

Figure S1

Vertices

- Metabolism
- Cell Organization and Biogenesis
- RNA Localization
- Transport
- Protein Degradation
- UNKNOWN
- Protein biosynthesis
- Stress Response
- Carbohydrate Metabolism
- Sporulation
- Signal transduction
- Protein transport
- DNA Repair

Experimental Systems

- TWO-HYBRID
- PCA
- RECONSTITUTED COMPLEX
- CO-PURIFICATION
- DOSAGE RESCUE
- SYNTHETIC RESCUE
- CO-CRYSTAL STRUCTURE
- AFFINITY CAPTURE-WESTERN
- SYNTHETIC GROWTH DEFECT
- AFFINITY CAPTURE-MS
- SYNTHETIC HAPLOINSUFFICIENCY
- DOSAGE GROWTH DEFECT
- PHENOTYPIC ENHANCEMENT
- PHENOTYPIC SUPPRESSION
- SYNTHETIC LETHALITY
- BIOCHEMICAL ACTIVITY
- PROTEIN-PEPTIDE

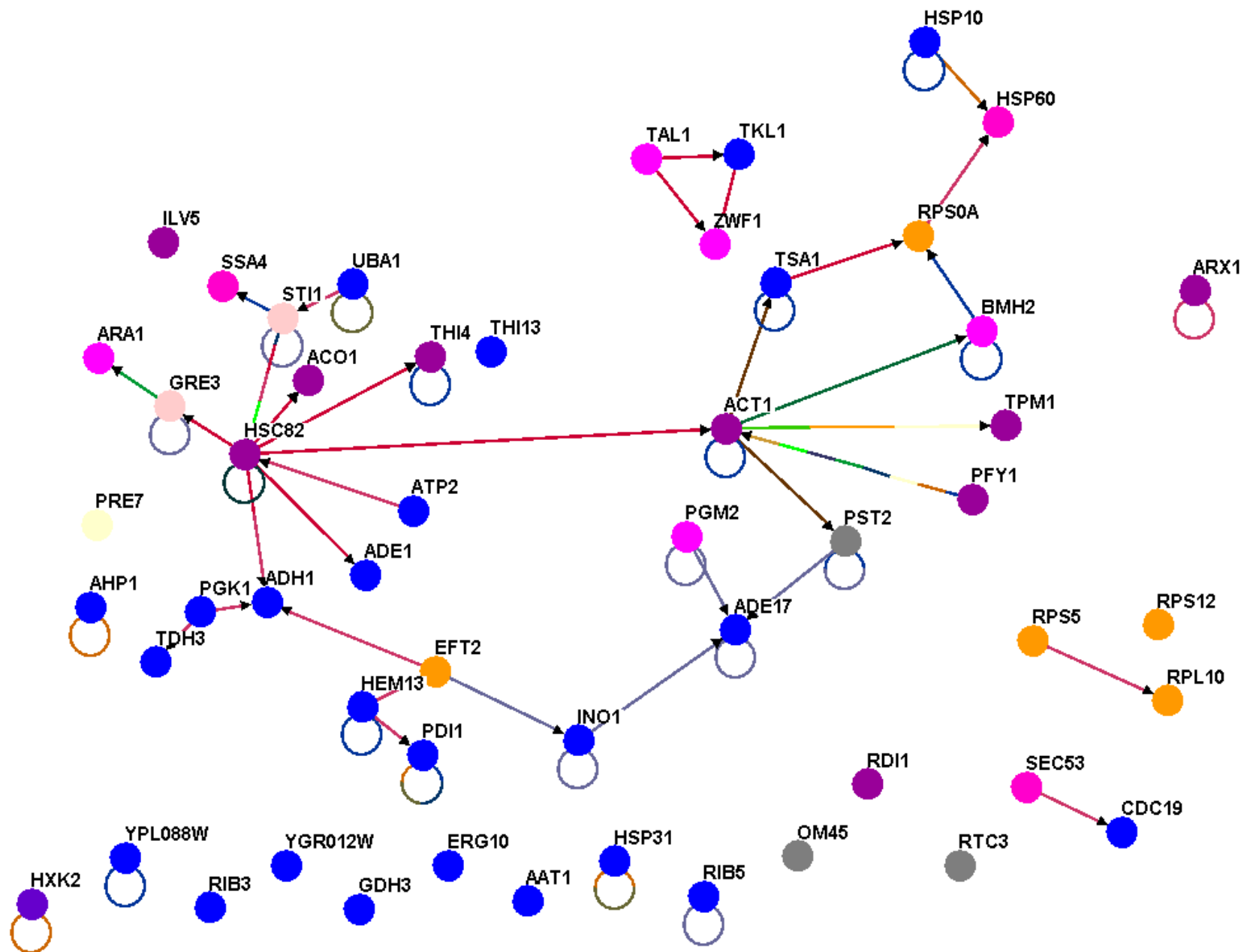


Table S1. 2D-DIGE experimental design of total cytoplasmic extracts gels (pH 3–11 NL IPG strips).

Gel	Cy2	Cy3	Cy5
1	50 µg Internal standard	50 µg yeast 1	50 µg hypha 4
2	50 µg Internal standard	50 µg hypha 3	50 µg yeast 2
3	50 µg Internal standard	50 µg yeast 3	50 µg hypha 2
4	50 µg Internal standard	50 µg hypha 1	50 µg yeast 4

Table S2: LC-MS/MS-identified proteins from *Candida albicans* acidic subproteome.

Accession Protein number name	Peptide Sequence	MH+ peptide	DeltaM	charge z	Probability P (pro) P (pep)	Score XC	MW
CA2474 Pdc11	R.NIVEFHSDYTK.I	1352,64811	1,73980	2	1,00E-30	150,34	62402,0
	R.FGGVYVGSLSKPEVK.E	1566,85262	0,81910	2	1,26E-04	3,55	947,5
	K.KIDLSLHPNDPESQTEVIETVEK.L	2621,33047	1,56429	3	7,71E-05	3,78	1325,4
	K.IDLSLHPNDPESQTEVIETVEK.L	2493,23550	0,75630	2	1,00E-30	5,37	1849,1
	K.LISEASNPVILVDACAIR.H	1941,04741	0,34917	2	1,15E-12	4,56	858,2
	K.NISQTSAFIADINSAPAEIDR.C	2233,10952	0,64374	2	4,58E-10	5,48	1551,2
	K.LINT@PAAPSTPLTQEYLWTK.V	2324,15739	1,63173	2	1,22E-14	6,85	2095,9
	R.PVYIGLPSNLVDMK.V	2324,15739	1,63173	2	2,88E-06	4,88	880,9
	R.MVEVMLPTMDAPANLVAQAK.L	1545,83453	1,71812	2	3,21E-08	4,15	1139,1
	K.WECNNTYLFVLNNDGYTIER.L	2129,08033	1,59530	2	4,65E-12	5,79	1095,7
	K.VDTVFGLPGDFNLALLDK.I	2521,14529	1,69064	2	6,41E-11	5,12	2015,7
	K.AQYNDIQPWNNLQLLPLFNAK.D	1934,02696	1,66316	2	2,00E-09	4,95	861,3
	K.NSIGISQVLWGSIGYTVGATCGAAMAAQELDPK.R	2500,29832	1,77248	2	7,77E-09	5,33	1434,1
	K.ESVESADLILSIGALLSDFNTGSFSYGYK.T	3365,65047	1,54302	3	4,43E-13	6,72	1166,7
	R.EGDIIITETGTSAFGIVQSR.F	3083,50955	1,54237	3	2,66E-09	5,23	1545,9
CA3534 Ssb1	R.SANITISNSIGR.L	2094,07134	1,86133	2	1,16E-05	3,35	418,7
	R.TFTTVADHQTTVQFPVYQGER.V	1232,65934	1,69152	2	1,11E-15	78,35	66408,6
	R.VTPSFVAFTSEER.L	2425,17826	1,55291	3	3,81E-07	4,39	1454,5
	R.IINEPTAAAIAYGLGAGK.S	1469,72709	0,45043	2	6,94E-08	5,02	1161,9
	K.TFSPQEISSMVLTK.M	1729,94831	0,84777	2	1,34E-06	3,48	566,9
	R.VNCTENTLLGEFDLK.N	1567,80362	1,82425	2	6,74E-13	6,37	2696,6
	K.DKIEAALS DALQTLEIEESSADDYR.K	1752,84731	-0,09955	2	1,68E-06	4,06	1081,7
	K.NIPPMQAGEPVLEAIFEVDANGILK.V	2782,32650	0,90507	2	3,99E-08	5,37	2472,9
CA4474 Ssc1	K.DASITVAGSSGLSDAEIEK.M	2665,39057	1,65761	2	1,11E-15	70,35	69705,5
	K.STNGDTHLGGEDFDIALVR.Y	1849,90254	1,60960	2	1,25E-07	4,33	502,0
	R.GEQYSPQQIGGFILNK.M	2016,96212	1,79531	2	1,11E-15	70,35	69705,5
	R.AQFEQLVEPLIK.K	1778,90717	-0,15514	2	2,46E-07	6,19	3781,7
	R.AQFEQLVEPLIK.K	1414,79404	1,75794	2	5,17E-12	3,56	1273,6
	R.AQFEQLVEPLIK.K	1778,90717	-0,15514	2	2,59E-05	4,42	1463,4
	R.AQFEQLVEPLIK.K	1414,79404	1,75794	2	6,24E-06	4,05	1528,2

CA0828 Ipf17186	K.GINPDEAVAMGAAIQGGILAGEVK.D	2281,18566	0,78887	2	1,34E-13	7,02	3385,1	
	K.GVPQIEVTFDIDTDGIK.V	1960,02735	0,68125	2	2,58E-09	5,22	950,5	
	K.DVVLLDVTPLSLGIETMGGVFAR.L	2402,29996	0,80790	2	1,11E-15	6,60	1956,7	
					1,11E-15	60,34	25795,0	
	K.GGVVSAVCHGPAIFENLNDPK.T	2181,07575	0,79586	2	9,07E-07	5,05	559,2	
	K.KASDLDPNDYDIFFGSAGHGTLFDYPNAK.D	3175,46434	1,01929	3	1,11E-15	6,90	1741,9	
	K.ASDLDPNDYDIFFGSAGHGTLFDYPNAK.D	3047,36937	1,16839	3	2,00E-07	3,16	255,4	
CA0127 Hxk2	K.TGVFVVEALHPFEVFR.K	1846,98503	0,74653	3	1,76E-08	3,61	727,9	
	K.KITGFTDIGEDILGVTDIMK.K	2166,13625	1,70047	2	3,82E-11	5,67	3373,0	
	K.ITGFTDIGEDILGVTDIMK.K	2038,04129	0,83145	2	4,37E-12	6,25	2213,8	
					1,11E-15	30,35	53382,7	
	R.TKYDVQIDEESPRPGQQTFEK.M	2495,20487	-0,46837	3	1,08E-07	3,78	1004,5	
	K.IEEDPFENLSDVADLFR.E	2008,94983	-0,04109	2	5,64E-11	6,40	2711,1	
	R.DIYEWPADVKDPIIIVPAEDGSGVGAAVIAALTEK.R	3622,88907	1,43854	3	1,11E-15	6,95	2795,3	
CA4362 Atp2					5,55E-15	120,30	53909,4	
	K.KPIHAEPSPFVEQSTAAEILETGIK.V	2692,41922	1,66569	3	2,20E-08	4,68	2062,9	
	R.IPSAVGYQPTLATDMGLLQER.I	2260,16419	1,66454	2	1,26E-11	5,84	980,9	
	K.NGDQDLVLEVAQHLGENTVR.A	2207,10510	0,80726	2	2,33E-12	5,64	2209,4	
	R.VALTGLTIAEYFR.D	1453,80494	1,70866	2	3,50E-08	4,81	1915,4	
	R.FLSQPFAVAEVFTGIPGR.L	1936,03271	-0,10064	2	6,02E-11	5,33	1465,6	
	K.YDNLPENAFYMGVGGIEDVVAK.A	2344,11658	1,63700	2	1,45E-11	6,00	1824,5	
	K.TVFIQELINNIK.A	1502,85771	0,35786	2	2,90E-07	5,12	2237,4	
	K.SLQDIIAILGMDLSEADK.L	2061,04201	1,63266	2	1,74E-09	5,53	1544,4	
	K.SLQDIIAILGMDLSEADKLTVER.A	2659,38587	0,67389	3	3,01E-13	3,36	1175,7	
	R.AVIGAVVDVQFDEGNLPAILNALT.K.N	2680,49199	0,81921	2	6,81E-09	5,63	1046,2	
	R.VALTGLTIAEYFRDEEGQDVLLFIDNIFR.F	3357,73653	1,53885	3	4,40E-10	4,88	1850,8	
	R.LLDASVVGQEHYDVATGVQQTLQAYK.S	2833,43666	1,95059	3	1,41E-08	4,08	449,1	
	CA3015 Ipf10029					9,99E-15	40,29	47858,4
		K.TVLVYGHYDVQPALK.D	1702,91628	-0,08427	2	2,02E-08	4,54	2073,9
		K.KVDQVTISDNYWLGTTKPVLTLYGLR.G	2867,53017	0,73872	3	1,18E-09	5,25	1550,7
		R.FPSLSLHGIEGAFSGAGAK.T	1845,94937	1,93395	2	9,99E-15	5,72	2155,9
K.ELGTQPPPQDANLQLPPIVLR.F		2452,35583	1,60125	2	9,09E-08	4,25	426,1	
CA2875 Ssa1					2,55E-14	156,34	70027,8	
	K.VDEIVLVGGSTR.I	1244,68449	0,79311	2	3,23E-06	3,34	1197,5	
	K.DAVVTVPAYFNDSQR.Q	1681,81803	-0,18074	2	2,58E-04	3,77	479,2	

