422.51
cpar2_406360	contig006372 normoxia hypoxia	266.614	133.232
cpar2_603600	contig005504 normoxia hypoxia	766.574	382.976
cpar2_405310	contig006372 normoxia hypoxia	13474	6729.04
cpar2_504110	contig006139 normoxia hypoxia	167.14	83.4097
cpar2_804630	contig005807 normoxia hypoxia	274.622	136.75
cpar2_107150	contig005569 normoxia hypoxia	231.37	115.1
cpar2_404000	contig006372 normoxia hypoxia	143.931	71.5676
cpar2_805560	contig005807 normoxia hypoxia	837.353	416.131
cpar2_602180	contig005504 normoxia hypoxia	192.414	95.5529
cpar2_104690	contig005569 normoxia hypoxia	4170.87	2071.15
cpar2_202560	contig005809 normoxia hypoxia	548.328	272.123
cpar2_803590	contig005807 normoxia hypoxia	1251	620.472
cpar2_503100	contig006139 normoxia hypoxia	79.8966	39.5531
cpar2_800470	contig005807 normoxia hypoxia	5567.94	2755.41
cpar2_400090	contig006372 normoxia hypoxia	84.35	41.668
cpar2_603240	contig005504 normoxia hypoxia	392.183	193.641
cpar2_502910	contig006139 normoxia hypoxia	440.37	217.34
cpar2_109630	contig005569 normoxia hypoxia	17901.2	8827.28
cpar2_407770	contig006372 normoxia hypoxia	3503.39	1724.39
cpar2_400810	contig006372 normoxia hypoxia	1537.44	756.655
cpar2_407650	contig006372 normoxia hypoxia	389.032	191.395
cpar2_407520	contig006372 normoxia hypoxia	1371.49	673.844
cpar2_402770	contig006372 normoxia hypoxia	3119.59	1532.69
cpar2_200930	contig005809 normoxia hypoxia	223.536	109.692
cpar2_406500	contig006372 normoxia hypoxia	2034.82	997.162
cpar2_807770	contig005807 normoxia hypoxia	635.217	311.252
cpar2_406020	contig006372 normoxia hypoxia	348.679	170.573
cpar2_501650	contig006139 normoxia hypoxia	462.293	226.141
cpar2_703920	contig006110 normoxia hypoxia	303.64	148.471
cpar2_102390	contig005569 normoxia hypoxia	154.82	75.6906
cpar2_204170	contig005809 normoxia hypoxia	345.418	168.855
cpar2_109420	contig005569 normoxia hypoxia	3893.33	1902.37
cpar2_400800	contig006372 normoxia hypoxia	3871.09	1891.46
cpar2_500300	contig006139 normoxia hypoxia	109.238	53.3577
cpar2_700990	contig006110 normoxia hypoxia	56.963	27.774
cpar2_502070	contig006139 normoxia hypoxia	309.662	150.862
cpar2_402380	contig006372 normoxia hypoxia	423.485	206.234
cpar2_102840	contig005569 normoxia hypoxia	13699.4	6657.7
cpar2_303730	contig005806 normoxia hypoxia	932.223	452.915
cpar2_502040	contig006139 normoxia hypoxia	945.271	458.478
cpar2_502390	contig006139 normoxia hypoxia	566.056	274.186
cpar2_303610	contig005806 normoxia hypoxia	98.9827	47.8698
cpar2_400480	contig006372 normoxia hypoxia	176.745	85.4476
cpar2_102660	contig005569 normoxia hypoxia	491.666	237.387
cpar2_208140	contig005809 normoxia hypoxia	328.853	158.681

cpar2_205320	contig005809 normoxia hypoxia	292.332	140.959
cpar2_602850	contig005504 normoxia hypoxia	9104.99	4387.67
cpar2_205980	contig005809 normoxia hypoxia	175.321	84.426
cpar2_210770	contig005809 normoxia hypoxia	802.12	385.938
cpar2_303030	contig005806 normoxia hypoxia	638.972	306.762
cpar2_704040	contig006110 normoxia hypoxia	950.596	455.899
cpar2_502520	contig006139 normoxia hypoxia	312.612	149.626
cpar2_703410	contig006110 normoxia hypoxia	1675.03	800.766
cpar2_303870	contig005806 normoxia hypoxia	572.769	273.056
cpar2_108460	contig005569 normoxia hypoxia	2080.2	991.342
cpar2_803400	contig005807 normoxia hypoxia	16916.8	8061.74
cpar2_602170	contig005504 normoxia hypoxia	399.562	189.92
cpar2_105340	contig005569 normoxia hypoxia	10096.2	4791.53
cpar2_101280	contig005569 normoxia hypoxia	852.465	404.453
cpar2_205700	contig005809 normoxia hypoxia	4987.22	2360.69
cpar2_806340	contig005807 normoxia hypoxia	165.089	78.1032
cpar2_302210	contig005806 normoxia hypoxia	347.214	163.583
cpar2_100130	contig005569 normoxia hypoxia	1538.51	724.049
cpar2_404830	contig006372 normoxia hypoxia	330.002	155.248
cpar2_210360	contig005809 normoxia hypoxia	1541.45	724.748
cpar2_807560	contig005807 normoxia hypoxia	16328.3	7674.33
cpar2_406640	contig006372 normoxia hypoxia	1104.31	518.882
cpar2_207910	contig005809 normoxia hypoxia	16049.5	7533.51
cpar2_210540	contig005809 normoxia hypoxia	17124.4	8033.77
cpar2_211390	contig005809 normoxia hypoxia	17071	8007.28
cpar2_203050	contig005809 normoxia hypoxia	80.2002	37.5457
cpar2_205470	contig005809 normoxia hypoxia	185.903	86.7835
cpar2_102040	contig005569 normoxia hypoxia	915.441	427.216
cpar2_603140	contig005504 normoxia hypoxia	3461.33	1614.92
cpar2_100560	contig005569 normoxia hypoxia	686.753	320.332
cpar2_102800	contig005569 normoxia hypoxia	2146.85	998.729
cpar2_100630	contig005569 normoxia hypoxia	166.318	77.1968
cpar2_107550	contig005569 normoxia hypoxia	357.498	165.73
cpar2_303100	contig005806 normoxia hypoxia	5126.31	2375.99
cpar2_210180	contig005809 normoxia hypoxia	1185.63	548.891
cpar2_213610	contig005809 normoxia hypoxia	377.452	174.306
cpar2_501280	contig006139 normoxia hypoxia	258.623	119.358
cpar2_805920	contig005807 normoxia hypoxia	1594.73	735.029
cpar2_400700	contig006372 normoxia hypoxia	413.059	190.258
cpar2_202080	contig005809 normoxia hypoxia	1062.8	489.212
cpar2_100240	contig005569 normoxia hypoxia	410.431	188.744
cpar2_702190	contig006110 normoxia hypoxia	1058.72	486.82
cpar2_207420	contig005809 normoxia hypoxia	146.99	67.5769
cpar2_204030	contig005809 normoxia hypoxia	914.205	420.235
cpar2_602130	contig005504 normoxia hypoxia	911.207	418.211
cpar2_402680	contig006372 normoxia hypoxia	1327.12	608.169

cpar2_402550	contig006372 normoxia	hypoxia	581.42	266.351
cpar2_500810	contig006139 normoxia	hypoxia	1527.4	698.834
cpar2_102440	contig005569 normoxia	hypoxia	786.832	359.54
cpar2_208030	contig005809 normoxia	hypoxia	263.707	120.456
cpar2_210200	contig005809 normoxia	hypoxia	132.05	60.2692
cpar2_108650	contig005569 normoxia	hypoxia	739.008	337.15
cpar2_208660	contig005809 normoxia	hypoxia	641.008	292.333
cpar2_105980	contig005569 normoxia	hypoxia	21715	9901.6
cpar2_109940	contig005569 normoxia	hypoxia	725.957	330.456
cpar2_302860	contig005806 normoxia	hypoxia	255.503	116.266
cpar2_109150	contig005569 normoxia	hypoxia	5428.59	2468.61
cpar2_405750	contig006372 normoxia	hypoxia	184.705	83.9061
cpar2_407620	contig006372 normoxia	hypoxia	199.687	90.6403
cpar2_202020	contig005809 normoxia	hypoxia	321.906	146.01
cpar2_208250	contig005809 normoxia	hypoxia	229.892	104.248
cpar2_212750	contig005809 normoxia	hypoxia	1308.15	591.934
cpar2_103270	contig005569 normoxia	hypoxia	184.67	83.4677
cpar2_302680	contig005806 normoxia	hypoxia	117.076	52.8712
cpar2_104370	contig005569 normoxia	hypoxia	16655.5	7520.2
cpar2_600780	contig005504 normoxia	hypoxia	427.645	192.775
cpar2_701710	contig006110 normoxia	hypoxia	222.009	99.8857
cpar2_404470	contig006372 normoxia	hypoxia	622.362	279.485
cpar2_801570	contig005807 normoxia	hypoxia	1533.92	688.701
cpar2_503970	contig006139 normoxia	hypoxia	630.506	282.532
cpar2_200010	contig005809 normoxia	hypoxia	145.998	65.4066
cpar2_301970	contig005806 normoxia	hypoxia	151.417	67.7531
cpar2_802020	contig005807 normoxia	hypoxia	334.594	149.557
cpar2_800990	contig005807 normoxia	hypoxia	1467.75	654.816
cpar2_106380	contig005569 normoxia	hypoxia	302.931	134.934
cpar2_503980	contig006139 normoxia	hypoxia	202.894	90.1284
cpar2_304310	contig005806 normoxia	hypoxia	26562.1	11790.4
cpar2_109370	contig005569 normoxia	hypoxia	940.916	417.116
cpar2_803580	contig005807 normoxia	hypoxia	695.701	308.162
cpar2_209350	contig005809 normoxia	hypoxia	2228.67	987.089
cpar2_209130	contig005809 normoxia	hypoxia	502.893	222.716
cpar2_109170	contig005569 normoxia	hypoxia	20592.8	9109.49
cpar2_103420	contig005569 normoxia	hypoxia	430.937	190.214
cpar2_102730	contig005569 normoxia	hypoxia	132.24	58.3673
cpar2_401360	contig006372 normoxia	hypoxia	132.786	58.5984
cpar2_501830	contig006139 normoxia	hypoxia	891.097	392.925
cpar2_500690	contig006139 normoxia	hypoxia	312.478	137.587
cpar2_101210	contig005569 normoxia	hypoxia	1338.28	588.962
cpar2_406240	contig006372 normoxia	hypoxia	839.251	369.062
cpar2_302160	contig005806 normoxia	hypoxia	19034.4	8370.3
cpar2_301550	contig005806 normoxia	hypoxia	107.905	47.2501
cpar2_801050	contig005807 normoxia	hypoxia	601.425	262.994

cpar2_703120	contig006110 normoxia hypoxia	124.391	54.3379
cpar2_402320	contig006372 normoxia hypoxia	169.594	73.7143
cpar2_302420	contig005806 normoxia hypoxia	604.547	262.399
cpar2_701770	contig006110 normoxia hypoxia	786.013	339.84
cpar2_701820	contig006110 normoxia hypoxia	14723.5	6351.75
cpar2_407920	contig006372 normoxia hypoxia	2254.15	971.371
cpar2_401120	contig006372 normoxia hypoxia	370.096	158.987
cpar2_107880	contig005569 normoxia hypoxia	348.474	149.217
cpar2_501680	contig006139 normoxia hypoxia	9241.33	3954.44
cpar2_211150	contig005809 normoxia hypoxia	209.355	89.4749
cpar2_800380	contig005807 normoxia hypoxia	648.759	277.238
cpar2_808240	contig005807 normoxia hypoxia	471.815	201.613
cpar2_208440	contig005809 normoxia hypoxia	994.104	423.03
cpar2_600560	contig005504 normoxia hypoxia	642.358	272.922
cpar2_105960	contig005569 normoxia hypoxia	10887	4600.65
cpar2_300460	contig005806 normoxia hypoxia	280.694	118.447
cpar2_403400	contig006372 normoxia hypoxia	261.056	110.127
cpar2_100790	contig005569 normoxia hypoxia	611.082	257.768
cpar2_104970	contig005569 normoxia hypoxia	550.515	232.123
cpar2_204350	contig005809 normoxia hypoxia	89.9807	37.7831
cpar2_801880	contig005807 normoxia hypoxia	12653.3	5306.72
cpar2_203410	contig005809 normoxia hypoxia	561.341	235.351
cpar2_500490	contig006139 normoxia hypoxia	90.1911	37.7363
cpar2_107540	contig005569 normoxia hypoxia	219.842	91.8489
cpar2_500540	contig006139 normoxia hypoxia	469.769	196.007
cpar2_400470	contig006372 normoxia hypoxia	6337.26	2642.96
cpar2_300030	contig005806 normoxia hypoxia	470.927	196.105
cpar2_802160	contig005807 normoxia hypoxia	220.532	91.834
cpar2_103040	contig005569 normoxia hypoxia	1038.31	432.282
cpar2_603570	contig005504 normoxia hypoxia	743.637	309.364
cpar2_602220	contig005504 normoxia hypoxia	177.213	73.6913
cpar2_101940	contig005569 normoxia hypoxia	252.192	104.741
cpar2_601420	contig005504 normoxia hypoxia	4776.87	1983.9
cpar2_808860	contig005807 normoxia hypoxia	1497.24	620.589
cpar2_601450	contig005504 normoxia hypoxia	405.022	167.577
cpar2_104610	contig005569 normoxia hypoxia	245.904	101.734
cpar2_300240	contig005806 normoxia hypoxia	16256.9	6717.05
cpar2_105650	contig005569 normoxia hypoxia	389.523	160.091
cpar2_108800	contig005569 normoxia hypoxia	147.35	60.4732
cpar2_106320	contig005569 normoxia hypoxia	14205.3	5821.5
cpar2_302470	contig005806 normoxia hypoxia	695.033	283.967
cpar2_807690	contig005807 normoxia hypoxia	1393.99	567.871
cpar2_304180	contig005806 normoxia hypoxia	682.835	277.994
cpar2_106560	contig005569 normoxia hypoxia	2188.08	889.767
cpar2_400160	contig006372 normoxia hypoxia	66.5819	27.0321
cpar2_702900	contig006110 normoxia hypoxia	483.331	194.896

cpar2_300620	contig005806 normoxia hypoxia	318.987	128.626
cpar2_802740	contig005807 normoxia hypoxia	456.259	183.61
cpar2_213170	contig005809 normoxia hypoxia	2667.53	1069.57
cpar2_103330	contig005569 normoxia hypoxia	165.79	66.2109
cpar2_108100	contig005569 normoxia hypoxia	1118.96	446.568
cpar2_109290	contig005569 normoxia hypoxia	924.107	368.015
cpar2_106990	contig005569 normoxia hypoxia	116.975	46.3751
cpar2_700400	contig006110 normoxia hypoxia	933.19	369.362
cpar2_102810	contig005569 normoxia hypoxia	1010.66	399.738
cpar2_301560	contig005806 normoxia hypoxia	908.025	356.585
cpar2_110080	contig005569 normoxia hypoxia	671.994	262.917
cpar2_211970	contig005809 normoxia hypoxia	1659.14	648.948
cpar2_200870	contig005809 normoxia hypoxia	739.588	288.392
cpar2_106430	contig005569 normoxia hypoxia	218.493	85.0827
cpar2_107920	contig005569 normoxia hypoxia	1405.6	545.953
cpar2_206430	contig005809 normoxia hypoxia	895.811	347.21
cpar2_404080	contig006372 normoxia hypoxia	195.913	75.9206
cpar2_601570	contig005504 normoxia hypoxia	1334.88	516.566
cpar2_104130	contig005569 normoxia hypoxia	5019.26	1942.19
cpar2_807840	contig005807 normoxia hypoxia	738.377	285.073
cpar2_703850	contig006110 normoxia hypoxia	1795.44	692.225
cpar2_107970	contig005569 normoxia hypoxia	1522.42	585.936
cpar2_101990	contig005569 normoxia hypoxia	429.582	165.298
cpar2_400600	contig006372 normoxia hypoxia	1651.07	635.188
cpar2_210320	contig005809 normoxia hypoxia	1252.95	480.865
cpar2_602580	contig005504 normoxia hypoxia	18479.2	7090.27
cpar2_302480	contig005806 normoxia hypoxia	1799.75	686.712
cpar2_702010	contig006110 normoxia hypoxia	450.177	171.731
cpar2_110140	contig005569 normoxia hypoxia	724.762	275.633
cpar2_803150	contig005807 normoxia hypoxia	5161.5	1962.06
cpar2_807830	contig005807 normoxia hypoxia	179.189	67.9972
cpar2_701010	contig006110 normoxia hypoxia	629.738	238.62
cpar2_300530	contig005806 normoxia hypoxia	181.599	68.7506
cpar2_100620	contig005569 normoxia hypoxia	1285.95	486.811
cpar2_101040	contig005569 normoxia hypoxia	306.3	115.91
cpar2_208450	contig005809 normoxia hypoxia	1060.11	400.743
cpar2_201840	contig005809 normoxia hypoxia	2583.05	970.217
cpar2_108920	contig005569 normoxia hypoxia	654.013	245.467
cpar2_300230	contig005806 normoxia hypoxia	1024.92	384.655
cpar2_808200	contig005807 normoxia hypoxia	1744.54	651.788
cpar2_803710	contig005807 normoxia hypoxia	659.505	245.835
cpar2_209010	contig005809 normoxia hypoxia	382.152	141.758
cpar2_203600	contig005809 normoxia hypoxia	875.097	323.279
cpar2_503440	contig006139 normoxia hypoxia	3845.54	1410.57
cpar2_600750	contig005504 normoxia hypoxia	1416.34	518.636
cpar2_207080	contig005809 normoxia hypoxia	855.025	312.967

cpar2_209410	contig005809 normoxia hypoxia	15659.6	5704.97
cpar2_702780	contig006110 normoxia hypoxia	386.854	139.63
cpar2_808020	contig005807 normoxia hypoxia	1588.85	573.158
cpar2_109550	contig005569 normoxia hypoxia	192.961	69.3323
cpar2_109430	contig005569 normoxia hypoxia	1234.4	442.668
cpar2_105600	contig005569 normoxia hypoxia	903.681	323.895
cpar2_402340	contig006372 normoxia hypoxia	151.126	54.0821
cpar2_402390	contig006372 normoxia hypoxia	841.692	300.227
cpar2_207190	contig005809 normoxia hypoxia	426.291	151.333
cpar2_302150	contig005806 normoxia hypoxia	867.747	304.871
cpar2_401430	contig006372 normoxia hypoxia	9930.47	3485.05
cpar2_208220	contig005809 normoxia hypoxia	236.404	82.8634
cpar2_208480	contig005809 normoxia hypoxia	185.936	65.0931
cpar2_303760	contig005806 normoxia hypoxia	354.134	122.314
cpar2_303940	contig005806 normoxia hypoxia	24389.8	8392.41
cpar2_701380	contig006110 normoxia hypoxia	137.196	47.07
cpar2_301230	contig005806 normoxia hypoxia	513.977	176.058
cpar2_701580	contig006110 normoxia hypoxia	15749.9	5354.4
cpar2_303360	contig005806 normoxia hypoxia	727.602	246.478
cpar2_304090	contig005806 normoxia hypoxia	464.222	155.909
cpar2_801860	contig005807 normoxia hypoxia	305.002	102.34
cpar2_602160	contig005504 normoxia hypoxia	12587	4215.07
cpar2_202720	contig005809 normoxia hypoxia	195.685	65.4752
cpar2_403460	contig006372 normoxia hypoxia	1063.59	348.526
cpar2_304170	contig005806 normoxia hypoxia	530.14	173.188
cpar2_803410	contig005807 normoxia hypoxia	10315.2	3337.84
cpar2_103030	contig005569 normoxia hypoxia	1388.28	448.063
cpar2_211380	contig005809 normoxia hypoxia	1100.45	355.158
cpar2_702290	contig006110 normoxia hypoxia	17049.9	5486.25
cpar2_500930	contig006139 normoxia hypoxia	7253.93	2301.11
cpar2_700570	contig006110 normoxia hypoxia	2701.38	852.853
cpar2_406160	contig006372 normoxia hypoxia	109.522	34.0648
cpar2_103780	contig005569 normoxia hypoxia	836.095	257.24
cpar2_201820	contig005809 normoxia hypoxia	644.104	197.448
cpar2_100200	contig005569 normoxia hypoxia	1396.82	424.473
cpar2_503670	contig006139 normoxia hypoxia	230.929	69.454
cpar2_213570	contig005809 normoxia hypoxia	14029.5	4216.39
cpar2_209450	contig005809 normoxia hypoxia	13242.6	3944.63
cpar2_803630	contig005807 normoxia hypoxia	3373.35	1004.15
cpar2_211140	contig005809 normoxia hypoxia	353.533	105.233
cpar2_107930	contig005569 normoxia hypoxia	959.45	283.987
cpar2_701730	contig006110 normoxia hypoxia	779.181	230.185
cpar2_803140	contig005807 normoxia hypoxia	1561.37	460.749
cpar2_600210	contig005504 normoxia hypoxia	2514.9	738.188
cpar2_208740	contig005809 normoxia hypoxia	4372.95	1281.07
cpar2_200290	contig005809 normoxia hypoxia	4520.23	1316.65

cpar2_802460	contig005807 normoxia	hypoxia	11061.1	3210.75
cpar2_405570	contig006372 normoxia	hypoxia	12413.5	3593.28
cpar2_404800	contig006372 normoxia	hypoxia	134.079	38.2835
cpar2_203160	contig005809 normoxia	hypoxia	745.28	212.56
cpar2_803420	contig005807 normoxia	hypoxia	11486.2	3252.93
cpar2_403070	contig006372 normoxia	hypoxia	554.125	154.824
cpar2_105160	contig005569 normoxia	hypoxia	5802.44	1607.82
cpar2_700410	contig006110 normoxia	hypoxia	185.708	51.2909
cpar2_303000	contig005806 normoxia	hypoxia	40.0078	10.8705
cpar2_800530	contig005807 normoxia	hypoxia	5460.99	1455.38
cpar2_703320	contig006110 normoxia	hypoxia	113.955	30.2093
cpar2_700110	contig006110 normoxia	hypoxia	67.1014	17.547
cpar2_300770	contig005806 normoxia	hypoxia	59.8463	15.4632
cpar2_602990	contig005504 normoxia	hypoxia	2094.3	528.003
cpar2_501010	contig006139 normoxia	hypoxia	48.6012	12.1512
cpar2_106530	contig005569 normoxia	hypoxia	239.956	59.7524
cpar2_502050	contig006139 normoxia	hypoxia	925.308	230.025
cpar2_104710	contig005569 normoxia	hypoxia	4204.49	1007.28
cpar2_603050	contig005504 normoxia	hypoxia	478.331	113.262
cpar2_501380	contig006139 normoxia	hypoxia	1503.37	355.541
cpar2_403360	contig006372 normoxia	hypoxia	219.822	51.3017
cpar2_401720	contig006372 normoxia	hypoxia	460.027	102.527
cpar2_401740	contig006372 normoxia	hypoxia	261.934	56.8134
cpar2_300630	contig005806 normoxia	hypoxia	683.447	144.112
cpar2_402910	contig006372 normoxia	hypoxia	3140.96	612.689
cpar2_211610	contig005809 normoxia	hypoxia	3709.49	707.099
cpar2_502800	contig006139 normoxia	hypoxia	110.548	19.6833
cpar2_600600	contig005504 normoxia	hypoxia	613.308	103.759
cpar2_700940	contig006110 normoxia	hypoxia	2321.84	374.471
cpar2_300120	contig005806 normoxia	hypoxia	42.796	6.29889
cpar2_402900	contig006372 normoxia	hypoxia	785.712	114.742
cpar2_703250	contig006110 normoxia	hypoxia	311.815	44.9128
cpar2_603010	contig005504 normoxia	hypoxia	103.572	14.9002
cpar2_205880	contig005809 normoxia	hypoxia	5599.72	711.115
cpar2_600590	contig005504 normoxia	hypoxia	577.625	68.1127
cpar2_212720	contig005809 normoxia	hypoxia	69.1262	7.87235
cpar2_402880	contig006372 normoxia	hypoxia	59.1941	6.50228
cpar2_213050	contig005809 normoxia	hypoxia	4560.47	493.132
	contig005807 normoxia	hypoxia	358.554	29.0646
cpar2_801290	contig005807 normoxia	hypoxia	158.483	8.4106

fold change in FPKM

ncbi.org

In.fold	chtest_stat	p_value	C.a. ortholog	C.a. ortholog gene name
4.52638	-99.6584	0		
3.92845	-33.1573	0	orf19.638	FDH1
3.14997	-7.73209	1.07E-14	orf19.1652	POX1-3
2.73053	-40.0432	0	orf19.1327	RBT1
2.68414	-9.25489	0		
2.64038	-37.9978	0	orf19.3932.1	
2.5763	-25.7444	0		
2.56767	-12.5718	0	orf19.5615	AYR2
2.46313	-57.4379	0	orf19.4210	
2.4463	-34.8372	0	orf19.7021	GPH1
2.40032	-18.7341	0	orf19.3232	
2.30437	-13.0091	0	orf19.4255	ECM331
2.26263	-25.1962	0	orf19.4591	CAT2
2.26125	-12.9589	0	orf19.2397	
2.2433	-11.6261	0	orf19.4682	HGT17
2.10359	-46.5261	0	orf19.1290	XKS1
2.10047	-20.0361	0	orf19.4041	PEX4
2.08875	-50.658	0	orf19.3053	
2.05537	-12.1519	0		
2.03674	-84.2951	0	orf19.5437	RHR2
2.00718	-50.427	0	orf19.5293	
1.96978	-185.907	0	orf19.3651	PGK1
1.95735	-33.0277	0		
1.95421	-10.8773	0		
1.94536	-20.3936	0	orf19.55	
1.93674	-15.2179	0	orf19.6844	ICL1
1.91987	-12.8151	0	orf19.6445	EC11
1.90759	-33.2151	0	orf19.5806	ALD5
1.88607	-13.7702	0		

1.8716	-77.7057	0	orf19.6882OSM1
1.82946	-16.6131	0	
1.82842	-67.782	0	orf19.1631ERG6
1.8208	-27.7689	0	
1.80592	-19.5054	0	orf19.1288FOX2
1.80341	-69.8565	0	orf19.2765PGA62
1.79292	-38.8694	0	orf19.5323MDH1-3
1.75947	-45.3166	0	orf19.4530.1
1.75677	-23.9457	0	
1.74726	-9.29849	0	orf19.1655PXP2
1.74404	-24.8264	0	orf19.1704FOX3
1.74033	-16.4379	0	
1.72521	-9.21054	0	orf19.7093HGT13
1.67117	-8.6751	0	orf19.7447JEN1
1.66645	-25.9383	0	orf19.4657
1.65633	-15.1642	0	orf19.6066
1.64207	-27.4219	0	orf19.1598ERG24
1.63943	-18.3476	0	orf19.7350RCT1
1.63493	-22.8526	0	
1.63197	-44.1231	0	orf19.944 IFG3
1.62459	-38.8299	0	orf19.1743ACS1
1.61279	-143.362	0	orf19.903 GPM1
1.61112	-17.2336	0	orf19.6679
1.60994	-18.4608	0	orf19.7520POT1
1.60763	-7.32502	2.39E-13	orf19.7379FAA2
1.60521	-103.922	0	orf19.7043ACB1
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1.58033	-68.5709	0	orf19.4980HSP70
1.5761	-11.3978	0	
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1.56832	-8.84601	0	orf19.4157SPS20
1.55778	-53.719	0	orf19.3672GAL10
1.54919	-21.4503	0	orf19.5727
1.54197	-44.0967	0	
1.53786	-36.3859	0	
1.53376	-57.1423	0	orf19.922 ERG11
1.53076	-22.3018	0	orf19.338
1.52986	-11.6945	0	orf19.742 ALD6
1.52576	-14.6905	0	
1.51513	-12.9636	0	
1.50817	-14.3878	0	
1.49242	-74.1967	0	orf19.7466ACC1
1.48642	-102.407	0	orf19.2803HEM13
1.47938	-37.8596	0	orf19.7284ASR2
1.47514	-18.5346	0	orf19.1653
1.46812	-16.7104	0	orf19.7446OPI3

1.46256	-133.305	0	orf19.6745TPI1
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1.44654	-48.9444	0	orf19.3171ACH1
1.44426	-180.608	0	orf19.395 ENO1
1.44373	-27.7836	0	orf19.7196
1.43277	-9.22884	0	orf19.7310
1.41899	-20.3212	0	orf19.3306
1.41814	-12.3854	0	
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1.41546	-19.8084	0	orf19.4737TPO3
1.41133	-9.38622	0	orf19.6518
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1.40097	-9.32596	0	orf19.541
1.39889	-67.396	0	orf19.7676XYL2
1.3933	-41.7853	0	orf19.1756GPD1
1.38589	-13.857	0	orf19.952
1.37783	-159.245	0	orf19.4618FBA1
1.3715	-8.61827	0	orf19.4679AGP2
1.34422	-8.76776	0	orf19.843
1.34337	-22.4001	0	orf19.5611
1.34233	-85.2483	0	orf19.3575CDC19
1.34097	-21.2117	0	orf19.3684
1.33875	-41.9562	0	orf19.2841PGM2
1.33595	-19.1433	0	orf19.854 UGA11
1.33435	-16.098	0	orf19.842 ASR3
1.32765	-32.1635	0	orf19.767 ERG3
1.32675	-67.0356	0	orf19.1064ACS2
1.32086	-242.424	0	orf19.6814TDH3
1.31771	-22.1004	0	orf19.6229CAT1
1.31095	-6.18312	6.28E-10	
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1.29067	-61.2444	0	orf19.3888PGI1
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1.28535	-11.7659	0	orf19.5862
1.28107	-17.7673	0	orf19.6877PNG2
1.23251	-6.25678	3.93E-10	orf19.4384HXT5
1.23117	-54.8198	0	orf19.4631ERG251
1.22074	-40.6707	0	orf19.734 GLK1
1.20926	-11.5897	0	orf19.1562
1.20844	-19.5634	0	orf19.7221SET3
1.20399	-20.0059	0	orf19.6800POS5
1.19725	-8.5672	0	orf19.3931SFC1
1.19641	-106.036	0	orf19.542 HXK2

1.19433	-9.65496	0	orf19.6073HMX1
1.18616	-58.6294	0	orf19.316CHSP12
1.18349	-20.9254	0	orf19.5158
1.1797	-29.3863	0	orf19.4274PUT1
1.17922	-67.3798	0	orf19.5117OLE1
1.17578	-9.17741	0	
1.1721	-20.6217	0	orf19.5379ERG4
1.16975	-12.5078	0	orf19.6830
1.16461	-10.5107	0	orf19.4982
1.16252	-20.2568	0	orf19.260 SLD1
1.15897	-25.0581	0	orf19.909.1
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1.15478	-6.34466	2.23E-10	
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1.15144	-7.23965	4.50E-13	orf19.1369
1.14836	-34.9866	0	orf19.2897SOU2
1.13854	-169.291	0	orf19.3997ADH1
1.13592	-39.0718	0	orf19.406 ERG1
1.13464	-15.931	0	orf19.6709
1.12962	-53.8482	0	orf19.5949FAS2
1.12867	-52.4869	0	orf19.979 FAS1
1.12379	-12.3768	0	orf19.4763
1.12357	-18.5813	0	orf19.5622GLC3
1.11342	-45.8765	0	orf19.3967PFK1
1.10911	-49.2567	0	orf19.2496
1.10728	-19.3988	0	orf19.4527HGT1
1.10552	-6.73277	1.66E-11	orf19.5498EFH1
1.10301	-30.2199	0	orf19.5525
1.102	-73.3438	0	orf19.5024GND1
1.10082	-9.093	0	orf19.169 CHO2
1.1005	-12.4496	0	orf19.5986THI4
1.09589	-9.82541	0	orf19.692
1.0954	-10.6723	0	orf19.7106
1.09118	-9.47206	0	orf19.473 TPO4
1.09031	-43.1211	0	orf19.3419MAE1
1.09017	-8.76404	0	orf19.2633HGT14
1.08681	-18.5171	0	orf19.2737
1.0862	-32.3436	0	orf19.2396IFR2
1.08528	-32.33	0	orf19.2977
1.08328	-9.08641	0	orf19.5673OPT7
1.08135	-13.9952	0	orf19.4639
1.07881	-39.6171	0	orf19.1591ERG10
1.07371	-25.2785	0	orf19.6816
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1.07162	-29.2632	0	orf19.1974TFS1
1.07067	-33.8142	0	orf19.6202RBT4

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1.05616	-26.1872	0	orf19.4754ZWF1
1.0444	-9.09674	0	orf19.6557
1.04382	-42.2431	0	orf19.6757GCY1
1.04184	-10.9838	0	orf19.2952EXG2
1.04047	-14.5395	0	orf19.6057
1.04005	-31.7161	0	orf19.7312ERG13
1.03685	-30.2661	0	orf19.5178ERG5
1.03485	-18.6108	0	orf19.1917
1.02605	-15.4233	0	orf19.118 FAD2
1.02373	-9.14646	0	orf19.7517CHT1
1.01888	-12.9277	0	orf19.246
1.01718	-18.2983	0	orf19.4451RIA1
1.01651	-15.9807	0	orf19.2248ARE2
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1.01308	-11.0162	0	orf19.2752ADR1
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0.994324	-16.7429	0	orf19.3921
0.989833	-21.5173	0	orf19.250 SLC1
0.988034	-40.2987	0	orf19.2770SOD1
0.982356	-31.3906	0	orf19.7459
0.979243	-13.0562	0	orf19.4445
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0.978465	-27.7301	0	orf19.3616ERG9
0.97758	-9.47813	0	orf19.4090
0.973883	-10.8837	0	orf19.3307
0.973642	-12.4997	0	orf19.4816
0.973154	-16.6784	0	orf19.4043
0.96983	-21.4935	0	orf19.6322ARD
0.966294	-16.8811	0	orf19.6287AAT21
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0.958309	-12.8116	0	orf19.7645
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0.954756	-9.23214	0	orf19.732
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0.949238	-6.01134	1.84E-09	orf19.5000CYB2
0.946199	-14.3255	0	orf19.1891 Apr-01
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0.907179	-13.0999	0	orf19.4520
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0.90235	-15.491	0	orf19.1785
0.899179	-9.35974	0	orf19.510
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0.89361	-47.1019	0	orf19.704&CYB5
0.891151	-9.24944	0	orf19.5216
0.885679	-7.56967	3.75E-14	orf19.200&HNM1
0.875722	-23.9828	0	orf19.610&MVD
0.875497	-9.50822	0	orf19.3051
0.872346	-22.4749	0	orf19.483&URA1
0.871667	-11.6063	0	orf19.405 VCX1
0.871044	-8.27376	2.22E-16	orf19.500&OSM2
0.866126	-8.11957	4.44E-16	orf19.6456
0.860631	-14.2004	0	orf19.564&MET15
0.85762	-12.1803	0	orf19.157CERG7
0.854809	-15.205	0	orf19.3679
0.854062	-10.6196	0	orf19.1721NCE103
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0.85122	-11.425	0	orf19.665&DUR3
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0.844201	-24.2186	0	orf19.3649
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0.843137	-30.5059	0	orf19.177&MP65
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0.837515	-5.68119	1.34E-08	orf19.445&GAP4
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0.836279	-6.67166	2.53E-11	orf19.757CUGA3
0.835785	-4.94826	7.49E-07	orf19.171&SGA1
0.834269	-8.39965	0	orf19.4066
0.833488	-38.3595	0	orf19.238 CCP1
0.832161	-20.7339	0	orf19.7592FAA4
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0.829735	-14.5507	0	orf19.534&TPS3
0.828889	-26.3661	0	orf19.5197APE2
0.826005	-30.2368	0	orf19.6731.1
0.823865	-6.1842	6.24E-10	orf19.299C XOG1
0.821398	-4.95015	7.42E-07	orf19.607CENA2
0.820136	-5.6385	1.72E-08	orf19.581&EBP7
0.819472	-10.7318	0	orf19.217
0.817509	-22.2137	0	orf19.717&PRE5
0.810736	-4.38566	1.16E-05	
0.809954	-18.1802	0	orf19.1031HMG1
0.807758	-9.61439	0	orf19.4740
0.807214	-5.42858	5.68E-08	orf19.5026
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0.806109	-8.24102	2.22E-16	orf19.132&ECM38
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0.800944	-8.94472	0	orf19.1505
0.79961	-21.1095	0	orf19.4886
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0.795662	-10.7832	0	orf19.163
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0.775888	-8.31225	0	orf19.7270
0.77242	-101.319	0	orf19.2877PDC11
0.76894	-16.7777	0	orf19.648&FMP45
0.766149	-13.8003	0	orf19.633&PGA25
0.76332	-7.46061	8.62E-14	orf19.899
0.762773	-11.2251	0	orf19.747&NTH1
0.761768	-9.63445	0	orf19.3226
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0.736697	-20.0814	0	orf19.691 GPD2
0.736392	-9.88363	0	orf19.276
0.736233	-8.38753	0	orf19.277 THI6
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0.734616	-7.00519	2.47E-12	orf19.7364
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0.724767	-8.33548	0	orf19.6443
0.722942	-7.59781	3.02E-14	orf19.792
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0.720132	-13.5555	0	orf19.4777 DAK2
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0.716171	-5.79455	6.85E-09	orf19.2853
0.7154	-6.00451	1.92E-09	orf19.6276
0.714583	-6.577	4.80E-11	orf19.5728
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0.712747	-13.7764	0	orf19.6403
0.706776	-29.1879	0	
0.70662	-25.0849	0	orf19.528C PST3
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0.699397	-6.53954	6.17E-11	orf19.6973
0.698646	-5.27079	1.36E-07	
0.697499	-6.0545	1.41E-09	
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0.695763	-8.88504	0	orf19.146C SMP2
0.69444	-5.98072	2.22E-09	orf19.1600
0.693074	-23.9875	0	orf19.565C PRO3
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-0.69036	8.45592	0	orf19.6662
-0.69057	5.83699	5.32E-09	orf19.4929
-0.69089	38.1476	0	orf19.1052
-0.69281	4.14689	3.37E-05	orf19.401C PCL5

-0.69355	51.973	0	orf19.5466RPS24
-0.69371	6.53851	6.21E-11	orf19.1886RCL1
-0.69396	11.09	0	orf19.4211FET3
-0.69433	46.5141	0	orf19.5996RPS19A
-0.69507	5.18477	2.16E-07	orf19.5454DAL1
-0.69724	6.66188	2.70E-11	orf19.4889
-0.69822	6.12138	9.28E-10	orf19.1050
-0.69869	4.83058	1.36E-06	orf19.154
-0.69925	11.6584	0	orf19.7203
-0.69997	5.59304	2.23E-08	orf19.3459
-0.70002	26.0416	0	orf19.5493GSP1
-0.70062	9.44842	0	orf19.4375
-0.70122	14.2808	0	
-0.70309	3.61636	0.000299	orf19.5429
-0.70346	30.2016	0	orf19.7509ATP17
-0.70524	3.72448	0.000196	orf19.2743
-0.70572	8.03515	8.88E-16	orf19.124 CIC1
-0.70616	8.51846	0	orf19.5277
-0.70702	54.3625	0	orf19.6085RPL16A
-0.70886	24.0969	0	orf19.5351TIF11
-0.70897	15.9649	0	orf19.2694TYS1
-0.70932	8.03391	8.88E-16	orf19.25
-0.71065	15.106	0	orf19.2183KRE30
-0.71068	22.7833	0	orf19.5660.1
-0.711892	6.10668	1.02E-09	orf19.7561DEF1
-0.71325	18.4512	0	orf19.2275
-0.71337	10.3104	0	orf19.6752
-0.71499	7.65208	1.98E-14	orf19.1388
-0.71504	8.81147	0	orf19.4146SMD3
-0.71545	7.14428	9.05E-13	orf19.7194
-0.71561	5.10231	3.36E-07	orf19.292
-0.71571	7.62204	2.49E-14	orf19.551
-0.71616	25.6016	0	orf19.3358LSC1
-0.71619	25.5291	0	orf19.2707QCR9
-0.71651	4.28997	1.79E-05	orf19.1794
-0.7183	3.10374	0.001911	
-0.719116	7.2428	4.39E-13	
-0.71951	8.47347	0	orf19.4177HIS5
-0.72157	48.2987	0	orf19.236 RPL9B
-0.72187	12.6032	0	orf19.923 THR1
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-0.72872	7.53911	4.73E-14	orf19.4771

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-0.73802	17.178	0	orf19.6531NUC2
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-0.75408	7.74825	9.33E-15	orf19.7419HNT2
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-0.75632	54.1545	0	orf19.667. RPL37B
-0.75685	55.968	0	orf19.2329RPS17B
-0.75703	55.8902	0	orf19.827. RPL39
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-0.76877	8.18067	2.22E-16	orf19.2471GIM5
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-0.77878	13.1854	0	orf19.685 YHM1
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-0.78066	10.551	0	orf19.4191RLP24
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-0.78355	7.12502	1.04E-12	orf19.445CZCF23
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-0.78906	5.99357	2.05E-09	orf19.6983
-0.78985	6.23645	4.48E-10	orf19.1735
-0.79059	7.92356	2.22E-15	orf19.2621
-0.79084	6.69759	2.12E-11	orf19.6197
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-0.8144	21.3009	0	orf19.2311RPL82
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-0.8385	12.9156	0	orf19.596. NOP10
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-0.8544	14.7183	0	orf19.5064MRPL3
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-0.86311	7.59597	3.06E-14	orf19.2667RPF1
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-0.8787	7.55912	4.06E-14	orf19.315&UTP20
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-0.88258	7.48696	7.04E-14	orf19.23 RTA3
-0.88387	60.9367	0	orf19.701&RPS18
-0.88918	9.47135	0	orf19.755 MRPL37
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-0.95309	21.3034	0	orf19.6696TIM9
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-0.95507	10.4346	0	orf19.252
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-0.95792	68.5714	0	orf19.3415RPL32
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-0.97996	13.0919	0	orf19.3064MRPL27
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-1.09484	7.66854	1.73E-14	orf19.4962
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-1.13089	20.8138	0	orf19.2511MRPL33
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-1.22046	23.0201	0	orf19.3223.1
-1.22579	29.2827	0	orf19.5597.1
-1.22774	38.6458	0	orf19.2785ATP7
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-1.23693	61.7034	0	orf19.3268TMA19
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-2.06364	51.8374	0	
-2.13776	16.6866	0	orf19.716
-2.17258	5.77574	7.66E-09	orf19.4508LYS22
-2.20867	5.34603	8.99E-08	orf19.5634FRP1
-2.22441	46.9245	0	
-2.51256	13.0279	0	orf19.1930CFL5
-2.93616	8.29782	0	orf19.3738PGA22

C.a. ortholog description

Putative formate dehydrogenase, oxidizes formate to produce CO₂; Mig1p regulated; induced in stationary phase; predicted acyl-CoA oxidase; farnesol regulated; protein detected by mass spec in stationary phase; Cell wall protein with similarity to Hwp1p, required for virulence; cell-wall attached; predicted

Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related gene regulation; *S. cerevisiae* ortholog CLD1 has phospholipase A2 activity, has role in cardiolipin metabolism; Putative glycogen phosphorylase; gene regulated by Ssk1p, Mig1p, and Tup1p; fluconazole sensitive; Putative transporter; mutation confers hypersensitivity to toxic ergosterol analog; fungal-specific; GPI-anchored protein; mainly at plasma membrane, also at cell wall; caspofungin induced; Major carnitine acetyl transferase localized in peroxisomes and mitochondria; involved in iron homeostasis; Predicted membrane transporter, member of the anion:cation symporter (ACS) family, major in yeast; Putative glucose transporter of the major facilitator superfamily; the *C. albicans* glucose transporter; Predicted ORF in Assemblies 19, 20 and 21; increased expression in response to prostaglandin; Predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in both intermediate and stationary phase; Protein detected by mass spec in exponential and stationary phase cultures; identified in electron microscopy

Putative glycerol 3-phosphatase; roles in osmotic tolerance, glycerol accumulation in response to stress

Phosphoglycerate kinase; enzyme of glycolysis; localizes to cell wall and to cytoplasm; and

S. cerevisiae ortholog IZH2 has role in cellular zinc ion homeostasis, response to toxin and oxidative stress; Isocitrate lyase; enzyme of glyoxylate cycle; required for wild-type virulence in murine system; Protein similar to *S. cerevisiae* Eci1p, which is involved in fatty acid oxidation; transposon insertion; Protein described as an aldehyde dehydrogenase; decreased expression in fluconazole-resistant

Putative flavoprotein subunit of fumarate reductase; soluble protein in hyphae; fungal-spec

Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in ergosterol biosy

Predicted 3-hydroxyacyl-CoA epimerase, required for fatty acid beta-oxidation; upregulated

Putative GPI-anchored protein; fluconazole-induced; transcriptionally regulated by iron; ex

Predicted malate dehydrogenase; farnesol regulated

ORF Predicted by Annotation Working Group; regulated by Nrg1p, Tup1p

Putative acyl-CoA oxidase; enzyme of fatty acid beta-oxidation; induced during macrophag

Putative peroxisomal 3-oxoacyl CoA thiolase; expression is regulated upon white-opaque :

Predicted sugar transporter, involved in glycerol utilization; member of the major facilitator

Lactate transporter; transcriptionally induced by lactic acid, activated by Cat8p; alkaline do

S. cerevisiae ortholog NEM1 has phosphoprotein phosphatase activity and has role in regi

S. cerevisiae ortholog HFD1 localizes to endosome, lipid particle, integral to mitochondrial

C-14 sterol reductase, has a role in ergosterol biosynthesis; mutation confers increased se

Soluble protein in hyphae; fluconazole-induced; mRNA abundance is elevated in a *cyr1* or

Putative D-amino acid oxidase

Putative acetyl-CoA synthetase, similar to *S. cerevisiae* Acs1p; upregulated in the presenc

Surface protein that binds host complement Factor H and FHL-1; phosphoglycerate mutas

Putative peroxisomal 3-oxoacyl CoA thiolase; transcription is regulated by Nrg1p and Mig1

Predicted acyl CoA synthetase; expression is regulated upon white-opaque switching; tran

Protein described as similar to a region of acyl-coenzyme-A-binding protein; amphotericin

Predicted acyl CoA synthetase; upregulated upon phagocytosis; transcription is regulated

Putative hsp70 chaperone; role in entry into host cells; heat-shock, amphotericin B, Cd, ke

Ortholog of *S. cerevisiae* YGL159W

Predicted ORF in Assemblies 19, 20 and 21; protein detected by mass spec in stationary p

UDP-glucose 4-epimerase, required for galactose utilization; mutant shows cell wall defect

Lanosterol 14-alpha-demethylase, member of cytochrome P450 family that functions in erg

Protein detected by mass spec in stationary phase cultures; Hog1p-downregulated; shows

Putative aldehyde dehydrogenase; expression is regulated upon white-opaque switching; |

Protein with similarity to acetyl-coenzyme-A carboxylases; regulated by Efg1p; amphoteric

Coproporphyrinogen III oxidase; antigenic in human/mouse; localizes to yeast-form cell su

Gene regulated by cAMP and by osmotic stress; greater mRNA abundance observed in a

Putative phosphatidylethanolamine N-methyltransferase of phosphatidylcholine biosynthes

Triose-phosphate isomerase; antigenic in mouse or human; mutation affects filamentous growth

Acetyl-coA hydrolase; acetate utilization; nonessential; soluble protein in hyphae; antigenic
Enolase (2-phospho-D-glycerate-hydrolyase), enzyme of glycolysis and gluconeogenesis;
Protein described as a vacuolar protease; upregulated in the presence of human neutrophil
Protein similar to *S. cerevisiae* Gin3p; transcription is upregulated in response to treatment
S. cerevisiae ortholog HOP1 has four-way junction DNA binding, has role in synaptonemal

Protein of the Pex5p family; required for PTS1-mediated peroxisomal protein import, fatty acid
Possible role in polyamine transport; MFS-MDR family; transcription induced by Sfu1p, repressed

Multidrug efflux pump of the plasma membrane; MDR family member of the MFS (major facilitator
Predicted enzyme of sphingolipid biosynthesis; upregulated in biofilm

Protein described as similar to D-xylulose reductase; immunogenic in mouse; soluble protein
Protein similar to *S. cerevisiae* glycerol-3-phosphate dehydrogenase (enzyme of glycerol k

Putative fructose-bisphosphate aldolase, enzyme of glycolysis; antigenic in murine or human
Protein described as an amino acid permease; hyphal downregulated; regulated upon white
Putative DNA repair exonuclease; fungal-specific (no human or murine homolog)

S. cerevisiae ortholog GRE2 has methylglyoxal reductase (NADPH-dependent) activity, 3-oxo
Putative pyruvate kinase; on yeast-form cell surface; soluble in hyphae; antigenic; Gcn4p,
S. cerevisiae ortholog SPS19 has 2,4-dienoyl-CoA reductase (NADPH) activity, has role in
Ortholog of *S. cerevisiae* PGM2

Predicted ORF in Assemblies 19, 20 and 21; macrophage-induced gene; overlaps orf19.8!
Gene regulated by cAMP and by osmotic stress; greater mRNA abundance observed in a
C-5 sterol desaturase; introduces C-5(6) double bond into episterol in ergosterol biosynthesis
Probable acetyl-CoA synthetase; antigenic during murine systemic infection; antigenic in human
Glyceraldehyde-3-phosphate dehydrogenase; enzyme of glycolysis; NAD-linked; binds fibronectin
Catalase; role in resistance to oxidative stress, neutrophils, peroxide; role in murine system

Predicted ORF in Assemblies 19, 20 and 21; alpha-factor induced

Protein described as glucose-6-phosphate isomerase, enzyme of glycolysis; antigenic in human
Putative delta-1-pyrroline-5-carboxylate dehydrogenase; alkaline upregulated; protein detected
Putative transketolase; localizes to surface of yeast-form cells, but not hyphae; soluble protein
Protein described as related to arginases; downregulated upon adherence to polystyrene;
Putative peptide:N-glycanase; gene contains highly variable numbers of 12-bp repeats; transcribed
Protein described as a sugar transporter; transcription upregulated in response to treatment
C-4 sterol methyl oxidase with a role in ergosterol biosynthesis; ketoconazole-induced; amino
Putative glucokinase; transcription is regulated upon yeast-hyphal switch; transcriptionally
Predicted ORF in Assemblies 19, 20 and 21; transcription is repressed in response to alpha-factor
Putative NAD-dependent histone deacetylase; mutations affect filamentous growth; genetically
Protein likely to be essential for growth, based on an insertional mutagenesis strategy; similar
Putative succinate-fumarate transporter; gene is alkaline upregulated; transcription is upregulated
Protein described as hexokinase II; antigenic in human; downregulated in the presence of

Heme oxygenase; acts in utilization of heme iron; gene transcriptionally activated by heat, Heat-shock protein; induced upon osmotic/oxidative/cadmium stress, fluphenazine treatment
Protein with similarity to a human gene associated with colon cancer and to orf19.5158; re
Alkaline upregulated by Rim101p

Fatty acid desaturase (stearoyl-CoA desaturase), essential protein involved in oleic acid synthesis

Protein described as similar to sterol C-24 reductase; shows Mob2p-dependent hyphal regulation
Putative enoyl-CoA hydratase

Sphingolipid delta-8 desaturase, catalyzes desaturation at carbon-8 in the long-chain base
Predicted ORF in Assembly 20 and 21; gene has intron

Malate synthase; enzyme of the glyoxylate cycle; peroxisomal; no mammalian homolog; transcriptionally repressed

Alkaline downregulated

Protein similar to Sou1p; not required for utilization of L-sorbose

Alcohol dehydrogenase; at yeast-form but not hyphal cell surface; soluble in hyphae; immunogenic

Squalene epoxidase, catalyzes epoxidation of squalene to 2,3(S)-oxidosqualene in the ergosterol pathway

Alpha subunit of fatty-acid synthase; required for virulence in mouse systemic infection and in yeast
Beta subunit of fatty-acid synthase; multifunctional enzyme; fluconazole-induced; amphoterpilin-induced
Protein not essential for viability

Protein described as similar to 1,4-glucan branching enzyme; fluconazole-induced; shows similarity to
Alpha subunit of phosphofructokinase (PFK), which is Pfk1p, Pfk2p heteromultimer; PFK is essential for growth
Predicted ORF in Assemblies 19, 20 and 21; fluconazole-downregulated

High-affinity glucose transporter, member of major facilitator superfamily; transcription induced by glucose
Transcriptional activator; minor role in transcriptional regulation, compared to Efg1p; regulated by glucose

Protein abundance is affected by URA3 expression in the CAI-4 strain background; regulated by glucose

Putative 6-phosphogluconate dehydrogenase; soluble protein in hyphae; farnesol-, macrophage-inducible
Putative phosphatidyl-ethanolamine N-methyltransferase; fungal-specific (no human or murine homolog)

Protein repressed during the mating process; fungal-specific (no human or murine homolog)

S. cerevisiae ortholog VPS70 has role in protein targeting to vacuole

Putative sperimidine transporter; fungal-specific (no human or murine homolog)

Malic enzyme, mitochondrial; transcription regulated by Mig1p and Tup1p; shows colony morphology-related gene expression

Putative glucose transporter of the major facilitator superfamily; the *C. albicans* glucose transporter is essential for growth
Ortholog of *S. cerevisiae* YDR109C

Increased transcription is observed upon benomyl treatment; transcription is upregulated in hyphae

Putative oligopeptide transporter; possibly transports GSH and related compounds; induced by hydrogen peroxide
Predicted ORF in Assemblies 19, 20 and 21; protein detected by mass spec in exponential phase

Protein similar to acetyl-CoA acetyltransferase; role in ergosterol biosynthesis; soluble in hyphae
S. cerevisiae ortholog YJR096W has aldehyde reductase activity, has role in arabinose catabolism

Putative glutathione peroxidase; peroxide-induced; induced in response to peroxide, exogenous hydrogen peroxide
Transcription is regulated upon yeast-hyphal switch; shows colony morphology-related gene expression

Protein with similarity to plant pathogenesis-related proteins; required for virulence in mouse

Putative glucose-6-phosphate dehydrogenase; antigenic in murine infection; activity induced by nitric oxide
Predicted ORF in Assemblies 19, 20 and 21; transcriptionally activated by Mnl1p under weakly repressing conditions
Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to toxic ergosterol
GPI-anchored cell wall protein, similar to *S. cerevisiae* exo-1,3-beta-glucosidase Exg2p; protein is secreted
S. cerevisiae ortholog ECM31 has 3-methyl-2-oxobutanoate hydroxymethyltransferase activity
Similar to *S. cerevisiae* ergosterol biosynthesis protein Erg13p; transposon mutation affects growth
Putative C-22 sterol desaturase; fungal C-22 sterol desaturases are cytochrome P450 enzymes

Delta-12 fatty acid desaturase, involved in production of linoleic acid, which is a major component of cell membranes
Chitinase; putative N-terminal catalytic domain; has secretory signal sequence; lacks S/T repeats
S. cerevisiae ortholog YIL108W localizes to cytoplasm

Putative translation elongation factor; genes encoding ribosomal subunits, translation factors, and other proteins
Acyl CoA:sterol acyltransferase (ASAT); uses cholesterol and oleoyl-CoA substrates; protein is secreted

Putative transcription factor with zinc finger DNA-binding motif; similar to *S. cerevisiae* Adr1p
Predicted ORF in Assemblies 19, 20 and 21; induced in core stress response; induced by H₂O₂
Beta subunit of phosphofructokinase (PFK), which is a heteromultimer of Pfk1p and Pfk2p
Ortholog of *S. cerevisiae* FSH3

Putative fatty acyltransferase; protein repressed during the mating process

Cytosolic copper- and zinc-containing superoxide dismutase, involved in protection from oxidative stress
Predicted ORF in Assemblies 19, 20 and 21; fluconazole-induced; ketoconazole-repressed
Putative protein of unknown function; Plc1p-regulated; expression is upregulated early upon stress

Mitochondrial carnitine carrier protein

Putative farnesyl-diphosphate farnesyl transferase (squalene synthase) involved in the sterol biosynthetic pathway
Predicted membrane transporter, member of the fucose:proton symporter (FHS) family, member of the FHS family
S. cerevisiae ortholog FMO1 has role in protein folding and localizes to endoplasmic reticulum
Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide

Predicted ORF in Assemblies 19, 20 and 21; transcription is induced in response to alpha-D-glucose
D-arabitol dehydrogenase, NAD-dependent (ArDH); enzyme of D-arabitol and D-arabinose biosynthesis
Protein detected by mass spec in exponential and stationary phase cultures; Gcn4p-regulated

S. cerevisiae ortholog LRO1 has phospholipid:diacylglycerol acyltransferase activity and has a role in lipid metabolism
Biotin protein ligase; catalyzes covalent attachment of biotin to biotin-dependent enzymes

Putative protein of unknown function; mRNA binds to She3p; transcription is induced in high glucose
Predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in both intermediate and stationary phase
Protein described as glycogen synthesis initiator; regulated by Efg1p and Efh1p; Hog1p-dependent
Protein described as precursor protein of cytochrome b2; transcriptionally regulated by iron
Vacuolar aspartic proteinase; mRNA abundance is equivalent in yeast-form and mycelial cultures
Protein similar to *S. cerevisiae* Ydr531wp; transposon mutation affects filamentous growth
Putative NAD-specific glutamate dehydrogenase; fungal-specific (no human or murine homolog)

Carboxypeptidase Y; transcriptionally regulated at yeast-hyphal transition or macrophage infection

Predicted ORF in Assemblies 19, 20 and 21; ketoconazole-induced; amphotericin B represses
Putative NADH:quinone oxidoreductase; similar to 1,4-benzoquinone reductase; immunogenic
Predicted ORF in Assemblies 19, 20 and 21; decreased expression in response to prostaglandin

S. cerevisiae ortholog OPY2 has role in cell cycle arrest in response to pheromone, osmotic stress
Protein of unknown function expressed during stationary phase; transcription is regulated by Gcn2p
S. cerevisiae ortholog YDR248C localizes to cytoplasm

3-Keto sterol reductase of ergosterol biosynthesis; acts in C-4 sterol demethylation with Erg11p

Protein involved in regulation of unsaturated fatty acid biosynthesis; controls the expression of ERG11
Transcriptional regulator of ergosterol biosynthetic genes and sterol uptake; binds ERG2 p
Cytochrome b(5); not essential for viability; similar to *S. cerevisiae* Cyb5p; transcriptionally repressed

Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to toxic ergosterol
Mevalonate diphosphate decarboxylase; functional homolog of *S. cerevisiae* Erg19p; possibly essential
Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related gene regulation
Dihydroorotate dehydrogenase (DHODH); enzyme of de novo pyrimidine biosynthesis; putative essential
Putative H⁺/Ca²⁺ antiporter; fungal-specific (no human or murine homolog)
Protein described as mitochondrial fumarate reductase; regulated by Ssn6p, Gcn2p, and Cln2p

O-acetylhomoserine O-acetylserine sulfhydrylase; involved in sulfur amino acid biosynthesis
2,3-epoxysqualene-lanosterol cyclase (lanosterol synthase), catalyzes the conversion of 2,3-epoxysqualene to lanosterol
Predicted ORF in Assemblies 19, 20 and 21; protein detected by mass spec in stationary phase
Carbonic anhydrase involved in the conversion of carbon dioxide to bicarbonate; essential for growth
Predicted ORF in Assemblies 19, 20 and 21; transcription is induced in response to alpha-amanitin
Putative urea transporter; transcription is upregulated in clinical isolates from HIV+ patients

Protein described as glycogen synthase; enzyme of glycogen metabolism; transcription downregulated
S. cerevisiae ortholog FES1 has adenyl-nucleotide exchange factor activity, has role in transcription

Cell surface mannoprotein; mycelial antigen; possible role in cell-wall glucan metabolism; immunogenic
Putative peptidyl-prolyl cis-trans isomerase; macrophage/pseudohyphal-repressed; heavy metal sensitive
Putative amino acid permease; hyphal induced; regulated by Gcn2p and Gcn4p; shows colony morphology

Protein with similarity to *S. cerevisiae* Ykr070wp; transposon mutation affects filamentous growth
Putative transcription factor with zinc cluster DNA-binding motif, required for utilization of glucose
Putative glucoamylase; fungal-specific (no human or murine homolog)
Predicted ORF in Assemblies 19, 20 and 21; Hog1p-downregulated
Similar to cytochrome-c peroxidase N terminus; transcription is negatively regulated by Rir1p
Predicted acyl CoA synthase

Protein described as similar to regulatory subunit of serine/threonine phosphoprotein phosphatase

Protein described as regulatory subunit of trehalose-phosphate synthase; regulated by Efg
Neutral arginine-, alanine-, leucine-specific metallo-aminopeptidase; expected to be secreted

Exo-1,3-beta-glucanase, major exoglucanase; member of family 5 glycosyl hydrolases; aff
Putative sodium transporter; transcription upregulated in response to ciclopirox olamine; al
Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to toxic ergo

Alpha6 subunit of the 20S proteasome; regulated by Gcn4p; induced in response to amino

HMG-CoA reductase; enzyme of sterol pathway; inhibited by lovastatin; gene not transcrip
S. cerevisiae ortholog PTH1 has aminoacyl-tRNA hydrolase activity, has role in mitochond
Putative transcription factor with zinc finger DNA-binding motif

Similar to D-xylose reductases; antigenic in murine systemic infection; soluble protein in hy
Alkaline upregulated; possibly an essential gene, disruptants not obtained by UAU1 methc

Predicted ORF in Assemblies 19, 20 and 21; induced by hypoxia

Copper transporter of the plasma membrane; P1-type ATPase (CPx type); mediates Cu re
Protein similar to S. cerevisiae Dap1p, which is a protein related to mammalian membrane

Predicted membrane transporter, member of the drug:proton antiporter (14 spanner) (DHA
S. cerevisiae ortholog PAN6 has pantoate-beta-alanine ligase activity, has role in pantothe

Predicted ORF in Assemblies 19, 20 and 21; protein level decreased in stationary phase c