	R.TTPSFVAFTDTER.L	1471,70635	-1,52883	2	2,48E-05	2,35	607,7
	R.IINEPTAAAIAYGLDK.K	1659,89521	1,25725	2	5,12E-05	4,69	1022,1
	R.ARFEELCADLFR.S	1526,74206	-0,06991	2	9,06E-06	3,38	1352,8
	R.FEELCADLFR.S	1299,60384	1,10393	2	5,82E-06	4,04	1528,3
	K.AVGIDLGTTYSCVAHFANDRVEIANDQGNR.T	3376,63391	1,75290	3	7,00E-12	4,77	1161,0
	K.KSETFSTYADNQPGVLIQVFEGER.A	2715,32605	0,84457	2	1,08E-09	6,39	1600,1
	R.LVNFFIQEFK.R	1284,69869	1,21413	2	7,79E-06	4,03	1078,9
	R.SINPDEAVAYGAAVQAAILSGDTSSK.T	2535,25730	0,85127	2	1,04E-11	6,76	1884,8
	K.SETFSTYADNQPGVLIQVFEGER.A	2587,23109	0,75667	2	5,69E-10	6,40	1417,0
	K.TFSPEEISSMILGK.M	1538,77707	0,06319	2	1,55E-07	3,94	1364,2
	R.TLSSSAQTSIEIDSLYEGIDFYTSITR.A	2997,45752	0,85683	2	4,13E-10	4,92	1280,2
	K.AVGIDLGTTYSCVAHFANDR.V	2167,02371	1,92470	2	1,79E-04	2,55	96,9
	K.TQDLLLLDVAPLSLGIETAGGIMTK.L	2569,41572	1,67677	2	1,48E-09	5,94	758,8
	R.TLSSSAQTSIEIDSLYEGIDFYTSITR.A	2997,45752	0,81047	2	7,31E-09	4,90	1124,4
	R.GVPQIEVTFDIDANGILNVSALEK.G	2542,33991	1,73231	2	3,59E-13	5,08	2359,8
CA4959 Hsp90					2,55E-14	120,34	80773,3
	K.TVKEEVTETEELNK.T	1648,82759	-0,43488	2	1,28E-07	4,05	1279,3
	K.FTVTLDETNER.L	1324,63794	-0,12540	2	4,12E-08	3,42	1224,8
	R.TGQFGWSANMER.I	1383,61101	0,88163	2	3,91E-06	3,66	1287,1
	R.LFLKEDQLEYLEEK.R	1796,93166	-0,13763	2	1,50E-07	5,04	2268,3
	K.HSEFVAYPIQLVVTKE.E	1730,94758	-0,07900	2	3,44E-14	4,90	1172,5
	R.YQALSDPSQLESEPELFI.R	2222,09755	0,79357	2	9,73E-12	6,24	2999,2
	K.MIETFNEISEDQEQFNQFYTAFSK.N	2946,31383	1,51447	3	3,02E-09	5,00	1138,6
	K.NFEVLFMVDPIDEYAMTQLK.E	2403,16108	1,61153	2	3,59E-08	6,22	2083,9
	R.RVFITDDAEELIPEWLSFIK.G	2421,27004	1,74706	2	4,49E-10	5,10	902,9
	R.VFITDDAEELIPEWLSFIK.G	2265,16893	1,62642	2	1,25E-10	4,58	883,0
	K.DLTTLLFDTALLTSGFTLDEPSNFAHR.I	2995,50474	1,85067	2	3,59E-07	5,77	702,1
	K.VETHEFTAIEISQLMSLIINTVYSNK.E	2867,44954	0,81956	2	2,55E-14	6,80	2284,0
CA4220 Ipf8762					6,88E-14	40,32	21481,5
	K.YFVGFDDNVK.T	1203,56807	0,82784	2	2,51E-06	3,08	924,2
	K.QENELIITVTQETEK.D	1774,90690	0,77011	2	9,98E-13	5,05	1336,2
	K.FEKPVNFDDISAEIGEQQGVQVTLPK.V	2760,40905	1,41594	3	6,48E-10	4,87	1121,2
	R.RDDFFDDFWK.N	1390,60624	1,76740	2	1,63E-04	3,67	1413,3
CA3771 Sou1					6,99E-14	10,29	30019,1
	K.VASVTGSSGGIGWAVAEFAQAGADVAIWYNSKPADA	3722,84492	1,55936	3	6,46E-13	5,89	864,9

CA1230 SsA4					1,07E-13	70,35	70281,2
	K.AGKPVIQVEYK.G	1231,70450	1,68731	2	2,27E-05	3,44	549,2
	K.SQVEEIVLVGGSTR.I	1473,79075	1,73788	2	1,88E-06	3,59	1019,1
	K.AIDETISWLDASQAASTEYEDK.R	2572,15731	0,79975	2	3,70E-12	6,42	2636,4
	K.TFSPEEISSMVLTK.M	1568,78764	0,84023	2	1,68E-06	4,10	973,1
	K.SINPDEAVAYGAAVQAAILTGDTSSK.T	2549,27295	0,72206	2	1,12E-13	6,92	2750,3
	K.SINPDEAVAYGAAVQAAILTGDTSSK.T	2549,27295	0,79877	2	7,37E-12	6,56	2745,7
	K.TQDILLLDVAPLSLGIETAGGIMTK.L	2569,41572	1,67677	2	1,48E-09	5,94	758,8
	R.GEHNVLIFDLGGGTFDVSLLAIDEGIFEVK.A	3204,64632	1,54446	3	4,00E-06	3,07	479,4
CA0622 Lsp1					1,31E-13	20,26	35569,3
	R.AEAESLVAEAQLSNITR.E	1801,92903	0,74813	2	2,75E-06	5,03	1784,9
	K.ALLELLDESPVTPGETRPAYDGYEASK.Q	2921,44147	1,78079	3	1,31E-13	4,81	957,5
CA1983 Ilv5					1,58E-13	20,33	44854,5
	K.DALKPVFEELYESVK.N	1766,92109	1,31292	2	9,15E-12	4,30	740,9
	R.GTIIMDLLSDAAQSETWFHIKQLTEGK.T	3129,59251	1,71109	3	4,70E-08	6,61	1069,4
CA5558 Ipf1969					2,04E-13	10,32	17179,5
	K.HDDDIFNQLLEDFPEFK.E	2121,97638	1,82070	2	2,04E-13	6,45	2409,3
CA5242 Pdx1					2,70E-13	20,31	46030,8
	K.LFVENFENSLLSQIPANK.L	2063,08078	1,27397	2	8,05E-11	5,09	913,9
	K.FPQFAQSPTASSIYDKYDVFEILSAPVTK.N	3364,66237	1,66097	3	2,70E-13	6,23	2076,8
CA2162 Pdb1					3,11E-13	30,32	41268,2
	K.ELEDFAFPDTDEVILR.A	1793,89561	0,75754	2	9,90E-07	4,53	776,3
	K.AAIRDPNPVVFLENEIAYGETFK.V	2593,32968	0,82117	2	2,99E-11	5,58	1627,4
	R.DPNPVVFLENEIAYGETFK.V	2182,07028	0,38029	2	3,11E-13	6,48	3089,8
CA5409 Cof1					4,10E-13	30,29	15841,9
	R.SGVTVADESILTAFNDLK.L	1766,88069	-0,12741	2	1,02E-09	5,76	2837,2
	K.TQIVVEQTSTEQEYDAFLEKLPENECR.Y	3256,53146	1,60789	3	4,10E-13	5,81	1148,0
	K.IVFFTWSPDTAPVR.A	1635,85295	1,61814	2	1,58E-06	4,42	1227,0
CA4909 Tuf1					7,89E-13	20,30	46676,0
	R.GITISTAHVEYETK.N	1548,79041	1,24185	2	1,98E-06	3,45	1338,5
	R.DLEQPFLLPVEDVFSISGR.G	2161,11756	-0,12583	2	2,78E-12	5,69	1524,1
CA5546 Tub1.3					1,62E-12	20,34	49936,5
	R.NLDIARPNFSSLNLIQVVSSTASLR.F	2999,62726	0,58330	3	9,76E-06	4,06	696,3
	R.PNFSSLNLIQVVSSTASLR.F	2317,25104	0,38267	2	1,62E-12	6,72	2807,7
CA5948 Ipf3496					1,79E-12	10,23	37427,0

CA6010 Trx1	R.YNNMLYSSAIDVLADDILK.K	2158,07365	0,87746	2	1,79E-12	4,68	2097,5
					1,80E-12	10,30	11480,0
CA0782 Ipf16253	K.IDVDQLGSLAQEYNVSSMPTLILFK.N	2781,43791	0,87464	2	1,80E-12	6,08	2214,7
					2,84E-12	20,34	30263,5
	K.AVSTALLLSDAELENTEFIK.V	2035,09576	1,58526	2	1,39E-10	5,85	2005,9
CA0870 Ipp1	K.YAIFAQLLADGYVISDQVIK.G	2298,23801	0,83686	2	2,84E-12	6,46	3099,6
					6,07E-12	40,28	32108,2
	K.VIVIDVNDPLAPK.L	1392,80969	0,65982	2	5,40E-04	3,38	888,8
	K.LNDIEDVETHLPGLLR.A	1833,97050	-0,03661	2	6,07E-12	5,31	1707,3
	K.TILNMIVEVPR.W	1284,73442	0,89626	2	4,10E-06	3,78	1854,8
CA0988 Pmi40	K.VLGVMALLDEGETDWK.V	1775,88841	1,72433	2	2,07E-09	5,63	2681,3
					1,16E-11	20,26	48836,0
	K.SVLYDPPIAEFSVLQTIQIFDK.S	2282,19548	1,67697	2	1,16E-11	4,50	1069,8
	K.TLATVPELNEIIGQELVDEFISGIK.L	2728,46550	0,72872	2	3,86E-09	5,12	866,7
CA3284 Ade6					1,80E-11	10,32	150714,8
	K.ELGLALDQGEIDYLINAFK.E	2122,10666	1,26849	2	1,80E-11	6,34	2930,4
CA1738 Mge1					1,84E-11	10,30	27217,8
	K.DLLDSLDFNLALGHVK.E	1883,98615	1,80580	2	6,76E-11	5,59	2494,5
CA5050 Bmh2					1,95E-11	30,30	29461,8
	K.AVASSGQELSVEER.N	1461,71798	1,67441	2	1,70E-06	3,37	1007,0
	K.QAFDDAVADLETLSSESYK.D	2116,95570	0,79541	2	7,99E-11	5,87	1743,1
	K.ICEDILSVLSDHLITSAQTGESK.V	2516,25490	1,27362	2	1,95E-11	5,81	1801,5
CA0425 Pph21					2,44E-11	10,31	40915,7
	K.LFTDLFDYFPITALVDNK.V	2132,09504	-0,05813	2	2,44E-11	6,29	2495,9
CA5729 Uba1					2,58E-11	20,30	114199,3
	K.NGFINLALPFIGFSEPIK.S	1977,08441	1,86669	2	8,13E-05	3,48	981,6
	R.GDIPGVVAFYGGGLIAQEVK.N	2046,12700	1,66205	2	2,58E-11	5,96	2094,4
CA4150 Rpt3					4,16E-11	10,28	45855,2
	R.NDPLSGAVIAAIMQEAGLR.A	1926,01132	1,74213	2	4,16E-11	5,63	2845,0
CA1239 Hsp60					6,32E-11	80,26	60088,7
	R.IIENAGEEGAVIVGK.I	1498,81115	1,14393	2	1,72E-09	4,87	2593,9
	K.AITLEDKFEDLGAK.L	1549,81081	1,73861	2	3,96E-07	4,35	1186,9
	R.AAVEEGILPGGGTALIK.A	1595,90030	0,81191	2	4,84E-08	4,63	1122,9
	R.RGSQAAVEAVIEFLQK.N	1745,95446	1,75763	2	4,61E-06	3,87	1180,5
	K.VEFENPLILLSEK.K	1530,84139	-0,09107	2	5,25E-09	4,12	2408,3

	R.GSQAAVEAVIEFLQK.N	1589,85335	1,67910	2	3,28E-07	5,16	2539,9
	K.NGLVDASGVASLLATTECAIVDAPQPK.G	2697,37641	1,77553	2	6,32E-11	4,74	1552,3
CA3333 Cdc48					6,98E-11	20,28	90934,5
	K.NSPSIIFIDEIDSIAPK.R	1858,97967	-0,14218	2	2,43E-06	4,29	1816,3
	R.AAAPTUVFLDELDSIAK.A	1759,94764	1,64454	2	1,49E-09	5,57	1588,1
CA6170 Ccp1					1,09E-10	10,32	40729,0
	K.HNSGYDGPWGPSFNQFTNVFYTTLLGDWHVK.K	3584,66583	1,68489	3	1,09E-10	6,32	1829,7
CA4127 Ahp1					1,20E-10	40,26	19245,8
	K.ALGYTDEENYVIFATDPNASISK.E	2518,19839	0,75573	2	8,73E-10	5,14	1473,3
	K.SLFPNNTVVVTAVPGAFTPTCTEQHIPDYLK.H	3416,71954	1,50887	3	1,27E-09	3,97	722,2
	K.ELGDGFVADLTSAGMGLR.L	1808,88472	1,18890	2	3,06E-06	5,05	1373,4
	R.YASIVVNGEITYLETEDSLGFSEISSAETILK.R	3478,73632	1,65475	3	1,20E-10	3,96	911,1
CA5546 Tsa1B					1,35E-10	10,30	11469,9
	K.TAVVDGVFEEVTLEQYK.G	1926,96950	-0,13249	2	1,35E-10	5,60	3009,2
CA1117 Arp3					1,46E-10	10,21	46618,3
	R.GLEDLDFYIGDEALEAASGSQYGLHYPIK.H	3171,51570	1,97363	3	1,46E-10	4,21	758,7
CA3796 Sgt2					1,70E-10	10,27	36438,6
	K.EVAEDYAESMDVAIDCIADAFEVNKEDDSK.T	3378,45122	1,74058	3	1,70E-10	5,48	1177,5
CA2939 Tif1					1,98E-10	40,32	44571,2
	R.SGVQIVVGTTPGR.V	1169,66370	-0,13403	2	5,42E-05	2,87	838,5
	R.GIFGYGYETPSAIQQR.A	1786,87587	0,79912	2	2,25E-09	4,45	1226,4
	K.MFILDEADEMLSSGFK.E	1832,84450	-0,05501	2	2,36E-10	6,45	3607,9
	R.LLPETTQIVLLSATMPQDVLEVTTK.F	2740,50526	0,80276	2	1,98E-10	5,28	897,6
CA1755 Pdi1					3,53E-10	10,25	62996,7
	K.LAPTWEELAEIFGSNK.D	1804,91159	-0,10073	2	3,53E-10	5,01	1131,3
CA2582 Tal1					3,53E-10	40,30	35650,4
	K.LLEQLYNSTEEVPK.Q	1662,85849	0,79425	2	4,27E-08	4,56	1085,1
	K.ATGTTIVTDTGEFEQIAK.Y	1881,94401	-0,22712	2	4,43E-08	4,82	2023,6
	K.NPEYASVIDVAIEYAK.D	1781,89561	0,82095	2	3,53E-10	5,99	2174,8
	K.DAVTLLTELESR.F	1346,71619	0,75297	2	2,43E-04	3,88	1384,7
CA4765 Adh1					4,08E-10	10,16	46035,7
	K.ATDGGPHGAINVSVSEK.A	1638,80819	0,58574	2	4,08E-10	3,13	840,6
CA0685 Ado1					7,80E-10	10,26	38230,6
	K.TNKPLVLNFSAPFIAQFFK.Q	2182,20592	1,70524	2	1,82E-07	5,09	1500,7
CA4181 Hom6					1,72E-09	20,29	38812,4