Predicted ORF in Assemblies 19, 20 and 21; transcription detected in high-resolution tiling

Predicted ORF in Assemblies 19, 20 and 21; protein level decreased in stationary phase c

Predicted ORF in Assemblies 19, 20 and 21; regulated by Tsa1p, Tsa1Bp in minimal medic

Predicted membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA

S. cerevisiae ortholog YJR008W localizes to cytoplasm, nucleus

Putative alcohol dehydrogenase; soluble protein in hyphae; expression is regulated upon v

Structural protein of cell wall; 1,3-beta-glucan-linked; O-glycosylated by Pmt1p; N-mannos

Protein described as hydantoin utilization protein A; induced upon adherence to polystyren

Putative transcription factor with a role in colony morphology and virulence; functionally co

Protein similar to pyruvate decarboxylase; antigenic; at hyphal cell surface, not yeast-form

Protein induced during the mating process; mutation confers hypersensitivity to toxic ergos

Putative GPI-anchored protein of unknown function; fluconazole-downregulated

Neutral trehalase; hyphal induction in homozygous null mutant is delayed but not reduced

S. cerevisiae ortholog NPC2 has role in intracellular sterol transport and localizes to funga

Putative transcription factor; downregulated upon adherence to polystyrene; reduced mRN

GPI-anchored cell surface protein of unknown function; fluconazole-induced; possibly an e

Predicted membrane protein; estradiol-induced; increased transcription is associated with

Predicted ORF in Assemblies 19, 20 and 21; induced upon biofilm formation

Regulator of sorbose utilization; putative GPI-anchor; predicted helix-loop helix domain; hy

Alkaline upregulated by Rim101p

Predicted ORF in Assemblies 19, 20 and 21; possibly an essential gene, disruptants not of
Putative transcription factor with zinc finger DNA-binding motif

Protein detected by mass spec in stationary phase cultures; transcription is induced upon ;
Phosphomannose isomerase; cell wall biosynthesis enzyme; drug target; functional homol

Predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in response to tre

Similar to glycerol 3-P dehydrogenases; regulated by Ssn6p, Nrg1p, Efg1p; induced upon
Plasma membrane-localized protein of unknown function; increased transcription is observ
Putative thiamin-phosphate pyrophosphorylase, hydroxyethylthiazole kinase; fungal-specif
Putative protein of unknown function; homozygous transposon insertion causes decreasec

S. cerevisiae ortholog MLH3 has role in reciprocal meiotic recombination, mismatch repair
S. cerevisiae ortholog YGR111W has role in regulation of cell size and localizes to cytopla
S. cerevisiae ortholog NPY1 has NAD⁺ diphosphatase activity, has role in NADH metaboli
Putative glucanase; induced during cell wall regeneration

Protein described as a putative cysteine peroxidase; transcriptionally induced by interactio
Protein described as similar to dihydroxyacetone kinase; transcription is decreased upon y
Putative transaldolase; protein detected by mass spec in exponential and stationary phase

S. cerevisiae ortholog SIL1 has adenylyl-nucleotide exchange factor activity, has role in SRF

Putative flavodoxin; biofilm induced; fungal-specific (no human or murine homolog); protei
Putative D-amino acid oxidase; transcription is regulated upon yeast-hyphal switch
Predicted ORF in Assemblies 19, 20 and 21; greater mRNA abundance observed in a *cyr1*
Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p

Putative transporter; fungal-specific (no human or murine homolog)
Transcription is regulated by Nrg1p

Protein induced during the mating process; alkaline upregulated
Putative quinolinate phosphoribosyl transferase, involved in NAD biosynthesis
Putative protein of unknown function, transcription is upregulated in clinical isolates from H

Predicted histone H2B
Protein similar to *S. cerevisiae* Pcl5p and other cyclins for Pho85p kinase; Gcn4p-induced

Predicted ribosomal protein; hyphal downregulated; genes encoding cytoplasmic ribosomal subunits, translation factors, and translation initiation factors
Predicted ORF in Assemblies 19, 20 and 21; essential; downregulated during core stress response
Multicopper oxidase; required for growth under low-iron conditions; null mutant shows decreased growth
Putative ribosomal protein; protein level decreased in stationary phase cultures
Predicted ORF in Assemblies 19, 20 and 21; transcription is regulated by Nrg1p and Mig1p
Predicted membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA)

S. cerevisiae ortholog UTP30 localizes to nucleolus, 90S preribosome

S. cerevisiae ortholog MRP7 has structural constituent of ribosome and localizes to mitochondrion
Predicted ORF in Assemblies 19, 20 and 21; possibly an essential gene, disruptants not viable
Small RAN G-protein; essential; prenylation not predicted; overproduction complements viability
S. cerevisiae ortholog NNT1 has role in nicotinamide metabolic process, chromatin silencing

S. cerevisiae ortholog DIA2 has role in invasive growth in response to glucose limitation, S-phase arrest
Mitochondrial ATPase complex subunit; downregulated by Efg1p; flucytosine induced; caseinase

Predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in both intermediate and late stages

Protein similar to *S. cerevisiae* ribosomal protein Rpl16Ap; transposon mutation affects filamentous growth
Translation initiation factor eIF1a; possibly transcriptionally regulated upon hyphal formation
Putative tRNA-Tyr synthetase; genes encoding ribosomal subunits, translation factors, and translation initiation factors
S. cerevisiae ortholog TRM10 has tRNA (guanine) methyltransferase activity, has role in tRNA modification
YEF3-subfamily ABC family protein, predicted not to be a transporter; downregulated during hyphal growth
S. cerevisiae ortholog TIM11 has structural molecule activity and has role in ATP synthesis
Protein required for filamentous growth and for escape from epithelial cells and dissemination
S. cerevisiae ortholog MNP1 has role in aerobic respiration and localizes to mitochondrion
S. cerevisiae ortholog RSM10 has structural constituent of ribosome and localizes to mitochondrion
Predicted ORF in Assemblies 19, 20 and 21; induced upon biofilm formation
Protein described as a core snRNP protein; induced upon adherence to polystyrene
Protein not essential for viability; decreased transcription is observed upon fluphenazine treatment

Protein described as succinate-CoA ligase subunit; transcriptionally regulated by iron; expression induced upon iron limitation
Putative ubiquinol cytochrome c reductase; shows colony morphology-related gene regulation

Predicted ORF in Assemblies 19, 20 and 21; Gcn4p-regulated

Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and translation initiation factors
Putative homoserine kinase; fungal-specific (no human or murine homolog); transcription induced upon nitrogen limitation
S. cerevisiae ortholog LSM7 has RNA binding and has role in nuclear-transcribed mRNA catabolic process
Putative ribosomal protein, transcription is upregulated in clinical isolates from HIV+ patients
Protein not essential for viability

Predicted ORF in Assemblies 19, 20 and 21; possibly an essential gene, disruptants not viable
S. cerevisiae ortholog RUB1 has protein tag, has role in protein neddylation and localizes to nucleus

Protein described as aconitate hydratase 2; regulated by Gcn4p; repressed in response to
Putative ribosomal protein

S. cerevisiae ortholog MRPS8 has structural constituent of ribosome and localizes to mitochondrion

S. cerevisiae ortholog CMC2 has role in mitochondrial respiratory chain complex assembly

S. cerevisiae ortholog COX18 has membrane insertase activity, has role in protein insertion
Protein described as NADH-ubiquinone oxidoreductase; identified in detergent-resistant membrane

Putative succinate dehydrogenase; localized to the mitochondrial membrane

Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors

S. cerevisiae ortholog MRPS18 has structural constituent of ribosome and localizes to mitochondrion
ATP synthase alpha subunit; antigenic in human/mouse; at hyphal surface, not yeast; soluble

Protein described as aconitase; Gcn4p-regulated; amino acid starvation (3-AT treatment),

Decreased mRNA abundance observed in *cyr1* homozygous mutant hyphae; induced by human hyphae
Putative dihydroxyacid dehydratase; fungal-specific (no human or murine homolog); upregulated

Predicted ORF in Assemblies 19, 20 and 21; induced upon low-level peroxide stress

Protein described as succinate dehydrogenase, enzyme of citric acid cycle; downregulated

Putative ribosomal protein; macrophage/pseudohyphal-induced after 16 h; genes encoding

Ribosomal protein L37

Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors

Ribosomal protein L39; transcription is induced upon germ tube formation; shows colony non-reproducible

Putative transcription factor; zinc finger; similar to *S. cerevisiae* Crz1p; homozygous *crz1*, 100% identical

Protein similar to *S. cerevisiae* Dsl1p, which is a member of the t-SNARE complex of the endoplasmic reticulum

Protein described as NADH-ubiquinone oxidoreductase; identified in detergent-resistant membrane

Protein described as ketol-acid reductoisomerase; antigenic during human or murine infection

General amino acid permease; antigenic in human, mouse; 10-12 transmembrane regions

Protein described as 2-oxoglutarate dehydrogenase; regulated by Efg1p under yeast-form

S. cerevisiae ortholog VPS25 has role in negative regulation of transcription from RNA polymerase II promoter

Predicted ORF in Assemblies 19, 20 and 21; macrophage/pseudohyphal-repressed gene

Putative translation release factor 1, which interacts with stop codons and promotes release of ribosomes

Putative molybdopterin-converting factor; fungal-specific (no human or murine homolog)

Transcription is regulated by Mig1p

Transcription is regulated by Mig1p

Succinate dehydrogenase, membrane subunit; transcriptionally regulated by iron; expressed in yeast

S. cerevisiae ortholog SWS2 has role in regulation of sporulation resulting in formation of ascospores

Vacuolar membrane transporter: MRP subfamily of ABC family; similar to *S. cerevisiae* Bpt1p

Protein described as a subunit of RNA polymerases I, II, and III; regulated by Gcn4p; repressed

Putative mitochondrial carrier protein; fungal-specific (no human or murine homolog)

Predicted ORF in Assemblies 19, 20 and 21; essential; *S. cerevisiae* ortholog is essential; Saccharopine dehydrogenase (biosynthetic); enzyme of alpha-amino adipate lysine biosynthesis
S. cerevisiae ortholog YSY6 localizes to endoplasmic reticulum

Predicted zinc-finger protein of unknown function

Putative zinc-finger transcription factor, similar to *A. nidulans* FarA and FarB; activates gene
S. cerevisiae ortholog RSM24 has structural constituent of ribosome and localizes to mitochondria
Protein regulated by Gcn4p; repressed in response to amino acid starvation (3-aminotriazole)
Conserved acidic ribosomal protein, likely to be involved in regulation of translation elongation

S. cerevisiae ortholog PER1 has role in GPI anchor biosynthetic process, cellular manganese
Protein similar to *S. cerevisiae* translation initiation factor; upregulated in highly virulent strains
Predicted ORF in Assemblies 19, 20 and 21; repressed by nitric oxide

S. cerevisiae ortholog SMB1 has role in nuclear mRNA splicing, via spliceosome and localizes to nucleus
Ortholog of *S. cerevisiae* DHH1

Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors
Mitochondrial dicarboxylate transporter; possibly an essential gene, disruptants not obtained

S. cerevisiae ortholog MRPL39 has structural constituent of ribosome and localizes to mitochondria
Predicted ORF in Assemblies 19, 20 and 21; alkaline downregulated

S. cerevisiae ortholog AIM8 has role in cellular zinc ion homeostasis and localizes to mitochondria

S. cerevisiae ortholog IPK1 has inositol pentakisphosphate 2-kinase activity, has role in inositol
Predicted ORF in Assemblies 19, 20 and 21; similar to isoleucyl-tRNA synthetase; isoleucyl-tRNA synthetase
Predicted ORF in Assemblies 19, 20 and 21; repressed by nitric oxide

S. cerevisiae ortholog MNN11 has alpha-1,6-mannosyltransferase activity, has role in protein
Essential protein involved in tRNA export from the nucleus and ribosomal small subunit biogenesis
Predicted ribosomal protein; macrophage/pseudohyphal-induced after 16 h; downregulated
Protein described as component of mitochondrial ribosome; decreased expression in hyphae
Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced

Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors
S. cerevisiae ortholog URM1 has protein tag and has role in protein urmylation, invasive growth
Protein described as similar to ribosomal protein S21; regulated by Nrg1p, Tup1p; shows cell cycle
Similar to oxidoreductases; transcriptionally regulated by iron; expression greater in high iron
Membrane-localized protein

S. cerevisiae ortholog IMG1 has structural constituent of ribosome and localizes to mitochondria
Protein described as homoaconitase; regulated by Gcn4p, Gcn2p; induced in response to amino acid
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21
Protein described as acetolactate synthase; regulated by Gcn4p; induced in response to amino acid
Ribosomal protein 6A; localizes to cell surface of yeast cells but not hyphae; genes encoding
S. cerevisiae ortholog FLX1 has FAD transmembrane transporter activity, has role in FAD
Predicted ORF in Assemblies 19, 20 and 21; macrophage/pseudohyphal-induced

S. cerevisiae ortholog FAR11 has role in re-entry into mitotic cell cycle after pheromone arrest
S. cerevisiae ortholog RAD17 has double-stranded DNA binding, has role in double-strand break recombination
S. cerevisiae ortholog MRPL11 has structural constituent of ribosome and localizes to mitochondrion
ORF Predicted by Annotation Working Group; flucytosine induced
Putative ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors
Transcription factor with zinc cluster DNA-binding motif involved in control of glycolysis; ortholog of S. cerevisiae YMR166C

Ortholog of S. cerevisiae RPS11B and RPS11A

S. cerevisiae ortholog RPA49 has role in transcription of nuclear rRNA large RNA polymerase II

S. cerevisiae ortholog YCR016W localizes to nucleolus

Predicted ORF in Assemblies 19, 20 and 21; downregulated in core stress response; protein
Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to tubercidin
Macrophage/pseudohyphal-induced after 16 h

Predicted ORF in Assemblies 19, 20 and 21; essential for growth

Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to 5-fluorouracil

S. cerevisiae ortholog CBP6 localizes to mitochondrion

Protein of RGS superfamily; not essential for viability

Putative ribosomal protein L14; promoter bound directly by Tbf1p

S. cerevisiae ortholog MRPL44 has structural constituent of ribosome and localizes to mitochondrion

Putative L-aspartate 4-P-transferase; fungal-specific (no human or murine homolog); regulated by TOR

Predicted malate dehydrogenase; macrophage-induced protein

Ortholog of S. cerevisiae UTP11

Predicted ORF in Assemblies 19, 20 and 21; possibly an essential gene, disruptants not viable

Protein likely to be essential for growth; similar to S. cerevisiae Utp20p, which is a putative GTPase

Described as a Gag-related protein; hyphal induced; downregulation correlates with clinical resistance to antifungals

Protein described as ubiquinone reductase; transcriptionally induced by interaction with mitochondrial proteins

Protein described as a nucleolar protein with role in ribosomal assembly; hyphal induced

Similar to S. cerevisiae Rta1p (role in 7-aminocholesterol resistance) and Rsb1p (flippase)

Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors

Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related gene regulation

S. cerevisiae ortholog TGL2 has triglyceride lipase activity, has role in triglyceride catabolism

S. cerevisiae ortholog RPL26B has structural constituent of ribosome, RNA binding, has role in translation

S. cerevisiae ortholog MRP10 has structural constituent of ribosome, has role in mitochondrial protein import

S. cerevisiae ortholog TOM6 has protein channel activity, has role in protein import into mitochondrion

Gene induced by hypoxia and ketoconazole

Predicted membrane transporter, member of the monocarboxylate porter (MCP) family, member of the RND family

S. cerevisiae ortholog YAR1 has role in ribosomal small subunit biogenesis, cellular response to stress

Putative ferric reductase; transcription is activated by Mac1p under copper starvation; Plc1

F1F0 ATP synthase complex subunit; gene has intron

Putative tRNA-Arg synthetase; essential; genes encoding ribosomal subunits, translation f
S. cerevisiae ortholog GPI18 has dolichyl-phosphate-mannose-glycolipid alpha-mannosylt
Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced

Membrane-localized protein

ORF Predicted by Annotation Working Group; flucytosine induced

Major type I protein arginine methyltransferases (PRMT) involved in asymmetric dimethyla

3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase; enzyme of aromatic amino acid I

S. cerevisiae ortholog UPS1 has role in cardiolipin metabolic process and localizes to extri

S. cerevisiae ortholog BUD20 has role in cellular bud site selection and localizes to nucleu

Predicted ORF in Assembly 20 and 21; gene has intron

S. cerevisiae ortholog Mrps35p is a structural constituent of ribosome and localizes to mitc

Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in

Protein similar to isoleucyl-tRNA synthetase, the target of drugs including the cyclic beta-a

Putative F0-ATP synthase subunit 4; macrophage/pseudohyphal-induced

S. cerevisiae ortholog TIM8 has protein transporter activity, has role in protein import into r

Predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in both intermedi

3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase; enzyme of aromatic amino acid I

S. cerevisiae ortholog FMP37 localizes to mitochondrion

S. cerevisiae ortholog TIM10 has unfolded protein binding, protein transporter activity and

S. cerevisiae ortholog MRPL31 has structural constituent of ribosome and localizes to mitc

Putative component of the large (60S) ribosomal subunit

Putative translation elongation factor; genes encoding ribosomal subunits, translation factc

S. cerevisiae ortholog RSM19 has structural constituent of ribosome and localizes to mitoc

S. cerevisiae ortholog RSM27 has structural constituent of ribosome and localizes to mitoc

F1-ATP synthase complex subunit; flucytosine induced; caspofungin repressed; macropha

Protein not essential for viability; protein level decreased in stationary phase cultures

Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; protein detected by mas:

S. cerevisiae ortholog GOT1 has role in Golgi to endosome transport, ER to Golgi vesicle-

Putative mitochondrial ATP synthase; shows colony morphology-related gene regulation b:

Putative ribosomal protein

Protein described as a mitochondrial ribosomal protein; induced upon adherence to polyst

Protein described as similar to fumarate hydratase, enzyme of citric acid cycle; fluconazole

Putative mitochondrial ribosomal protein

Predicted membrane transporter, member of the monocarboxylate porter (MCP) family, ma

S. cerevisiae ortholog MRPL51 has structural constituent of ribosome, has role in aerobic |

Predicted ORF in Assemblies 19, 20 and 21; caspofungin repressed; protein level decreas

Protein similar to S. cerevisiae Snq2p transporter; member of PDR subfamily of ABC famil

Putative protein of glycine catabolism; downregulated by Efg1p; Hog1p-induced; upregulat

Ortholog of *S. cerevisiae* RPL31A and RPL31B

S. cerevisiae ortholog TRM82 has tRNA (guanine-N7-)-methyltransferase activity, has role in transcription factor involved in control of glucose-regulated gene expression
Protein described as transcription factor involved in control of glucose-regulated gene expression
Protein not essential for viability; similar to *S. cerevisiae* Crd1p, which is cardiolipin synthase
S. cerevisiae ortholog FYV4 localizes to mitochondrion

Predicted ORF in Assemblies 19, 20 and 21; clade-associated gene expression

S. cerevisiae ortholog MRPS17 has structural constituent of ribosome and localizes to mitochondrion

S. cerevisiae ortholog MRPL28 has structural constituent of ribosome and localizes to mitochondrion

S. cerevisiae ortholog PXR1 has telomerase inhibitor activity, has role in box C/D snoRNA biogenesis

Protein with similarity to the ribosomal protein portion of *S. cerevisiae* Rpl40Bp; shows colony morphology-related gene regulation
Protein not essential for viability

Ortholog of *S. cerevisiae* LRP1

Minor protein arginine methyltransferases (PRMT) involved in methylation of arginine residues

Mitochondrial ADP/ATP carrier protein involved in ATP biosynthesis; possible lipid raft component

S. cerevisiae ortholog MRPL17 has structural constituent of ribosome and localizes to mitochondrion
Predicted mitochondrial ribosomal protein

Omega-3 fatty acid desaturase, involved in production of alpha-linolenic acid, which is a major component of cell membranes
ORF Predicted by Annotation Working Group; shows colony morphology-related gene regulation

S. cerevisiae ortholog MRPL22 has structural constituent of ribosome and localizes to mitochondrion
Ortholog of *S. cerevisiae* YDR115W

Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors
ORF predicted by Annotation Working Group; increased expression observed in an *ssr1* hypomorph

Predicted ORF in Assemblies 19, 20 and 21; decreased expression in response to prostaglandin
Putative ribosomal protein S28B

S. cerevisiae ortholog RPL22B has structural constituent of ribosome, has role in translational control
High-affinity iron permease (ferric citrate, ferrioxamines E or B, transferrin); required for mitochondrial iron import
Ammonium permease; Mep1p is a more efficient ammonium permease than Mep2p, when both are present
S. cerevisiae ortholog MRPS12 localizes to ribosome, mitochondrion

S. cerevisiae ortholog MRPL15 has structural constituent of ribosome and localizes to mitochondrion
ATP phosphoribosyl transferase; enzyme of histidine biosynthesis; fungal-specific (no human ortholog)

Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors

S. cerevisiae ortholog RPL33A has structural constituent of ribosome, has role in translational control
Predicted ORF in Assemblies 19, 20 and 21; soluble protein in hyphae; protein level decreased in hyphae

S. cerevisiae ortholog JJJ3 has role in peptidyl-diphthamide biosynthetic process from peptidyl-diphthamide
Predicted ORF in Assembly 20 and 21; gene has intron

Predicted ORF in Assemblies 19, 20 and 21; repressed by nitric oxide

Protein described as 12kDa subunit of mitochondrial NADH-ubiquinone oxidoreductase; gene essential for viability

Putative subunit of the F1F0-ATPase complex; shows colony morphology-related gene regulation

S. cerevisiae ortholog ATP16 has ATPase activity, hydrogen ion transporting ATP synthase

Cell wall protein, ortholog of *S. cerevisiae* Tma19p (Ykl065cp)

Protein described as a ribosomal protein; downregulation correlates with clinical development of ALS family protein; hypermutable contingency gene; growth-regulated, downregulated in bud
Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; macrophage/pseudohyphal-induced
Ortholog of *S. cerevisiae* RPL39

S. cerevisiae ortholog IMG2 has structural constituent of ribosome and localizes to mitochondria

Protein with Mob2p-dependent hyphal regulation; fluconazole-induced

Phosphoenolpyruvate carboxykinase; role in gluconeogenesis; regulated by hyphal switch
Nucleoside permease; adenosine and guanosine are substrates, whereas cytidine, adenine and uridine are not
Putative transporter of the major facilitator superfamily (MFS); similar to Nag4p; required for growth on glucose
Putative polyamine transport protein; fungal-specific (no human or murine homolog)
Copper transporter; probably multimeric; transcribed if copper limited; induced by Mac1p, Irf1p
Putative high-affinity, high-capacity xanthine-uric acid/H⁺ symporter; similar to *A. nidulans* Xan1p

ORF Predicted by Annotation Working Group; macrophage/pseudohyphal-induced

NADP-glutamate dehydrogenase; hyphal downregulated expression; transcription is regulated by Nrg1p

Major cell-surface ferric reductase under low-iron conditions; 7 transmembrane regions and a cytoplasmic tail

Protein described as isocitrate dehydrogenase subunit; transcription is upregulated in response to iron
Predicted ORF in Assemblies 19, 20 and 21; induced by Rgt1p

Alternative oxidase; induced by antimycin A, some oxidants; growth- and carbon-source-regulated
Surface antigen on elongating hyphae and buds; no obvious hyphal defects in mutant; strongly induced by iron
Protein described as a putative precursor of a hyphal surface antigen; putative GPI-anchored

Predicted ORF in Assemblies 19, 20 and 21; regulated by Nrg1p, Tup1p; transcription is repressed by Tup1p
Putative homocitrate synthase; fungal-specific (no human or murine homolog); repressed by Tup1p
Predicted ferric reductase; gene alkaline-induced directly by Rim101p; iron-chelation-induced

Protein similar to ferric reductase Fre10p; expression greater in low iron; negatively regulated by Tup1p
Putative GPI-anchored protein of unknown function

ced during macrophage infection; fluconazole-downregulated; downregulated by Efg1p un
ry phase cultures
ed glycosylation; Tup1p repressed; serum, hyphal and alkaline induced; farnesol, alpha fac

lation by Ssn6p

c process and localizes to mitochondrion

le-induced; localizes to cell surface of hyphal cells, but not yeast-form cells; *S. cerevisiae* (

pecific (no human or murine homolog)

; Plc1p-regulated; repressed by Rim101p, Hog1p; colony morphology-related gene regulat
ntracellular acetyl-CoA transport; transcriptionally induced in macrophage; farnesol-upregu
or facilitator superfamily (MFS); amphotericin B, caspofungin repressed

nsporter family comprises 20 members; 12 probable membrane-spanning segments; indu
andins

ate and mature biofilms

stracts from biofilm and planktonic cells

onse to salt; regulated by macrophage, stress response, yeast-hyphal switch, pheromone,

tigenic during murine or human systemic infection; biofilm, Hog1p, GCN-induced; downreg

l localizes to plasma membrane

emic infection; no mammalian homolog; gene induced upon phagocytosis by macrophage

mutation affects filamentous growth; expression is regulated upon white-opaque switching

ssistant isolate, or in hyphae; biofilm induced; fluconazole-downregulated; protein abundan

specific (no human or murine homolog); caspofungin repressed; protein detected by mass spectrometry; methylation at position C-24; mutation confers nystatin resistance; fluconazole-induced upon phagocytosis; transcription is regulated by Mig1p and by white-opaque switching; transcription greater in high iron; induced during cell wall regeneration; Cyr1p or Ras1p downregulated

yeast infection; expression is opaque specific; has putative peroxisome targeting signal; white-opaque switching

superfamily; 12 transmembrane; gene has intron; oxidative stress-induced via Cap1p; expression downregulated by Rim101p; localizes to plasma membrane; similar to *S. cerevisiae* Jen1p; involved in regulation of lipid biosynthetic process, nuclear envelope organization, ascospore formation, and outer membrane

increased sensitivity to dyclonine

ras1 null mutant and decreased mRNA abundance in an efg1 null mutant; regulated by Nrg1p

secreted by human neutrophils; fluconazole-downregulated; regulated by Nrg1p and Mig1p; shows antigenicity; antigenic in murine, human infection; biofilm-, fluconazole-, or amino acid starvation (3- to 5-fold)

secreted; farnesol regulated

transcription is upregulated in both intermediate and mature biofilms

B repressed; regulated by Nrg1p, Tup1p

regulated by Nrg1p and Mig1p

fluconazole-induced; farnesol-downregulated in biofilm; farnesol-induced; surface localized

stationary phase cultures

filamentation and increased filamentation; fluconazole- and ketoconazole-induced; protein detected by mass spec

involved in ergosterol biosynthesis; target of azole antifungals; may contribute to drug resistance; azole-induced; colony morphology-related gene regulation by Ssn6p

protein detected by mass spec in stationary phase cultures; transcription is upregulated in stationary phase

in B repressed; caspofungin repressed; intron in 5'-UTR

secreted; surface, not hyphae; soluble in hyphae; iron-regulated expression; macrophage-downregulated; expression greater in cyr1 or ras1 homozygous null mutant than in wild type; protein detected by mass spec in stationary phase

secreted; downregulation correlates with clinical development of fluconazole resistance; amphotericin B

rowth; biofilm-induced; macrophage-downregulated protein; detected by mass spec in exp

in human; induced on polystyrene adherence; farnesol-, ketoconazole-induced; no huma
major cell-surface antigen; binds host plasmin/plasminogen; immunoprotective; phagocyt
ils

t with ciclopirox olamine; positively regulated by Sfu1p; Hog1p, fluconazole-downregulated
l complex assembly, meiotic recombination checkpoint and localizes to lateral element

acid beta-oxidation; similar to *S. cerevisiae* Pas10p peroxisomal targeting receptor; macro
regulated upon white-opaque switching; decreased expression in hyphae compared to yeast

icilitator superfamily) of transporters; preferred substrate may be mycophenolic acid; funga

in hyphae; Hog1p-induced; induced during cell wall regeneration; caspofungin or flucor
iosynthesis); biofilm-induced expression; regulated by Efg1p; regulated by Tsa1p, Tsa1Bp

an infection; regulated by yeast-hyphal switch; induced by Efg1p, Gcn4p, Hog1p, biofilm g
te-opaque switching; induced in core caspofungin response, during cell wall regeneration,

methylbutanal reductase activity, has role in filamentous growth, ergosterol metabolic proc
Hog1p regulated; induced on polystyrene adherence; downregulated upon phagocytosis, i
fatty acid catabolic process, ascospore formation and localizes to peroxisomal matrix

54.1, which is a region annotated as a blocked reading frame

cyr1 or ras1 homozygous null mutant than in wild type

osis; clinically-isolated homozygous null mutants show azole resistance, defects in hyphal g
uman; upregulated by Efg1p; macrophage-induced protein; soluble protein in hyphae; gen
ronectin and laminin; at surface of yeast-form cells and hyphae; soluble in hyphae; antigen
nic virulence; regulated by iron, ciclopirox olamine, fluconazole, growth, carbon source, pH

uman; regulated by Efg1p; induced in biofilm, upon adherence to polystyrene; downregula
ected by mass spec in exponential and stationary phase cultures

rotein in hyphae; transcription regulated by Nrg1p, Mig1p, and Tup1p; antigenic in human or
regulated by Gcn2p and Gcn4p

nscription is upregulated under treatment with caspofungin, ciclopirox olamine, ketoconaz
nt with ciclopirox olamine; Snf3p-induced; alkaline downregulated; shows colony morpholo
photeracin B, caspofungin repressed; possibly an essential gene, disruptants not obtained
regulated by Efg1p; fluconazole-induced; induced in core stress response; shows colony i
a pheromone in SpiderM medium

c evidence suggests that Set3p and Hos2p function together as a complex involved in regi
ilar to *S. cerevisiae* Pos5p, which is a mitochondrial NADH kinase involved in the oxidative
gulated in both intermediate and mature biofilms

human neutrophils; regulated by Efg1p; fluconazole-induced; shows colony morphology-re

low iron, or hemin; negatively regulated by Efg1p; expression greater in low iron; upregulated in low iron, CDR1 and CDR2 overexpression, or ssn6 or ssk1 homozygous null mutation; regulated by Gcn4p, Cyr1p; induced in response to amino acid starvation; macrophage-induced; required for aerobic hyphal growth and chlamyospore formation; subject to hypoxia-induced regulation; fluconazole-induced; caspofungin repressed

phosphorylated moiety of ceramides during glucosylceramide synthesis, which is important for virulence; transcription is induced upon phagocytosis by macrophage; regulated upon white-opaque switch

mutagenic in human or mouse; complements *S. cerevisiae* adh1 adh2 adh3 mutation; regulates ergosterol biosynthetic pathway; essential; target of allylamine antifungal drugs; uses NADH

induced in rat oropharyngeal infection models; regulated by Efg1p; fluconazole-induced; amphotericin B, caspofungin repressed; macrophage/pseudohyphal-induced; fungal-specific (no human homolog)

colony morphology-related gene regulation by Ssn6p; protein detected by mass spectrometry; activated by fructose 2,6-bisphosphate or AMP, inhibited by ATP; activity reduced on hypoxia

regulated by progesterone and by drugs including chloramphenicol and benomyl; likely essential for filamentous growth, phenotypic switching; homodimerizes; has APSES domain and activated by Efg1p and Efh1p; repressed by Rgt1p; protein detected by mass spec in exponential phase; macrophage-induced protein; antigenic in mouse; protein detected by mass spec in exponential phase (human homolog); amphotericin B repressed; protein detected by mass spec in stationary phase cultures

colony morphology-related gene regulation by Ssn6p

transmembrane transporter family comprises 20 members; 12 probable membrane-spanning segments; expressed in response to treatment with ciclopirox olamine, alpha pheromone; regulated by oxidative stress

induced upon biofilm formation; Hog1p-induced; expression of OPT6, -7, or -8 does not suppress growth in planktonic and stationary phase cultures

expressed in hyphae; changes in protein abundance associated with azole resistance; fluconazole or ketoconazole-induced; involved in catabolic process, D-xylose catabolic process, cellular response to oxidative stress and local response to neutrophils and macrophage blood fractions; downregulated during infection of macrophages; regulated by Ssn6p

essential for systemic and rabbit corneal infections; not required for filamentation; mRNA binds to Sfrp1

ed by O₂ or oxidizing agents H₂O₂ or menadione; caspofungin repressed; macrophage in
ak acid stress

osterol analog; farnesol-downregulated; protein detected by mass spec in stationary phase
redicted Kex2p substrate; induced during cell wall regeneration; possibly an essential gene
ivity, has role in pantothenate biosynthetic process and localizes to mitochondrion
s filamentous growth; repressed by amphotericin B, caspofungin; detected by mass spectr
ymes of ergosterol biosynthesis, catalyze formation of the C-22(23) double bond in the ste

ponent of membranes

egion and N-glycosylation motifs of Chs2p and Chs3p; alkaline downregulated; expression

rs, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage
berberine derivative drug inhibits enzyme activity; 7 putative transmembrane regions; ketc

1p but mutant phenotype suggests that it has a different set of target genes; transposon m
heavy metal (cadmium) stress via Hog1p; oxidative stress-induced via Cap1p; induced by
; PFK is activated by fructose 2,6-bisphosphate or AMP, inhibited by ATP; downregulated u

oxidative stress and required for full virulence; alkaline upregulated by Rim101p; upregulate
d

on infection of reconstituted human epithelium (RHE), while expression of the *C. dubliniens*

rol biosynthesis pathway; likely to be essential for growth; regulated by fluconazole and lo
ajor facilitator superfamily (MFS)
ilum membrane

pheromone in SpiderM medium

3 catabolism; D-arabitol is a marker for active infection in humans; has conserved YXXXK
ated

as role in lipid storage, triglyceride biosynthetic process

including acetyl CoA carboxylase and pyruvate carboxylase

gh iron, decreased upon yeast-hyphal switch; downregulation correlates with clinical develo
ate and mature biofilms

ownregulated; shows colony morphology-related gene regulation by Ssn6p; increased exp
r; expression greater in high iron; alkaline downregulated; shows colony morphology-relate
ells but is elevated at lower growth temperatures; upregulated in the presence of human n
; downregulated in core stress response

nolog); transcription is regulated by Nrg1p, Mig1p, Tup1p, and Gcn4p

esponse; upregulated in the presence of human neutrophils; regulated by Gcn2p and Gcn

ssed

enic in mice; benomyl treatment induces transcription; oxidative stress-induced via Cap1p
plandins

sensory signaling pathway and localizes to integral to membrane, plasma membrane, fung
by Tup1p, Efg1p

g25p and Erg26p; possible drug target, essential for viability; functional homolog of *S. cere*

in of the Ole1p delta-9-fatty acid desaturase

romoter; has Zn(2)-Cys(6) binuclear cluster; induced upon ergosterol depletion, by azoles
regulated by iron; expression greater in high iron; fluconazole-induced; shows colony mor

osterol analog; shows colony morphology-related gene regulation by Ssn6p; clade-associ
ible drug target; transcriptionally regulated by carbon source, yeast-hyphal switch, growth
lation by Ssn6p

tative bipartite mitochondrial targeting motif, membrane spanning region; transcription is re

3cn4p; Hog1p-downregulated; protein detected by mass spec in stationary phase cultures

sis; immunogenic; Hog1p, biofilm, possibly adherence-induced; brown colony color of hom
,3-oxidosqualene to lanosterol in sterol biosynthesis; fluconazole-induced; possibly an ess
hase cultures

for pathogenesis in host niches with limited CO₂, wild-type white-opaque switching; biofilr
pheromone in SpiderM medium

s with oral candidiasis; alkaline downregulated; amphotericin B induced; shows colony mo

wnregulated upon yeast-hyphal switch and regulated by Efg1p; strong oxidative stress ind
nslation and localizes to cytosolic ribosome, cytosol

has adhesin motif; O-glycosylation but no predicted N-glycosylation; induced by heat, upor
metal (cadmium) stress-induced; heterozygous null mutant displays sensitivity to virgineor
lony morphology-related gene regulation by Ssn6p; detected at plasma membrane of yea:

growth; Hog1p-downregulated; shows colony morphology-related gene regulation by Ssn6
gamma-aminobutyrate (GABA) as a nitrogen source

n101p or alkaline pH; transcription induced by interaction with macrophage or low iron; ox

phatase 1; fluconazole-induced; caspofungin repressed; transcriptionally activated by Mnl:

1p; biofilm-repressed expression; regulated by Tsa1p, Tsa1Bp under H₂O₂ stress conditions, purified from cell wall and intracellular fractions; protein repressed during the mating phase

ffects sensitivity to inhibitors of chitin and glucan synthesis; not required for yeast-to-hyphal transition; alkaline upregulated by Rim101p; repressed upon high-level peroxide stress; upregulated in response to ergosterol analog; oxidative stress-induced via Cap1p

acid starvation (3-aminotriazole treatment)

tionally regulated in response to lovastatin and fluconazole
rial translation and localizes to mitochondrion

hyphae; transcriptionally induced by macrophage interaction and by Mnl1p under weak acidic conditions

istance; similar to proteins of Menkes and Wilson disease; copper-induced; Tbf1p-activated; progesterone receptors involved in response to DNA damage; induced in core

.2) family, major facilitator superfamily (MFS)
nate biosynthetic process and localizes to cytoplasm, nucleus
cultures

array experiments

ultures

at 37 deg; shows colony morphology-related gene regulation by Ssn6p

.1) family, major facilitator superfamily (MFS)

white-opaque switching; fluconazole-induced; antigenic during murine systemic infection; regulated; tandem repeats; heterozygous mutant has cell wall defects; hyphal repressed; Hog1p-activated; regulated by Gcn2p and Gcn4p
complements *S. cerevisiae* aft1 mutant growth defect

cells; soluble in hyphae; regulated by Gcn4p, Efg1p, Efh1p; fluconazole-, farnesol-, biofilm inhibitor, ergosterol analog and to amphotericin B; alkaline downregulated; repressed by alpha pheromone

overall; not required for virulence in mouse systemic infection; homodimeric enzyme; possible vacuole lumen

IA abundance detected in homozygous null mutant; macrophage/pseudohyphal-repressed
essential gene, disruptants not obtained by UAU1 method

CDR1 and CDR2 overexpression or fluphenazine treatment; gene has putative drug-resistance function

hyphal induced; induced during cell wall regeneration; shows colony morphology-related gene

obtained by UAU1 method

yeast-hyphal transition; benomyl or caspofungin induced
log of *S. cerevisiae* and *E. coli* phosphomannose isomerase; Gcn4p-regulated; repressed
treatment with ciclopirox olamine; transcription is induced in response to alpha pheromone in

osmotic and oxidative stress (via Hog1p), cell wall regeneration, macrophage/pseudohyphal
induced in an azole-resistant strain that overexpresses MDR1
specific (no human or murine homolog)
filamentous growth-inducing conditions, but does not block true hyphal

and localizes to MutLbeta complex
cytoplasm, nucleus
secretory process and localizes to peroxisome

interacts with macrophage; fluconazole induced; Fkh2p-downregulated; caspofungin repressed
yeast-hyphal switch; fluconazole-induced; caspofungin repressed; protein detected by mass
spectrometry in stationary phase cultures; biofilm induced; oxidative stress-induced via Cap1p; induced by nitric oxide in yeast

gamma-dependent cotranslational protein targeting to membrane, translocation and localizes to cell
wall; protein detected by mass spec in stationary phase cultures

expressed at lower level in *ras1* homozygous null mutant than in wild type; expression upregulated by hypoxia, by

HIV+ patients with oral candidiasis

; suppresses toxicity of *C. albicans* Gcn4p overproduction in *S. cerevisiae* via increased PI

al subunits, translation factors, and tRNA synthetases are downregulated upon phagocytosis response; *S. cerevisiae* ortholog is essential for increased prostaglandin E2 production; functional homolog of *S. cerevisiae* Fet3p; ketoconazole

repressed; macrophage/pseudohyphal-repressed
(MFS) family, major facilitator superfamily (MFS)

mitochondrial large ribosomal subunit

obtained by UAU1 method

ability of *S. cerevisiae* gsp1 mutant; macrophage/pseudohyphal-induced; not transcriptionally regulated at rDNA and localizes to cytoplasm

CF-dependent proteasomal ubiquitin-dependent protein catabolic process, protein ubiquitination; cyclosporin A repressed

late and mature biofilms

filamentous growth; genes encoding cytoplasmic ribosomal subunits are downregulated upon infection; genes encoding ribosomal subunits, translation factors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage; protein Rna15p methylated and localizes to cytoplasm, nucleus

regulates core stress response; mutation confers hypersensitivity to amphotericin B

; coupled proton transport, protein oligomerization, cristae formation

induction in an RHE model; transcription induced in oral candidiasis clinical isolates; induced by

mitochondrial small ribosomal subunit

adhesion; induced upon adherence to polystyrene

expression greater in high iron; fluconazole-induced
regulation by Ssn6p

actors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophages; regulated by Tup1p; amphotericin B repressed; regulated by Gcn2p and Gcn4p
catabolic process, nuclear mRNA splicing, via spliceosome, maturation of SSU-rRNA
associated with oral candidiasis

obtained by UAU1 method
localizes to cytoplasm

amino acid starvation (3-aminotriazole treatment); transcriptionally regulated by iron; expr

chondrial small ribosomal subunit

/ and localizes to mitochondrial intermembrane space, nucleus

n into mitochondrial membrane from inner side and localizes to integral to mitochondrial in
membrane fraction (possible lipid raft component); alkaline downregulated

ctors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophagi
chondrial small ribosomal subunit

ble in hyphae; induced by ciclopirox olamine, ketoconazole or flucytosine; downregulated l

amphotericin B, phagocytosis, farnesol induced; fluconazole-downregulated; expression g

heavy metal (cadmium) stress; Hog1p regulated

ulated in biofilm; *S. cerevisiae* ortholog is Gcn4p regulated; repressed by nitric oxide; mac

l by Efg1p; repressed by nitric oxide

g cytoplasmic ribosomal subunits, translation factors, and tRNA synthetases are downregu

ctors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophagi
morphology-related gene regulation by Ssn6p

not crz2, null mutation suppresses fluconazole resistance of homozygous cka2 null (defect
:ndoplasmic reticulum

membrane fraction (possible lipid raft component); predicted N-terminal acetylation; repress

tion; regulated by Gcn4p; amino acid starvation (3-aminotriazole) induced; biofilm induced

; regulated by nitrogen source; alkaline, GlcNAc, phagocytosis upregulated; not required f

but not hyphal growth conditions; transcription is upregulated in an RHE model of oral car

mymerase II promoter by glucose, protein targeting to vacuole and localizes to ESCRT II cor

and macrophage-induced protein

se of nascent peptides from ribosomes

ion greater in high iron

a cellular spore and localizes to cytoplasm

t1p and Ycf1p; may transport organic anions conjugated to glutathione, glucuronate, or sul

ressed in response to amino acid starvation (3-aminotriazole treatment); heterozygous null i

heterozygous mutation confers hypersensitivity to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU) biosynthesis pathway; functionally complements *S. cerevisiae* lys1 mutation; fungal-specific (no human ortholog)

genes required for fatty acid degradation; induced by oleate; null mutant displays carbon source utilization defect

mitochondrial small ribosomal subunit; upregulated upon alkaline treatment; macrophage-induced protein; interacts with Rpp2Bp; one of four similar *C. albicans* ribosomal proteins (Rpp1Ap, Rpp2Ap, Rpp3Ap, Rpp4Ap)

essential for iron homeostasis and localizes to endoplasmic reticulum, fungal-type vacuole membrane; more abundant in more virulent strain; antigenic in human; flucytosine induced; translation-repressed

localizes to U1 snRNP, U2-type prespliceosome, U4/U6 x U5 tri-snRNP complex, U5 snRNP

ribosomal proteins, and tRNA synthetases are downregulated upon phagocytosis by murine macrophages; identified by UAU1 method

mitochondrial large ribosomal subunit

mitochondrial matrix

inositol phosphate biosynthetic process, nuclear-transcribed mRNA catabolic process, non-selenocysteine tRNA synthetase is the target of drugs including the cyclic beta-amino acid icofungipen/ICF

involved in glycosylation and localizes to alpha-1,6-mannosyltransferase complex

cellular homeostasis; physically interacts with TAP-tagged Nop1p

downregulated upon phagocytosis by murine macrophage; transcription is positively regulated by Tbf1p; more abundant in yeast-form cells

ribosomal proteins, and tRNA synthetases are downregulated upon phagocytosis by murine macrophages; growth in response to glucose limitation, cell budding, tRNA wobble position uridine thiolatic acid; involved in colony morphology-related gene regulation by Ssn6p; transcription is positively regulated by Ssn6p

mitochondrial large ribosomal subunit

essential for amino acid starvation (3-aminotriazole treatment); upregulated in the presence of human Assembled 21 based on comparative genome analysis

essential for amino acid starvation (3-aminotriazole treatment); protein detected by mass spec in stationary phase; cytoplasmic ribosomal subunits are downregulated upon phagocytosis by murine macrophages; transport and localizes to mitochondrion

rest

I break repair, DNA damage checkpoint, reciprocal meiotic recombination and localizes to mitochondrial large ribosomal subunit

ctors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage homolog of *S. cerevisiae* Gal4p, but not involved in the regulation of galactose utilization genes

ase I transcript, regulation of cell size, RNA elongation from RNA polymerase I promoter and

in detected by mass spec in exponential and stationary phase cultures

n (7-deazaadenosine); transcription is upregulated in both intermediate and mature biofilm

ytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)

chondrial large ribosomal subunit

lated by Gcn2p and Gcn4p

btained by UAU1 method

: snoRNA-binding protein; downregulated in core stress response; mutation confers resistance to development of fluconazole resistance; repressed by nitric oxide, 17-beta-estradiol, ethyl acetate; macrophage; alkaline downregulated; repressed by nitric oxide; clade-associated gene expression

; putative membrane protein; putative drug-responsive regulatory site; induced by fluphenazine; tRNA synthetases are downregulated upon phagocytosis by murine macrophage homolog of *S. cerevisiae* Gal4p; regulation by Ssn6p

: process and localizes to mitochondrion

role in translation and localizes to cytosolic large ribosomal subunit

mitochondrial respiratory chain complex assembly, mitochondrial translation and localizes to mitochondrial matrix and localizes to mitochondrial outer membrane translocase complex

major facilitator superfamily (MFS); alkaline upregulated by Rim101p; possibly an essential gene for response to oxidative stress, response to osmotic stress and localizes to cytoplasm

p-regulated; transcription is negatively regulated by Rim101p

actors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage
transferase activity and has role in GPI anchor biosynthetic process

tion of arginine residues; involved in nuclear export of Npl3p
biosynthesis; GCN-regulated; feedback-inhibited by phenylalanine when heterologously pr
insic to mitochondrial inner membrane, mitochondrial intermembrane space
IS

chondrial small ribosomal subunit; the snoRNA CD39 is encoded within the MRPS35 intron
Assembly 21 based on comparative genome analysis
amino acid cofungipen/PLD-118/BAY-10-8888 and mupirocin; detected by mass spec in ex

mitochondrial inner membrane and localizes to mitochondrial intermembrane space protein
ate and mature biofilms
biosynthesis; GCN-regulated; feedback-inhibited by tyrosine when produced in *S. cerevisiae*

has role in protein import into mitochondrial inner membrane
chondrial large ribosomal subunit

ors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage
chondrial small ribosomal subunit
chondrial small ribosomal subunit
ge/pseudohyphal-induced

s spec in exponential and stationary phase cultures
mediated transport and localizes to Golgi membrane, endoplasmic reticulum, ER to Golgi

y Ssn6p; flucytosine induced; caspofungin repressed; macrophage/pseudohyphal-induced

ylene

downregulated; downregulated by Efg1p; transcriptionally regulated by iron; expression (

major facilitator superfamily (MFS); possibly an essential gene, disruptants not obtained by U
respiration and localizes to mitochondrial large ribosomal subunit

ed in stationary phase cultures

y; transposon mutation affects filamentation; benomyl-induced transcription; detected at ye
ted by Rim101p at acid pH; transcription is activated in the presence of elevated CO₂; prot

in tRNA methylation and localizes to nucleus
expression; repressed by Rgt1p
expression; transcription is upregulated in clinical isolates from HIV+ patients with oral candidiasis

mitochondrial small ribosomal subunit
mitochondrial large ribosomal subunit
3'-end processing, negative regulation of telomere maintenance via telomerase and localizes to nucleus
colony morphology-related gene regulation by Ssn6p; transcription is positively regulated by Tpk1

transmembrane protein
transmembrane protein; 3 predicted transmembrane helices; flucytosine induced; ketoconazole-induced; d

mitochondrial large ribosomal subunit

major component of membranes; caspofungin induced; Plc1p-regulated; shows colony morphology
regulation by Ssn6p

mitochondrial large ribosomal subunit

transmembrane protein, and tRNA synthetases are downregulated upon phagocytosis by murine macrophages
homozygous null mutant; transcription is upregulated in both intermediate and mature biofilm
pigment

transmembrane protein and localizes to cytosolic large ribosomal subunit
essential for virulence, low-iron growth; iron, amphotericin B, caspofungin, ciclopirox, Hog1p regulated
expression; Mep2p has additional regulatory role; not essential for viability; 11 predicted transmembrane

mitochondrial large ribosomal subunit
transmembrane protein (human, murine homolog); upregulated in biofilm; acid upregulated/alkaline downregulated by Hsp90

transmembrane protein, and tRNA synthetases are downregulated upon phagocytosis by murine macrophages
transmembrane protein and localizes to cytosolic large ribosomal subunit
essential for virulence, low-iron growth; iron, amphotericin B, caspofungin, ciclopirox, Hog1p regulated
expression; Mep2p has additional regulatory role; not essential for viability; 11 predicted transmembrane
transmembrane protein and localizes to cytoplasm, nucleus

transmembrane protein has intron

transmembrane protein; regulation by Ssn6p; farnesol-, macrophage-downregulated protein abundance
transmembrane protein; activity, rotational mechanism and has role in ATP synthesis coupled proton transport

ent of fluconazole resistance; shows colony morphology-related gene regulation by Ssn6p; biofilm; two variable repeat regions; expression in *S. cerevisiae* does not confer adhesiveness; metal-induced; intron in 5'-UTR

mitochondrial large ribosomal subunit

, carbon source; repressed on glucose; induced by fluconazole, phagocytosis, H₂O₂; precise, guanine, uridine, uracil are not; similar to a nucleoside permease of *S. pombe*; possibly involved in wild-type mouse virulence and cycloheximide resistance; in gene cluster that includes genes

macrophage interaction, alkaline pH via Rim101p; 17-beta-estradiol downregulated; complexed with UapA; member of the Nucleobase-Ascorbate Transporter/Nucleobase-Cation Symporter (NACS) family

regulated by Nrg1p, Plc1p; downregulated by Efg1p; upregulated by Rim101p at pH 8; cyclopirox olamine

has a secretion signal predicted; repressed by Tup1p, Rim101p, Ssn6p, Hog1p, caspofungin

response to treatment with cyclopirox olamine; transcriptionally regulated by iron; expression generally

upregulated; one of two isoforms (Aox1p and Aox2p); involved in cyanide-resistant respiratory chain; variation in number of repeat domains; upregulated in filaments; alkaline upregulated by Rim101p; induced by cyclopirox olamine, ketoconazole, or by Rim101p at pH 8; regulated during plasmid shuffle

repressed in response to alpha pheromone in SpiderM medium

induced by nitric oxide and by hypoxia; protein level decreased in stationary phase cultures; induced by CCAAT-binding factor; fluconazole-downregulated; cyclopirox olamine and hypoxia induced

regulated by Sfu1p; cyclopirox olamine, flucytosine induced; amphotericin B repressed; transcript

in yeast, not hyphal, growth conditions; predicted to be cytosolic
TOR induced; Rfg1p-, Rim101p-regulated

Gph1p is a stress-regulated protein of glycogen metabolism
induced by Ssn6p; induced by ketoconazole and by hypoxia
induced in biofilm; Hog1p-downregulated
induced at low (0.2%, compared to 2%) glucose in rich media

GCN4, HOG1, NRG1, TUP1; antigenic in murine systemic infection
induced upon phagocytosis; possible N-glycosylation at N349

; farnesol regulated; Pex5p-dependent peroxisomal localization
expression is affected by URA3 expression in the CAI-4 strain background

c in stationary phase cultures

luced; transcription increased in azole-resistant strain

ranscriptional activation by oleate requires Ctf1p
egulated; transcription is positively regulated by Tbf1p

ressed in rich medium, 2% glucose

rg1p, Tup1p, Tbf1p, Ssn6p

s colony morphology-related gene regulation by Ssn6p
aminotriazole treatment) induced, farnesol-downregulated

l in yeast-form and hyphal cells; antigenic in host

y mass spec in stationary phase cultures

· or biofilm-induced; subject to hypoxic regulation

both intermediate and mature biofilms

ted; not Rfg1p regulated, farnesol-induced; possibly essential
tationary phase cultures

ericin B repressed; caspofungin repressed

ponential and stationary phase cultures; possibly an essential gene

n or murine homolog

osis, biofilm-regulated; farnesol-downregulated; possibly essential

l

phage/pseudohyphal-repressed

-form cells; regulated by Nrg1p; fungal-specific

al-specific (no human or murine homolog)

razole-induced; Mnl1p-induced in weak acid stress

under H₂O₂ stress conditions

rowth, or fluconazole; phagocytosis-repressed; fungal-specific

or by flucytosine; fungal-specific (no human or murine homolog)

ress and localizes to cytoplasm, nucleus

farnesol treatment; mutation affects filamentation

growth and virulence; Efg1p-repressed; fluconazole-induced

ie contains an intron

ic during infection; farnesol-downregulated

l, Rim101p, Ssn6p, Hog1p, farnesol, core stress response

ited in the presence of human neutrophils, upon phagocytosis

r murine infection; possibly essential (by UAU1 method)

ole or hypoxia; gene of core caspofungin response

ogy-related gene regulation by Ssn6p; possibly essential gene

by UAU1 method

morphology-related gene regulation by Ssn6p

ulation of white-opaque switching, morphogenesis, and virulence

stress response

elated gene regulation by Ssn6p

ated by Rim101p at pH 8
; repressed by Hog1p, flucytosine, elevated CO2
iced protein, macrophage-downregulated gene

oxic regulation; fluconazole-induced; caspofungin repressed

ketoconazole and hypoxia induced

witching; biofilm-repressed; strong oxidative stress induced

ated by growth phase, carbon source; fluconazole-, farnesol-induced
as a reducing cofactor, while *S. cerevisiae* Erg1p uses NADPH

sin B repressed
(human or murine homolog)

try in stationary phase cultures
hal induction; phagocytosis-downregulated; fluconazole-induced

al for growth, based on an insertional mutagenesis strategy
cidic region; EFG1 and EFH1 genetically interact
al and stationary phase cultures
and stationary phase cultures

ressed in rich medium with 2% glucose

stress (via Cap1p) and osmotic stress (via Hog1p)

s defect of mutant lacking Opt1p, -2p, or -3p; fungal-specific

toconazole induced; macrophage-downregulated protein
lizes to cytoplasm, nucleus
crophages

ie3p and is localized to hyphal tips

duced; induced in core stress response; regulated by Gcn2p, Gcn4p

3 cultures

3, disruptants not obtained by UAU1 method

ometry in exponential and stationary phase cultures

rol side chain; transposon mutation affects filamentous growth

n not detected in yeast-form or hyphal cells

onazole-induced

utation affects filamentous growth

Mnl1p under weak acid stress; macrophage-downregulated

upon phagocytosis or hyphal growth; fluconazole-induced

3d in the presence of human blood

sis ortholog is not upregulated; not required for viability

vastatin; amphotericin B, caspofungin repressed

motif of short-chain alcohol-polyol-sugar dehydrogenases

opment of fluconazole resistance; Ras1p-regulated

ression in response to prostaglandins

ed gene regulation by Ssn6p

eutrophils; detected by mass spec in stationary phase cultures

14p; putative N-glycosylation

; fungal-specific (no human/murine homolog), farnesol-downregulated

al-type vacuole

evisiae Erg27p

, anaerobicity; macrophage/pseudohyphal-repressed
morphology-related gene regulation by Ssn6p

ated gene expression
phase, antifungals; gene has intron

regulated upon yeast-hyphal switch, or by Nrg1p, Mig1p, Tup1p

ozygous mutant in Pb(2+) medium is visual selection marker
essential gene, disruptants not obtained by UAU1 method

n induced; activated by Mnl1p under weak acid stress

morphology-related gene regulation by Ssn6p

luced; shows colony morphology-related gene regulation by Ssn6p

germ tube formation, wall regeneration; diagnostic marker
ne
st-form and germ tube by mass spectrometry

ip; induced during cell wall regeneration; possibly essential gene

xygen-induced activity

1p under weak acid stress; regulated by Nrg1p, Tup1p

ons

rocess; Hog1p-, farnesol-induced; possibly essential

transition or for virulence in mouse systemic infection
oral candidiasis clinical isolates; possibly essential gene

stress; farnesol-induced

ed; suppresses Cu sensitivity of *S. cerevisiae* cup1 null mutant
stress response; Hog1p regulated; clade-associated expression

regulated by Nrg1p, Tup1p; macrophage-downregulated protein
1p, fluconazole, hypoxia induced; iron, Efg1p, Plc1p regulated

n-induced; repressed upon amino acid starvation
ne in SpiderM medium; possibly essential gene (by UAU1 method)

sible regulatory cAMP-dependent phosphorylation at S10 and S213

; possibly an essential gene, disruptants not obtained by UAU1 method

onsive regulatory site; similar to *S. cerevisiae* Wwm1p

ne regulation by Ssn6p; transcription activated by Tbf1p

by 3-AT; induced on adherence to polystyrene, phagocytosis

γ SpiderM medium

ial growth, core stress response; possibly essential (UAU1 method)

γphal formation in liquid media

is spec in stationary phase cultures
hb1 mutant

endoplasmic reticulum

' ketoconazole and during growth in the mouse cecum

ho85p-dependent phosphorylation and degradation of Gcn4p

sis by murine macrophage; transcription activated by Tbf1p

ole, caspofungin, amphotericin B repressed

ally regulated during white-opaque or yeast-hyphal switching

ination, regulation of DNA replication

γ phagocytosis by murine macrophage

nregulated upon phagocytosis by murine macrophage

detected by mass spec in stationary phase cultures

fluconazole, high cell density; hyphally regulated

ge; repressed by nitric oxide

expression greater in high iron

inner membrane

expression; transcription is positively regulated by Tbf1p

regulated by Efg1p, caspofungin; possibly essential

expression greater in high iron; antigenic in human or murine infection

macrophage-induced protein; farnesol-downregulated

internalized upon phagocytosis by murine macrophage

expression

expression sensitive to CK2 kinase inhibition; Rim101p-downregulated at pH 8

expression repressed by nitric oxide; plasma membrane-localized

expression; macrophage-downregulated protein; no human or murine homolog

expression required for virulence in mouse systemic infection; fungal-specific

expression; detected by mass spec in stationary phase cultures

expression complex

expression required for virulence in mouse peritonitis model

expression mutant exhibits resistance to parnafungin

5-FU), and tubercidin (7-deazaadenosine)
human or murine homolog)

ce utilization defects and slightly reduced virulence

pp1Bp, Rpp2Ap, Rpp2Bp)

ne

related genes are downregulated upon phagocytosis

ge; colony morphology-related gene regulation by Ssn6p

stability; rapid decay and localizes to nucleus
LD-118/BAY-10-8888 and mupirocin

; intron in 5'-UTR

ge

ion, cellular response to oxidative stress
by Tbf1p

whole blood or polymorphonuclear (PMN) cells

early phase cultures
prophage; possibly essential

checkpoint clamp complex

e
es; caspofungin repressed

nd localizes to DNA-directed RNA polymerase I complex

s

ance to 5-fluorocytosine (5-FC) and parnafungin
nyl estradiol
ession

azine, estradiol, ketoconazole, caspofungin
ge; repressed by nitric oxide

ondrial small ribosomal subunit

gene, disruptants not obtained by UAU1 method

ge; downregulated by growth in the mouse cecum

roduced in *S. cerevisiae*; Aro3p and Aro4p catalyze the same reaction

in

ponential and stationary phase cultures

1 transporter complex

ae; fungal-specific; Aro3p and Aro4p catalyze the same reaction

transport vesicle

greater in high iron

JAU1 method

east-form cell plasma membrane by mass spec
tein detected by mass spec in stationary phase cultures

zes to nucleoplasm, nucleolus
Tbf1p

lowregulated by Efg1p

phology-related gene regulation by Ssn6p

ge
ns

ated; complements *S. cerevisiae* *ftr1* iron transport
lbrane regions; low mRNA abundance; hyphal downregulated

Rim101p; regulated by Gcn2p, Gcn4p; strain CA9 is a *his1* mutant

ge

)
ess; ALS family includes adhesins, cell-surface glycoproteins

licted ATP-dependent, dimeric; predicted PKC phosphorylation sites
processed by Kex2p
enes encoding enzymes of GlcNAc catabolism

lements *S. cerevisiae* ctr1 ctr3 copper transport mutant
NAT/NCS2) family

x olamine and ketoconazole induced; transcript repressed by hypoxia

; ciclopirox olamine induced; not required for filamentous growth

reater in high iron

pathway that is absent from *S. cerevisiae*
y Rim101p; ciclopirox induced; Efg1p- and Cph1p-regulated
anktonic growth; induced during cell wall regeneration

:d by ketoconazole
induced; colony morphology-related gene regulation by Ssn6p

tion is positively regulated by Tbf1p

f

Legend**Cpar2 ID** Cpar2 ID**Cpar ID** Cpar ID**C. albicans O** C. albicans ortholog**log2(FC)micro** log fold change in gene expression from the microarray data from the
log fold change in gene expression from the**log2(FC)micro** microarray data from the second oligo**C. albicans.g** C. albicans ortholog gene name**Description** Description of C. albicans ortholog, from CandidaGenomeDatabase.c