	R.ISGLEVEGPTSFPVESLIPK.E	2099,12706	1,66197	2	2,00E-08	5,40	2155,9
	K.DLIATGDKVDKIEGIFSGTLSYIFNEFSK.T	3207,64599	1,66057	3	2,63E-06	5,76	1620,3
CA4844 Pdr13					2,21E-09	20,32	58494,5
	K.VLQLINEPSAALLAHLSDNEDR.L	2418,26233	1,56121	3	3,81E-04	2,67	540,7
	K.LASNISFLFPETTNIIPSLDSK.A	2478,31263	1,60359	2	5,58E-09	6,48	1074,7
CA5078 Ipf15297					2,58E-09	10,18	20310,4
	K.APELIPVFTFNLK.L	1488,84608	1,76422	2	2,58E-09	3,64	967,7
CA5487 Met12					8,27E-09	10,23	71412,6
	K.WGTPESIADLTQVFINYLSGK.V	2339,19179	0,75871	2	8,27E-09	4,61	816,8
CA0386 Ipf4065					9,17E-09	10,31	13130,8
	K.GAENDFVIFIDDADLLAK.Y	1965,98040	-0,10591	2	9,17E-09	6,20	1814,9
CA4551 Apt1					1,24E-08	10,19	20864,1
	R.GFLFGPTLALALNAGFVVR.K	2060,16914	-0,33316	2	7,90E-06	3,70	320,8
CA0495 Ucf1					1,50E-08	10,25	23638,5
	K.EFDELEQFESFVR.D	1674,76459	1,70510	2	1,50E-08	5,00	2329,2
CA2300 Pma1					1,52E-08	10,21	97582,7
	R.SAADIVFLAPGLSAIIDALK.T	1985,13175	-0,13537	2	1,52E-08	4,11	1043,4
CA3874 Eno1					2,43E-08	10,17	47202,6
	R.GNPTVEVDFTTDK.G	1422,67472	0,81551	2	2,43E-08	3,45	943,4
CA5015 Uso6					8,53E-08	10,26	128561,4
	K.LSLIEQPLLVEDYLEVLK.E	2227,28356	0,79096	2	5,09E-07	3,05	472,7
CA2480 Cct7	Unknown				2,89E-07	10,20	60384,3
	K.LPIGDLATQYFADR.N	1579,81148	-0,13879	2	2,89E-07	4,02	832,9
CA6179 Efb1					1,02E-06	20,16	34586,4
	K.AAFNYQFDATR.E	1303,60658	1,76982	2	1,02E-06	2,78	837,4
	K.IPVLEQELVR.A	1195,70450	1,46742	2	2,66E-05	2,78	1024,2
CA3978 Cpr3					6,98E-06	10,23	20965,4
	K.KIESCGTSSGTPSASVVEESGAEK.-	2639,23528	-0,59170	3	6,98E-06	4,67	1765,8
CA2122 Cpy1	Carboxypeptidase Y				3,00E-05	10,20	60975,1
	K.ELPVLIYAGDKDFICNWLGNQAWTNR.L	3093,52514	0,63565	3	3,00E-05	3,93	1538,7
CA0748 Tfs1					3,27E-05	10,20	29328,1
	K.WSEYLHWLVTDLK.L	1689,86352	0,80701	2	3,27E-05	3,99	1606,5
CA5986 Ino1					5,13E-05	10,21	57743,1
	K.ISIHNVCEDSLATPLIIDLVVATEFATR.V	3210,70791	1,44715	3	5,13E-05	4,28	721,7
CA1765 Ape2					5,98E-05	20,20	107294,4

	K.GEETIDFQVNEK.T	1408,65907	0,25296	2	5,98E-05	3,76	1223,9
	K.VWESYVSDSLQHALTLDALR.A	2303,16664	-0,15677	3	1,44E-04	3,23	1120,6
CA5255 Act1					7,77E-15	10,41	41582,8
	R.TTGIVLDSGDGVTHVVPYAGFSLPHGILR.I	3091,65747	1,51925	3	7,77E-15	8,21	1987,1
CA1116 Cct5					4,00E-14	10,31	59798,3
	R.SQDDEIGDGTGTVVVLASALLDQALELIDK.G	3085,57861	1,32568	3	4,00E-14	6,16	2259,8
CA2120 Pup3					1,70E-13	20,27	22636,6
	R.NIEPSTLANLVSSSLYER.R	1993,02368	-0,15071	2	3,11E-13	5,46	2369,3
	R.FGPWFVSPIVAGLSSK.D	1691,91553	0,79956	2	1,70E-13	4,63	1919,9
CA4897 Tub2.3					4,72E-12	10,31	49965,3
	K.LPQPSYAELNNLVSSVMSGVTTSLR.Y	2663,37085	1,70435	2	4,72E-12	6,20	1621,7
CA2956 Egd2					2,95E-11	10,22	19498,0
	R.GNLIYAIDSPDVYR.S	1595,80640	1,74845	2	2,95E-11	4,42	1257,1
CA0692 Pgm2					2,37E-09	10,29	61762,7
	K.VDEYLTNEIQFVLELLK.F	2066,10571	-0,09627	2	2,37E-09	5,89	2873,2
CA0585 Ade5,7					3,31E-09	10,28	85951,5
	K.QLLSSINQGLLLGLAHITGGGLVENIPR.A	2883,64136	1,66377	3	3,31E-09	5,60	785,2
CA3897 Pfy1					3,76E-07	20,28	13800,0
	K.HEAEGVICVR.T	1169,57324	0,74147	2	3,76E-07	3,20	903,0
	K.QTILIAHYPSGVQPGEATTLVEK.L	2452,30811	1,65476	3	1,20E-04	5,69	876,8
CA5714 Tsa1					8,08E-08	20,22	21846,3
	R.LLEAFQFTEK.Y	1225,64636	1,74761	2	1,64E-04	2,43	588,4
	R.DYGVLIIEEGVALR.G	1562,80603	0,78274	2	8,08E-08	4,48	1471,9
CA5732 Tif51					1,01E-13	20,31	17121,5
	K.VHLVAIDIFTGK.K	1312,76233	1,75263	2	1,63E-07	4,24	1550,8
	K.LQSEFDEGKDLIVTIISAMGEEAAISYK.E	3057,53369	0,85998	2	1,53E-13	6,26	2005,1
CA5826 Mdh11					5,74E-06	10,19	35982,2
	K.LNPNVDELALFDVVNVPVGVGADLSHINSDSK.T	3248,64331	1,58911	3	2,80E-04	3,23	608,8
CA0838 Tfp1					3,42E-05	10,27	66681,6
	R.EILSNAEELEQVVQLVGK.S	1998,07532	0,76093	2	3,42E-05	5,40	1273,9
eorf19.4900	orf19.4900 CGDID:CAL0006195 Assembly 21, Chromosome 1 (2276430, 2278916) CDS, translat				6,03E-05	8,14	97452,9
	K.TTTTSTAEIILYCKNFIR.L	2148,06418	1,32932	2	6,03E-05	2,89	547,3

Table S3: MALDI-TOF/TOF-identified proteins from the 4.5 to 5.5 2-DE gel (Figure 2) of *Candida albicans* acidic subproteome.

Protein name, accession number, pIs, Mr, protein coverage, matched peaks/unmatched peaks and protein score are derived from the Mascot results page based on CGD database.

Gel number	Protein Name	Accession No.	Protein MW	Protein PI	Matched peaks/ unmatched peaks	Protein Score	Coverage %
2	F1 beta subunit of F1F0-ATPase complex	CA4362 CaATP2	53966.3	5.06	26/39	247	67%
7	Microsomal ATPase (by homology)	CA3333 CaCDC48	91219.5	4.91	23/40	168	32%
8	Microsomal ATPase (by homology)	CA3333 CaCDC48	91219.5	4.91	25/37	180	35%
11	DnaK-type molecular chaperone (by homology)	CA0915 CaKAR2	74599.0	4.81	27/38	240	39%
13	Drug resistance	CA4844 CaPDR13	58608.4	4.79	15/19	160	35%
14	Heat shock protein of HSP70 family	CA2857 CaSSA1	70198.7	4.96	19/24	179	33%
15	Heat shock protein of HSP70 family	CA2857 CaSSA1	70198.7	4.96	29/36	258	46%
16	Cahsp70 mRNA for heat shock	CA1230 CaSSA4	70452.1	5.06	23/42	190	37%
17	Cahsp70 mRNA for heat shock	CA1230 CaSSA4	70452.1	5.06	29/36	272	43%
18	Cahsp70 mRNA for heat shock	CA1230 CaSSA4	70452.1	5.06	33/32	339	57%
19	Cahsp70 mRNA for heat shock	CA1230 CaSSA4	70452.1	5.06	16/33	129	25%
21	Stress-induced protein (by homology)	CA0265 CaSTI1	66545.0	5.22	19/40	131	33%
22	Similar to <i>Saccharomyces cerevisiae</i> Pab1p mRNA polyadenylate-binding protein (by homology)	CA5065 CaPAB1	70658.9	5.21	17/25	155	30%
23	Vacuolar ATPase subunit (by homology)	CA0838 CaTFP1	67081.0	5.12	28/37	270	55%
24	Mitochondrial heat shock protein 70-related protein (by homology)	CA4474 CaSSC1	69876.5	5.48	29/36	272	45%
25	Mitochondrial heat shock protein 70-related protein (by	CA4474 CaSSC1	69876.5	5.48	31/34	289	43%

homology)							
26 Heat shock protein 70	CA3534 CaSSB1	66579.5	5.25	30/35	308	54%	
27 Pyruvate decarboxylase (by homology)	CA2474 CaPDC11	62744.1	5.39	20/45	164	47%	
28 Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehyd	CA4875 CaLAT1	50145.0	5.73	12/53	74	25%	
29 Inositol-1-phosphate synthase	CA5986 CaINO1	57857.1	5.35	15/31	124	32%	
30 Metalloprotease	CA3015 lpf10029	48029.4	5.05	10/36	91	30%	
31 F1 beta subunit of F1F0-ATPase complex	CA4362 CaATP2	53966.0	5.06	16/40	117	38%	
32 F1 beta subunit of F1F0-ATPase complex	CA4362 CaATP2	53966.0	5.06	27/38	249	67%	
33 F1 beta subunit of F1F0-ATPase complex	CA4362 CaATP2	53966.0	5.06	19/30	170	49%	
34 Pyruvate dehydrogenase complex protein X (by homology)	CA5242 CaPDX1	46030.8	5.34	8/46	55	24%	
36 Unknown function	CA3313 lpf8811	38529.8	4.84	17/28	181	49%	
37 Response to oxidative stress	CA4928 SUF1	43029.3	4.93	15/27	135	41%	
40 Isopropyl malate dehydrogenase	CA5618 CaLEU2	40232.1	5.16	12/49	103	47%	
41 Argininosuccinate synthetase (by homology)	CA5818 CaARG1	55660.6	5.54	12/53	73	27%	
43 Succinate-CoA ligase beta subunit (by homology)	CA0664 CaLSC2	44670.0	4.88	16/49	140	43%	
44 Translation initiation factor eIF3, p39 subunit	CA4166 CaTIF34	38322.1	5.25	16/42	156	49%	
46 Enolase I (2-phosphoglycerate dehydratase)	CA3874 CaENO1	47202.5	5.54	13/47	107	36%	
50 Translation elongation factor TU (by homology)	CA4909 CaTUF1	46904.1	5.67	12/40	86	34%	
52 Homo-isocitrate dehydrogenase (by homology)	CA1737 CaLYS12	40871.1	5.64	8/21	68	26%	
53 Ketol-acid reducto-isomerase (by homology)	CA1983 CaLV5	44969.0	6.17	25/40	248	59%	

54	Actin (by homology)	CA5255 CaACT1	41811.0	5.54	10/47	75	31%
56	Nascent polypeptide associated complex protein alpha subunit (by homology)	CA2956 CaEGD2	19498	4.7	7/52	50	36%
59	Protein degradation	CA4319 CaRPN10	30375	4.74	8/46	69	40%
62	Unknown function	CA3190 lpf11603	34394.3	5.39	9/48	71	35%
63	Unknown function	CA4220 lpf8762	21481.5	5.15	12/32	154	59%
64	Derepression of telomeric silencing (by homology)	CA5773 CaDOT5	29176.8	4.91	9/28	98	43%
66	Unknown function	CA0782 lpf16253	30320.6	5.11	11/33	110	32%
67	Unknown function	CA4220 lpf8762	21481.5	5.15	7/30	74	34%
69	Homoserine dehydrogenase (by homology)	CA4181 CaHOM6	38926.4	5.2	17/48	170	56%
71	Similar to cytochrome-c peroxidase N-terminus	CA6170 CaCCP1	40786	5.8	18/47	134	46%
75	Translation initiation factor eIF4E, cap binding protein	CA6023 CaCDC33	24280.3	5.18	16/49	166	55%
76	Rho GDP dissociation inhibitor (by homology)	CA6089 CaRDI1	22947.9	5.15	21/44	245	73%
80	ThiJ/PfpI protein family	CA0828 lpf17186	25910	4.68	6/58	50	38%
81	Adenylyl cyclase and stress responsive	CA5526 ARS2	27761.6	5.43	8/32	77	34%
82	Adenine phosphoribosyltransferase	CA4551 CaAPT1	20864.1	5.26	8/44	85	42%
83	Protein described as a putative cysteine peroxidase	CA4416 PRX1	27482.0	6.66	13/26	135	58%
87	Unknown function	CA5078 lpf15297	20424.4	5.11	16/42	213	91%
88	Translation initiation factor eIF-5A, 3-prime end	CA3752 CaTIF51.3	17236.0	4.88	8/57	52	31%
91	Putative alkyl hydroperoxide reductase	CA4127 CaAhp1	19359.8	5.16	8/57	68	52%
92	Cofilin (by homology)	CA5409 CaCOF1	15899.0	5.08	13/52	174	84%
93	Profilin, binds to actin	CA3897 CaPFY1	13857	5.26	7/58	82	69%

Table S4. FunSpec analysis of *C. albicans* yeast-to-hypha differentially abundant proteins identified. Analysis of three lists of proteins: a) more abundant proteins in hyphal cells; b) less abundant proteins in hyphal cells and c) all differentially expressed proteins.

Table S4.a. Funspec analysis: results from more abundant proteins in *C. albicans* hyphal cells. Input Cluster (n=30):

Systematic Name	Common Name	Essential		Publications
YAL012W	CYS3	no	41	(Literature on CYS3) (SGD) (MIPS)
YBR256C	RIB5	yes	12	(Literature on RIB5) (SGD) (MIPS)
YCL043C	PDI1	yes	77	(Literature on PDI1) (SGD) (MIPS)
YDL135C	RDI1	no	16	(Literature on RDI1) (SGD) (MIPS)
YDR044W	HEM13	yes	37	(Literature on HEM13) (SGD) (MIPS)
YDR099W	BMH2	no	65	(Literature on BMH2) (SGD) (MIPS)
YER103W	SSA4	no	148	(Literature on SSA4) (SGD) (MIPS)
YFL039C	ACT1	yes	772	(Literature on ACT1) (SGD) (MIPS)
YFL045C	SEC53	yes	38	(Literature on SEC53) (SGD) (MIPS)
YGL253W	HXK2	no	264	(Literature on HXK2) (SGD) (MIPS)
YGR214W	RPS0A	no	30	(Literature on RPS0A) (SGD) (MIPS)
YHR087W	RTC3	no	10	(Literature on RTC3) (SGD) (MIPS)
YHR104W	GRE3	no	29	(Literature on GRE3) (SGD) (MIPS)
YIL138C	TPM2	no	38	(Literature on TPM2) (SGD) (MIPS)
YJL153C	INO1	no	167	(Literature on INO1) (SGD) (MIPS)
YJR123W	RPS5	yes	32	(Literature on RPS5) (SGD) (MIPS)
YKL106W	AAT1	no	14	(Literature on AAT1) (SGD) (MIPS)
YKL210W	UBA1	yes	31	(Literature on UBA1) (SGD) (MIPS)
YLR075W	RPL10	yes	33	(Literature on RPL10) (SGD) (MIPS)
YLR259C	HSP60	yes	97	(Literature on HSP60) (SGD) (MIPS)
YLR354C	TAL1	no	27	(Literature on TAL1) (SGD) (MIPS)
YML028W	TSA1	no	84	(Literature on TSA1) (SGD) (MIPS)
YMR105C	PGM2	no	57	(Literature on PGM2) (SGD) (MIPS)
YMR186W	HSC82	no	185	(Literature on HSC82) (SGD) (MIPS)
YOL086C	ADH1	no	324	(Literature on ADH1) (SGD) (MIPS)
YOR020C	HSP10	yes	29	(Literature on HSP10) (SGD) (MIPS)
YOR027W	STI1	no	71	(Literature on STI1) (SGD) (MIPS)
YOR122C	PFY1	yes	63	(Literature on PFY1) (SGD) (MIPS)
YPL028W	ERG10	yes	33	(Literature on ERG10) (SGD) (MIPS)
YPL240C	HSP82	no	292	(Literature on HSP82) (SGD) (MIPS)

Genes Not Found:
CIP1

Number of Genes in each Database: 6603

k: number of genes from the input cluster in given category.

f: number of genes total in given category.