Cpar2.ID	Cpar.ID	C.albicans	log.FC..mi	log.FC..mi	P_value1	P_value
cpar2_404850	cpar2047		6.47635191	6.44895041	7.44E-13	3.39E-12
cpar2_503990	cpar4494	orf19.5437	5.17316511	5.16321915	7.44E-13	7.44E-13
cpar2_100830	cpar5643		4.666202	4.54598068	1.31E-10	6.67E-09
cpar2_301400	cpar3264	orf19.7021	4.25035488	3.32958476	1.14E-09	5.70E-05
cpar2_402640	cpar1351		3.98178548	3.57019977	5.86E-11	1.49E-08
cpar2_403510	cpar3326	orf19.1327	3.95713826	3.17604269	5.83E-10	2.49E-08
cpar2_209460	cpar608	orf19.6882	3.94134233	3.77195543	1.70E-10	1.14E-09
cpar2_602950	cpar5357	orf19.3651	3.88105666	4.0827703	9.03E-11	2.29E-10
cpar2_203450	cpar4091	orf19.638	3.84802441	1.15538968	1.04E-08	5.17E-05
cpar2_103450	cpar2798	orf19.2803	3.71054693	3.52765836	3.12E-10	4.12E-10
cpar2_807620	cpar4305	orf19.1653	3.62215513	3.6071771	2.67E-11	1.83E-10
cpar2_207210	cpar517	orf19.395	3.53319816	3.62348652	2.11E-11	6.34E-11
cpar2_404310	cpar655	orf19.5323	3.51997563	3.27303635	6.42E-11	6.61E-11
cpar2_211810	cpar1245	orf19.903	3.51485514	3.19295116	2.17E-11	5.86E-11
cpar2_502580	cpar427	orf19.3997	3.49801764	3.51188868	2.52E-11	4.45E-11
cpar2_201490	cpar1554		3.47910836	3.58326342	1.73E-10	5.47E-08
cpar2_804310	cpar5421	orf19.4737	3.43884546	3.02214589	6.38E-11	1.02E-09
cpar2_603610	cpar5292	orf19.4210	3.43133312	3.33259385	5.96E-09	1.78E-08
cpar2_401230	cpar1881	orf19.4618	3.37422097	3.28358887	2.14E-11	1.20E-10
cpar2_704060	cpar903		3.315065	3.07628164	3.02E-09	8.78E-09
cpar2_300740	cpar3422		3.28335138	2.48486791	1.20E-10	1.01E-05
cpar2_502810	cpar450	orf19.2496	3.26825801	2.63707834	6.61E-11	1.04E-06
cpar2_109010	cpar5561	orf19.3053	3.22264571	3.14364085	1.93E-10	3.25E-09
cpar2_808670	cpar560	orf19.6814	3.21848472	3.32867459	8.19E-10	1.27E-09
cpar2_400970	cpar1907	orf19.4631	3.20558083	3.22801921	2.52E-11	2.67E-11
cpar2_501020	cpar3013	orf19.2877	3.20319417	3.06423286	6.61E-11	5.16E-10
cpar2_105550	cpar1643	orf19.767	3.123409	3.29068162	1.30E-08	4.77E-08
cpar2_100710	cpar5633	orf19.4255	3.111385209	3.03185978	1.64E-10	9.50E-10
cpar2_406210	cpar2182	orf19.1862	3.11057684	3.111007325	9.59E-10	7.11E-09
cpar2_203720	cpar4062	orf19.4784	3.10516694	2.47093343	6.71E-10	1.85E-07
cpar2_206020	cpar4399	orf19.542	3.05835159	2.44064505	5.29E-10	3.37E-07
cpar2_303740	cpar2497	orf19.922	3.01325405	3.15746476	6.40E-09	1.11E-08
cpar2_404240	cpar4393	orf19.1354	3.00985166	2.9401639	6.38E-11	1.83E-10
cpar2_108280	cpar3566	orf19.4530.1	2.9931372	2.90090437	3.33E-09	1.28E-08
cpar2_807980	cpar5389	orf19.6745	2.96742923	2.8231501	1.70E-10	1.83E-10
cpar2_204260	cpar4011	orf19.734	2.94039721	2.75215353	1.70E-10	7.14E-10
cpar2_808490	cpar577	orf19.7459	2.92843561	2.94327502	4.45E-11	6.42E-11
cpar2_200280	cpar1742	orf19.7676	2.91765566	2.83917006	3.37E-10	1.45E-07
cpar2_209240	cpar623	orf19.3575	2.91508468	2.98361359	4.97E-10	5.21E-10
cpar2_602260	cpar1204	orf19.3419	2.8815231	3.05382259	2.15E-08	2.93E-08
cpar2_304060	cpar3708	orf19.944	2.86651713	2.57170187	6.34E-11	6.61E-11
cpar2_405010	cpar2063	orf19.1631	2.83012804	2.60854836	2.56E-09	0.00029733
	cpar394		2.82161034	2.7053241	1.79E-07	3.45E-05

cpar2_800220	cpar3883	orf19.2841	2.8024598	2.81141698	6.42E-11	7.87E-11
cpar2_402940	cpar1322	orf19.5293	2.79257611	2.83354414	2.60E-09	1.56E-08
cpar2_703030	cpar5690	orf19.6540	2.75863603	2.58943299	7.87E-11	5.16E-10
cpar2_101070	cpar2474	orf19.3967	2.71531383	2.59059377	1.83E-10	6.24E-08
cpar2_405780	cpar2140		2.6888037	2.82233884	2.82E-10	3.37E-10
cpar2_808660	cpar561	orf19.6816	2.68115296	2.55967166	7.22E-11	9.33E-11
cpar2_407170	cpar357	orf19.1756	2.6732674	2.61393973	1.65E-10	3.37E-10
cpar2_804060	cpar1607	orf19.7466	2.62301406	2.07035079	6.35E-08	0.00048485
cpar2_701390	cpar1159		2.62147092	2.48459099	1.96E-10	1.75E-09
cpar2_210480	cpar2721	orf19.406	2.60473096	2.4152933	4.34E-09	1.01E-06
cpar2_109780	cpar2652	orf19.3306	2.60201524	2.55140423	1.15E-10	1.65E-10
cpar2_301610	cpar3285	orf19.7085	2.56211617	2.33599419	2.82E-10	6.38E-10
cpar2_204880	cpar258	orf19.3888	2.56001852	2.38980474	2.01E-10	5.61E-08
cpar2_808820	cpar545	orf19.6800	2.5236999	2.76849822	8.10E-11	1.75E-10
cpar2_804740	cpar5463	orf19.5112	2.51027622	2.42358495	1.31E-08	2.18E-07
cpar2_502820	cpar451		2.46640417	2.01801447	1.28E-07	1.40E-06
cpar2_301300	cpar3254		2.45454307	2.39270983	1.70E-10	1.71E-07
cpar2_405900	cpar2151	orf19.1598	2.42283194	2.44518394	1.30E-09	3.72E-09
cpar2_210700	cpar2743		2.41605727	2.64549448	5.71E-08	9.31E-08
cpar2_206900	cpar2409	orf19.5117	2.40301218	2.15310455	6.67E-09	2.15E-08
cpar2_702400	cpar5751	orf19.7043.1	2.39206731	2.43208737	7.45E-09	1.29E-08
cpar2_500850	cpar2996	orf19.1290	2.38599028	2.30059681	3.66E-08	4.64E-07
cpar2_108000	cpar5018	orf19.55	2.343972	2.19412024	8.61E-07	1.25E-06
cpar2_103400	cpar2803	orf19.338	2.3424362	2.26280008	1.49E-10	2.28E-08
cpar2_202130	cpar4220	orf19.6992	2.27189928	1.91661623	2.90E-08	7.88E-08
cpar2_106140	cpar4836	orf19.3672	2.21414597	2.2187789	6.72E-10	1.13E-09
cpar2_400570	cpar1945	orf19.4657	2.17400458	2.11601698	1.09E-08	1.52E-08
cpar2_302650	cpar2029	orf19.979	2.1688985	1.99481719	1.15E-07	1.70E-07
cpar2_209770	cpar2250	orf19.6877	2.16606776	2.05988922	4.96E-10	6.72E-10
cpar2_213720	cpar1102	orf19.1917	2.15606902	2.24629902	2.23E-09	2.73E-09
cpar2_400960	cpar1908	orf19.4639	2.14227903	2.09250196	3.03E-10	2.09E-08
cpar2_209220	cpar621	orf19.2308	2.11477572	2.19292932	5.01E-10	1.28E-09
cpar2_106960	cpar4917	orf19.1064	2.07700435	1.96849121	1.99E-08	5.20E-08
cpar2_502980	cpar466	orf19.5379	2.07388803	2.09497916	3.53E-08	4.66E-08
	cpar1157		2.0585244	2.05749839	9.51E-10	1.00E-09
cpar2_401300	cpar1874	orf19.4591	2.04383151	1.84598651	3.99E-07	4.51E-07
cpar2_802250	cpar5083	orf19.2396	2.04223794	2.13910679	2.55E-08	4.30E-08
cpar2_703970	cpar911	orf19.5178	2.04017919	1.51959636	1.54E-09	3.87E-08
cpar2_405810	cpar2143	orf19.1743	2.02054677	1.87992157	2.21E-07	1.70E-06
cpar2_804260	cpar5416	orf19.4735	1.98463334	1.88875302	5.55E-10	3.85E-09
cpar2_401550	cpar3468		1.98102891	2.13464972	1.52E-09	2.79E-08
cpar2_802240	cpar5084	orf19.2397	1.9773227	1.49720569	1.44E-08	1.28E-07
cpar2_101620	cpar5252	orf19.3171	1.97229	2.0228975	2.32E-06	2.34E-06
cpar2_211700	cpar2290	orf19.909.1	1.95362206	1.9956911	8.88E-08	1.42E-07
cpar2_600270	cpar787	orf19.5615	1.93826685	1.27662507	5.04E-06	1.41E-05
cpar2_601230	cpar3664	orf19.5727	1.9334286	2.03613919	7.01E-07	1.07E-06
cpar2_701400	cpar1158	orf19.7312	1.93098527	1.82970524	2.60E-09	3.97E-08
cpar2_402140	cpar3527	orf19.5673	1.9182409	1.81179214	7.11E-09	3.53E-08
cpar2_808750	cpar552	orf19.6757	1.9090069	1.73802203	3.04E-09	1.09E-07
cpar2_807400	cpar4326	orf19.5949	1.90310894	1.58496318	4.14E-07	4.93E-07
cpar2_500350	cpar2946	orf19.2769	1.87975053	1.79798719	1.19E-07	1.25E-07
cpar2_203520	cpar4083	orf19.5024	1.8742637	1.84858811	2.63E-07	2.52E-06
cpar2_105770	cpar4560	orf19.6057	1.86429833	1.84248889	8.08E-09	7.68E-08
cpar2_212810	cpar1014	orf19.1591	1.85824727	1.35644797	1.44E-07	4.10E-06
cpar2_402900	cpar1326	orf19.5635	1.85031561	1.3898651	2.45E-08	2.96E-08
cpar2_703370	cpar971		1.83693351	1.75834182	4.50E-09	2.55E-08
cpar2_105460	cpar1652	orf19.775	1.83627378	1.58963648	1.11E-08	2.60E-08
cpar2_807310	cpar4335	orf19.6007	1.83593559	1.73248719	2.09E-08	2.64E-08

cpar2_806350	cpar2002	orf19.3605	1.81974208	1.87391285	4.15E-09	1.71E-07
cpar2_201370	cpar1542	orf19.7284	1.81636781	1.91541713	1.27E-09	2.16E-09
cpar2_212860	cpar1019	orf19.2023	1.80872648	1.76766595	1.14E-09	1.52E-08
cpar2_301770	cpar3301	orf19.4754	1.796803	1.46641791	2.95E-09	1.38E-06
cpar2_301310	cpar3255		1.78351613	1.63230387	1.50E-07	5.83E-07
cpar2_100090	cpar5573	orf19.4043	1.77620467	1.67695646	9.56E-08	1.04E-06
cpar2_700580	cpar57	orf19.7221	1.76954846	1.79884819	2.60E-08	2.48E-07
cpar2_403180	cpar3358	orf19.2765	1.76544389	1.58037895	2.68E-07	0.00015659
cpar2_102630	cpar3406	orf19.288	1.76473087	1.72289273	1.82E-07	2.55E-07
cpar2_212160	cpar3743	orf19.5801	1.75382328	1.55363526	6.31E-07	6.70E-06
cpar2_208360	cpar1410	orf19.5054	1.73536841	1.67159238	5.67E-09	6.40E-09
cpar2_300120	cpar2874	orf19.7114	1.73226775	1.53450213	1.33E-07	3.00E-07
cpar2_805790	cpar1818	orf19.7446	1.73092965	1.66921599	1.20E-08	5.46E-05
cpar2_700380	cpar38	orf19.4980	1.72623441	1.37820034	0.00076701	0.00266069
cpar2_403160	cpar1301		1.7148897	1.63531154	3.13E-08	3.53E-08
cpar2_100530	cpar5617	orf19.1974	1.70907236	1.65728496	5.13E-08	4.06E-07
cpar2_300320	cpar2894		1.70464639	1.80382248	3.85E-09	4.12E-08
cpar2_801560	cpar5153	orf19.3240	1.6991798	1.57428201	2.87E-07	0.0043045
cpar2_106620	cpar4883	orf19.2952	1.68962738	1.53539804	3.08E-07	4.56E-06
cpar2_210630	cpar2736	orf19.5818	1.68226391	1.52766293	1.02E-08	3.76E-08
cpar2_406760	cpar2238	orf19.3616	1.67428978	1.83340539	8.96E-08	4.35E-07
cpar2_102080	cpar4692	orf19.260	1.66632453	1.51571389	1.14E-06	9.86E-06
cpar2_704260	cpar883	orf19.5158	1.6615278	1.65943417	1.57E-07	3.19E-07
cpar2_209600	cpar594	orf19.4128	1.65857955	1.37840276	1.04E-06	9.08E-06
cpar2_202280	cpar4205	orf19.489	1.64947347	1.47412368	8.61E-09	2.15E-06
cpar2_108230	cpar745		1.64737004	-0.13129391	1.28E-07	0.29367997
cpar2_406800	cpar390	orf19.2242	1.64101656	1.56465695	7.05E-08	1.47E-07
cpar2_804900	cpar4671	orf19.4836	1.63820199	1.34130425	5.80E-08	4.92E-07
cpar2_803840	cpar1585		1.6350345	1.35211086	7.54E-08	2.32E-05
cpar2_402910	cpar1325	orf19.5636	1.62649713	1.46591332	8.79E-06	2.00E-05
cpar2_108320	cpar180	orf19.4526	1.61506007	1.47895065	1.05E-06	1.18E-06
cpar2_404120	cpar4381		1.60735194	0.47654545	2.55E-08	0.00947727
cpar2_302800	cpar2587	orf19.4246	1.59643975	1.53712311	3.53E-09	1.83E-08
cpar2_106980	cpar4919	orf19.1067	1.59539546	1.38180198	3.22E-09	2.07E-08
cpar2_208430	cpar1404	orf19.5063	1.58357439	1.43446055	3.48E-08	2.86E-07
cpar2_602960	cpar5356	orf19.3649	1.57629283	1.50024078	9.80E-08	2.60E-05
cpar2_501170	cpar3028	orf19.2897	1.5748993	1.45413243	1.11E-07	2.64E-07
cpar2_201730	cpar4259	orf19.4982	1.56662583	1.8876948	5.47E-09	9.55E-09
cpar2_600530	cpar813	orf19.5622	1.54505418	1.16424456	1.23E-06	0.00014527
cpar2_207280	cpar2339	orf19.391	1.54448192	1.24819378	2.58E-08	5.97E-08
cpar2_100920	cpar1163	orf19.3921	1.54023589	1.59107657	8.30E-08	2.21E-07
cpar2_808260	cpar5646	orf19.6731.1	1.52861892	1.54937215	5.53E-08	6.15E-08
cpar2_106210	cpar4843	orf19.3679	1.50871172	1.44230123	4.40E-06	9.92E-06
cpar2_212450	cpar981	orf19.1505	1.50430548	1.38808262	1.36E-08	5.80E-08
cpar2_206270	cpar669	orf19.3278	1.50104458	1.35862055	1.15E-07	2.57E-06
cpar2_700920	cpar91		1.49799651	1.43680203	2.03E-07	9.05E-06
cpar2_204270	cpar4010	orf19.11	1.4978132	1.461119403	1.25E-07	1.00E-06
cpar2_302890	cpar2579	orf19.6679	1.49744528	1.30912089	1.01E-06	1.50E-05
cpar2_106650	cpar4886	orf19.2948	1.49440304	1.56648032	7.96E-08	1.76E-07
cpar2_211270	cpar3141	orf19.842	1.49102942	1.67736372	9.57E-09	7.72E-08
cpar2_202940	cpar4141	orf19.4979	1.48796659	1.03220633	1.40E-06	0.00189092
cpar2_202640	cpar4171	orf19.4953	1.48414827	1.32604515	2.09E-07	1.08E-06
cpar2_500390	cpar2950	orf19.2770.1	1.48089826	1.04864268	6.15E-08	3.60E-06
cpar2_601670	cpar1379	orf19.5525	1.46300541	1.67961952	9.49E-09	3.94E-08
cpar2_204280	cpar4009	orf19.9	1.45453177	1.04218625	2.38E-05	0.00024598
cpar2_703660	cpar942	orf19.1340	1.45311785	1.2960274	1.14E-06	9.75E-06
cpar2_211260	cpar3142	orf19.843	1.44771262	1.2330268	5.80E-08	2.74E-06
cpar2_209840	cpar2257	orf19.5216	1.43929208	1.44204246	1.30E-07	4.64E-06

cpar2_109890	cpar5489	orf19.6026	1.43659379	1.15917073	7.08E-07	1.84E-05
cpar2_109870	cpar5491		1.43286711	1.38979031	5.66E-07	2.97E-06
cpar2_109530	cpar3203	orf19.6105	1.43255817	1.31600743	7.82E-08	4.92E-07
	cpar5534	orf19.3038	1.43174911	1.33134502	8.03E-08	7.50E-06
cpar2_301730	cpar3297	orf19.4752	1.43170263	1.23808047	7.08E-07	3.17E-05
cpar2_406050	cpar2166	orf19.1390	1.43131591	1.10392504	4.65E-07	6.73E-05
cpar2_102580	cpar4739		1.42489392	1.27122261	2.95E-05	0.00010109
cpar2_202600	cpar4175	orf19.4371	1.42352684	1.46838535	2.99E-08	2.94E-07
cpar2_211230	cpar3145		1.42236305	1.16604599	1.45E-07	2.78E-07
cpar2_103440	cpar2799	orf19.7597	1.41834242	0.91081355	2.68E-06	3.06E-05
cpar2_208580	cpar1390		1.41488606	1.22475715	1.74E-05	0.00032049
cpar2_207460	cpar2358	orf19.4740	1.41435305	1.59608973	2.87E-08	6.75E-08
cpar2_803090	cpar4799	orf19.2531	1.41079793	1.44346571	9.57E-09	2.54E-08
cpar2_407410	cpar3799	orf19.1779	1.40901696	1.16089891	1.61E-06	2.95E-06
cpar2_208800	cpar834	orf19.6202	1.40236066	1.57140485	6.35E-08	4.77E-07
cpar2_602050	cpar1225	orf19.5576	1.39812118	1.30554543	2.87E-07	1.67E-06
cpar2_101350	cpar2447	orf19.4317	1.3943731	1.16848352	0.00020636	0.00098032
cpar2_211280	cpar3140	orf19.847	1.38564354	1.15452328	5.40E-08	2.59E-07
cpar2_104530	cpar5235	orf19.541	1.38330918	1.02356094	1.85E-07	0.00029869
cpar2_201200	cpar1525		1.38086745	1.19027946	4.70E-07	1.24E-05
cpar2_601530	cpar3583	orf19.5611	1.37509459	1.40979455	7.32E-07	1.87E-06
cpar2_201990	cpar4233	orf19.6117	1.37477338	1.50762544	9.55E-07	2.63E-06
cpar2_601690	cpar1381	orf19.5523	1.37345817	1.2171583	1.55E-07	1.85E-06
cpar2_300190	cpar2881	orf19.7106	1.37239201	1.24965959	9.77E-08	6.96E-07
cpar2_106080	cpar4830	orf19.2977	1.36885767	1.38062514	5.68E-08	5.00E-06
cpar2_206650	cpar706	orf19.4444	1.3479189	1.22643345	7.84E-08	2.34E-07
cpar2_109770	cpar2651	orf19.3307	1.34653676	1.16485755	0.00299279	0.00635921
cpar2_407630	cpar3819	orf19.35	1.3419863	0.93995994	1.43E-07	8.92E-06
cpar2_805340	cpar4627		1.34166338	0.97620357	1.54E-05	0.00053968
cpar2_805040	cpar4657	orf19.4886	1.34073015	1.26355072	8.90E-08	6.62E-05
cpar2_803890	cpar1590	orf19.4833	1.33846513	1.09208529	1.02E-07	1.28E-07
cpar2_807870	cpar5400	orf19.6189	1.32191059	1.00163946	8.95E-07	9.10E-07
cpar2_704270	cpar882	orf19.5157	1.31888916	1.2545858	6.01E-08	1.19E-05
cpar2_800970	cpar3954	orf19.2608	1.31768097	1.03896877	5.27E-06	2.81E-05
cpar2_703940	cpar914	orf19.7196	1.31562469	1.19457931	0.00017574	0.00146255
cpar2_404840	cpar2046	orf19.7417	1.3150654	1.39683423	3.14E-07	1.39E-05
cpar2_101480	cpar5365	orf19.3974	1.31264944	1.3986465	1.25E-07	4.18E-05
cpar2_101160	cpar2465		1.31177413	1.51908973	5.66E-08	8.27E-08
cpar2_603130	cpar5339	orf19.90	1.30668058	1.14826483	6.57E-07	2.91E-05
cpar2_104140	cpar5197	orf19.810	1.3054927	1.06511528	5.70E-07	4.26E-05
cpar2_804750	cpar5464		1.30443337	1.37915792	1.05E-06	0.00019139
cpar2_211400	cpar1863	orf19.854	1.30280991	0.93215875	8.37E-07	1.88E-05
cpar2_103510	cpar2792	orf19.274	1.29627993	0.88221512	2.80E-06	4.53E-05
cpar2_700830	cpar82	orf19.4871	1.29464377	1.0653419	2.35E-07	1.24E-06
cpar2_806400	cpar2007		1.29440932	1.34068489	4.56E-06	4.56E-06
cpar2_212150	cpar3742	orf19.5799	1.29009897	1.31501239	5.44E-08	1.21E-06
cpar2_211730	cpar2287	orf19.5777	1.28846504	1.27245293	4.08E-07	5.72E-06
cpar2_703570	cpar951	orf19.6557	1.27966029	0.91935414	9.55E-08	4.22E-05
cpar2_700290	cpar29	orf19.7209	1.27848043	1.25583248	8.03E-06	3.19E-05
cpar2_501370	cpar3046		1.27783341	1.08755594	2.76E-06	6.88E-05
cpar2_109500	cpar3206	orf19.6066	1.27771062	1.0378625	4.91E-07	5.19E-07
cpar2_102830	cpar3387	orf19.238	1.27751323	1.17781674	1.57E-07	7.43E-06
cpar2_602940	cpar5358	orf19.3653	1.27612808	1.0057738	9.78E-06	0.00011252
cpar2_402820	cpar1334	orf19.5665	1.27086254	1.20168268	1.81E-06	3.45E-05
cpar2_700100	cpar10	orf19.2157	1.26287614	1.16015446	1.46E-05	1.89E-05
cpar2_109160	cpar4542	orf19.3325	1.26068021	0.91297956	8.62E-06	6.23E-05
cpar2_102400	cpar4722		1.26060598	0.86110213	5.01E-05	0.00017919
cpar2_400130	cpar2012	orf19.2737	1.25981986	1.28651775	8.47E-08	4.56E-07

cpar2_101670	cpar5247	orf19.3160	1.25950016	1.20244428	1.28E-07	1.38E-06
cpar2_603150	cpar5337	orf19.86	1.25897317	1.17740966	6.74E-08	1.19E-05
cpar2_802940	cpar739	orf19.2525	1.25518898	1.06987229	2.76E-06	2.28E-05
cpar2_406710	cpar2233	orf19.2248	1.25240441	1.12618183	7.15E-06	3.17E-05
cpar2_805070	cpar4654	orf19.4894	1.24617707	1.1295488	9.62E-06	1.94E-05
cpar2_809000	cpar527	orf19.6771	1.24455896	1.14001774	2.33E-07	9.43E-06
cpar2_210500	cpar2723	orf19.409	1.24176416	1.07704333	2.87E-07	2.85E-05
cpar2_103490	cpar2794	orf19.276	1.23796282	1.00921818	7.36E-06	2.94E-05
	cpar2596		1.23768632	1.02526203	8.47E-08	5.05E-05
cpar2_803600	cpar4748	orf19.4763	1.23579699	0.97843398	4.76E-06	0.00167442
cpar2_703300	cpar5663	orf19.7049	1.22413633	1.02605961	2.06E-05	3.43E-05
cpar2_807090	cpar4356	orf19.7357	1.22263693	0.97979996	2.34E-07	2.88E-06
cpar2_402150	cpar3528	orf19.5644	1.21909184	1.14106363	7.73E-07	1.05E-06
cpar2_208020	cpar206	orf19.4450.1	1.21832674	1.08337974	7.96E-07	6.09E-05
cpar2_801410	cpar3998	orf19.3732	1.21562316	1.14847543	3.19E-07	5.10E-05
cpar2_401500	cpar3464	orf19.2691	1.21526744	1.16012815	0.00011222	0.0010505
cpar2_701420	cpar1153	orf19.7310	1.21407631	1.32221083	6.06E-08	1.98E-07
cpar2_101230	cpar2459	orf19.4274	1.21345682	1.26827142	1.33E-07	1.20E-06
cpar2_704100	cpar899	orf19.5129	1.20763661	1.33925812	3.42E-07	6.08E-07
	cpar4631		1.20515867	1.13970061	3.90E-06	1.54E-05
cpar2_109030	cpar5563	orf19.3051	1.20510751	0.91955434	1.04E-06	0.00011009
cpar2_208070	cpar211	orf19.4449	1.20242135	0.99995315	2.04E-06	2.94E-05
cpar2_301660	cpar3290	orf19.4816	1.19546203	1.14155428	1.51E-06	0.000111302
cpar2_300570	cpar4276		1.19348178	1.06084469	2.59E-06	1.17E-05
cpar2_206090	cpar4406	orf19.1843	1.18893796	0.66789292	0.00027849	0.00473111
cpar2_301330	cpar3257		1.18345903	0.89900079	7.40E-06	1.79E-05
cpar2_502100	cpar3118	orf19.6656	1.18041011	1.17341698	1.15E-06	6.63E-06
cpar2_206920	cpar2410	orf19.5114	1.17319767	1.15183836	1.57E-05	2.50E-05
cpar2_603270	cpar5326	orf19.1177	1.17190824	0.97265669	8.50E-07	9.89E-07
cpar2_212470	cpar983	orf19.1509	1.16799276	1.16349709	5.13E-06	7.54E-06
cpar2_300610	cpar4272	2	1.16773226	0.89425216	5.10E-07	8.48E-06
cpar2_805590	cpar4602	orf19.5180	1.16383638	1.19421603	7.48E-07	1.70E-06
cpar2_107500	cpar4972	orf19.2475	1.16367379	1.10175456	1.69E-05	1.84E-05
cpar2_209210	cpar4567		1.16033371	1.18194854	0.00016718	0.0005763
cpar2_106950	cpar4916		1.1586954	0.98754846	9.29E-07	1.01E-05
cpar2_502970	cpar465		1.1535424	1.05549792	1.25E-06	2.42E-05
cpar2_105370	cpar1660	orf19.6852	1.1525068	1.111936783	3.73E-06	5.86E-06
cpar2_700910	cpar90	orf19.4777	1.14973624	1.24648339	7.08E-07	1.21E-06
cpar2_701130	cpar112		1.14859947	1.44902621	1.31E-06	1.58E-06
cpar2_804650	cpar5454		1.14116839	1.04744979	1.76E-06	1.99E-05
cpar2_107310	cpar4953	orf19.2458	1.13935566	0.9166968	1.39E-05	0.00049843
cpar2_110160	cpar3781	orf19.6023	1.1390465	0.72303087	1.16E-05	0.00140383
cpar2_100040	cpar5568	orf19.583	1.13659439	0.94925495	0.00089244	0.00394929
cpar2_203550	cpar4080	orf19.5282	1.13351942	0.6088986	0.00016276	0.01574212
cpar2_803350	cpar4773	orf19.6261	1.13306078	1.34378495	1.92E-07	2.21E-07
cpar2_211870	cpar1251	orf19.891	1.12830615	0.92619618	4.19E-07	3.91E-06
cpar2_806890	cpar3631	orf19.6951	1.12804285	1.04179468	4.95E-07	1.08E-05
cpar2_603730	cpar5282	orf19.118	1.12676025	1.21182892	4.19E-07	1.95E-06
cpar2_404220	cpar4391	orf19.7438	1.12148781	0.96257098	2.76E-07	1.48E-05
	cpar1731		1.11992153	1.10639582	7.03E-06	9.87E-06
cpar2_204160	cpar4021	orf19.5285	1.11844418	1.13903827	3.85E-06	6.41E-06
cpar2_801840	cpar5125		1.1183667	0.91370604	1.42E-06	5.41E-06
cpar2_602070	cpar1223	orf19.5575	1.11426793	1.06007143	5.21E-07	4.27E-06
cpar2_403470	cpar3330	orf19.3369	1.11114521	1.04743816	6.57E-07	1.07E-06
cpar2_207000	cpar2418		1.10913399	1.01066939	8.13E-06	0.00016969
cpar2_401730	cpar3486	orf19.1416	1.10892619	0.76359079	1.12E-06	2.67E-05
cpar2_700090	cpar9	orf19.2156	1.10857503	0.92260048	1.08E-05	2.54E-05
cpar2_806210	cpar1989	orf19.2175	1.1082706	0.90367669	2.57E-06	9.73E-06

cpar2_104460	cpar5228	orf19.6868	1.10748642	0.91670354	5.19E-07	1.63E-05
cpar2_805300	cpar4632	orf19.6559	1.10359691	0.83678801	2.94E-07	4.23E-06
cpar2_703380	cpar970		1.09864715	1.25564393	2.30E-05	2.99E-05
cpar2_105300	cpar1666	orf19.5197	1.09765808	1.03082002	3.88E-06	6.12E-05
cpar2_803760	cpar1577	orf19.7479	1.09179839	1.05416284	5.22E-06	7.40E-06
cpar2_203560	cpar4079		1.09146279	1.01928631	3.19E-06	1.27E-05
cpar2_503710	cpar4466	orf19.1702	1.08684373	1.23815054	9.87E-06	2.52E-05
cpar2_205680	cpar337	orf19.6366	1.08655405	0.836123	1.55E-05	0.0001697
cpar2_700630	cpar62	orf19.7229	1.08544139	1.09184001	4.69E-06	5.52E-06
cpar2_808380	cpar1855	orf19.5862	1.08469776	0.92680449	1.71E-06	9.62E-06
cpar2_208500	cpar1398	orf19.5069	1.08322638	0.89801337	5.08E-06	0.00066233
cpar2_500950	cpar3006	orf19.1801	1.08248864	0.87782626	1.51E-06	0.0008395
cpar2_401990	cpar3513	orf19.5295	1.08074915	1.00562215	2.48E-07	1.67E-05
cpar2_213920	cpar1120	orf19.2003	1.07982187	0.84142577	4.83E-06	0.00282944
cpar2_802660	cpar5068	orf19.169	1.07855922	1.12044764	4.68E-07	1.92E-06
cpar2_800370	cpar3897	orf19.7499	1.07804288	0.85538381	3.33E-07	1.48E-06
cpar2_210890	cpar2762	orf19.1563	1.07589507	0.87973635	4.98E-07	0.00010651
cpar2_106800	cpar4901	orf19.4540	1.07588602	0.81065147	4.81E-06	2.28E-05
cpar2_301160	cpar3240	orf19.6492	1.07254148	1.00176008	1.21E-05	1.93E-05
cpar2_500730	cpar2984	orf19.3822	1.07031586	1.22296169	5.72E-06	1.25E-05
cpar2_802980	cpar743		1.06631845	0.94416523	7.63E-06	0.00043154
cpar2_702740	cpar5719	orf19.6472	1.06403934	1.12418957	2.02E-06	4.69E-06
cpar2_110070	cpar3790	orf19.6018	1.06279295	0.94059815	7.33E-07	1.06E-06
cpar2_102250	cpar4707	orf19.6973	1.05778619	0.86737417	9.21E-07	6.06E-06
cpar2_104660	cpar1729	orf19.5498	1.05441148	1.09506586	2.07E-06	2.49E-06
cpar2_100080	cpar5572	orf19.4044	1.0535801	0.64843446	1.74E-05	6.36E-05
cpar2_104170	cpar5200	orf19.4112	1.0528109	1.02262803	3.71E-07	1.64E-06
	gb_cpmt9	gb_cpmt9	1.0517888	0.97200654	0.00102089	0.00552761
cpar2_500840	cpar2995		1.05164029	0.81554872	1.07E-06	4.44E-05
cpar2_406820	cpar392	orf19.3612	1.04207703	0.59184355	7.77E-07	0.00023554
	cpar2674		1.03544474	1.01736143	0.001405	0.00244716
cpar2_503350	cpar4431	orf19.5408	1.03516112	0.776727	2.33E-07	0.00030614
cpar2_403410	cpar3336		1.03359157	1.2163016	5.70E-07	6.35E-07
cpar2_402200	cpar3534	orf19.5650	1.02871534	0.93988883	4.66E-06	2.16E-05
cpar2_206490	cpar691	orf19.3554	1.02544298	1.06661752	1.11E-05	1.91E-05
cpar2_200520	cpar1765		1.0250309	-0.0180824	0.0002372	0.94452731
	gb_cpmt8	gb_cpmt8	1.01986425	0.77933253	0.00198289	0.00613651
cpar2_303330	cpar2536	orf19.1940	1.01679989	0.77565508	1.09E-06	9.52E-05
cpar2_801590	cpar5150	orf19.4756	1.01657282	0.94454472	9.24E-07	0.00028016
cpar2_214120	cpar1139	orf19.1458	1.01271392	1.04405592	2.68E-06	4.02E-05
cpar2_700310	cpar31	orf19.7210	1.01077093	0.87634453	2.06E-06	3.30E-05
cpar2_108530	cpar764	orf19.3008	1.00903833	0.81045782	6.12E-06	4.66E-05
cpar2_105500	cpar1648	orf19.778	1.0066371	0.60582976	2.35E-06	7.65E-05
cpar2_213530	cpar1084	orf19.2107.1	0.99996819	1.05277216	2.90E-06	6.74E-06
cpar2_603340	cpar5319	orf19.2767	0.99897655	1.03312404	1.23E-05	1.79E-05
cpar2_700950	cpar94	orf19.4774	0.97375339	1.10048894	5.97E-06	9.78E-06
	cpara5831_part		0.9710509	1.011199679	3.11E-06	1.63E-05
cpar2_102340	cpar4716		0.95116154	1.07043473	9.44E-05	0.0001414
cpar2_702150	cpar5776	orf19.6403	0.94843892	1.06633693	6.68E-06	0.00011497
cpar2_105130	cpar1682	orf19.1891	0.94745453	1.05022983	2.75E-05	3.52E-05
cpar2_804590	cpar5448	orf19.1152	0.93941802	1.05239874	5.66E-06	5.73E-06
cpar2_600730	cpar1453		0.88207419	1.00804682	4.72E-06	1.17E-05
cpar2_103000	cpar3372	orf19.250	0.8816599	1.09353319	1.68E-05	9.45E-05
cpar2_102970	cpar3375	orf19.246	0.86156462	1.08515021	3.49E-06	1.01E-05
cpar2_209310	cpar630	orf19.815	0.85653902	1.00142988	1.40E-06	3.69E-06
cpar2_204030	cpar4032	orf19.6314	-0.73704343	-1.0221705	7.35E-05	0.00015021
cpar2_302480	cpar2318	orf19.2651	-0.78524671	-1.1125585	2.04E-05	2.19E-05
cpar2_801570	cpar5152	orf19.4758	-0.86287725	-1.00049288	4.06E-06	4.69E-06

cpar2_603240	cpar5329	orf19.124	-0.868008	-1.00753134	0.00038241	0.00055311
cpar2_104130	cpar5196	orf19.3579	-0.90725054	-1.03509284	1.68E-05	1.70E-05
cpar2_300230	cpar2885	orf19.7019	-0.91102454	-1.00359387	6.51E-06	2.20E-05
cpar2_404540	cpar634	orf19.5926	-0.92125558	-1.09216182	1.57E-05	2.29E-05
cpar2_102760	cpar3394	orf19.341	-0.93771739	-1.10452198	2.78E-06	3.11E-05
cpar2_300460	cpar4287	orf19.6909	-0.95246036	-1.04102437	1.01E-05	2.77E-05
	cpar2343		-0.95505513	-1.00858902	9.68E-05	0.0003651
cpar2_805710	cpar1810	orf19.2170	-0.9556372	-1.00032948	2.79E-06	6.29E-06
cpar2_106180	cpar4840	orf19.3676	-0.95884418	-1.09662077	4.45E-05	6.57E-05
cpar2_110140	cpar3783	orf19.3297	-0.96895281	-1.0456698	1.97E-06	1.55E-05
cpar2_600460	cpar806		-0.9742035	-1.302528	2.74E-05	7.46E-05
cpar2_401120	cpar1892	orf19.4159	-0.9857161	-1.00095727	1.18E-05	0.0001128
cpar2_803710	cpar1572	orf19.7486	-0.98670917	-1.17491015	4.76E-06	6.47E-06
cpar2_201600	cpar1565	orf19.5010	-0.99682304	-1.02270696	0.00056365	0.00086579
cpar2_205600	cpar329	orf19.6435	-1.00052201	-0.76752815	7.01E-07	1.13E-05
cpar2_204120	cpar4025	orf19.6313	-1.00090072	-0.59064809	0.00018823	0.0004701
cpar2_300650	cpar3413	orf19.7097	-1.00239059	-0.93508859	5.10E-05	0.00010138
cpar2_602600	cpar1172	orf19.3414	-1.00421894	-0.78963407	1.94E-05	0.00055941
cpar2_809030	cpar525	orf19.6766	-1.00690392	-1.00160763	0.00013541	0.0002846
cpar2_106330	cpar4855	orf19.3691	-1.00735104	-0.87890856	0.00182759	0.00371725
cpar2_108920	cpar5553	orf19.3064	-1.00746121	-0.73563227	9.78E-06	0.00012945
cpar2_303760	cpar2495	orf19.920	-1.01358345	-1.21260162	1.49E-05	0.00011386
cpar2_200380	cpar1752	orf19.7624	-1.01756065	-0.75627825	4.94E-05	0.00245849
cpar2_500810	cpar2992	orf19.1789.1	-1.01880826	-1.06976528	1.31E-05	2.22E-05
cpar2_107970	cpar5015	orf19.4060	-1.02323807	-1.05306966	3.94E-05	4.27E-05
cpar2_401050	cpar1899	orf19.4640	-1.02468977	-0.83766907	4.82E-05	0.00032035
cpar2_110080	cpar3789	orf19.3291	-1.0280834	-0.81292447	3.81E-05	0.0004701
cpar2_101190	cpar2463	orf19.4268	-1.02984352	-0.97568591	0.00011287	0.00149928
cpar2_205810	cpar4587	orf19.6418	-1.03025015	-0.78790511	0.00010651	0.00081464
cpar2_300210	cpar2883	orf19.7104	-1.03087945	-0.77548257	0.00013635	0.00020792
cpar2_704180	cpar891	orf19.5143	-1.03185971	-0.9862721	2.49E-06	0.00011417
cpar2_603490	cpar5304	orf19.1199	-1.03290759	-0.8910037	0.00092062	0.00139663
cpar2_108800	cpar5541	orf19.3043	-1.03457506	-0.92670771	1.30E-05	4.37E-05
cpar2_213940	cpar1122	orf19.1996	-1.03969309	-0.53122589	1.66E-05	0.00046889
cpar2_213180	cpar1049	orf19.2067	-1.04243488	-0.80999858	1.15E-06	4.95E-05
cpar2_802830	cpar728	orf19.2546	-1.04263165	-0.90309478	7.08E-07	3.93E-05
cpar2_204740	cpar244	orf19.1860	-1.04578722	-1.09742284	1.25E-06	1.59E-06
cpar2_204570	cpar227	orf19.5850	-1.04761719	-0.96260293	0.00030565	0.00053653
cpar2_102040	cpar4688	orf19.1710	-1.051173	-0.62692922	1.17E-05	0.00109623
cpar2_301670	cpar3291	orf19.4815	-1.05327646	-0.83551325	0.00039201	0.00165984
cpar2_101430	cpar2439	orf19.3962	-1.0556598	-0.77587653	0.00050582	0.00106315
cpar2_211970	cpar1261	orf19.1517	-1.05593826	-0.97970613	3.49E-05	5.19E-05
cpar2_104510	cpar5233		-1.06028184	-1.02083431	1.11E-05	1.32E-05
cpar2_103390	cpar2804	orf19.2812	-1.0607525	-1.15839201	1.51E-06	1.53E-06
cpar2_303940	cpar3696	orf19.930	-1.0609692	-0.94577715	4.69E-06	1.68E-05
cpar2_400810	cpar1923	orf19.2694	-1.06142528	-0.7098302	1.59E-06	0.00018494
cpar2_803150	cpar4793	orf19.3223	-1.06269163	-0.87057849	2.32E-06	9.60E-06
	cpar1296		-1.06451734	-0.74466328	0.00023634	0.00072168
cpar2_100180	cpar5582	orf19.4029	-1.06683832	-0.77165441	4.36E-05	0.0002084
cpar2_210460	cpar2719	orf19.403	-1.06942375	-0.75133146	3.11E-07	4.56E-05
	cpar5370		-1.06944682	-0.99962214	0.00097563	0.00260362
cpar2_300300	cpar2892	orf19.7011	-1.07410224	-1.08052314	3.26E-05	6.53E-05
cpar2_208260	cpar1420	orf19.1233	-1.07483853	-0.89093646	4.23E-06	3.20E-05
	cpara5841_part		-1.07502996	-0.79908639	7.72E-07	0.00087135
cpar2_407650	cpar3821	orf19.25	-1.07634075	-1.01351175	3.66E-06	2.04E-05
cpar2_212220	cpar3177	orf19.5827	-1.07795674	-0.90385015	1.40E-05	0.00025126
cpar2_208860	cpar838	orf19.2778	-1.07955202	-0.86568734	2.24E-06	0.00101148
cpar2_109810	cpar5497	orf19.3303	-1.08345072	-0.07068774	0.00256997	0.64514046

cpar2_303100	cpar2559		-1.08503126	-1.02666464	3.85E-05	0.00016282
cpar2_802080	cpar5101	orf19.4401	-1.09940537	-0.67653915	0.00019641	0.00076792
cpar2_404450	cpar642	orf19.7411	-1.10053858	-1.03358464	6.63E-06	1.20E-05
cpar2_700510	cpar50	orf19.7238	-1.10353459	-0.92052322	0.00062933	0.00209803
cpar2_110400	cpar3757	orf19.4551	-1.10401983	-1.02723633	2.60E-06	5.95E-06
cpar2_104620	cpar5244	orf19.24	-1.10554519	-0.60906299	2.31E-05	0.00050582
cpar2_304180	cpar3720	orf19.962	-1.10590584	-1.1527349	1.50E-06	2.90E-06
cpar2_303750	cpar2496	orf19.921	-1.10719528	-0.66688805	9.32E-06	0.00190633
cpar2_703290	cpar5664	orf19.7050	-1.10769946	-0.79253159	1.97E-05	0.00099002
cpar2_400470	cpar5529	orf19.4602	-1.10789947	-0.8838067	4.19E-07	0.00017193
cpar2_104610	cpar5243	orf19.23	-1.1092031	-0.96545292	8.66E-06	0.00850904
cpar2_105190	cpar1677	orf19.5198	-1.11286881	-0.93502862	0.00122207	0.0052334
cpar2_501560	cpar3065	orf19.2649	-1.11629382	-1.05117814	4.99E-05	0.00015119
cpar2_803560	cpar4752	orf19.4813	-1.12134643	-1.03706249	4.29E-05	6.50E-05
cpar2_700790	cpar78	orf19.5232	-1.12254148	-0.72272706	0.00015125	0.00868071
cpar2_301060	cpar3230	orf19.7062	-1.12389066	-1.16911826	6.88E-05	8.02E-05
cpar2_802010	cpar5108	orf19.4393	-1.12710385	-1.1249004	2.15E-06	1.90E-05
cpar2_201820	cpar4250	orf19.3755	-1.12980813	-0.93651857	8.79E-06	9.20E-06
cpar2_401740	cpar3487	orf19.1415	-1.13000042	-1.06140761	5.43E-07	1.64E-06
cpar2_802430	cpar5045	orf19.3744	-1.13186134	-0.96120006	4.17E-06	1.75E-05
cpar2_109420	cpar3214	orf19.3358	-1.13198296	-1.06451985	1.71E-07	2.24E-05
cpar2_108760	cpar5537	orf19.3034	-1.13423615	-0.82027835	4.61E-06	0.00010069
cpar2_500060	cpar2918	orf19.3099	-1.13452587	-0.85052533	8.50E-06	0.00017548
cpar2_301490	cpar3273	orf19.7069	-1.13791778	-1.00604878	0.00019641	0.00069564
cpar2_100620	cpar5625	orf19.3941	-1.14027743	-1.00629432	4.30E-06	3.30E-05
cpar2_209010	cpar852	orf19.6209	-1.14184351	-0.79516412	9.20E-06	1.63E-05
cpar2_109590	cpar3197	orf19.6092	-1.14220342	-1.00354183	3.88E-06	0.00012099
cpar2_601560	cpar1368	orf19.2143	-1.14409251	-0.70912198	2.57E-06	1.75E-05
cpar2_701340	cpar133	orf19.7332	-1.14838738	-1.15009666	3.11E-05	8.45E-05
cpar2_801050	cpar3962	orf19.2859	-1.14848231	-1.45075509	2.02E-05	4.67E-05
cpar2_700110	cpar11	orf19.2160	-1.15348164	-0.99952847	0.00042213	0.00337084
cpar2_502460	cpar415	orf19.3902	-1.15427401	-1.1223724	2.96E-06	2.37E-05
cpar2_109290	cpar4529	orf19.3341	-1.15613614	-0.6210813	3.01E-05	0.00074968
cpar2_213060	cpar1038		-1.15853052	-1.01104644	1.65E-05	2.78E-05
cpar2_806790	cpar3621	orf19.7384	-1.16000818	-0.99528543	0.00020758	0.00039049
cpar2_803140	cpar4794	orf19.3223.1	-1.16521303	-0.98710869	5.35E-06	7.70E-06
cpar2_204310	cpar4006	orf19.1815	-1.16648219	-1.27818769	2.39E-05	8.45E-05
cpar2_101940	cpar5263		-1.17394682	-1.0177098	8.33E-06	0.00010688
cpar2_404800	cpar2042		-1.17631225	-1.09943731	1.04E-06	4.91E-06
cpar2_405290	cpar2091	orf19.6000	-1.18402715	-1.19956062	2.96E-06	1.94E-05
cpar2_100560	cpar5620	orf19.4304	-1.19123255	-1.11607899	5.78E-05	0.00021398
cpar2_106500	cpar4872	orf19.2941	-1.19524524	-1.0491385	2.00E-06	9.86E-06
cpar2_701670	cpar5820	orf19.597	-1.19579151	-0.98826244	8.47E-08	2.32E-06
cpar2_304320	cpar3734	orf19.6662	-1.19876291	-1.15166249	4.14E-07	5.67E-06
cpar2_107130	cpar4935	orf19.1047	-1.19922701	-1.13711017	0.00020583	0.00028206
cpar2_702780	cpar5715	orf19.6477	-1.20022274	-1.09044821	7.13E-05	0.00014466
cpar2_207780	cpar2390	orf19.6229	-1.20188744	-1.02663974	1.86E-05	3.00E-05
cpar2_504190	cpar4514	orf19.7635	-1.20283141	-0.95498186	2.19E-05	0.00110898
cpar2_601450	cpar3575	orf19.3478	-1.20466833	-0.71485819	8.67E-05	0.00204917
cpar2_704090	cpar900	orf19.5126	-1.20769158	-0.87197094	6.62E-05	0.00013797
cpar2_100490	cpar5613	orf19.1979	-1.2091685	-0.86807863	3.52E-06	5.55E-06
cpar2_404990	cpar2061	orf19.1633	-1.21242127	-0.882922	3.41E-05	0.00103036
cpar2_808860	cpar541	orf19.6794	-1.21417728	-0.9543263	1.64E-06	2.77E-06
cpar2_304090	cpar3711	orf19.947	-1.21556613	-0.97548144	5.80E-08	2.48E-06
cpar2_211740	cpar2286	orf19.909	-1.21627335	-0.80395434	2.68E-06	6.47E-06
cpar2_209350	cpar619	orf19.2311	-1.22023984	-1.0264499	2.20E-07	1.45E-06
cpar2_806290	cpar1997	orf19.1403	-1.22511472	-1.07043649	4.50E-06	8.50E-06
cpar2_100300	cpar5594	orf19.4335	-1.22561663	-0.71321703	5.05E-06	3.15E-05

cpar2_603140	cpar5338	orf19.88	-1.22778387	-1.31308143	0.00019572	0.00044451
cpar2_109620	cpar3194	orf19.6086	-1.22805421	-0.75889339	5.75E-06	2.21E-05
cpar2_108600	cpar771	orf19.3015	-1.24033171	-1.06760575	7.47E-05	0.00063382
cpar2_700840	cpar83	orf19.4872	-1.24118263	0.0010042	0.00077499	0.99668554
cpar2_109610	cpar3195	orf19.6090	-1.24156619	-0.86565682	5.57E-06	0.00178516
cpar2_801860	cpar5123	orf19.4933	-1.24232654	-1.24230848	2.17E-05	0.00015058
cpar2_406400	cpar2202	orf19.2287	-1.25320319	-0.91433736	8.91E-07	0.00021013
cpar2_600870	cpar1467	orf19.5728	-1.26098321	-1.47363595	1.18E-07	2.16E-07
cpar2_403880	cpar142		-1.26530663	-0.63772799	0.00022803	0.01040976
cpar2_807590	cpar4308	orf19.5933	-1.27208705	-0.98013536	8.64E-07	6.45E-06
cpar2_102800	cpar3390	orf19.6165	-1.27370505	-0.96233058	1.96E-07	7.01E-06
cpar2_106430	cpar4865	orf19.2934	-1.27616643	-1.03642773	4.07E-05	0.00028788
cpar2_600780	cpar1458	orf19.5628	-1.28134948	-1.06734005	6.44E-06	1.46E-05
cpar2_203300	cpar4106	orf19.558	-1.2881475	-1.38129458	1.07E-07	6.54E-07
cpar2_500540	cpar2965	orf19.1235	-1.29381977	-1.13020351	1.37E-06	6.71E-06
cpar2_601950	cpar1235		-1.30221899	-1.36868342	1.59E-06	3.73E-06
cpar2_405970	cpar2158	orf19.1378	-1.31161116	-1.35744805	9.71E-06	5.81E-05
cpar2_210360	cpar2709	orf19.1480	-1.32144309	-1.17624961	4.40E-07	9.50E-06
cpar2_204580	cpar228	orf19.637	-1.32782745	-1.07520319	1.06E-06	1.42E-05
cpar2_108740	cpar5535	orf19.3037	-1.33988137	-1.09315741	1.87E-05	0.0003259
cpar2_804630	cpar5452	orf19.4889	-1.34655033	-1.58230573	4.06E-06	1.30E-05
cpar2_200290	cpar1743	orf19.7678	-1.34741206	-1.52280574	1.25E-07	3.60E-07
cpar2_208740	cpar828	orf19.2785	-1.35279569	-1.30899213	1.14E-06	2.63E-06
cpar2_208170	cpar222		-1.35559547	-1.29073575	1.08E-05	2.52E-05
cpar2_601840	cpar1284	orf19.5517	-1.356585	-1.19742016	2.72E-07	3.31E-07
cpar2_104710	cpar1724	orf19.5491.1	-1.35734374	-1.25043076	1.28E-06	1.61E-06
cpar2_212720	cpar1005	orf19.4506	-1.35840702	-1.74251423	2.86E-07	4.68E-07
cpar2_400160	cpar2015	orf19.2751	-1.36865602	-0.77327786	1.85E-07	0.00039159
cpar2_808200	cpar5652	orf19.6724	-1.36965755	-1.33018195	1.68E-07	1.00E-06
cpar2_405940	cpar2155	orf19.4093	-1.3700925	-1.14431292	9.70E-05	0.00165313
cpar2_803580	cpar4750	orf19.1839	-1.37053429	-1.22141611	0.00010109	0.00025033
cpar2_803630	cpar4745	orf19.4826	-1.37821682	-1.02277529	2.91E-07	2.32E-06
cpar2_206630	cpar704	orf19.3544	-1.38179649	-1.21328957	4.50E-07	4.06E-06
cpar2_404940	cpar2056	orf19.7392	-1.39960355	-0.98259826	6.09E-05	0.00019799
cpar2_801250	cpar3982	orf19.3733	-1.40015146	-1.46185374	4.12E-08	1.09E-06
cpar2_802460	cpar5048	orf19.3268	-1.40173935	-1.23849959	3.82E-07	3.70E-05
cpar2_212700	cpar1003	orf19.1826	-1.40915385	-0.96261148	0.00079437	0.00251062
cpar2_110250	cpar3772	orf19.2998	-1.41039966	-0.91282325	6.56E-06	0.00077832
cpar2_101270	cpar2455	orf19.4281	-1.41046044	-0.40653975	0.00127776	0.00242755
cpar2_203690	cpar4066	orf19.1164	-1.42286108	-1.2105506	6.08E-05	0.00015588
cpar2_701510	cpar1968	orf19.7296	-1.43494821	-1.327921	1.48E-06	6.49E-06
cpar2_501380	cpar3047	orf19.4716	-1.43702581	-1.35611167	5.74E-08	1.33E-07
cpar2_101990	cpar4683	orf19.252	-1.44461868	-1.27906692	6.54E-08	5.23E-06
cpar2_203160	cpar4119	orf19.2360	-1.44923021	-1.26323377	2.68E-06	4.28E-05
cpar2_100870	cpar2490	orf19.3931	-1.47491804	-1.20377932	1.21E-06	0.00010046
cpar2_100130	cpar5577	orf19.4040	-1.50401165	-1.61131552	4.12E-08	6.50E-08
cpar2_400190	cpar2018	orf19.2747	-1.50936773	-1.50419423	8.74E-07	1.56E-06
cpar2_207080	cpar2426	orf19.385	-1.52021818	-1.44374507	4.14E-07	1.91E-06
cpar2_703320	cpar5661	orf19.6570	-1.52485774	-1.64072401	7.57E-07	1.82E-05
cpar2_807740	cpar496		-1.52785294	-1.26860887	0.00728471	0.01027588
cpar2_100200	cpar5584	orf19.4026	-1.54587024	-1.51146122	1.29E-07	1.86E-06
cpar2_500690	cpar2980	orf19.3846	-1.56983774	-1.19358965	1.70E-07	0.00014043
cpar2_301640	cpar3288	orf19.4779	-1.59901657	-1.6848911	2.79E-08	0.00163749
cpar2_208160	cpar220	orf19.655	-1.60278841	-1.39491506	9.78E-06	2.04E-05
cpar2_703950	cpar913	orf19.769	-1.60724266	-1.41082625	5.13E-06	7.96E-05
cpar2_214100	cpar1137	orf19.1453	-1.60992883	-1.50370591	0.00167672	0.00297367
	cpar1427		-1.64136534	-1.31743732	0.00084405	0.00693865
cpar2_500490	cpar2960		-1.64929335	-1.61859802	7.74E-06	1.82E-05

cpar2_300580	cpar4275		-1.68866033	-1.6222074	8.47E-08	1.94E-07
cpar2_600600	cpar1440	orf19.715	-1.69360623	-1.79499946	1.28E-07	1.80E-07
cpar2_211610	cpar2299	orf19.5791	-1.70722411	-1.43778781	7.74E-08	2.68E-07
cpar2_205890	cpar4580	orf19.6417	-1.76274048	-1.69794769	9.78E-06	1.52E-05
cpar2_601420	cpar3645	orf19.3475	-1.78862758	-1.46167005	1.20E-08	2.94E-07
cpar2_504080	cpar4503	orf19.5447	-1.8525023	-1.74208064	1.31E-08	7.19E-08
cpar2_600590	cpar1439	orf19.716	-1.8582817	-2.11500866	4.48E-06	5.27E-06
cpar2_406240	cpar2185	orf19.1613	-1.86276749	-1.47492623	3.13E-08	1.31E-06
cpar2_703250	cpar5668		-1.87931922	-1.02771914	4.23E-09	0.00045863
cpar2_301750	cpar3299		-1.91150046	-1.79985247	1.36E-09	1.01E-05
	cpara5830_part		-1.97716116	-1.49605354	7.70E-06	6.54E-05
cpar2_106530	cpar4875	orf19.2962	-1.99632448	-1.60937514	6.57E-07	2.14E-05
cpar2_802720	cpar5074	orf19.3232	-2.01194717	-2.04988303	3.52E-08	1.35E-06
cpar2_300620	cpar4271	orf19.7077	-2.02267151	-1.56884871	1.79E-08	9.61E-08
cpar2_808020	cpar5385	orf19.6173	-2.03442209	-2.18076218	4.52E-09	7.98E-09
cpar2_106690	cpar4890	orf19.2942	-2.0364818	-1.48535455	1.68E-07	1.85E-07
cpar2_106700	cpar4891		-2.1046684	-1.73014595	2.37E-06	3.49E-06
cpar2_603010	cpar5351		-2.2791652	-2.49296187	1.65E-10	1.70E-10
cpar2_603050	cpar5347		-2.38575263	-2.35356164	6.72E-10	2.60E-07
cpar2_207540	cpar2366		-2.42835396	-2.48421329	5.54E-09	3.13E-08
cpar2_800530	cpar3911	orf19.7514	-2.68577961	-2.82785379	1.18E-07	1.60E-07
cpar2_802670	cpar5069	orf19.171	-2.70740101	-2.0596585	1.06E-06	1.39E-05
cpar2_700940	cpar93	orf19.4773	-2.7804229	-2.65252683	1.76E-10	4.97E-10
cpar2_300630	cpar4270		-2.81821506	-3.00827126	1.65E-10	1.69E-08
cpar2_602990	cpar5353	orf19.3646	-2.81892084	-2.89578541	1.65E-10	4.63E-10
cpar2_108370	cpar749	orf19.4527	-3.23412579	-3.56574044	2.17E-09	1.02E-08

first oligo

org

C.albicans Description

NA	NA
RHR2	Putative glycerol 3-phosphatase; roles in osmotic tolerance, glycerol accumulation
NA	NA
GPH1	Putative glycogen phosphorylase; gene regulated by Ssk1p, Mig1p, and Tup1p; flu
NA	NA
RBT1	Putative cell wall protein with similarity to Hwp1p, required for virulence; predicted t
OSM1	Putative flavoprotein subunit of fumarate reductase; soluble protein in hyphae; fung
PGK1	Phosphoglycerate kinase; enzyme of glycolysis; localizes to cell wall and to cytoplasm
FDH1	Putative formate dehydrogenase, oxidizes formate to produce CO ₂ ; induced during
HEM13	Coproporphyrinogen III oxidase; antigenic in human, mouse; localizes to yeast-form
	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation W
ENO1	Enolase (2-phospho-D-glycerate-hydrolyase), enzyme of glycolysis and gluconeog
MDH1-3	Predicted malate dehydrogenase; farnesol regulated
GPM1	Surface protein that binds host complement Factor H and FHL-1; phosphoglycerate
ADH1	Alcohol dehydrogenase; at yeast-form but not hyphal cell surface; soluble in hypha
NA	NA
TPO3	Possible role in polyamine transport; MFS-MDR family; transcription induced by Sft
	Predicted ORF in Assemblies 19, 20 and 21
FBA1	Putative fructose-bisphosphate aldolase; enzyme of glycolysis; antigenic in murine
NA	NA
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21; fluconazole-downregulated
	Predicted ORF in Assemblies 19, 20 and 21; identified in extracts from biofilm and
TDH3	Glyceraldehyde-3-phosphate dehydrogenase; enzyme of glycolysis; binds fibronect
ERG251	Predicted ORF in Assemblies 19, 20 and 21; ketoconazole-induced; amphotericin B
PDC11	Protein similar to pyruvate decarboxylase; antigenic; at hyphal cell surface, not yea
ERG3	C-5 sterol desaturase; introduces C-5(6) double bond into episterol in ergosterol bi
ECM331	GPI-anchored protein; mainly at plasma membrane, also at cell wall; caspofungin ii
	Possible stress protein; increased transcription is associated with CDR1 and CDR2
CRP1	Copper transporter of the plasma membrane; P1-type ATPase (CPx type); mediate
HXK2	Protein described as hexokinase II; antigenic in human; downregulated in the pres
ERG11	Lanosterol 14-alpha-demethylase, member of cytochrome P450 family that functio
UCF1	Transcriptionally regulated by iron or by yeast-hyphal switch; expression greater in
	ORF Predicted by Annotation Working Group; regulated by Nrg1p, Tup1p
TPI1	Triose-phosphate isomerase; glycolysis/gluconeogenesis; antigenic in mouse or hu
GLK1	Putative glucokinase; transcription is regulated upon yeast-hyphal switch; transcrip
	Predicted ORF in Assemblies 19, 20 and 21; fluconazole-induced; ketoconazole-re
XYL2	Protein described as similar to D-xylulose reductase; immunogenic in mouse; solub
CDC19	Putative pyruvate kinase; on yeast-form cell surface; soluble in hyphae; antigenic; (
MAE1	Malic enzyme, mitochondrial; transcription regulated by Mig1p and Tup1p; shows c
IFG3	Putative D-amino acid oxidase
ERG6	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in ergostero
NA	NA