The p-values represent the probability that the intersection of a given list with any given functional

category occurs by chance. The Bonferroni-correction divides the p-value threshold, that would be deemed significant for an individual test, by the number of tests conducted and thus accounts for spurious significance due to multiple testing over the categories of a database.

MIPS Functional Classification (459 categories)

Category	p-value	In Category from Cluster	k	f
protein folding and stabilization [14.01]	1.369e-07	PDI1 SSA4 HSP60 HSC82 HSP10 STI1 HSP82	7	93
sugar, glucoside, polyol and carboxylate anabolism [01.05.02.04]	1.644e-05	SEC53 INO1 TAL1 PGM2	4	35
unfolded protein response (e.g. ER quality control) [32.01.07]	0.0002439	SSA4 HSC82 HSP10 STI1	4	69
protein binding [16.01]	0.0002595	BMH2 SSA4 TPM2 UBA1 HSC82 HSP10 STI1 PFY1	8	391
sugar, glucoside, polyol and carboxylate catabolism [01.05.02.07]	0.0004519	SEC53 GRE3 TAL1 PGM2	4	81
metabolism of energy reserves (e.g. glycogen, trehalose) [02.19]	0.001995	BMH2 PGM2 HSP82	3	56
budding, cell polarity and filament formation [43.01.03.05]	0.002405	RDI1 BMH2 ACT1 RPS0A TPM2 PFY1	6	312
actin dependent transport [20.09.14.02]	0.004543	ACT1	1	1
pentose-phosphate pathway [02.07]	0.005611	TAL1 PGM2	2	25
protein targeting, sorting and translocation [14.04]	0.008	SSA4 ACT1 SEC53 HSP60 HSP10	5	281
bud / growth tip [42.29]	0.008551	ACT1 TPM2	2	31
metabolism of secondary monosaccharides [01.20.01.01]	0.009067	INO1	1	2
degradation of aspartate [01.01.06.01.02]	0.009067	AAT1	1	2
biosynthesis of aspartate [01.01.06.01.01]	0.009067	AAT1	1	2
actin cytoskeleton [42.04.03]	0.0091	RDI1 TPM2 PFY1	3	96
exocytosis [20.09.16.09.03]	0.009655	ACT1 TPM2	2	33
cell growth / morphogenesis [40.01]	0.009953	BMH2 ACT1 STI1 PFY1	4	189
biosynthesis of cysteine [01.01.09.03.01]	0.01805	CYS3	1	4
biosynthesis of asparagine [01.01.06.02.01]	0.01805	AAT1	1	4
GTPase inhibitor (GIP) [18.02.01.02.01]	0.02252	RDI1	1	5
metabolism of glutamate [01.01.03.02]	0.02252	AAT1	1	5
PROTEIN WITH BINDING FUNCTION OR COFACTOR REQUIREMENT (structural or catalytic) [16]	0.02252	ACT1	1	5
protein transport [20.01.10]	0.0254	ACT1 SEC53 HSP60	3	141
protein modification [14.07]	0.02553	PDI1 SEC53	2	55
aminosaccharide catabolism [01.05.09.07]	0.02696	PGM2	1	6
aminosaccharide anabolism [01.05.09.04]	0.02696	PGM2	1	6
small GTPase mediated signal transduction [30.01.05.05.01]	0.02818	RDI1 BMH2	2	58

osmotic and salt stress response [32.01.03]	0.02909	ACT1 PFY1	2 59
cell cycle dependent actin filament reorganization [10.03.05.03]	0.03139	ACT1	1 7
biosynthesis of homocysteine [01.01.06.05.01.01]	0.03139	CYS3	1 7
stress response [32.01]	0.03626	UBA1 HSP60 HSP82	3 162
development of asco- basidio- or zygosporangium [43.01.03.09]	0.03856	BMH2 ACT1 HSP82	3 166
enzyme inhibitor [18.02.01.02]	0.04455	STI1	1 10

MIPS Phenotypes (142 categories)

Category	p-value	In Category from Cluster	k f
Actin cytoskeleton mutants [52.30.10]	0.001275	ACT1 RPL10 PFY1	3 48
Rapamycin sensitivity [112.30.10]	0.009067	BMH2	1 2
Heat-sensitivity (ts) [12.05]	0.01243	ACT1 SEC53 RPL10 PFY1 HSP82	5 313
Formamide or formaldehyde sensitivity [12.25]	0.01357	ADH1	1 3
Slow-growth (slg) [12.15]	0.0213	PDI1 RPS0A RPL10 PFY1	4 237
other stress response defects [62.99]	0.04018	UBA1	1 9
other cell wall mutants [52.15.99]	0.04297	RPL10 PFY1	2 73

MIPS Subcellular Localization (48 categories)

Category	p-value	In Category from Cluster	k f
actin cytoskeleton [730.01]	0.003774	ACT1 TPM2 PFY1	3 70
cytoplasm [725]	0.005026	CYS3 RIB5 PDI1 RDI1 HEM13 BMH2 SSA4 SEC53 HXK2 RPS0A RTC3 GRE3 TPM2 INO1 RPS5 UBA1 RPL10 TAL1 TSA1 PGM2 HSC82 ADH1 STI1 PFY1 ERG10 HSP82	26 4208
cytoskeleton [730]	0.01222	ACT1 TPM2 PFY1	3 107
ER lumen [735.05]	0.04018	PDI1	1 9

MIPS Protein Complexes (1142 categories)

Category	p-value	In Category from Cluster	k f
Complex Number 17, probably cell polarity and structure [550.1.17]	3.712e-05	ACT1 HSC82 ADH1	3 15

Complex Number 244 [550.2.244]	5.393e-05	CYS3 UBA1 PGM2 ERG10	4 47
Complex Number 175, probably signalling [550.1.175]	5.97e-05	HSC82 HSP82	2 3
Complex Number 406 [550.2.406]	0.0001191	UBA1 STI1	2 4
Complex Number 171, probably signalling [550.1.171]	0.0005494	HSC82 ADH1	2 8
Complex Number 454 [550.2.454]	0.0005494	PGM2 STI1	2 8
Complex Number 191, probably transcription/DNA maintanance/chromatin structure [550.1.191]	0.00128	ACT1 ADH1	2 12
Complex Number 34, probably intermediate and energy metabolism [550.1.34]	0.001509	HSC82 ADH1	2 13
Complex Number 378 [550.2.378]	0.00202	SEC53 PGM2	2 15
Complex Number 283 [550.2.283]	0.003253	SEC53 UBA1	2 19
Cytoplasmic ribosomes [500.40]	0.004543	RPL10	1 1
Actins [140.20.10]	0.004543	ACT1	1 1
Hexokinase 2 [225]	0.004543	HXK2	1 1
Complex Number 203, probably transcription/DNA maintanance/chromatin structure [550.1.203]	0.005176	ACT1 ADH1	2 24
Actin-associated proteins [140.20.20]	0.005611	TPM2 PFY1	2 25
Complex Number 62 [550.2.62]	0.006061	UBA1 PGM2	2 26
Complex Number 56, probably intermediate and energy metabolism [550.1.56]	0.009067	ADH1	1 2
Complex Number 8 [550.2.8]	0.009067	SEC53	1 2
Complex Number 492 [550.2.492]	0.009067	TAL1	1 2
Complex Number 358 [550.2.358]	0.009067	ERG10	1 2
Complex Number 18 [550.2.18]	0.009067	BMH2	1 2
Complex Number 477 [550.2.477]	0.009067	ERG10	1 2
Complex Number 58, probably intermediate and energy metabolism [550.1.58]	0.01357	ADH1	1 3
Complex Number 266 [550.2.266]	0.01357	STI1	1 3
Complex Number 65, probably membrane biogenesis and traffic [550.1.65]	0.01357	ADH1	1 3
Complex Number 222, probably transcription/DNA maintanance/chromatin structure [550.1.222]	0.01357	ADH1	1 3
Complex Number 242 [550.2.242]	0.01357	STI1	1 3
Complex Number 285 [550.2.285]	0.01357	UBA1	1 3
Complex Number 175 [550.2.175]	0.01357	STI1	1 3
Complex Number 51, probably intermediate and energy metabolism [550.1.51]	0.01357	CYS3	1 3
Complex Number 60 [550.2.60]	0.01805	PGM2	1 4
Complex Number 168 [550.2.168]	0.01805	TAL1	1 4
Complex Number 95, probably protein synthesis turnover [550.1.95]	0.01805	ADH1	1 4
Complex Number 130 [550.2.130]	0.01805	SEC53	1 4
Complex Number 167, probably signalling [550.1.167]	0.01805	ACT1	1 4
Complex Number 114, probably protein synthesis turnover [550.1.114]	0.01805	ADH1	1 4
Complex Number 194 [550.2.194]	0.01805	TAL1	1 4

Complex Number 75 [550.2.75]	0.01805	UBA1	1 4
Complex Number 5 [550.2.5]	0.01805	CYS3	1 4
Complex Number 214, probably transcription/DNA maintenance/chromatin structure [550.1.214]	0.02136	HEM13 ADH1	2 50
Complex Number 462 [550.2.462]	0.02252	STI1	1 5
Complex Number 341 [550.2.341]	0.02553	SEC53 UBA1	2 55
Complex Number 52, probably intermediate and energy metabolism [550.1.52]	0.02696	ACT1	1 6
Complex Number 352 [550.2.352]	0.02696	SEC53	1 6
Complex Number 410 [550.2.410]	0.02696	UBA1	1 6
cytoplasmic ribosomal small subunit [500.40.20]	0.02729	RPS0A RPS5	2 57
Complex Number 53, probably intermediate and energy metabolism [550.1.53]	0.03139	ADH1	1 7
Complex Number 3, probably cell cycle [550.1.3]	0.03139	ACT1	1 7
Complex Number 544 [550.2.544]	0.03139	PGM2	1 7
Complex Number 298 [550.2.298]	0.03139	PGM2	1 7
Complex Number 68, probably membrane biogenesis and traffic [550.1.68]	0.03139	TSA1	1 7
Complex Number 161, probably signalling [550.1.161]	0.03139	BMH2	1 7
Complex Number 348 [550.2.348]	0.03579	SEC53	1 8
Complex Number 174 [550.2.174]	0.03579	PDI1	1 8
Complex Number 229, probably transcription/DNA maintenance/chromatin structure [550.1.229]	0.03579	ACT1	1 8
Complex Number 363 [550.2.363]	0.03579	STI1	1 8
Complex Number 304 [550.2.304]	0.04018	ERG10	1 9
Complex Number 52, tIF2 (7) [550.3.52]	0.04018	ACT1	1 9
Complex Number 143 [550.2.143]	0.04018	PGM2	1 9
Complex Number 194, probably transcription/DNA maintenance/chromatin structure [550.1.194]	0.04018	ADH1	1 9
Complex Number 525 [550.2.525]	0.04018	PGM2	1 9
Complex Number 85, probably protein synthesis turnover [550.1.85]	0.04018	SSA4	1 9
Complex Number 532 [550.2.532]	0.04455	STI1	1 10
Complex Number 459 [550.2.459]	0.04455	SEC53	1 10
Complex Number 344 [550.2.344]	0.04455	PDI1	1 10
Complex Number 31 [550.2.31]	0.04455	STI1	1 10
Complex Number 34 [550.2.34]	0.04889	PDI1	1 11
Complex Number 296 [550.2.296]	0.04889	PGM2	1 11
Complex Number 511 [550.2.511]	0.04889	PGM2	1 11
Complex Number 88 [550.2.88]	0.04889	TAL1	1 11
Complex Number 319 [550.2.319]	0.04889	RTC3	1 11
Complex Number 412 [550.2.412]	0.04889	UBA1	1 11
Complex Number 230, probably transcription/DNA maintenance/chromatin structure [550.1.230]	0.04889	ADH1	1 11
Complex Number 284 [550.2.284]	0.04889	PGM2	1 11

MIPS Protein Classes (149 categories)

Category	p-value	In Category from Cluster	k	f
HSP90 family [101.31]	1.996e-05	HSC82 HSP82	2	2
other ATPases [41.61]	0.00023	HSP60 HSC82 HSP82	3	27
GroEL-related proteins (HSP60 family) [101.11.11]	0.004543	HSP60	1	1
RHO-GDIs [91.51]	0.004543	RDI1	1	1
Actins [11]	0.004543	ACT1	1	1
GroES-related proteins [101.11.21]	0.004543	HSP10	1	1
14-3-3 proteins [101.81]	0.009067	BMH2	1	2
Ubiquitin-activating enzymes (E1) [191.21]	0.02252	UBA1	1	5
DnaK subfamily [101.21.11]	0.04889	SSA4	1	11

GO Molecular Function (1533 categories)