PGM2 Protein not essential for viability; similar to *S. cerevisiae* Pgm2p, which is phosphoglycerate kinase; predicted ORF in Assemblies 19, 20 and 21

PFK2 Beta subunit of phosphofructokinase (PFK), which is a heteromultimer of Pfk1p and Pfk2p

PFK1 Alpha subunit of phosphofructokinase (PFK), which is Pfk1p, Pfk2p heteromultimer

NA Predicted ORF in Assemblies 19, 20 and 21

GPD1 Protein similar to *S. cerevisiae* glycerol-3-phosphate dehydrogenase (enzyme of glycolysis)

ACC1 Protein with similarity to acetyl-coenzyme-A carboxylases; regulated by Efg1p; amphotropic

NA

ERG1 Squalene epoxidase, catalyzes epoxidation of squalene to 2,3(S)-oxidosqualene in ergosterol biosynthesis; predicted ORF in Assemblies 19, 20 and 21

PGI1 Protein described as glucose-6-phosphate isomerase, enzyme of glycolysis; antigenic

POS5 Protein likely to be essential for growth, based on an insertional mutagenesis strategy

TKL1 Putative transketolase; localizes to surface of yeast-form cells, but not hyphae; soluble

NA

NA

ERG24 C-14 sterol reductase, has a role in ergosterol biosynthesis; mutation confers increased growth

NA

OLE1 Fatty acid desaturase (stearoyl-CoA desaturase), essential protein involved in oleic acid biosynthesis

ACB1 Protein described as similar to a region of acyl-coenzyme-A-binding protein; amphipathic

XKS1 Predicted ORF in Assemblies 19, 20 and 21; increased expression in response to oxidative stress

Predicted ORF in Assemblies 19, 20 and 21

Predicted ORF in Assemblies 19, 20 and 21; Hog1p-downregulated; shows colony morphology defect

Predicted membrane transporter, member of the drug:proton antiporter (12 spanning)

GAL10 UDP-glucose 4-epimerase, required for galactose utilization; mutant shows cell wall defects

FAS1 Beta subunit of fatty-acid synthase; multifunctional enzyme; fluconazole-induced; a predicted ORF in Assemblies 19, 20 and 21; transcription is upregulated in response to stress

Predicted ORF in Assemblies 19, 20 and 21

Predicted ORF in Assemblies 19, 20 and 21; protein detected by mass spec in experiment

Predicted ORF in Assemblies 19, 20 and 21

ACS2 Probable acetyl-CoA synthetase, similar to known fungal acetyl-CoA synthetases; essential

ERG4 Protein described as similar to sterol C-24 reductase; shows Mob2p-dependent hyphal growth

NA

CAT2 Major carnitine acetyl transferase localized in peroxisomes and mitochondria; involved in carnitine shuttle

IFR2 Increased transcription is observed upon benomyl treatment; transcription is upregulated in response to stress

ERG5 Putative C-22 sterol desaturase; fungal C-22 sterol desaturases are cytochrome P₄₅₀

ACS1 Putative acetyl-CoA synthetase, similar to *S. cerevisiae* Acs1p; upregulated in the presence of stress

Predicted ORF in Assemblies 19, 20 and 21

NA

Predicted membrane transporter, member of the anion:cation symporter (ACS) family

ACH1 Acetyl-coA hydrolase; acetate utilization; nonessential; soluble protein in hyphae; a predicted ORF in Assembly 20 and 21; gene has intron

AYR2 Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related growth defect

Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation W)

ERG13 Protein similar to *S. cerevisiae* Erg13p, which is involved in ergosterol biosynthesis

OPT7 Putative oligopeptide transporter; possibly transports GSH and related compounds

GCY1 Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to temperature

FAS2 Alpha subunit of fatty-acid synthase; required for virulence in mouse systemic infection

Predicted ORF in Assemblies 19, 20 and 21; hyphal-induced expression; greater morphological defects

GND1 Putative 6-phosphogluconate dehydrogenase; soluble protein in hyphae; farnesol-, fluconazole-induced

Predicted ORF in Assemblies 19, 20 and 21

ERG10 Protein similar to acetyl-CoA acetyltransferase; role in ergosterol biosynthesis; soluble

PGA7 Protein described as a putative precursor of a hyphal surface antigen; putative GPI anchor

NA

Predicted ORF in Assemblies 19, 20 and 21

Predicted ORF in Assemblies 19, 20 and 21; decreased expression in response to stress

ASR2 Predicted ORF in Assemblies 19, 20 and 21
 HGT7 Gene regulated by cAMP and by osmotic stress; greater mRNA abundance observ
 ZWF1 Putative glucose transporter, major facilitator superfamily; glucose-, fluconazole-, S
 NA Putative glucose-6-phosphate dehydrogenase; antigenic in murine infection; activit
 NA
 SET3 Predicted ORF in Assemblies 19, 20 and 21; transcription is induced in response tc
 PGA62 Protein similar to *S. cerevisiae* Set3p, which is an NAD-dependent histone deacety
 Putative GPI-anchored protein; fluconazole-induced; transcriptionally regulated by
 Predicted ORF in Assemblies 19, 20 and 21
 RNR21 Protein described as similar to ribonucleoside-diphosphate reductase; regulated by
 Putative quinolinate phosphoribosyl transferase, involved in NAD biosynthesis
 CSA1 Surface antigen on elongating hyphae and buds; no obvious hyphal defects in mut
 OPI3 Putative phosphatidylethanolamine N-methyltransferase of phosphatidylcholine bio
 HSP70 Putative hsp70 chaperone; role in sensitivity to beta-defensins; heat-shock, ampho
 NA
 TFS1 Transcription is regulated upon yeast-hyphal switch; shows colony morphology-rele
 NA
 ERG27 3-Keto sterol reductase of ergosterol biosynthesis; acts in C-4 sterol demethylation
 EXG2 Protein similar to *S. cerevisiae* Exg2p, which is an exo-1,3-beta-glucosidase; predic
 SUR2 Protein described as similar to ceramide hydroxylase; predicted enzyme of sphingc
 ERG9 Putative farnesyl-diphosphate farnesyl transferase (squalene synthase) involved in
 SLD1 Sphingolipid delta-8 desaturase, catalyzes desaturation at carbon-8 in the long-cha
 Protein with slight similarity to a human gene associated with colon cancer and to c
 Predicted ORF in Assemblies 19, 20 and 21
 DAP1 Protein similar to *S. cerevisiae* Dap1p, which is a protein related to mammalian me
 NA
 PRB1 Putative endoprotease B; regulated by heat, carbon source (GlcNAc-induced), nitrc
 URA1 Dihydroorotate dehydrogenase (DHODH); enzyme of de novo pyrimidine biosynthe
 NA
 RBT5 GPI-anchored cell wall protein involved in hemoglobin utilization; expression is regi
 HSP30 Protein described as similar to heat shock protein; fluconazole-downregulated; am
 NA
 GPM2 Predicted ORF in Assemblies 19, 20 and 21; similar to *S. cerevisiae* Ykr070wp; trai
 Protein described as phosphoglycerate mutase; decreased expression in hyphae c
 Predicted ORF in Assemblies 19, 20 and 21; ciclopirox olamine induced; regulated
 Predicted ORF in Assemblies 19, 20 and 21
 SOU2 Protein similar to Sou1p; not required for utilization of L-sorbose
 Predicted ORF in Assemblies 19, 20 and 21
 GLC3 Protein described as similar to 1,4-glucan branching enzyme; fluconazole-induced;
 UPC2 Transcriptional regulator of ergosterol biosynthetic genes and sterol uptake; binds I
 Predicted ORF in Assemblies 19, 20 and 21
 ORF Predicted by Annotation Working Group
 Predicted ORF in Assemblies 19, 20 and 21; protein detected by mass spec in stat
 Predicted ORF in Assemblies 19, 20 and 21
 GSY1 Protein described as glycogen synthase; enzyme of glycogen metabolism; transcrip
 NA
 Gene transcription regulated by Mig1p and Tup1p; possibly spurious ORF (Annotat
 Predicted ORF in Assemblies 19, 20 and 21
 SNO1 Protein of unknown function expressed during stationary phase; transcription is reg
 ASR3 Gene regulated by cAMP and by osmotic stress; greater mRNA abundance observ
 KNS1 Protein not essential for viability; similar to *S. cerevisiae* Kns1p, which is a protein l
 Predicted ORF in Assemblies 19, 20 and 21
 SOD1 Cytosolic copper- and zinc-containing superoxide dismutase, involved in protection
 Protein abundance is affected by URA3 expression in the CAI-4 strain background;
 Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation W
 Predicted ORF in Assemblies 19, 20 and 21; protein level decreased in stationary p
 Putative DNA repair exonuclease; fungal-specific (no human or murine homolog)
 Predicted ORF in Assemblies 19, 20 and 21

ERG2	C-8 sterol isomerase; enzyme of ergosterol biosynthesis pathway; converts fecoste
NA	NA
MVD	Mevalonate diphosphate decarboxylase; functional homolog of <i>S. cerevisiae</i> Erg19
TPS2	Trehalose-6-phosphate (Tre6P) phosphatase; mutation causes heat sensitivity, Tre
MSN4	Putative zinc finger transcription factor; similar to <i>S. cerevisiae</i> Msn4p, but not a sig
PMI1	Phosphomannose isomerase; cell wall biosynthesis enzyme; drug target; functiona
NA	NA
TAL1	Predicted ORF in Assemblies 19, 20 and 21; biofilm induced; oxidative stress-induc
NA	NA
PGA12	Putative GPI-anchored protein of unknown function
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
CSP37	Plasma membrane, hyphal cell wall protein; role in progression of murine systemic
MP65	Cell surface mannoprotein; mycelial antigen; possible role in cell-wall glucan metat
RBT4	Similar to plant pathogenesis-related proteins; required for virulence in mouse syst
	Protein similar to <i>S. cerevisiae</i> Ydr531wp; transposon mutation affects filamentous
GRE3	Similar to D-xylose reductases; antigenic in murine systemic infection; soluble prot
YIM1	Protein similar to protease of mitochondrial inner membrane; increased transcriptio
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
PHO15	Protein described as 4-nitrophenyl phosphatase; hyphal downregulated; induced in
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
MLS1	Malate synthase; enzyme of the glyoxylate cycle; peroxisomal; no mammalian hom
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; hsix putative membrane-spanning reg
ADH5	Putative alcohol dehydrogenase; soluble protein in hyphae; expression is regulat
	Protein described as a vacuolar protease; upregulated in the presence of human n
TSA1	Protein of TSA/alkyl hydroperoxide peroxidase C (AhPC) family; similar to thiol-dep
PUT2	Alkaline upregulated; protein detected by mass spec in exponential and stationary
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
UGA11	Predicted ORF in Assemblies 19, 20 and 21; macrophage-induced gene; overlaps
TFC4	Predicted ORF in Assemblies 19, 20 and 21; transcriptionally activated by Mnl1p u
ERO1	Protein described as similar to <i>S. cerevisiae</i> Ero1p, which has a role in formation o
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; induced upon biofilm formation
	Predicted ORF in Assemblies 19, 20 and 21; transcriptionally activated by Mnl1p u
	Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide in yhb1 mutan
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
CCP1	Similar to cytochrome-c peroxidase N terminus; transcription is negatively regulat
FAT1	Predicted enzyme of sphingolipid biosynthesis; upregulated in biofilm
	Predicted ORF in Assemblies 19, 20 and 21
DAC1	N-acetylglucosamine-6-phosphate (GlcNAcP) deacetylase; enzyme of N-acetylgluc
	Protein described as glycogen synthesis initiator; regulated by Efg1p and Efh1p; H
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21

HSP12 Heat-shock protein; induced upon osmotic/oxidative/cadmium stress, fluphenazine
Protein described as glutathione peroxidase; macrophage-downregulated gene

LYS12 Protein described as mitochondrial homoisocitrate dehydrogenase; clade-associate

ARE2 Acyl CoA:sterol acyltransferase (ASAT); uses cholesterol and oleoyl-CoA substrate

UBI4 Protein of unknown function, has similarity to *S. cerevisiae* Yer010cp, which is a pr
Ubiquitin precursor (polyubiquitin), contains three tandem repeats of the ubiquitin p
Predicted membrane protein; similar to *S. cerevisiae* Ynr018Wp
Predicted ORF in Assemblies 19, 20 and 21; increased transcription is observed in

NA NA
Protein not essential for viability

CYB5 Cytochrome b(5); not essential for viability; similar to *S. cerevisiae* Cyb5p; transcrip
Predicted ORF in Assemblies 19, 20 and 21
Predicted ORF in Assemblies 19, 20 and 21
ORF Predicted by Annotation Working Group

ERG25 Putative C-4 methyl sterol oxidase with role in C4-demethylation of ergosterol bios
Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation W
Protein similar to *S. cerevisiae* Gin3p; transcription is upregulated in response to tr

PUT1 Alkaline upregulated by Rim101p
Predicted ORF in Assemblies 19, 20 and 21

NA NA
Predicted ORF in Assemblies 19, 20 and 21; shows colony morphology-related ger
Predicted ORF in Assemblies 19, 20 and 21
Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide

NA NA

ALG6 Putative glucosyltransferase involved in cell wall mannan biosynthesis; transcrip
NA NA

DUR3 Putative protein of unknown function, transcription is upregulated in clinical isolates
Predicted ORF in Assemblies 19, 20 and 21
Predicted ORF in Assemblies 19, 20 and 21

ROD1 Protein not essential for viability; similar to *S. cerevisiae* Rod1p, which is a membra
NA NA
Protein described as a putative cysteine peroxidase; transcriptionally induced by in

PGA26 Putative GPI-anchored protein of unknown function; transcriptionally regulated by ii
NA NA
NA NA
NA NA
Predicted ORF in Assemblies 19, 20 and 21

DAK2 Protein described as similar to dihydroxyacetone kinase; transcription is decreased
NA NA
NA NA
Putative transcription factor with zinc finger DNA-binding motif
Predicted ORF in Assemblies 19, 20 and 21
Putative indoleamine 2,3-dioxygenase (IDO); IDO is the rate-limiting enzyme of try
Predicted ORF in Assemblies 19, 20 and 21; decreased expression in hyphae com

BPH1 Protein not essential for viability; similar to *S. cerevisiae* Bph1p, which is a putative
Predicted ORF in Assemblies 19, 20 and 21
Predicted ORF in Assemblies 19, 20 and 21

FAD2 Delta-12 fatty acid desaturase, involved in production of linoleic acid, which is a ma

UBA1 Protein similar to *S. cerevisiae* Uba1p, which is a ubiquitin-activating enzyme that i
NA NA

PST3 Putative flavodoxin; biofilm induced; fungal-specific (no human or murine homolog)
NA NA
Predicted ORF in Assemblies 19, 20 and 21

MOH1 Protein similar to *S. cerevisiae* Moh1p; transcription is induced in response to alph
NA NA

COX11 Protein repressed during the mating process; transcription is regulated by Nrg1p

NAG1 Glucosamine-6-phosphate deaminase; enzyme of N-acetylglucosamine utilization;
Predicted ORF in Assemblies 19, 20 and 21; induced by nitric oxide

	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; protein level decreased in stationary phase
NA	NA
APE2	Neutral arginine-, alanine-, leucine-specific metallo-aminopeptidase; expected to be
NTH1	Neutral trehalase; hyphal induction in homozygous null mutant is delayed but not repressed
NA	NA
ARF3	Transcription is filament induced; Tup1p regulated (see Locus History Note for Assemblies 19, 20 and 21)
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
	Protein described as related to arginases; downregulated upon adherence to polysaccharide
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; transcription is induced in response to carbon source
HNM1	Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to carbon source
CHO2	Putative phosphatidyl-ethanolamine N-methyltransferase; fungal-specific (no human ortholog)
	Putative nicotinic acid mononucleotide adenylyltransferase, involved in NAD salvage
ECM3	Predicted ORF in Assemblies 19, 20 and 21
UBC8	Protein similar to <i>S. cerevisiae</i> Ubc8p; transcription is induced in response to alpha-factor
	Predicted ORF in Assemblies 19, 20 and 21
SCS7	Protein described as ceramide hydroxylase; transcription is regulated by Nrg1p; transcription is induced in response to alpha-factor
NA	NA
CYP1	Peptidyl-propyl cis-trans isomerase (PPIase); activity is cyclosporin A sensitive; soluble protein
LRO1	Predicted ORF in Assemblies 19, 20 and 21; nonessential; similar to <i>S. cerevisiae</i> Lro1p
	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p
EFH1	Transcriptional activator; minor role in transcriptional regulation, compared to Efg1p
MUM2	Protein similar to <i>S. cerevisiae</i> Mum2p; transcription is induced in response to alpha-factor
	Predicted ORF in Assemblies 19, 20 and 21
NA	Mitochondrial gene
NA	NA
PST2	Putative NADH:quinone oxidoreductase; similar to 1,4-benzoquinone reductase; involved in iron homeostasis
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
PRO3	Protein induced during the mating process; alkaline upregulated
AAT1	Protein described as aspartate aminotransferase; soluble protein in hyphae; macrophage-inducible
NA	NA
NA	Mitochondrial gene
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; fungal-specific
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
COQ4	Protein described as having role in coenzyme Q biosynthesis; transcriptionally induced in response to alpha-factor
PIL1	Echinocandin-binding protein; localizes to cell surface of hyphae, but not yeast-form
STF2	Protein involved in ATP biosynthesis; decreased expression in hyphae compared to yeast-form
PGA59	Putative GPI-anchored protein of unknown function; shows colony morphology-related phenotype
AOX1	Alternative oxidase; low abundance; constitutively expressed; one of two isoforms of alternative oxidase
NA	NA
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
Apr-01	Vacuolar aspartic proteinase; mRNA abundance is equivalent in yeast-form and mycelium
	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p; induced in response to alpha-factor
NA	NA
SLC1	Protein repressed during the mating process
	Predicted ORF in Assemblies 19, 20 and 21; fungal-specific (no human or murine ortholog)
DCK1	Putative guanine nucleotide exchange factor required for embedded filamentous growth
RPB8	Protein described as a subunit of RNA polymerases I, II, and III; regulated by Gcn4p
CAM1-1	Putative translation elongation factor; genes encoding ribosomal subunits, translation factors
	Predicted ORF in Assemblies 19, 20 and 21; alkaline downregulated

	Predicted ORF in Assemblies 19, 20 and 21
ATP4	Predicted ORF in Assemblies 19, 20 and 21; macrophage/pseudohyphal-induced
YML6	Protein described as a mitochondrial ribosomal protein; induced upon adherence to
ARG11	Protein induced during the mating process
	Putative spermidine export pump; fungal-specific (no human or murine homolog)
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
PHM7	Putative transporter; fungal-specific (no human or murine homolog); Hog1p-downregulated
ABP140	Protein similar to <i>S. cerevisiae</i> actin-binding protein Abp140p; induced upon biofilm
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
MRPL6	Putative mitochondrial ribosomal protein
DIM1	Protein likely to be essential for growth, based on an insertional mutagenesis strategy
	Predicted ORF in Assemblies 19, 20 and 21
MNT4	Transcriptionally regulated by iron; expression greater in low iron; similar to mannose
	Predicted ORF in Assemblies 19, 20 and 21
SUR7	Protein required for wild-type cell wall, plasma membrane, cytoskeletal organization
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; ketoconazole-repressed
MRPL27	Putative ribosomal protein
RMT2	Minor protein arginine methyltransferases (PRMT) involved in methylation of arginine
	Predicted ORF in Assemblies 19, 20 and 21
LYS1	Saccharopine dehydrogenase (biosynthetic); enzyme of alpha-aminoadipate lysine
ARO4	3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase; enzyme of aromatic amino acid
PWP1	Predicted ORF in Assemblies 19, 20 and 21; downregulated in core stress response
HMT1	Major type I protein arginine methyltransferases (PRMT) involved in asymmetric dimethylation
UTP13	Predicted ORF in Assemblies 19, 20 and 21; downregulated in core stress response
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21; similar to mucins and to a <i>Leishmania</i> mucin
	Predicted ORF in Assemblies 19, 20 and 21
NOP5	Protein similar to <i>S. cerevisiae</i> Nop5p protein of small nucleolar ribonucleoprotein complex
	Predicted ORF in Assemblies 19, 20 and 21
CHA1	Protein similar to serine/threonine dehydratases, catabolic; negatively regulated by
	Predicted ORF in Assemblies 19, 20 and 21
TRP2	Predicted ORF in Assemblies 19, 20 and 21; regulated by Gcn2p and Gcn4p
LSC2	Protein described as beta subunit of succinate-CoA ligase; transcription regulated by
NOC2	Protein similar to <i>S. cerevisiae</i> Noc2p; transposon mutation affects filamentous growth
	Protein described as NADH-ubiquinone oxidoreductase; identified in detergent-resistant membrane
YTM1	Protein similar to <i>S. cerevisiae</i> Ytm1p, which is involved in biogenesis of the large ribosomal subunit
HAS1	Functional homolog of <i>S. cerevisiae</i> Has1p, which is a nucleolar protein of the DEAD-box family
ARO3	3-Deoxy-D-arabinoheptulosonate-7-phosphate synthase; enzyme of aromatic amino acid
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
PET9	Protein involved in ATP biosynthesis; identified in detergent-resistant membrane fraction
TYS1	Putative tRNA-Tyr synthetase; genes encoding ribosomal subunits, translation factors
ATP3	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; caspofungin repressed
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
PCL2	Cyclin homolog; reduced expression observed upon depletion of Cln3p; farnesol repressed
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
ADE4	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
BUB2	Predicted ORF in Assemblies 19, 20 and 21; described as similar to <i>S. cerevisiae</i> Bub2p
	Putative protein of unknown function, transcription is upregulated in clinical isolates
	Predicted ORF in Assemblies 19, 20 and 21

NA	NA
YVH1	Putative dual specificity phosphatase (phosphoserine/threonine and phosphotyrosine); Predicted ORF in Assemblies 19, 20 and 21
NPL3	Putative RNA-binding protein, ortholog of <i>S. cerevisiae</i> Npl3p; nuclear export is factor
CTN1	Predicted carnitine acetyl transferase; required for growth on nonfermentable carbon source
RTA2	Putative floppase; required for sphingolipid long chain base release; mediates calcium signaling; Predicted ORF in Assemblies 19, 20 and 21
NOP15	Protein described as a nucleolar ribosome biogenesis factor; hyphal-induced expression
MDH1-1	Predicted malate dehydrogenase; macrophage-induced protein
RTA3	Similar to <i>S. cerevisiae</i> Rta1p (role in 7-amincholesterol resistance) and Rsb1p (flippase)
NOP4	Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to 5-fluorouracil
PCL1	Cyclin homolog; expression induced upon filamentous growth; transcription is induced by cAMP
GUA1	Predicted ORF in Assemblies 19, 20 and 21; soluble protein in hyphae; flucytosine induced
CSI2	Protein essential for growth; transposon mutation affects filamentous growth
RPA135	Predicted ORF in Assemblies 19, 20 and 21; decreased expression in response to oxidative stress
CIT1	Protein described as citrate synthase; soluble protein in hyphae; biofilm induced; essential for growth; Predicted ORF in Assemblies 19, 20 and 21
FRE10	Major cell-surface ferric reductase under low-iron conditions; 7 transmembrane region; Predicted ORF in Assemblies 19, 20 and 21
LSC1	Protein described as succinate-CoA ligase subunit; transcriptionally regulated by iron
RLI1	Member of RNase L inhibitor (RLI) subfamily of ABC family; predicted not to be a transporter
TRP4	Predicted enzyme of amino acid biosynthesis; upregulated in biofilm; regulated by iron; Predicted ORF in Assemblies 19, 20 and 21
URA7	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; protein detected in hyphae
KEL1	Predicted membrane transporter, member of the monocarboxylate porter (MCP) family; Protein containing a Kelch repeat domain, similar to <i>S. cerevisiae</i> Kel1p; not required for growth; Predicted ORF in Assemblies 19, 20 and 21
ELF1	Protein required for wild-type morphology, growth; Walker A and B (ATP/GTP binding sites)
SRP40	Predicted ORF in Assemblies 19, 20 and 21; macrophage/pseudohyphal-induced
NAG4	Putative transporter; fungal-specific; similar to Nag3p and to <i>S. cerevisiae</i> Ypr156C; Predicted ORF in Assemblies 19, 20 and 21; decreased transcription is observed under oxidative stress; Putative tRNA-Arg synthetase; essential; <i>S. cerevisiae</i> ortholog is essential; genes essential for growth
NA	NA
NOG1	Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to 5-fluorouracil; Predicted ORF; described as 12kDa subunit of mitochondrial NADH-ubiquinone oxidoreductase; Predicted ORF in Assemblies 19, 20 and 21
NA	NA
NA	NA
CDR1	Multidrug transporter of ATP-binding cassette (ABC) superfamily; transports phospholipids
GAP1	General amino acid permease; antigenic in human, mouse; 10-12 transmembrane region
SCW4	Putative cell wall protein; exogenously expressed protein is a substrate for Kex2p protease; Predicted ORF in Assemblies 19, 20 and 21; Gcn4p-regulated
ERB1	Putative protein of unknown function, transcription is upregulated in clinical isolates; Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to 5-fluorouracil; Predicted ORF in Assemblies 19, 20 and 21
CAT1	Catalase; role in resistance to oxidative stress, neutrophils, peroxide; role in murine host defense
DRS1	Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to 5-fluorouracil
NIP7	Protein described as a nucleolar protein with role in ribosomal assembly; hyphal induced; Predicted ORF in Assemblies 19, 20 and 21
GIT1	Putative glycerophosphoinositol permease; fungal-specific (no human or murine homolog)
UTP4	Predicted ORF in Assemblies 19, 20 and 21; physically interacts with TAP-tagged proteins
FESUR1	Protein described as ubiquinone reductase; transcriptionally induced by interaction with iron
MRP17	Predicted mitochondrial ribosomal protein
STP4	Putative transcription factor with zinc finger DNA-binding motif; induced in core casein
RPL82	Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, transcribed in hyphae; Predicted ORF in Assemblies 19, 20 and 21
TNA1	Putative nicotinic acid transporter; fungal-specific (no human or murine homolog); cAMP regulated

ILV5	Protein described as ketol-acid reductoisomerase; antigenic during human or murine
LEU4	Putative 2-isopropylmalate synthase; regulated by Nrg1p, Mig1p, Tup1p, Gcn4p;
ARX1	Predicted ORF in Assemblies 19, 20 and 21; downregulated during core stress response
	Protein not essential for viability; possibly spurious ORF (Annotation Working Group)
	Predicted ORF in Assemblies 19, 20 and 21; repressed by nitric oxide
FAD3	Omega-3 fatty acid desaturase, involved in production of alpha-linolenic acid, which
RPA12	Protein described as DNA-directed RNA polymerase I; induced upon adherence to
	Predicted ORF in Assemblies 19, 20 and 21
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21; increased transcription is observed upon
KGD1	Protein described as 2-oxoglutarate dehydrogenase; regulated by Efg1p under yeast
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
GUT1	Protein described as glycerol kinase; downregulated upon adherence to polystyrene
HOM3	Putative L-aspartate 4-P-transferase; fungal-specific (no human or murine homolog)
NA	NA
SUP35	Translation factor eRF3; shows prion-like aggregation in some, not all, studies; part
	Protein described as succinate dehydrogenase, enzyme of citric acid cycle; downregulated
SDH2	Succinate dehydrogenase, Fe-S subunit; localizes to surface of yeast-form cells, but
	Protein described as poly(A)-binding protein; regulated by Gcn4p; induced in response
	Predicted membrane transporter, member of the drug:proton antiporter (12 spanner)
	Predicted ORF in Assemblies 19, 20 and 21
ATP7	Putative subunit of the F1F0-ATPase complex; shows colony morphology-related growth
NA	NA
	Similar to alcohol dehydrogenases; increased transcription is observed upon benzoate
ATP14	ORF Predicted by Annotation Working Group; macrophage/pseudohyphal-induced
LYS22	Putative homocitrate synthase; fungal-specific (no human or murine homolog); repressed
	Predicted membrane transporter, member of the monocarboxylate porter (MCP) family
FUM12	Protein described as similar to fumarate hydratase, enzyme of citric acid cycle; flucan
NOP7	Pescadillo homolog required for filament-to-yeast switching; mutation confers hypobiont
RPA190	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced
IDH1	Predicted ORF in Assemblies 19, 20 and 21; soluble protein in hyphae; protein levels
	Predicted ORF in Assemblies 19, 20 and 21
	Predicted ORF in Assemblies 19, 20 and 21
IDP2	Putative isocitrate dehydrogenase; expression is regulated upon white-to-opaque switch
	Ortholog of <i>S. cerevisiae</i> Tma19p (Ykl065cp)
MDM34	Putative transcription factor with zinc finger DNA-binding motif; macrophage-downregulated
TSR2	Predicted ORF in Assemblies 19, 20 and 21; decreased expression in response to
	Predicted ORF in Assemblies 19, 20 and 21
GAR1	Predicted ORF in Assemblies 19, 20 and 21; mutation confers hypersensitivity to tunicamycin
	Predicted ORF in Assemblies 19, 20 and 21; similar to stomatin mechanoreception
GDH3	Protein described as similar to NADP-glutamate dehydrogenase; hyphal downregulated
	Predicted ORF in Assemblies 19, 20 and 21
URA2	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; macrophage/pseudohyphal
SFC1	Alkaline upregulated
ILV3	Putative dihydroxyacid dehydratase; fungal-specific (no human or murine homolog)
RGT1	Transcriptional repressor involved in the regulation of glucose transporter genes; highly
GCV2	Putative protein of glycine catabolism; downregulated by Efg1p; Hog1p-induced; upregulated
NUP	Nucleoside permease; adenosine and guanosine are substrates, whereas cytidine, uridine
NA	NA
HIS1	ATP phosphoribosyl transferase; enzyme of histidine biosynthesis; fungal-specific (no
LYS4	Protein described as homoaconitase; regulated by Gcn4p, Gcn2p; induced in response to
	Putative transporter; slightly similar to the Sit1p siderophore transporter; Gcn4p-regulated
PHO84	Protein similar to high-affinity phosphate transporters; expression is regulated upon
IFE1	Protein not essential for viability; similar to <i>S. cerevisiae</i> Yal061wp, which is a putative
SPT5	Protein similar to <i>S. cerevisiae</i> Spt5p transcription elongation factor; transposon mutagenesis
NA	NA
NA	NA