Category	p-value	In Category from Cluster	k	f
unfolded protein binding [GO:0051082]	2.183e-05	SSA4 HSP60 TSA1 HSC82 HSP10 HSP82	6	131
catalytic activity [GO:0003824]	0.0002281	CYS3 SEC53 HXK2 INO1 AAT1 UBA1 TAL1 ADH1 ERG10	9	492
isomerase activity [GO:0016853]	0.0002439	PDI1 SEC53 INO1 PGM2	4	69
ATPase activity, coupled [GO:0042623]	0.00128	HSC82 HSP82	2	12
chaperone binding [GO:0051087]	0.004357	HSP60 HSP10	2	22
5'-3' DNA helicase activity [GO:0043139]	0.004543	ACT1	1	1
ubiquitin activating enzyme activity [GO:0004839]	0.004543	UBA1	1	1
methylglyoxal reductase (NADH-dependent) activity [GO:0019170]	0.004543	ADH1	1	1
Hsp70 protein binding [GO:0030544]	0.009067	STI1	1	2
glucose 1-dehydrogenase (NADP+) activity [GO:0047935]	0.009067	GRE3	1	2
actin lateral binding [GO:0003786]	0.009067	TPM2	1	2
acetyl-CoA C-acetyltransferase activity [GO:0003985]	0.009067	ERG10	1	2
chaperone inhibitor activity [GO:0030190]	0.009067	STI1	1	2
N-acyltransferase activity [GO:0016410]	0.009067	ACT1	1	2
Rho GDP-dissociation inhibitor activity [GO:0005094]	0.009067	RDI1	1	2
actin monomer binding [GO:0003785]	0.009067	PFY1	1	2
ligase activity, forming carbon-nitrogen bonds [GO:0016879]	0.009067	ACT1	1	2
DNA replication origin binding [GO:0003688]	0.01332	BMH2 HSP60	2	39
protein domain specific binding [GO:0019904]	0.01357	BMH2	1	3
coproporphyrinogen oxidase activity [GO:0004109]	0.01357	HEM13	1	3

phosphomannomutase activity [GO:0004615]	0.01357	SEC53	1 3
small protein activating enzyme activity [GO:0008641]	0.01357	UBA1	1 3
Hsp90 protein binding [GO:0051879]	0.01357	STI1	1 3
lysine N-acetyltransferase activity [GO:0004468]	0.01357	ACT1	1 3
cystathionine gamma-lyase activity [GO:0004123]	0.01357	CYS3	1 3
pyridoxal phosphate binding [GO:0030170]	0.01535	CYS3 AAT1	2 42
transferase activity, transferring acyl groups [GO:0016746]	0.01805	ACT1	1 4
transferase activity, transferring groups other than amino-acyl groups [GO:0016747]	0.01805	ACT1	1 4
inositol-3-phosphate synthase activity [GO:0004512]	0.01805	INO1	1 4
ATP-dependent 5'-3' DNA helicase activity [GO:0043141]	0.02252	ACT1	1 5
riboflavin synthase activity [GO:0004746]	0.02252	RIB5	1 5
ribosome binding [GO:0043022]	0.02252	TSA1	1 5
aspartate transaminase activity [GO:0004069]	0.02252	AAT1	1 5
transaldolase activity [GO:0004801]	0.02696	TAL1	1 6
chaperone activator activity [GO:0030189]	0.03139	STI1	1 7
intramolecular transferase activity, phosphotransferases [GO:0016868]	0.03139	PGM2	1 7
binding [GO:0005488]	0.03439	INO1 UBA1 ADH1 STI1	4 275
peroxiredoxin activity [GO:0051920]	0.04018	TSA1	1 9
acetyltransferase activity [GO:0016407]	0.04455	ACT1	1 10
transferase activity, transferring nitrogenous groups [GO:0016769]	0.04889	AAT1	1 11
antioxidant activity [GO:0016209]	0.04889	TSA1	1 11

GO Biological Process (1695 categories)

Category	p-value	In Category from Cluster	k f
biopolymer biosynthetic process [GO:0043284]	1.115e-07	CYS3 HEM13 ACT1 HXK2 TAL1 HSC82 ADH1 ERG10	8 137
protein refolding [GO:0042026]	7.911e-07	HSP60 HSC82 HSP10 HSP82	4 17
protein folding [GO:0006457]	2.139e-06	PDI1 SSA4 HSP60 HSC82 HSP10 STI1 HSP82	7 139
'de novo' protein folding [GO:0006458]	4.668e-06	HSP60 HSC82 HSP82	3 8
actin polymerization and/or depolymerization [GO:0008154]	0.0001979	TPM2 PFY1	2 5
response to stress [GO:0006950]	0.0002074	SSA4 GRE3 HSP60 HSC82 STI1 HSP82	6 196
budding cell isotropic bud growth [GO:0007119]	0.0005494	ACT1 TPM2	2 8
response to osmotic stress [GO:0006970]	0.002099	ACT1 PFY1 HSP82	3 57

protein maturation [GO:0051604]	0.004543	HSP60	1 1
regulation of transcription by glucose [GO:0046015]	0.004543	HXK2	1 1
transsulfuration [GO:0019346]	0.004543	CYS3	1 1
mannose biosynthetic process [GO:0019307]	0.004543	SEC53	1 1
aspartate catabolic process [GO:0006533]	0.004543	AAT1	1 1
asparagine biosynthetic process from oxaloacetate [GO:0019266]	0.004543	AAT1	1 1
response to hydroperoxide [GO:0033194]	0.004543	TSA1	1 1
vacuole inheritance [GO:0000011]	0.004758	ACT1 TPM2	2 23
proteasome assembly [GO:0043248]	0.004758	HSC82 HSP82	2 23
glucose metabolic process [GO:0006006]	0.006061	HXK2 PGM2	2 26
response to oxidative stress [GO:0006979]	0.006938	ACT1 GRE3 TSA1	3 87
metabolic process [GO:0008152]	0.007406	SEC53 INO1 UBA1 TAL1 ADH1 ERG10	6 392
amino acid metabolic process [GO:0006520]	0.008551	CYS3 AAT1	2 31
aspartate biosynthetic process [GO:0006532]	0.009067	AAT1	1 2
fructose import [GO:0032445]	0.009067	HXK2	1 2
cysteine metabolic process [GO:0006534]	0.009067	CYS3	1 2
ethanol biosynthetic process during fermentation [GO:0043458]	0.009067	ADH1	1 2
glucose 6-phosphate utilization [GO:0006010]	0.009067	PGM2	1 2
inositol biosynthetic process [GO:0006021]	0.01357	INO1	1 3
actin nucleation [GO:0045010]	0.01357	PFY1	1 3
glucose import [GO:0046323]	0.01357	HXK2	1 3
mitochondrion inheritance [GO:0000001]	0.01466	ACT1 TPM2	2 41
mannose metabolic process [GO:0006013]	0.01805	HXK2	1 4
protein stabilization [GO:0050821]	0.01805	HSP60	1 4
intracellular transport [GO:0046907]	0.01805	PFY1	1 4
establishment of cell polarity [GO:0030010]	0.02136	ACT1 TPM2	2 50
positive regulation of telomere maintenance via telomerase [GO:0032212]	0.02252	HSP82	1 5
UDP-glucose metabolic process [GO:0006011]	0.02252	PGM2	1 5
vesicle transport along actin filament [GO:0030050]	0.02252	ACT1	1 5
chaperone-mediated protein complex assembly [GO:0051131]	0.02252	HSP60	1 5
D-xylose catabolic process [GO:0042843]	0.02252	GRE3	1 5
actin cable formation [GO:0045011]	0.02252	TPM2	1 5
sulfur amino acid metabolic process [GO:0000096]	0.02252	CYS3	1 5
exocytosis [GO:0006887]	0.02299	ACT1 TPM2	2 52
galactose catabolic process [GO:0019388]	0.02696	PGM2	1 6
actin filament reorganization during cell cycle [GO:0030037]	0.02696	ACT1	1 6
amino acid catabolic process to alcohol via Ehrlich pathway [GO:0000947]	0.02696	ADH1	1 6
glucose 1-phosphate utilization [GO:0006008]	0.02696	PGM2	1 6

contractile ring contraction involved in cytokinesis [GO:0000916]	0.02696	ACT1	1 6
actin filament organization [GO:0007015]	0.02729	RDI1 TPM2	2 57
arabinose catabolic process [GO:0019568]	0.03139	GRE3	1 7
fructose metabolic process [GO:0006000]	0.03139	HXK2	1 7
oxidation reduction [GO:0055114]	0.034	HEM13 GRE3 TSA1 ADH1	4 274
regulation of translation [GO:0006417]	0.03547	CYS3 HEM13 ACT1 HXK2 ADH1	5 410
cell redox homeostasis [GO:0045454]	0.03676	PDI1 TSA1	2 67
fermentation [GO:0006113]	0.04018	ADH1	1 9
chronological cell aging [GO:0001300]	0.04018	ACT1	1 9
protein secretion [GO:0009306]	0.04018	ACT1	1 9
protein import into mitochondrial intermembrane space [GO:0045041]	0.04455	HSP60	1 10
cellular cation homeostasis [GO:0030003]	0.04455	PGM2	1 10
cellular protein metabolic process [GO:0044267]	0.04455	HSP60	1 10
ascospore formation [GO:0030437]	0.04512	BMH2 ACT1	2 75
negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle [GO:0051436]	0.04889	BMH2	1 11
SRP-dependent cotranslational protein targeting to membrane, translocation [GO:0006616]	0.04889	SSA4	1 11

GO Cellular Component (569 categories)

Category	p-value	In Category from Cluster	k	f
cellular bud neck				
contractile ring [GO:0000142]	4.555e-05	ACT1 TPM2 PFY1	3	16
actin cable [GO:0030482]	0.000296	ACT1 TPM2	2	6
cytosol [GO:0005829]	0.0003974	RDI1 SEC53 HXK2 TSA1 ADH1 ERG10	6	221
small ribosomal subunit [GO:0015935]	0.00202	RPS0A RPS5	2	15
cytoskeleton [GO:0005856]	0.0091	ACT1 TPM2 PFY1	3	96
cytoplasm [GO:0005737]	0.01778	CYS3 RDI1 HEM13 BMH2 SSA4 ACT1 SEC53 RPS0A RTC3 GRE3 TPM2 INO1 RPS5 UBA1 RPL10 TAL1 TSA1 PGM2 HSC82 ADH1 STI1 PFY1 ERG10 HSP82	24	3973
actin cytoskeleton [GO:0015629]	0.02252	PFY1	1	5
actin filament [GO:0005884]	0.02696	ACT1	1	6
cytosolic small ribosomal subunit [GO:0022627]	0.03188	RPS0A RPS5	2	62

mitochondrial matrix [GO:0005759]	0.03294	AAT1 HSP60 HSP10	3	156
90S preribosome [GO:0030686]	0.04191	RPS0A RPS5	2	72

SMART Domains (345 categories)

Category	p-value	In Category from Cluster	k	f
HATPase_c	0.0007044	HSC82 HSP82	2	9
PROF	0.004543	PFY1	1	1
14_3_3	0.009067	BMH2	1	2
STI1	0.02252	STI1	1	5
ACTIN	0.04455	ACT1	1	10

PFam-A Domains (2168 categories)

Category	p-value	In Category from Cluster	k	f
HSP90	1.996e-05	HSC82 HSP82	2	2
HATPase_c	0.0004132	HSC82 HSP82	2	7
Inos-1-P_synth	0.004543	INO1	1	1
Profilin	0.004543	PFY1	1	1
NAD_binding_5	0.004543	INO1	1	1
Coprogen_oxidas	0.004543	HEM13	1	1
PMM	0.004543	SEC53	1	1
Rho_GDI	0.004543	RDI1	1	1
UBA_e1_C	0.004543	UBA1	1	1
Cpn10	0.004543	HSP10	1	1
Thiolase_C	0.009067	ERG10	1	2
14-3-3	0.009067	BMH2	1	2
PGM_PMM_III	0.009067	PGM2	1	2
Thiolase_N	0.009067	ERG10	1	2
Lum_binding	0.009067	RIB5	1	2
SBDS	0.009067	RTC3	1	2
Transaldolase	0.009067	TAL1	1	2
Hydrolase_3	0.009067	SEC53	1	2
Ribosomal_S7	0.009067	RPS5	1	2
Ribosomal_L16	0.009067	RPL10	1	2
Ribosomal_S2	0.01357	RPS0A	1	3
PGM_PMM_IV	0.01357	PGM2	1	3
PGM_PMM_II	0.01357	PGM2	1	3

PGM_PMM_I	0.01805	PGM2	1 4
UBACT	0.01805	UBA1	1 4
Hexokinase_2	0.01805	HXK2	1 4
Hexokinase_1	0.02252	HXK2	1 5
AhpC-TSA	0.02252	TSA1	1 5
Redoxin	0.02252	TSA1	1 5
ThiF	0.04018	UBA1	1 9
Cpn60_TCP1	0.04018	HSP60	1 9
Actin	0.04018	ACT1	1 9
Cys_Met_Meta_PP	0.04018	CYS3	1 9
Aminotran_1_2	0.04889	AAT1	1 11

Yeast Two Hybrid - Uetz (509 categories)

Category	p-value	In Category from Cluster	k f
YDR077W (SED1)	0.004543	HEM13	1 1
YLL050C (COF1)	0.004543	ACT1	1 1
YLR335W (NUP2)	0.004543	HSP10	1 1
YDR017C (KCS1)	0.004543	BMH2	1 1
YLR229C (CDC42)	0.009067	RDI1	1 2
YNR032W (PPG1)	0.01357	HSC82	1 3
YMR308C (PSE1)	0.04889	HSP10	1 11

Yeast Two Hybrid - Ito (core) (449 categories)

Category	p-value	In Category from Cluster	k f
YOR020C (HSP10)	0.004543	HSP10	1 1

Yeast Two Hybrid - Ito (full) (1532 categories)

Category	p-value	In Category from Cluster	k f
YPR001W (CIT3)	0.004543	SSA4	1 1
YNL173C (MDG1)	0.004543	HSP10	1 1
YIL118W (RHO3)	0.004543	RTC3	1 1
YJL190C (RPS22A)	0.004543	INO1	1 1
YKR055W (RHO4)	0.004543	RDI1	1 1
YLR343W	0.004543	SEC53	1 1

YMR101C (SRT1)	0.004543	CYS3	1	1
YOR020C (HSP10)	0.004543	HSP10	1	1
YNL176C	0.009067	RDI1	1	2
YCL043C (PDI1)	0.009067	TAL1	1	2
YBL066C (SEF1)	0.009067	BMH2	1	2
YBL056W (PTC3)	0.009067	HSP10	1	2
YNL189W (SRP1)	0.017	HEM13 SEC53 HSP10	3	121

Synthetic Genetic Array Analysis (8 categories)

Category p-value In Category from Cluster k f

MDS Proteomics Complexes (493 categories)

Category	p-value	In Category from Cluster	k	f
YBR055C (PRP6)	4.95e-05	CYS3 UBA1 PGM2 ERG10	4	46
YDL059C (RAD59)	0.00023	SEC53 UBA1 PGM2	3	27
YDR306C	0.0004132	PGM2 STI1	2	7
YOR212W (STE4)	0.001756	SEC53 PGM2	2	14
YJL068C	0.004543	TAL1	1	1
YGR223C	0.004543	ERG10	1	1
YPL026C (SKS1)	0.004543	ERG10	1	1
YOL062C (APM4)	0.004543	SEC53	1	1
YBR109C (CMD1)	0.005611	UBA1 PGM2	2	25
YGL058W (RAD6)	0.009067	UBA1	1	2
YPR178W (PRP4)	0.009067	STI1	1	2
YIL143C (SSL2)	0.009067	STI1	1	2
YML112W (CTK3)	0.01357	UBA1	1	3
YJL092W (HPR5)	0.01357	SEC53	1	3
YKL210W (UBA1)	0.01357	STI1	1	3
YNL053W (MSG5)	0.01357	TAL1	1	3
YMR199W (CLN1)	0.01357	PGM2	1	3
YIR034C (LYS1)	0.01357	TAL1	1	3
YPL149W (APG5)	0.01357	CYS3	1	3
YER066C-A	0.01805	STI1	1	4
YDR227W (SIR4)	0.02252	SEC53	1	5
YDR092W (UBC13)	0.02252	UBA1	1	5
YBR136W (MEC1)	0.02252	STI1	1	5
YMR059W (SEN15)	0.02467	SEC53 UBA1	2	54
YPR015C	0.02696	PGM2	1	6