NA	NA
	Predicted ORF in Assemblies 19, 20 and 21
IDH2	Protein described as isocitrate dehydrogenase subunit; transcription is upregulated
TSR1	Predicted ORF in Assemblies 19, 20 and 21; decreased expression in response to
	Described as a Gag-related protein; hyphal induced; downregulation correlates with
HGT19	Putative glucose/myo-inositol transporter of major facilitator superfamily; 12 transmembrane
	Predicted ORF in Assemblies 19, 20 and 21; regulated by Nrg1p, Tup1p; transcript
ILV2	Protein described as acetolactate synthase; regulated by Gcn4p; induced in response to
NA	NA
NA	NA
NA	NA
	Predicted ORF in Assemblies 19, 20 and 21; possibly spurious ORF (Annotation W)
	Putative transporter; mutation confers hypersensitivity to toxic ergosterol analog; function
	Protein with similarity to ferric reductases; transcription is activated by Mac1p under
STD1	Protein described as transcription factor involved in control of glucose-regulated genes
DIP5	Putative permease for dicarboxylic amino acids; mutation confers hypersensitivity to
NA	NA
PCK1	Phosphoenolpyruvate carboxykinase; role in gluconeogenesis; regulated by hyphal
DBP2	Predicted ORF in Assemblies 19, 20 and 21; flucytosine induced; downregulated in
AOX2	Alternative oxidase; induced by antimycin A, some oxidants; growth- and carbon-source
NA	NA
CTR1	Copper transporter; probably multimeric; transcribed if copper limited; induced by
HGT1	High-affinity glucose transporter, member of major facilitator superfamily; transcript

in response to salt; regulated by macrophage, stress response, yeast-hyphal switch, pheromone, conazole-induced; localizes to cell surface of hyphal cells, but not yeast-form cells; *S. cerevisiae* (

to be cell-wall attached and glycosylated; Tup1p repressed; serum, hyphal and alkaline induced; fungal-specific (no human or murine homolog); caspofungin repressed; protein detected by mass spectrometry; antigenic during murine or human systemic infection; biofilm, Hog1p, GCN-induced; downregulated by macrophage infection; fluconazole-downregulated; Mig1p regulated; downregulated by Efg1p on cell surface, not hyphae; soluble in hyphae; iron-regulated expression; macrophage-downregulated (working Group prediction)

phagocytosis; major cell-surface antigen; binds host plasmin and plasminogen; immunoprotective; phagocytosis; antigenic in murine, human infection; biofilm-, fluconazole-, or amino acid starvation (3-aminopropanoate); immunogenic in human or mouse; complements *S. cerevisiae* adh1 adh2 adh3 mutation; regulated

Tup1p, regulated upon white-opaque switching; decreased expression in hyphae compared to yeast

or human infection; regulated on yeast-hyphal switch; induced by Efg1p, Gcn4p, Hog1p, biofilm (

planktonic cells; protein detected by mass spec in exponential and stationary phase cultures; binds laminin and laminin; at surface of yeast-form cells and hyphae; soluble in hyphae; antigenic during infection; caspofungin repressed

yeast-form cells; soluble in hyphae; regulated by Gcn4p, Efg1p, Efh1p; fluconazole-, farnesol-, biofilm-induced; clinically-isolated homozygous null mutants show azole resistance, defects in hyphal growth; induced; Plc1p-regulated; repressed by Rim101p, Hog1p; colony morphology-related gene regulation; overexpression or fluphenazine treatment; transcription regulated by Sfu1p, Nrg1p, Tup1p; confers Cu resistance; similar to proteins of Menkes and Wilson disease; copper-induced; Tbf1p-activator; antigenic in human neutrophils; regulated by Efg1p; fluconazole-induced; shows colony morphology-related defects in ergosterol biosynthesis; target of azole antifungals; may contribute to drug resistance; azole-resistant; high iron, decreased upon yeast-hyphal switch; downregulation correlates with clinical development

in human; mutation affects filamentous growth; biofilm-induced; macrophage-downregulated protein; conditionally regulated by Efg1p; fluconazole-induced; induced in core stress response; shows colony morphology-related defects; repressed

major protein in hyphae; Hog1p-induced; induced during cell wall regeneration; caspofungin or flucanazole-resistant; Gcn4p, Hog1p regulated; induced on polystyrene adherence; downregulated upon phagocytosis; colony morphology-related gene regulation by Ssn6p

of ergosterol biosynthesis by methylating position C-24; mutation confers nystatin resistance; fluconazole-inc

glucomutase

PFK2p; PFK is activated by fructose 2,6-bisphosphate or AMP, inhibited by ATP; downregulated in hyphae; PFK is activated by fructose 2,6-bisphosphate or AMP, inhibited by ATP; activity reduced on hypoxia

glycerol biosynthesis); biofilm-induced expression; regulated by Efg1p; regulated by Tsa1p, Tsa1Bp; amphotericin B repressed; caspofungin repressed; intron in 5'-UTR

involved in the ergosterol biosynthetic pathway; essential; target of allylamine antifungal drugs; uses NADH

repressed by heavy metal (cadmium) stress via Hog1p; oxidative stress-induced via Cap1p; induced by hypoxia in human; regulated by Efg1p; induced in biofilm, upon adherence to polystyrene; downregulated in hyphae; similar to *S. cerevisiae* Pos5p, which is a mitochondrial NADH kinase involved in the oxidative phosphorylation pathway; stable protein in hyphae; transcription is regulated by Nrg1p, Mig1p, and Tup1p; antigenic in human

increased sensitivity to dyclonine

involved in acid synthesis; required for aerobic hyphal growth and chlamydospore formation; subject to hypoxia; amphotericin B repressed; regulated by Nrg1p, Tup1p; induced by prostaglandins

involved in morphology-related gene regulation by Ssn6p; protein detected by mass spec in stationary phase; belongs to the (DHA1) family, major facilitator superfamily (MFS)

involved in cell wall defects and increased filamentation; fluconazole-induced; protein detected by mass spec in stationary phase

repressed by amphotericin B, caspofungin repressed; macrophage/pseudohyphal-induced; fungal-specific (no human ortholog); sensitive to treatment with caspofungin, ciclopirox olamine or ketoconazole; gene of core caspofungin resistance

involved in exponential and stationary phase cultures

antigenic during murine systemic infection; antigenic in human; upregulated by Efg1p; macrophage-induced; involved in cell wall regulation; fluconazole-induced; caspofungin repressed

involved in intracellular acetyl-CoA transport; transcriptionally induced in macrophage; farnesol-upregulated in response to treatment with ciclopirox olamine, alpha pheromone; regulated by oxidative stress; involved in ergosterol biosynthesis, catalyze formation of the C-22(23) double bond in the sterol; involved in the presence of human neutrophils; fluconazole-downregulated; regulated by Nrg1p and Mig1p; show

involved in cell wall regulation; major facilitator superfamily (MFS); amphotericin B, caspofungin repressed

antigenic in human; induced on polystyrene adherence; farnesol-, ketoconazole-induced; no human ortholog

involved in cell wall regulation by Ssn6p

(Working Group prediction)

involved in cell wall regulation; transposon mutation affects filamentous growth; amphotericin B, caspofungin repressed; detected in hyphae; induced upon biofilm formation; Hog1p-induced; expression of OPT6, -7, or -8 does not suppress growth; involved in ergosterol biosynthesis; farnesol-downregulated; protein detected by mass spec in stationary phase; involved in cell wall regulation and rat oropharyngeal infection models; regulated by Efg1p; fluconazole-induced; amphotericin B repressed; mRNA abundance observed in a *cyr1* or *ras1* homozygous null mutant than in wild type

involved in cell wall regulation; macrophage-induced protein; antigenic in mouse; protein detected by mass spec in exponential phase

involved in cell wall regulation; stable in hyphae; changes in protein abundance associated with azole resistance; fluconazole or ketoconazole-induced; involved in cell wall regulation; -anchor; induced by ciclopirox olamine, ketoconazole, or by Rim101p at pH 8; regulated during pH shift

involved in prostaglandins

ed in a *cyr1* or *ras1* homozygous null mutant than in wild type; protein detected by mass spec in s
nf3p-induced, expressed at high glucose; upregulated in biofilm; *C. albicans* glucose transporter
y induced by O₂ or oxidizing agents H₂O₂ or menadione; caspofungin repressed; macrophage in

o alpha pheromone in SpiderM medium

lase; transposon mutation affects filamentous growth

iron; expression greater in high iron; induced during cell wall regeneration; *Cyr1p* or *Ras1p* downr

r tyrosol and cell density; transcription is upregulated in response to treatment with ciclopirox olam

ant; strain variation in number of repeat domains; upregulated in filaments; alkaline upregulated b
synthesis; downregulation correlates with clinical development of fluconazole resistance; amphot
tericin B, Cd, ketoconazole-induced; farnesol-downregulated in biofilm; farnesol-induced; surface

ated gene regulation by *Ssn6p*

with *Erg25p* and *Erg26p*; possible drug target, essential for viability; functional homolog of *S. cer*
cted *Kex2p* substrate; induced during cell wall regeneration

lipid biosynthesis; upregulated in biofilm; regulated by *Tsa1p*, *Tsa1Bp* under H₂O₂ stress conditic
the sterol biosynthesis pathway; likely to be essential for growth; regulated by fluconazole and lo
in base moiety of ceramides during glucosylceramide synthesis

rf19.5158; regulated by *Gcn4p*, *Cyr1p*; induced in response to amino acid starvation (3-aminotria

mbrane-associated progesterone receptors involved in response to DNA damage; induced in core

ogen, macrophage response, human neutrophils; putative D200-H232-S389 catalytic triad; similar
sis; putative bipartite mitochondrial targeting motif, membrane spanning region; transcription is re

lulated by *Rfg1p*, *Rim101p*, *Tbf1p*, iron; repressed by *Sfu1p*, *Hog1p*, *Tup1p*; induced by serum, alk
hotericin B induced

nsposon mutation affects filamentous growth; *Hog1p*-downregulated; shows colony morphology-r
ompared to yeast-form cells; macrophage/pseudohyphal-repressed; induced by high levels of per
by *Ssn6p*; induced by nitric oxide in *yhb1* mutant

shows colony morphology-related gene regulation by *Ssn6p*; protein detected by mass spec in s
ERG2 promoter; has Zn(2)-Cys(6) binuclear cluster; induced upon ergosterol depletion, by azoles

ionary phase cultures

otion downregulated upon yeast-hyphal switch and regulated by *Efg1p*; strong oxidative stress inc

tion Working Group prediction)

ulated by *Tup1p*, *Efg1p*

ed in a *cyr1* or *ras1* homozygous null mutant than in wild type; possibly spurious ORF (Annotati
kinase

from oxidative stress and required for full virulence; alkaline upregulated by *Rim101p*; upregulate
; regulated by *Efg1p* and *Efh1p*; repressed by *Rgt1p*; protein detected by mass spec in exponenti
(orking Group prediction)

hase cultures

rol to episterol; mutant is hypersensitive to multiple drugs; ketoconazole-induced

p; possible drug target; transcriptionally regulated by carbon source, yeast-hyphal switch, growth
6P accumulation, and decreased mouse virulence; possible drug target; two conserved phospho
nificant stress response regulator in *C. albicans*; partly complements STRE-activation defect of *S*
.l homolog of *S. cerevisiae* and *E. coli* phosphomannose isomerase; Gcn4p-regulated; repressed

ced via Cap1p; induced by nitric oxide in yhb1 mutant; protein detected by mass spec in exponen

infection; predicted P-loop, divalent cation binding, N-glycosylation sites; expressed in yeast and
olism; has adhesin motif; O-glycosylation but no predicted N-glycosylation; induced by heat, upo
emic, rabbit corneal infections; not required for filamentation; secretion signal; TUP1/RFG1/SSN6
growth; downregulated in core stress response
ain in hyphae; transcriptionally induced by macrophage interaction; transcriptionally induced by M
n is observed upon benomyl treatment; macrophage-downregulated gene

i core stress response; induced by heavy metal (cadmium) stress via Hog1p

olog; transcription is induced upon phagocytosis by macrophage; regulated upon white-opaque s

ions; similar to *S. cerevisiae* Yjl097p, which is required for growth
l upon white-opaque switching; fluconazole-induced; antigenic during murine systemic infection; r
eutrophils
endent peroxidases of oxidative stress signaling; antigenic; hyphal surface, nucleus; yeast-form r
phase cultures

orf19.854.1, which is a region annotated as a blocked reading frame
nder weak acid stress
f disulfide bonds in the endoplasmic reticulum; fluconazole-induced; transcriptionally activated by

nder weak acid stress

t

d by Rim101p or alkaline pH; transcription induced by interaction with macrophage or low iron; ox

:osamine utilization; required for wild-type hyphal growth and virulence in mouse systemic infectio
og1p-downregulated; shows colony morphology-related gene regulation by Ssn6p; increased exp

treatment, low iron, CDR1 and CDR2 overexpression, or *ssn6* or *ssk1* homozygous null mutation

and gene expression; protein level decreased in stationary phase cultures

; protoberberine derivative drug inhibits enzyme activity; 7 putative transmembrane regions; ketone protein of unknown function belonging to the prokaryotic RraA family; decreased transcription is observed in peptide that are processed to individual units; transcription is induced by stress; mRNA found in yeast

an azole-resistant strain that overexpresses MDR1

transcriptionally regulated by iron; expression greater in high iron; fluconazole-induced; shows colony morphology

synthesis intermediates, based on similarity to *S. cerevisiae* Erg25p; fluconazole-induced; upregulated (working Group prediction)

treatment with ciclopirox olamine; positively regulated by Sfu1p; Hog1p, fluconazole-downregulated

transcription regulation by Ssn6p

transcription is elevated in *chk1*, *nik1*, and *sln1* homozygous null mutants; repressed by nitric oxide

isolated from HIV+ patients with oral candidiasis; alkaline downregulated; amphotericin B induced; shows morphology

transcription regulation by Rgt1p

interaction with macrophage; fluconazole induced; Fkh2p-downregulated; caspofungin repressed transcription; expression greater in high iron; induced during cell wall regeneration; possibly spurious ORF

transcription upregulated upon yeast-hyphal switch; fluconazole-induced; caspofungin repressed; protein detected by mass spec

tryptophan catabolism via kynurenine pathway; enzyme inhibition by 1-methyl-D,L-tryptophan cause compared to yeast-form cells; regulated by Efg1p and Efh1p; intron in 5'-UTR; transcriptionally activated ortholog of human Chediak-Higashi syndrome protein and murine beige gene implicated in disease

major component of membranes

transcription essential for growth; protein level decreased in stationary phase cultures

transcription; protein detected by mass spec in stationary phase cultures

transcription a pheromone in SpiderM medium; transcriptionally activated by Mnl1p under weak acid stress

transcription required for wild-type hyphal growth and mouse virulence; converts glucosamine 6-P to fructose 6-P

phase cultures

secreted, purified from cell wall and intracellular fractions; protein repressed during the mating phase; reduced overall; not required for virulence in mouse systemic infection; homodimeric enzyme; possible

(assembly 19 correction)

tyrene; regulated by Gcn2p and Gcn4p

alpha pheromone in SpiderM medium

toxic ergosterol analog; shows colony morphology-related gene regulation by Ssn6p; clade-associated (in human or murine homolog); amphotericin B repressed; involved in the ergosterol biosynthesis pathway

beta pheromone in SpiderM medium

transcriptionally regulated by iron; expression greater in high iron; fluconazole-induced

soluble protein in hyphae; biofilm induced, macrophage-induced protein; downregulated upon treatment with Lro1p acyltransferase

regulates filamentous growth, phenotypic switching; homodimerizes; has APSES domain and a murine homolog; a pheromone in SpiderM medium; transcription is regulated by Tup1p

immunogenic in mice; benomyl treatment induces transcription; oxidative stress-induced via Cap1p

phage-induced protein; alkaline upregulated; amphotericin B repressed; gene used for strain identification

induced by interaction with macrophage

in yeast cells; biofilm induced; fungal-specific (no human or murine homolog)

expressed in yeast-form cells; downregulated by Efg1p; transcription is upregulated in clinical isolates from HIV-infected patients; gene regulation by Ssn6p

(Aox1p and Aox2p); involved in a cyanide-resistant respiratory pathway present in plants, protists, and fungi

secreted by yeast cells but is elevated at lower growth temperatures; upregulated in the presence of human neutrophils; induced in core stress response

homolog)

growth; activates Rac1p; contains a DOCKER domain; similar to adjacent DCK2 and to S. cerevisiae DCK2; repressed in response to amino acid starvation (3-aminotriazole treatment)

transcription factors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage

polystyrene

regulated; downregulated in response to 17-beta-estradiol, ethynyl estradiol
formation

ogy; similar to *S. cerevisiae* Dim1p, which is an 18S rRNA dimethylase involved in rRNA modification
syltransferases

1, endocytosis; localizes to eisosome subdomains of plasma membrane; four transmembrane mo

ne residues

· biosynthesis pathway; functionally complements *S. cerevisiae* lys1 mutation; fungal-specific (no l
io acid biosynthesis; GCN-regulated; feedback-inhibited by tyrosine when produced in *S. cerevisi*
e

nethylation of arginine residues; involved in nuclear export of Npl3p
e; physically interacts with TAP-tagged Nop1p

es microfilarial sheath protein

· complex; transposon mutation affects filamentous growth; macrophage/pseudohyphal-induced; pt

Rim101p; expression greater in low iron; regulated on white-opaque switching; filament induced;

by Mig1p and Tup1p; transcriptionally regulated by iron; expression greater in high iron; filament ir
wth; mutation confers hypersensitivity to 5-fluorouracil (5-FU), tubercidin (7-deazaadenosine); do
stant membrane fraction (possible lipid raft component); predicted N-terminal acetylation; repress
ribosomal subunit; transposon mutation affects filamentous growth; protein level decreased in stal
D-box ATP-dependent RNA helicase family that is involved in biogenesis of the ribosome, particu
io acid biosynthesis; GCN-regulated; feedback-inhibited by phenylalanine when heterologously pr

action (possible lipid raft component); 3 predicted transmembrane helices; flucytosine induced; ke
ors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage; proteir
essed; macrophage/pseudohyphal-induced

· regulated; periodic mRNA expression, peak at cell-cycle G1/S phase

3ub2p; mutation confers hypersensitivity to amphotericin B; induced upon adherence to polystyrene
; from HIV+ patients with oral candidiasis; predicted ORF in Assemblies 19, 20 and 21

ne phosphatase); similar to *S. cerevisiae* Yvh1p; required for wild-type growth rate and for wild-type

regulated by Hmt1p; transcription is upregulated in an RHE model of oral candidiasis
on sources but not for hyphal growth or virulence in mouse systemic model; transcription induced
neurin-dependent resistance to azoles; stress-associated protein; Ca²⁺, calcineurin-regulated; ke

ssion

ippase); putative membrane protein; putative drug-responsive regulatory site; induced by fluphen-
-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); downregulated in
ced in response to alpha pheromone in SpiderM medium
induced; macrophage-downregulated protein abundance; protein level decreased in stationary ph

prostaglandins

xpression greater in high iron; upregulated upon phagocytosis; Hog1p-downregulated; regulated l

ions and a secretion signal predicted; repressed by Tup1p, Rim101p, Ssn6p, Hog1p, caspofungir

on; expression greater in high iron; fluconazole-induced

ansporter

Gcn2p and Gcn4p; *S. cerevisiae* ortholog is Gcn4p regulated

by mass spec in exponential and stationary phase cultures

mily, major facilitator superfamily (MFS)

ed for adherence to buccal epithelial cells or virulence in mouse systemic infection; null mutant cc

rg) motifs, ABC transporter consensus; expressed in hyphal, pseudohyphal, and yeast form, upre

;p and Ygr138Cp; required for wild-type mouse virulence and wild-type cycloheximide resistance;
pon fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2
encoding ribosomal subunits, translation factors, and tRNA synthetases are downregulated upon

-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); decreased expre
idoreductase; gene has intron

holipids in an in-to-out direction; transcription induced by beta-estradiol, progesterone, corticoster
regions; regulated by nitrogen source; alkaline, GlcNAc, phagocytosis upregulated; not required f
rocessing in vitro; expression is regulated upon white-opaque switching; alkaline downregulated

; from HIV+ patients with oral candidiasis; predicted ORF in Assemblies 19, 20 and 21

-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); hyphal represser

systemic virulence; regulated by iron, ciclopirox olamine, fluconazole, growth, carbon source, pH
-fluorouracil (5-FU), tubercidin (7-deazaadenosine); transcription is positively regulated by Tbf1p;
duced

molog); alkaline downregulated; transcription is specific to white cell type; caspofungin repressed
lop1p

with macrophage; alkaline downregulated; repressed by nitric oxide; clade-associated gene expr

pofungin response; shows colony morphology-related gene regulation by Ssn6p; induced by 17-t
lation factors, and tRNA synthetases are downregulated upon phagocytosis by murine macropha

detected at germ tube plasma membrane by mass spectrometry; transcriptionally induced upon pl

re infection; regulated by Gcn4p; amino acid starvation (3-aminotriazole) induced; biofilm induced upregulated in the presence of human whole blood or polymorphonuclear (PMN) cells; macrophage response; decreased expression in response to prostaglandins (Miyamoto et al. 2004); transcriptionally activated by Mnl1p under weak acid stress

Chitin is a major component of membranes; caspofungin induced; Plc1p-regulated; shows colony morphology on polystyrene

Induced by benomyl treatment; possibly spurious ORF (Annotation Working Group prediction); transcription is upregulated in an RHE model of oral candidiasis but not hyphal growth conditions

Greater mRNA abundance observed in a *cyr1* homozygous null mutant than in wild type; regulated by Gcn2p and Gcn4p

Essentially complements *S. cerevisiae* sup35 mutant translation defect; species barrier with *S. cerevisiae*; regulated by Efg1p; repressed by nitric oxide; not hyphae; transcriptionally regulated by iron; expression greater in high iron; repressed by nitric oxide; response to amino acid starvation (3-aminotriazole treatment); protein detected by mass spec in exponential phase (DHA1) family, major facilitator superfamily (MFS)

Gene regulation by Ssn6p; farnesol-, macrophage-downregulated protein abundance

Induced by benomyl treatment; induced by nitric oxide; induced in core stress response; oxidative stress-induced

Repressed by nitric oxide; protein level decreased in stationary phase cultures; major facilitator superfamily (MFS); alkaline upregulated by Rim101p; 5-fluorouracil-downregulated; downregulated by Efg1p; transcriptionally regulated by iron; expression (sensitivity to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)

Protein level decreased in stationary phase cultures

Induced by benomyl treatment; shows colony morphology-related gene regulation by Ssn6p; protein detected by mass spec

Regulated gene
prostaglandins

Induced by tubercidin (7-deazaadenosine); macrophage/pseudohyphal-induced; protein; induced by Rgt1p; upregulated expression; transcription is regulated by Nrg1p, Plc1p; downregulated by Efg1p; upregulated

Pseudohyphal-induced; intron in 5'-UTR

Induced by benomyl treatment; upregulated in biofilm; *S. cerevisiae* ortholog is Gcn4p regulated; repressed by nitric oxide; macrophage response; zinc-cluster; similar to *S. cerevisiae* Rgt1p; upregulated by Rim101p at acid pH; transcription is activated in the presence of elevated CO₂; protons; adenine, guanine, uridine, uracil are not; similar to a nucleoside permease of *S. pombe*; possibly

(no human, murine homolog); upregulated in biofilm; acid upregulated/alkaline downregulated by Rim101p; response to amino acid starvation (3-aminotriazole treatment); upregulated in the presence of human whole blood; upregulated; fungal-specific (no human or murine homolog); transcriptionally activated by Mnl1p under conditions of white-opaque switching or biofilm formation; Hog1p, ciclopirox olamine or alkaline induced; caspofungin-induced; polyol dehydrogenase; benomyl treatment affects filamentous growth

l in response to treatment with ciclopirox olamine; transcriptionally regulated by iron; expression g
prostaglandins
n clinical development of fluconazole resistance; repressed by nitric oxide, 17-beta-estradiol, ethy
membrane segments, extended N terminus; expressed in rich medium, 2% glucose; phagocytosis-
ion is repressed in response to alpha pheromone in SpiderM medium
rse to amino acid starvation (3-aminotriazole treatment); protein detected by mass spec in station

orking Group prediction)

ingal-specific (no human or murine homolog)

r copper starvation; Plc1p-regulated; transcription is negatively regulated by Rim101p

ne expression; repressed by Rgt1p

o toxic ergosterol analog; transcriptionally induced upon phagocytosis by macrophage; Gcn4p-re

l switch, carbon source; repressed on glucose; induced by fluconazole, phagocytosis, H₂O₂; prec
l core stress response

urce-regulated; one of two isoforms (Aox1p and Aox2p); involved in cyanide-resistant respiratory

Mac1p, macrophage interaction, alkaline pH via Rim101p; 17-beta-estradiol downregulated; compl
ion induced by progesterone and by drugs including chloramphenicol and benomyl; likely essenti

upon phagocytosis or hyphal growth; fluconazole-induced
hal induction; phagocytosis-downregulated; fluconazole-induced

under H₂O₂ stress conditions

as a reducing cofactor, while *S. cerevisiae* Erg1p uses NADPH

Mnl1p under weak acid stress; macrophage-downregulated
induced in the presence of human neutrophils, upon phagocytosis
e stress response
in murine infection

toxic regulation; fluconazole-induced; caspofungin repressed

in cultures

stationary phase cultures

human or murine homolog)
response

fluconazole-induced protein; soluble protein in hyphae

isolated in biofilm; Hog1p-downregulated
osmotic stress (via Cap1p) and osmotic stress (via Hog1p)
involves side chain; transposon mutation affects filamentous growth
affects colony morphology-related gene regulation by Ssn6p

in murine homolog

detected by mass spec in exponential and stationary phase cultures
phenotypic defect of mutant lacking Opt1p, -2p, or -3p; fungal-specific
in cultures
cin B repressed

in stationary phase cultures

fluconazole induced; macrophage-downregulated protein
in planktonic growth; induced during cell wall regeneration

stationary phase cultures
family comprises 20 members; 12 TM regions predicted
induced; induced in core stress response; regulated by Gcn2p, Gcn4p

regulated; transcription is positively regulated by Tbf1p

ine; fluconazole or flucytosine induced

y Rim101p; ciclopirox induced; Efg1p- and Cph1p-regulated
ericin B repressed; caspofungin repressed
localized in yeast-form and hyphal cells; antigenic in host

evisiae Erg27p

ons
vastatin; amphotericin B, caspofungin repressed

zole treatment); macrophage-induced protein, macrophage-downregulated gene

σ stress response; Hog1p regulated; clade-associated expression

to (but does not replace) *S. cerevisiae* vacuolar B protease Prb1p
regulated upon yeast-hyphal switch, or by Nrg1p, Mig1p, Tup1p

caline pH, ketoconazole, ciclopirox olamine

related gene regulation by Ssn6p; induced during cell wall regeneration
oxidative stress, farnesol-induced

tationary phase cultures
, anaerobicity; macrophage/pseudohyphal-repressed

luced; shows colony morphology-related gene regulation by Ssn6p

Working Group prediction)

ind in the presence of human blood
al and stationary phase cultures

phase, antifungals; gene has intron
/drolase motifs; no human or murine homolog
i. cerevisiae msn2 msn4 double mutant
by 3-AT; induced on adherence to polystyrene, phagocytosis

tial and stationary phase cultures

hyphae; hyphal downregulated; lacks S. cerevisiae homolog
γ germ tube formation, wall regeneration; diagnostic marker
/HOG1 repressed; serum, hyphal, pheromone, alkaline-induced

nl1p under weak acid stress, farnesol-induced

witching; biofilm-repressed; strong oxidative stress induced

regulated by Nrg1p, Tup1p; macrophage-downregulated protein

nucleus, cytoplasm; biofilm, phagocytosis, peroxide induced

Mnl1p under weak acid stress

xygen-induced activity

n; gene is GlcNAc-induced
ression in response to prostaglandins

; repressed by Hog1p, flucytosine, elevated CO2

conazole-induced
erved upon benomyl treatment
ast-form and mycelial cells at similar abundance

phology-related gene regulation by Ssn6p

ted in biofilm and in azole-resistant strain

d

s colony morphology-related gene regulation by Ssn6p

(Annotation Working Group prediction)

is spec in stationary phase cultures

s increased hyphal growth; expressed in yeast-form cells and hyphae
ed by Mnl1p under weak acid stress
se syndromes involving defective lysosomal trafficking

6-P; reaction is reversible in vitro; gene is GlcNAc-induced

rocess; Hog1p-, farnesol-induced
sible regulatory cAMP-dependent phosphorylation at S10 and S213

ated gene expression

ent of biofilm with farnesol

cidic region; EFG1 and EFH1 genetically interact

; fungal-specific (no human/murine homolog), farnesol-downregulated

tification by multilocus sequence typing, farnesol-induced

IV+ patients with oral candidiasis

, and some fungi, although absent from *S. cerevisiae*

eutrophils; detected by mass spec in stationary phase cultures

ae Ylr422wp; regulated by Nrg1p

ion and processing; induced upon biofilm formation

tifs; mutant shows ectopic, chitin-rich cell wall

human or murine homolog)
ae; fungal-specific; Aro3p and Aro4p catalyze the same reaction

ysically interacts with TAP-tagged Nop1p

transposon mutation affects filamentous growth

duced
wnregulated during core stress response
ied by nitric oxide
tionary phase cultures
larly the small (40S) subunit; caspofungin-downregulated
duced in *S. cerevisiae*; Aro3p and Aro4p catalyze the same reaction

toconazole-induced; downregulated by Efg1p
1 detected by mass spec in stationary phase cultures

ae; fungal-specific (no human or murine homolog)

of virulence in mouse model of systemic infection

in macrophage; macrophage/pseudohyphal-repressed after 16 hr
itraconazole, caspofungin induced; Plc1p-regulated

azole, estradiol, ketoconazole, caspofungin
core stress response

ase cultures

by Efg1p under yeast-form but not hyphal growth conditions

; ciclopirox olamine induced; not required for filamentous growth

colonies exhibit slightly decreased filamentation ratio

regulated in biofilm; *S. pombe* homolog is ABC ATPase of mRNA export

gene cluster encodes enzymes of GlcNAc catabolism

phagocytosis by murine macrophage

expression in response to prostaglandins

oid, or cholesterol

of virulence in mouse systemic infection; fungal-specific

d; macrophage repressed

l, Rim101p, Ssn6p, Hog1p, farnesol, core stress response
downregulated during core stress response

l; macrophage/pseudohyphal-repressed

expression

beta-estradiol, ethynyl estradiol
gene

phagocytosis by macrophage

; macrophage-downregulated protein; no human or murine homolog
ge/pseudohyphal-repressed after 16h; fungal-specific

phology-related gene regulation by Ssn6p

ndidiasis; detected by mass spec in stationary phase cultures

ie Sup35p prion; gene not regulated by yeast-hyphal switch

ric oxide; induced during log phase (aerobic growth)
ntial and stationary phase cultures

ria Cap1p

greater in high iron

ec in exponential and stationary phase cultures

d by Rim101p at pH 8; ciclopirox olamine induced

:rophage-induced protein; farnesol-downregulated

tein detected by mass spec in stationary phase cultures
' processed by Kex2p

Rim101p; regulated by Gcn2p, Gcn4p; strain CA9 is a his1 mutant
whole blood or polymorphonuclear (PMN) cells
' weak acid stress
ofungin or stress repressed; upregulated in RHE model

reater in high iron

nyl estradiol

induced; *C. albicans* glucose transporter family has 20 members

ary phase cultures

gulated; upregulated by Rim101p at pH 8

dicted ATP-dependent, dimeric; predicted PKC phosphorylation sites

pathway that is absent from *S. cerevisiae*

lements *S. cerevisiae* ctr1 ctr3 copper transport mutant

al for growth, based on an insertional mutagenesis strategy