YGL208W (SIP2)	0.03139	SEC53	1 7
YOL126C (MDH2)	0.03139	PDI1	1 7
YPR165W (RHO1)	0.03579	ERG10	1 8
YIR005W (IST3)	0.03579	PGM2	1 8
YNL094W (APP1)	0.03579	PGM2	1 8
YNL311C	0.04018	STI1	1 9
YIR001C (SGN1)	0.04018	PDI1	1 9
YPR054W (SMK1)	0.04018	STI1	1 9
YDR398W (UTP5)	0.04018	SEC53	1 9
YAL021C (CCR4)	0.04018	STI1	1 9
YLR340W (RPP0)	0.04455	RTC3	1 10
YJR076C (CDC11)	0.04455	PDI1	1 10
YJL173C (RFA3)	0.04455	PGM2	1 10
YER100W (UBC6)	0.04455	UBA1	1 10
YLR222C (UTP13)	0.04889	PGM2	1 11
YDL101C (DUN1)	0.04889	PGM2	1 11

Cellzome Complexes (459 categories)

Category	p-value	In Category from Cluster	k	f
YAL029C (MYO4)	1.812e-05	ACT1 HSC82 ADH1	3	12
YGR123C (PPT1)	5.97e-05	HSC82 HSP82	2	3
YAL059W (ECM1)	0.0005494	HSC82 ADH1	2	8
YOR244W (ESA1)	0.000878	ACT1 ADH1	2	10
YNL127W	0.001509	HSC82 ADH1	2	13
YFR021W (AUT10)	0.009067	ADH1	1	2
YGL009C (LEU1)	0.009067	ADH1	1	2
YMR300C (ADE4)	0.01357	CYS3	1	3
YDR164C (SEC1)	0.01357	ADH1	1	3
YOR304W (ISW2)	0.01357	ADH1	1	3
YNL138W (SRV2)	0.01357	ACT1	1	3
YJL005W (CYR1)	0.01805	ACT1	1	4
YPR180W (AOS1)	0.01805	ADH1	1	4
YBR058C (UBP14)	0.01805	ADH1	1	4
YGL240W (DOC1)	0.02252	ACT1	1	5
YOR056C (NOB1)	0.02252	ADH1	1	5
YPL106C (SSE1)	0.02252	TSA1	1	5
YHR023W (MYO1)	0.02696	ACT1	1	6
YML126C (ERG13)	0.02696	ACT1	1	6
YAL034C (FUN19)	0.02696	ADH1	1	6
YDR099W (BMH2)	0.03139	BMH2	1	7
YDL042C (SIR2)	0.03139	ADH1	1	7

YBR207W (FTH1)	0.03139	ADH1	1 7
YLR196W (PWP1)	0.03579	ACT1	1 8
YPL082C (MOT1)	0.03579	ADH1	1 8
YOL090W (MSH2)	0.04018	HSC82	1 9
YFL024C (EPL1)	0.04018	ACT1	1 9
YBL087C (RPL23A)	0.04018	SSA4	1 9
YDR127W (ARO1)	0.04455	HSC82	1 10
YAL027W	0.04455	ADH1	1 10
YBR114W (RAD16)	0.04889	ADH1	1 11

Proteome Localization--Observed (11 categories)

Category	p-value	In Category from Cluster	k	f
cyto	0.0008793	CYS3 RIB5 HEM13 SSA4 GRE3 INO1 RPS5 RPL10 TAL1 TSA1 PGM2 HSC82 ADH1 HSP82	14	1321
mixed	0.009067	TPM2	1	2

Proteome Localization--Predicted+Observed (4 categories)

Category	p-value	In Category from Cluster	k	f
cyt	1.371e-05	CYS3 RIB5 RDI1 HEM13 BMH2 SSA4 ACT1 SEC53 HXK2 RPS0A RTC3 GRE3 TPM2 INO1 RPS5 UBA1 RPL10 TAL1 TSA1 PGM2 HSC82 ADH1 STI1 PFY1 ERG10 HSP82	26	3195

Deletions Consortium (Essentiality, Morphology) (11 categories)

Category	p-value	In Category from Cluster	k	f
essential	0.001959	RIB5 PDI1 HEM13 ACT1 SEC53 RPS5 UBA1 RPL10 HSP60 HSP10 PFY1 ERG10	12	1099

Yeast Fitness Data (1 category)

Category p-value In Category from Cluster k f

Published Complexes (7 categories)

Category	p-value	In Category from Cluster	k	f
Andersen et al. (2002) - Curr Bio 12:1-	0.0007876	PDI1 ACT1 RPS0A RPS5 HSP60	5	165

A tab-delimited version of the results can be downloaded [here](#). Note: This link will expire in 3 hours.

FunSpec was created by Jorg Grigull, Naveed Mohammad and Mark Robinson.

Table S4.b. FunSpec analysis: results from less abundant proteins in *C. albicans* hyphal cells. Input Cluster (n=29):

Systematic Name	Common Name	Essential		Publications	
YAL038W	CDC19	yes	117	(Literature on CDC19)	(SGD) (MIPS)
YAL062W	GDH3	no	31	(Literature on GDH3)	(SGD) (MIPS)
YAR015W	ADE1	no	83	(Literature on ADE1)	(SGD) (MIPS)
YBL041W	PRE7	yes	25	(Literature on PRE7)	(SGD) (MIPS)
YBR149W	ARA1	no	15	(Literature on ARA1)	(SGD) (MIPS)
YCL043C	PDI1	yes	77	(Literature on PDI1)	(SGD) (MIPS)
YCR012W	PGK1	yes	184	(Literature on PGK1)	(SGD) (MIPS)
YDL244W	THI13	no	9	(Literature on THI13)	(SGD) (MIPS)
YDR032C	PST2	no	11	(Literature on PST2)	(SGD) (MIPS)
YDR101C	ARX1	no	16	(Literature on ARX1)	(SGD) (MIPS)
YDR385W	EFT2	no	47	(Literature on EFT2)	(SGD) (MIPS)
YDR487C	RIB3	yes	11	(Literature on RIB3)	(SGD) (MIPS)
YDR533C	HSP31	no	14	(Literature on HSP31)	(SGD) (MIPS)
YGR012W		no	5	(Literature on YGR012W)	(SGD) (MIPS)
YGR144W	THI4	no	33	(Literature on THI4)	(SGD) (MIPS)
YGR192C	TDH3	no	119	(Literature on TDH3)	(SGD) (MIPS)
YGR214W	RPS0A	no	30	(Literature on RPS0A)	(SGD) (MIPS)
YHR087W	RTC3	no	10	(Literature on RTC3)	(SGD) (MIPS)
YIL136W	OM45	no	10	(Literature on OM45)	(SGD) (MIPS)
YJR121W	ATP2	no	114	(Literature on ATP2)	(SGD) (MIPS)
YLR075W	RPL10	yes	33	(Literature on RPL10)	(SGD) (MIPS)
YLR109W	AHP1	no	59	(Literature on AHP1)	(SGD) (MIPS)
YLR304C	ACO1	no	66	(Literature on ACO1)	(SGD) (MIPS)
YLR355C	ILV5	yes	47	(Literature on ILV5)	(SGD) (MIPS)
YMR120C	ADE17	no	26	(Literature on ADE17)	(SGD) (MIPS)
YNL241C	ZWF1	no	88	(Literature on ZWF1)	(SGD) (MIPS)
YOR369C	RPS12	no	12	(Literature on RPS12)	(SGD) (MIPS)
YPL088W		no	13	(Literature on YPL088W)	(SGD) (MIPS)
YPR074C	TKL1	no	70	(Literature on TKL1)	(SGD) (MIPS)

Genes Not Found:

SOU1

Number of Genes in each Database: 6603

k: number of genes from the input cluster in given category.

f: number of genes total in given category.

The p-values represent the probability that the intersection of a given list with any given functional category occurs by chance. The Bonferroni-correction divides the p-value threshold, that would be

deemed significant for an individual test, by the number of tests conducted and thus accounts for spurious significance due to multiple testing over the categories of a database.

MIPS Functional Classification (459 categories)

Category	p-value	In Category from Cluster	k	f
sugar, glucoside, polyol and carboxylate catabolism [01.05.02.07]	4.036e-08	CDC19 ARA1 PGK1 TDH3 ACO1 ZWF1 TKL1	7	81
glycolysis and gluconeogenesis [02.01]	2.717e-05	CDC19 PGK1 TDH3 ZWF1	4	41
biosynthesis of glutamate [01.01.03.02.01]	0.001888	GDH3 ACO1	2	15
pentose-phosphate pathway [02.07]	0.005249	ZWF1 TKL1	2	25
purine nucleotide/nucleoside/nucleobase anabolism [01.03.01.03]	0.007027	ADE1 ADE17	2	29
tricarboxylic-acid pathway (citrate cycle, Krebs cycle, TCA cycle) [02.10]	0.008004	GDH3 ACO1	2	31
propionate fermentation [02.16.11]	0.008765	ACO1	1	2
biosynthesis of glutamine [01.01.03.01.01]	0.008765	ZWF1	1	2
biosynthesis of vitamins, cofactors, and prosthetic groups [01.07.01]	0.012	THI13 RIB3 THI4	3	110
degradation of glutamate [01.01.03.02.02]	0.01746	GDH3	1	4
biosynthesis of isoleucine [01.01.11.02.01]	0.02177	ILV5	1	5
nitrogen, sulfur and selenium metabolism [01.02]	0.02315	GDH3 YGR012W	2	54
oxidative stress response [32.01.01]	0.02396	PST2 AHP1	2	55
biosynthesis of valine [01.01.11.03.01]	0.02607	ILV5	1	6
PROTEIN FATE (folding, modification, destination) [14]	0.03462	HSP31	1	8
biosynthesis of leucine [01.01.11.04.01]	0.03462	ILV5	1	8
metabolism of cysteine [01.01.09.03]	0.03886	YGR012W	1	9

MIPS Phenotypes (142 categories)

Category	p-value	In Category from Cluster	k	f
Pseudohyphae formation [52.10.20]	0.008004	GDH3 RPS0A	2	31
Methionine auxotrophy (Met) [42.10]	0.03886	ZWF1	1	9

MIPS Subcellular Localization (48 categories)

Category	p-value	In Category from Cluster	k	f
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cytoplasm [725]	0.02181	CDC19 GDH3 ADE1 PRE7 ARA1 PDI1 PGK1 PST2 ARX1 EFT2 RIB3 HSP31 THI4 TDH3 RPS0A RTC3 RPL10 AHP1 ACO1 ADE17 ZWF1 RPS12 YPL088W TKL1	24 4208
ER lumen [735.05]	0.03886	PDI1	1 9

MIPS Protein Complexes (1142 categories)

Category	p-value	In Category from Cluster	k f
Complex Number 435 [550.2.435]	0.000955	PST2 AHP1 ILV5	3 45
Complex Number 319 [550.2.319]	0.0009996	RTC3 AHP1	2 11
Cytoplasmic ribosomes [500.40]	0.004392	RPL10	1 1
D-arabinose dehydrogenase [143]	0.004392	ARA1	1 1
Pyruvate kinase [380]	0.008765	CDC19	1 2
Complex Number 488 [550.2.488]	0.008765	ACO1	1 2
Complex Number 293 [550.2.293]	0.008765	ACO1	1 2
Complex Number 28, probably intermediate and energy metabolism [550.1.28]	0.008765	TKL1	1 2
Complex Number 91, eEF2 (2) [550.3.91]	0.008765	EFT2	1 2
eEF2 [500.20.20]	0.008765	EFT2	1 2
Complex Number 110, probably protein synthesis turnover [550.1.110]	0.009578	PRE7 PGK1	2 34
Complex Number 111, probably protein synthesis turnover [550.1.111]	0.01013	PRE7 PGK1	2 35
Complex Number 27, probably intermediate and energy metabolism [550.1.27]	0.01312	PGK1	1 3
Complex Number 59, probably intermediate and energy metabolism [550.1.59]	0.01312	TDH3	1 3
Complex Number 170, probably signalling [550.1.170]	0.01711	PRE7 TDH3	2 46
Complex Number 67 [550.2.67]	0.01746	ILV5	1 4
Complex Number 83 [550.2.83]	0.01746	ACO1	1 4
Complex Number 294 [550.2.294]	0.01746	AHP1	1 4
Complex Number 422 [550.2.422]	0.01746	PST2	1 4
Complex Number 160 [550.2.160]	0.01746	AHP1	1 4
Complex Number 176 [550.2.176]	0.01746	ACO1	1 4
Complex Number 116, probably protein synthesis turnover [550.1.116]	0.01746	ARX1	1 4
Complex Number 244 [550.2.244]	0.01782	ARA1 ADE17	2 47
Complex Number 130, probably RNA metabolism [550.1.130]	0.02177	TDH3	1 5
Complex Number 341 [550.2.341]	0.02396	AHP1 ACO1	2 55
cytoplasmic ribosomal small subunit [500.40.20]	0.02561	RPS0A RPS12	2 57
Complex Number 38, Arx1 Complex (5) [550.3.38]	0.02607	ARX1	1 6
Complex Number 183 [550.2.183]	0.02607	AHP1	1 6

Complex Number 423 [550.2.423]	0.02607	AHP1	1 6
Complex Number 368 [550.2.368]	0.02607	PST2	1 6
Complex Number 396 [550.2.396]	0.02607	ACO1	1 6
Complex Number 549 [550.2.549]	0.02607	ACO1	1 6
Complex Number 256 [550.2.256]	0.02607	AHP1	1 6
Complex Number 35, probably intermediate and energy metabolism [550.1.35]	0.03036	ATP2	1 7
Complex Number 157 [550.2.157]	0.03036	ILV5	1 7
Complex Number 174 [550.2.174]	0.03462	PDI1	1 8
Complex Number 301 [550.2.301]	0.03462	ACO1	1 8
Complex Number 169, probably signalling [550.1.169]	0.03462	TDH3	1 8
Complex Number 89 [550.2.89]	0.03886	ARX1	1 9
Complex Number 194, probably transcription/DNA maintainance/chromatin structure [550.1.194]	0.03886	TDH3	1 9
Complex Number 344 [550.2.344]	0.04309	PDI1	1 10
Complex Number 34 [550.2.34]	0.0473	PDI1	1 11
Complex Number 328 [550.2.328]	0.0473	ILV5	1 11
Complex Number 230, probably transcription/DNA maintainance/chromatin structure [550.1.230]	0.0473	TDH3	1 11

MIPS Protein Classes (149 categories)

Category p-value In Category from Cluster k f

GO Molecular Function (1533 categories)

Category	p-value	In Category from Cluster	k f
catalytic activity [GO:0003824]	0.0001708	CDC19 GDH3 ADE1 YGR012W TDH3 ILV5 ADE17 ZWF1 TKL1	9 492
oxidoreductase activity [GO:0016491]	0.000328	GDH3 ARA1 PST2 TDH3 AHP1 ILV5 ZWF1 YPL088W	8 420
phosphoglycerate kinase activity [GO:0004618]	0.01312	PGK1	1 3
3,4-dihydroxy-2-butanone-4-phosphate synthase activity [GO:0008686]	0.01312	RIB3	1 3
glyceraldehyde-3-phosphate dehydrogenase activity [GO:0008943]	0.01312	TDH3	1 3
ketol-acid reductoisomerase activity [GO:0004455]	0.01312	ILV5	1 3
phosphoribosylaminoimidazolesuccinocarboxamide synthase activity [GO:0004639]	0.01312	ADE1	1 3

peptidase activity [GO:0008233]	0.01619	PRE7 ARX1 HSP31	3 123
cysteine synthase activity [GO:0004124]	0.01746	YGR012W	1 4
D-arabinose 1-dehydrogenase [NAD(P)+] activity [GO:0045290]	0.01746	ARA1	1 4
glutamate dehydrogenase activity [GO:0004352]	0.02177	GDH3	1 5
glucose-6-phosphate dehydrogenase activity [GO:0004345]	0.02177	ZWF1	1 5
magnesium ion binding [GO:0000287]	0.02497	CDC19 RIB3 ILV5	3 145
IMP cyclohydrolase activity [GO:0003937]	0.02607	ADE17	1 6
glutamate dehydrogenase (NADP+) activity [GO:0004354]	0.02607	GDH3	1 6
aconitate hydratase activity [GO:0003994]	0.02607	ACO1	1 6
phosphoribosylaminoimidazolecarboxamide formyltransferase activity [GO:0004643]	0.02607	ADE17	1 6
hydrogen-exporting ATPase activity, phosphorylative mechanism [GO:0008553]	0.03036	ATP2	1 7
transketolase activity [GO:0004802]	0.03036	TKL1	1 7
metalloexopeptidase activity [GO:0008235]	0.03036	ARX1	1 7
pyruvate kinase activity [GO:0004743]	0.03036	CDC19	1 7
binding [GO:0005488]	0.03078	GDH3 TDH3 ILV5 ZWF1	4 275
aryl-alcohol dehydrogenase activity [GO:0018456]	0.03462	YPL088W	1 8
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity [GO:0004365]	0.03886	TDH3	1 9
peroxiredoxin activity [GO:0051920]	0.03886	AHP1	1 9
lyase activity [GO:0016829]	0.04554	RIB3 ACO1	2 78
antioxidant activity [GO:0016209]	0.0473	AHP1	1 11
potassium ion binding [GO:0030955]	0.0473	CDC19	1 11

GO Biological Process (1695 categories)

Category	p-value	In Category from Cluster	k f
oxidation reduction [GO:0055114]	1.592e-05	GDH3 ARA1 TDH3 AHP1 ACO1 ILV5 ZWF1 YPL088W	8 274
mitochondrial genome maintenance [GO:0000002]	0.000626	THI4 ACO1 ILV5	3 39
metabolic process [GO:0008152]	0.001229	GDH3 YGR012W TDH3 ACO1 ILV5 ZWF1 TKL1	7 392
vacuolar protein catabolic process [GO:0007039]	0.002136	GDH3 PDI1 AHP1 ACO1	4 127
'de novo' IMP biosynthetic process [GO:0006189]	0.002728	ADE1 ADE17	2 18
glutamate biosynthetic process [GO:0006537]	0.003041	GDH3 ACO1	2 19
glycolysis [GO:0006096]	0.004318	CDC19 PGK1 TDH3	3 76
negative regulation of transcription by carbon catabolites [GO:0045013]	0.004392	ZWF1	1 1
glucose metabolic process [GO:0006006]	0.005671	TDH3 ZWF1	2 26

gluconeogenesis [GO:0006094]	0.006108	PGK1 TDH3	2 27
IMP biosynthetic process [GO:0006188]	0.008765	ADE17	1 2
cysteine biosynthetic process from serine [GO:0006535]	0.008765	YGR012W	1 2
purine nucleotide biosynthetic process [GO:0006164]	0.01187	ADE1 ADE17	2 38
thiamin biosynthetic process [GO:0009228]	0.0131	THI13 THI4	2 40
NADPH regeneration [GO:0006740]	0.01746	ZWF1	1 4
citrate metabolic process [GO:0006101]	0.01746	ACO1	1 4
biopolymer biosynthetic process [GO:0043284]	0.02153	CDC19 PGK1 TDH3	3 137
oxygen and reactive oxygen species metabolic process [GO:0006800]	0.02607	TDH3	1 6
response to hydrogen peroxide [GO:0042542]	0.02607	ZWF1	1 6
secondary metabolic process [GO:0019748]	0.03036	ADE1	1 7
propionate metabolic process [GO:0019541]	0.03036	ACO1	1 7
cell redox homeostasis [GO:0045454]	0.03453	PDI1 AHP1	2 67
response to metal ion [GO:0010038]	0.03886	AHP1	1 9
ATP metabolic process [GO:0046034]	0.03886	ATP2	1 9
pentose-phosphate shunt, oxidative branch [GO:0009051]	0.04309	ZWF1	1 10
response to water [GO:0009415]	0.0473	GDH3	1 11
pyruvate metabolic process [GO:0006090]	0.0473	CDC19	1 11

GO Cellular Component (569 categories)

Category	p-value	In Category from Cluster	k f
cytosol [GO:0005829]	3.56e-05	CDC19 PRE7 ARA1 RIB3 THI4 ACO1 ADE17	7 221
mitochondrial nucleoid [GO:0042645]	0.006108	ACO1 ILV5	2 27
soluble fraction [GO:0005625]	0.01854	GDH3 HSP31	2 48
mitochondrial proton-transporting ATP synthase, catalytic core [GO:0005754]	0.02177	ATP2	1 5
cytosolic small ribosomal subunit [GO:0022627]	0.02993	RPS0A RPS12	2 62
proton-transporting ATP synthase complex, catalytic core F(1) [GO:0045261]	0.04309	ATP2	1 10
proteasome core complex, beta-subunit complex [GO:0019774]	0.0473	PRE7	1 11

SMART Domains (345 categories)

Category p-value In Category from Cluster k f

AICARFT_IMPCHas	0.008765	ADE17	1 2
Gp_dh_N	0.01312	TDH3	1 3
ELFV_dehydrog	0.01312	GDH3	1 3
EFG_C	0.02607	EFT2	1 6

PFam-A Domains (2168 categories)

Category	p-value	In Category from Cluster	k f
Aldo_ket_red	0.00164	ARA1 YPL088W	2 14
IlvN	0.004392	ILV5	1 1
IlvC	0.004392	ILV5	1 1
SAICAR_synt	0.004392	ADE1	1 1
G6PD_C	0.004392	ZWF1	1 1
DHBP_synthase	0.004392	RIB3	1 1
PGK	0.004392	PGK1	1 1
Thi4	0.004392	THI4	1 1
G6PD_N	0.004392	ZWF1	1 1
AICARFT_IMPCHas	0.008765	ADE17	1 2
SBDS	0.008765	RTC3	1 2
Transketolase_N	0.008765	TKL1	1 2
Ribosomal_L16	0.008765	RPL10	1 2
ELFV_dehydrog_N	0.008765	GDH3	1 2
PK_C	0.008765	CDC19	1 2
PK	0.008765	CDC19	1 2
Transketolase_C	0.01312	TKL1	1 3
Gp_dh_N	0.01312	TDH3	1 3
Gp_dh_C	0.01312	TDH3	1 3
Ribosomal_S2	0.01312	RPS0A	1 3
MGS	0.01312	ADE17	1 3
ELFV_dehydrog	0.01312	GDH3	1 3
EFG_IV	0.01746	EFT2	1 4
Aconitase_C	0.01746	ACO1	1 4
DJ-1_PfpI	0.01746	HSP31	1 4
Aconitase	0.01746	ACO1	1 4
NMT1	0.01746	THI13	1 4
Transket_pyr	0.01746	TKL1	1 4
ATP-synt_ab_C	0.01746	ATP2	1 4
ATP-synt_ab	0.01746	ATP2	1 4
ATP-synt_ab_N	0.01746	ATP2	1 4
AhpC-TSA	0.02177	AHP1	1 5
Redoxin	0.02177	AHP1	1 5
Ribosomal_L7Ae	0.02607	RPS12	1 6

DAO	0.03036	THI4	1 7
EFG_C	0.03036	EFT2	1 7
PALP	0.03036	YGR012W	1 7
Flavodoxin_1	0.03036	PST2	1 7

Yeast Two Hybrid - Uetz (509 categories)

Category	p-value	In Category from Cluster	k f
YCR004C (YCP4)	0.004392	PST2	1 1
YOR226C (ISU2)	0.004392	YPL088W	1 1
YGR144W (THI4)	0.004392	THI4	1 1
YBR052C	0.004392	PST2	1 1
YDR032C (PST2)	0.008765	PST2	1 2

Yeast Two Hybrid - Ito (core) (449 categories)

Category	p-value	In Category from Cluster	k f
YNL189W (SRP1)	3.398e-06	RIB3 HSP31 THI4 TDH3 YPL088W	5 55
YLR267W (BOP2)	0.004392	GDH3	1 1
YPL088W	0.004392	YPL088W	1 1
YGR144W (THI4)	0.004392	THI4	1 1

Yeast Two Hybrid - Ito (full) (1532 categories)

Category	p-value	In Category from Cluster	k f
YNL189W (SRP1)	1.125e-05	GDH3 RIB3 HSP31 THI4 TDH3 YPL088W	6 121
YIL118W (RHO3)	0.004392	RTC3	1 1
YPL088W	0.004392	YPL088W	1 1
YMR010W	0.004392	HSP31	1 1
YOR226C (ISU2)	0.004392	CDC19	1 1
YOR110W (TFC7)	0.008765	PGK1	1 2
YLR267W (BOP2)	0.008765	GDH3	1 2
YGR144W (THI4)	0.008765	THI4	1 2
YNL116W	0.01312	THI4	1 3
YEL048C	0.01746	OM45	1 4
YJR091C (JSN1)	0.03223	HSP31 THI4 ZWF1 YPL088W	4 279

Synthetic Genetic Array Analysis (8 categories)

Category p-value In Category from Cluster k f

MDS Proteomics Complexes (493 categories)

Category	p-value	In Category from Cluster	k f
YDR369C (XRS2)	0.0003859	PST2 AHP1	2 7
YLR340W (RPP0)	0.0008201	RTC3 AHP1	2 10
YHR135C (YCK1)	0.0008939	PST2 AHP1 ILV5	3 44
YIL007C	0.004392	ACO1	1 1
YDR480W (DIG2)	0.01312	ACO1	1 3
YBR155W (CNS1)	0.01312	ILV5	1 3
YBR055C (PRP6)	0.01711	ARA1 ADE17	2 46
YGL090W (LIF1)	0.01746	AHP1	1 4
YGL115W (SNF4)	0.02177	PST2	1 5
YBR136W (MEC1)	0.02177	ACO1	1 5
YMR022W (QRI8)	0.02177	AHP1	1 5
YOL006C (TOP1)	0.02177	ACO1	1 5
YLR262C (YPT6)	0.02177	ACO1	1 5
YAR007C (RFA1)	0.02177	ACO1	1 5
YMR059W (SEN15)	0.02315	AHP1 ACO1	2 54
YNL312W (RFA2)	0.02607	AHP1	1 6
YDR499W (LCD1)	0.02607	ILV5	1 6
YOL126C (MDH2)	0.03036	PDI1	1 7
YPR017C (DSS4)	0.03462	ARX1	1 8
YIR001C (SGN1)	0.03886	PDI1	1 9
YJR076C (CDC11)	0.04309	PDI1	1 10

Cellzome Complexes (459 categories)

Category	p-value	In Category from Cluster	k f
YAR044W (OSH1)	0.008765	TDH3	1 2
YBR117C (TKL2)	0.008765	TKL1	1 2
YBR031W (RPL4A)	0.01248	ARX1 RPL10	2 39
YBR267W	0.01312	ARX1	1 3
YEL031W (SPF1)	0.01312	PGK1	1 3

YCR012W (PGK1)	0.01312	PGK1	1 3
YER036C (KRE30)	0.01746	ARX1	1 4
YDR075W (PPH3)	0.01746	TDH3	1 4
YHR170W (NMD3)	0.02177	ARX1	1 5
YOR014W (RTS1)	0.02607	TDH3	1 6
YDL042C (SIR2)	0.03036	TDH3	1 7
YNL313C	0.03036	ATP2	1 7
YIR001C (SGN1)	0.03036	TDH3	1 7
YAR007C (RFA1)	0.04309	PGK1	1 10
YBR114W (RAD16)	0.0473	TDH3	1 11
YAL007C (ERP2)	0.0473	ARX1	1 11

Proteome Localization--Observed (11 categories)

Category	p-value	In Category from Cluster	k	f
mixed (cyto / ER)	0.004988	PRE7 PST2 HSP31	3	80
mitochondria	0.01334	THI4 OM45 ATP2 ACO1 ILV5	5	330
cyto	0.01951	CDC19 GDH3 ADE1 PGK1 TDH3 RPL10 AHP1 ADE17 ZWF1 YPL088W TKL1	11	1321

Proteome Localization--Predicted+Observed (4 categories)

Category	p-value	In Category from Cluster	k	f
cyt	0.0476	CDC19 GDH3 ADE1 PRE7 ARA1 PGK1 THI13 EFT2 RIB3 TDH3 RPS0A RTC3 RPL10 AHP1 ADE17 ZWF1 RPS12 YPL088W TKL1	19	3195

Deletions Consortium (Essentiality, Morphology) (11 categories)

Category p-value In Category from Cluster k f

Yeast Fitness Data (1 category)

Category p-value In Category from Cluster k f

Published Complexes (7 categories)

Category	p-value	In Category from Cluster k	f
Andersen et al. (2002) - Curr Bio 12:1-	0.005483	PDI1 RPS0A ATP2 RPS12 4	165
Harnicharnpai et al. (2001) - Mol Cell 8:505-	0.009578	TDH3 RPL10	2 34

A tab-delimited version of the results can be downloaded [here](#). Note: This link will expire in 3 hours.

FunSpec was created by Jorg Grigull, Naveed Mohammad and Mark Robinson.

Table S4.c. FunSpec analysis: results from all differentially abundant proteins identified. Input Cluster (n=55):

Systematic Name	Common Name	Essential		Publications
YAL012W	CYS3	no	41	(Literature on CYS3) (SGD) (MIPS)
YAL038W	CDC19	yes	117	(Literature on CDC19) (SGD) (MIPS)
YAL062W	GDH3	no	31	(Literature on GDH3) (SGD) (MIPS)
YAR015W	ADE1	no	83	(Literature on ADE1) (SGD) (MIPS)
YBL041W	PRE7	yes	25	(Literature on PRE7) (SGD) (MIPS)
YBR149W	ARA1	no	15	(Literature on ARA1) (SGD) (MIPS)
YBR256C	RIB5	yes	12	(Literature on RIB5) (SGD) (MIPS)
YCL043C	PDI1	yes	77	(Literature on PDI1) (SGD) (MIPS)
YCR012W	PGK1	yes	184	(Literature on PGK1) (SGD) (MIPS)
YDL135C	RDI1	no	16	(Literature on RDI1) (SGD) (MIPS)
YDL244W	THI13	no	9	(Literature on THI13) (SGD) (MIPS)
YDR032C	PST2	no	11	(Literature on PST2) (SGD) (MIPS)
YDR044W	HEM13	yes	37	(Literature on HEM13) (SGD) (MIPS)
YDR099W	BMH2	no	65	(Literature on BMH2) (SGD) (MIPS)
YDR101C	ARX1	no	16	(Literature on ARX1) (SGD) (MIPS)
YDR385W	EFT2	no	47	(Literature on EFT2) (SGD) (MIPS)
YDR487C	RIB3	yes	11	(Literature on RIB3) (SGD) (MIPS)
YDR533C	HSP31	no	14	(Literature on HSP31) (SGD) (MIPS)
YER103W	SSA4	no	148	(Literature on SSA4) (SGD) (MIPS)
YFL039C	ACT1	yes	772	(Literature on ACT1) (SGD) (MIPS)
YFL045C	SEC53	yes	38	(Literature on SEC53) (SGD) (MIPS)
YGL253W	HXK2	no	264	(Literature on HXK2) (SGD) (MIPS)
YGR012W		no	5	(Literature on YGR012W) (SGD) (MIPS)
YGR144W	THI4	no	33	(Literature on THI4) (SGD) (MIPS)
YGR192C	TDH3	no	119	(Literature on TDH3) (SGD) (MIPS)
YGR214W	RPS0A	no	30	(Literature on RPS0A) (SGD) (MIPS)
YHR087W	RTC3	no	10	(Literature on RTC3) (SGD) (MIPS)
YHR104W	GRE3	no	29	(Literature on GRE3) (SGD) (MIPS)
YIL136W	OM45	no	10	(Literature on OM45) (SGD) (MIPS)
YIL138C	TPM2	no	38	(Literature on TPM2) (SGD) (MIPS)
YJL153C	INO1	no	167	(Literature on INO1) (SGD) (MIPS)
YJR121W	ATP2	no	114	(Literature on ATP2) (SGD) (MIPS)
YJR123W	RPS5	yes	32	(Literature on RPS5) (SGD) (MIPS)
YKL106W	AAT1	no	14	(Literature on AAT1) (SGD) (MIPS)
YKL210W	UBA1	yes	31	(Literature on UBA1) (SGD) (MIPS)
YLR075W	RPL10	yes	33	(Literature on RPL10) (SGD) (MIPS)
YLR109W	AHP1	no	59	(Literature on AHP1) (SGD) (MIPS)
YLR259C	HSP60	yes	97	(Literature on HSP60) (SGD) (MIPS)

YLR304C	ACO1	no	66	(Literature on ACO1)	(SGD) (MIPS)
YLR354C	TAL1	no	27	(Literature on TAL1)	(SGD) (MIPS)
YLR355C	ILV5	yes	47	(Literature on ILV5)	(SGD) (MIPS)
YML028W	TSA1	no	84	(Literature on TSA1)	(SGD) (MIPS)
YMR105C	PGM2	no	57	(Literature on PGM2)	(SGD) (MIPS)
YMR120C	ADE17	no	26	(Literature on ADE17)	(SGD) (MIPS)
YMR186W	HSC82	no	185	(Literature on HSC82)	(SGD) (MIPS)
YNL241C	ZWF1	no	88	(Literature on ZWF1)	(SGD) (MIPS)
YOL086C	ADH1	no	324	(Literature on ADH1)	(SGD) (MIPS)
YOR020C	HSP10	yes	29	(Literature on HSP10)	(SGD) (MIPS)
YOR027W	STI1	no	71	(Literature on STI1)	(SGD) (MIPS)
YOR122C	PFY1	yes	63	(Literature on PFY1)	(SGD) (MIPS)
YOR369C	RPS12	no	12	(Literature on RPS12)	(SGD) (MIPS)
YPL028W	ERG10	yes	33	(Literature on ERG10)	(SGD) (MIPS)
YPL088W		no	13	(Literature on YPL088W)	(SGD) (MIPS)
YPL240C	HSP82	no	292	(Literature on HSP82)	(SGD) (MIPS)
YPR074C	TKL1	no	70	(Literature on TKL1)	(SGD) (MIPS)

Genes Not Found:

Number of Genes in each Database: 6603

k: number of genes from the input cluster in given category.

f: number of genes total in given category.

The p-values represent the probability that the intersection of a given list with any given functional category occurs by chance. The Bonferroni-correction divides the p-value threshold, that would be deemed significant for an individual test, by the number of tests conducted and thus accounts for spurious significance due to multiple testing over the categories of a database.

MIPS Functional Classification (459 categories)

Category	p-value	In Category from Cluster	k	f
sugar, glucoside, polyol and carboxylate catabolism [01.05.02.07]	3.646e-11	CDC19 ARA1 PGK1 SEC53 TDH3 GRE3 ACO1 TAL1 PGM2 ZWF1 TKL1	11	81
sugar, glucoside, polyol and carboxylate anabolism [01.05.02.04]	8.943e-06	SEC53 INO1 TAL1 PGM2 TKL1	5	35
protein folding and stabilization [14.01]	1.025e-05	PDI1 SSA4 HSP60 HSC82 HSP10 STI1 HSP82	7	93
glycolysis and gluconeogenesis [02.01]	1.988e-05	CDC19 PGK1 TDH3 PGM2 ZWF1	5	41
pentose-phosphate pathway [02.07]	4.787e-05	TAL1 PGM2 ZWF1 TKL1	4	25

unfolded protein response (e.g. ER quality control) [32.01.07]	0.0002498	HSP31 SSA4 HSC82 HSP10 STI1	5	69
biosynthesis of vitamins, cofactors, and prosthetic groups [01.07.01]	0.002101	RIB5 THI13 HEM13 RIB3 THI4	5	110
oxygen and radical detoxification [32.07.07]	0.004262	AHP1 TSA1	2	12
protein binding [16.01]	0.00457	BMH2 HSP31 SSA4 TPM2 UBA1 HSC82 HSP10 STI1 PFY1	9	391
biosynthesis of glutamate [01.01.03.02.01]	0.006673	GDH3 ACO1	2	15
actin dependent transport [20.09.14.02]	0.00833	ACT1	1	1
oxidative stress response [32.01.01]	0.01057	PST2 AHP1 TSA1	3	55
metabolism of energy reserves (e.g. glycogen, trehalose) [02.19]	0.0111	BMH2 PGM2 HSP82	3	56
biosynthesis of glutamine [01.01.03.01.01]	0.01659	ZWF1	1	2
propionate fermentation [02.16.11]	0.01659	ACO1	1	2
biosynthesis of aspartate [01.01.06.01.01]	0.01659	AAT1	1	2
metabolism of secondary monosaccharides [01.20.01.01]	0.01659	INO1	1	2
degradation of aspartate [01.01.06.01.02]	0.01659	AAT1	1	2
purine nucleotide/nucleoside/nucleobase anabolism [01.03.01.03]	0.02396	ADE1 ADE17	2	29
tricarboxylic-acid pathway (citrate cycle, Krebs cycle, TCA cycle) [02.10]	0.02715	GDH3 ACO1	2	31
bud / growth tip [42.29]	0.02715	ACT1 TPM2	2	31
exocytosis [20.09.16.09.03]	0.0305	ACT1 TPM2	2	33
degradation of glutamate [01.01.03.02.02]	0.03291	GDH3	1	4
biosynthesis of asparagine [01.01.06.02.01]	0.03291	AAT1	1	4
biosynthesis of cysteine [01.01.09.03.01]	0.03291	CYS3	1	4
NAD/NADP binding [16.21.07]	0.03582	ARA1 INO1	2	36
PROTEIN WITH BINDING FUNCTION OR COFACTOR REQUIREMENT (structural or catalytic) [16]	0.04097	ACT1	1	5
metabolism of glutamate [01.01.03.02]	0.04097	AAT1	1	5
GTPase inhibitor (GIP) [18.02.01.02.01]	0.04097	RDI1	1	5
biosynthesis of isoleucine [01.01.11.02.01]	0.04097	ILV5	1	5
budding, cell polarity and filament formation [43.01.03.05]	0.04399	RDI1 BMH2 ACT1 RPS0A TPM2 PFY1	6	312
stress response [32.01]	0.04528	UBA1 HSP60 ZWF1 HSP82	4	162
actin cytoskeleton [42.04.03]	0.04538	RDI1 TPM2 PFY1	3	96
aminosaccharide catabolism [01.05.09.07]	0.04897	PGM2	1	6
aminosaccharide anabolism [01.05.09.04]	0.04897	PGM2	1	6
biosynthesis of valine [01.01.11.03.01]	0.04897	ILV5	1	6

MIPS Phenotypes (142 categories)

Category	p-value	In Category from Cluster	k f
Actin cytoskeleton mutants [52.30.10]	0.007259	ACT1 RPL10 PFY1	3 48
Rapamycin sensitivity [112.30.10]	0.01659	BMH2	1 2
Formamide or formaldehyde sensitivity [12.25]	0.02478	ADH1	1 3
Pseudohyphae formation [52.10.20]	0.02715	GDH3 RPS0A	2 31

MIPS Subcellular Localization (48 categories)

Category	p-value	In Category from Cluster	k f
cytoplasm [725]	0.000972	CYS3 CDC19 GDH3 ADE1 PRE7 ARA1 RIB5 PDI1 PGK1 RDI1 PST2 HEM13 BMH2 ARX1 EFT2 RIB3 HSP31 SSA4 SEC53 HXK2 THI4 TDH3 RPS0A RTC3 GRE3 TPM2 INO1 RPS5 UBA1 RPL10 AHP1 ACO1 TAL1 TSA1 PGM2 ADE17 HSC82 ZWF1 ADH1 STI1 PFY1 RPS12 ERG10 YPL088W HSP82 TKL1	46 4208
actin cytoskeleton [730.01]	0.02021	ACT1 TPM2 PFY1	3 70

MIPS Protein Complexes (1142 categories)

Category	p-value	In Category from Cluster	k f
Complex Number 244 [550.2.244]	2.086e-06	CYS3 ARA1 UBA1 PGM2 ADE17 ERG10	6 47
Complex Number 17, probably cell polarity and structure [550.1.17]	5.495e-06	ARX1 ACT1 HSC82 ADH1	4 15
Complex Number 175, probably signalling [550.1.175]	0.0002033	HSC82 HSP82	2 3
Complex Number 378 [550.2.378]	0.0002318	SEC53 PGM2 ADE17	3 15
Complex Number 406 [550.2.406]	0.0004044	UBA1 STI1	2 4
Complex Number 435 [550.2.435]	0.0004983	PST2 UBA1 AHP1 ILV5	4 45
Complex Number 341 [550.2.341]	0.001073	SEC53 UBA1 AHP1 ACO1	4 55
Complex Number 62 [550.2.62]	0.001242	PST2 UBA1 PGM2	3 26
Complex Number 171, probably signalling [550.1.171]	0.001847	HSC82 ADH1	2 8
Complex Number 454 [550.2.454]	0.001847	PGM2 STI1	2 8
Complex Number 194, probably transcription/DNA maintainance/chromatin structure [550.1.194]	0.002362	TDH3 ADH1	2 9
Complex Number 230, probably transcription/DNA maintainance/chromatin structure [550.1.230]	0.003571	TDH3 ADH1	2 11
Complex Number 319 [550.2.319]	0.003571	RTC3 AHP1	2 11
Complex Number 191, probably transcription/DNA maintainance/chromatin structure [550.1.191]	0.004262	ACT1 ADH1	2 12

Complex Number 34, probably intermediate and energy metabolism [550.1.34]	0.00501	HSC82 ADH1	2 13
Cytoplasmic ribosomes [500.40]	0.00833	RPL10	1 1
Hexokinase 2 [225]	0.00833	HXK2	1 1
D-arabinose dehydrogenase [143]	0.00833	ARA1	1 1
Actins [140.20.10]	0.00833	ACT1	1 1
Complex Number 49 [550.2.49]	0.00957	PST2 STI1	2 18
Complex Number 283 [550.2.283]	0.01064	SEC53 UBA1	2 19
cytoplasmic ribosomal small subunit [500.40.20]	0.01165	RPS0A RPS5 RPS12	3 57
Complex Number 267 [550.2.267]	0.01293	SEC53 ACO1	2 21
Complex Number 358 [550.2.358]	0.01659	ERG10	1 2
eEF2 [500.20.20]	0.01659	EFT2	1 2
Complex Number 56, probably intermediate and energy metabolism [550.1.56]	0.01659	ADH1	1 2
Complex Number 8 [550.2.8]	0.01659	SEC53	1 2
Complex Number 492 [550.2.492]	0.01659	TAL1	1 2
Complex Number 477 [550.2.477]	0.01659	ERG10	1 2
Complex Number 28, probably intermediate and energy metabolism [550.1.28]	0.01659	TKL1	1 2
Complex Number 91, eEF2 (2) [550.3.91]	0.01659	EFT2	1 2
Complex Number 18 [550.2.18]	0.01659	BMH2	1 2
Complex Number 293 [550.2.293]	0.01659	ACO1	1 2
Pyruvate kinase [380]	0.01659	CDC19	1 2
Complex Number 488 [550.2.488]	0.01659	ACO1	1 2
Complex Number 203, probably transcription/DNA maintainance/chromatin structure [550.1.203]	0.01672	ACT1 ADH1	2 24
Actin-associated proteins [140.20.20]	0.01808	TPM2 PFY1	2 25
Complex Number 65, probably membrane biogenesis and traffic [550.1.65]	0.02478	ADH1	1 3
Complex Number 222, probably transcription/DNA maintainance/chromatin structure [550.1.222]	0.02478	ADH1	1 3
Complex Number 175 [550.2.175]	0.02478	STI1	1 3
Complex Number 27, probably intermediate and energy metabolism [550.1.27]	0.02478	PGK1	1 3
Complex Number 285 [550.2.285]	0.02478	UBA1	1 3
Complex Number 266 [550.2.266]	0.02478	STI1	1 3
Complex Number 242 [550.2.242]	0.02478	STI1	1 3
Complex Number 58, probably intermediate and energy metabolism [550.1.58]	0.02478	ADH1	1 3
Complex Number 59, probably intermediate and energy metabolism [550.1.59]	0.02478	TDH3	1 3
Complex Number 51, probably intermediate and energy metabolism [550.1.51]	0.02478	CYS3	1 3
Complex Number 110, probably protein synthesis turnover [550.1.110]	0.03224	PRE7 PGK1	2 34
Complex Number 388 [550.2.388]	0.03224	PST2 SEC53	2 34

Complex Number 130 [550.2.130]	0.03291	SEC53	1 4
Complex Number 168 [550.2.168]	0.03291	TAL1	1 4
Complex Number 75 [550.2.75]	0.03291	UBA1	1 4
Complex Number 67 [550.2.67]	0.03291	ILV5	1 4
Complex Number 160 [550.2.160]	0.03291	AHP1	1 4
Complex Number 294 [550.2.294]	0.03291	AHP1	1 4
Complex Number 176 [550.2.176]	0.03291	ACO1	1 4
Complex Number 60 [550.2.60]	0.03291	PGM2	1 4
Complex Number 422 [550.2.422]	0.03291	PST2	1 4
Complex Number 95, probably protein synthesis turnover [550.1.95]	0.03291	ADH1	1 4
Complex Number 114, probably protein synthesis turnover [550.1.114]	0.03291	ADH1	1 4
Complex Number 83 [550.2.83]	0.03291	ACO1	1 4
Complex Number 194 [550.2.194]	0.03291	TAL1	1 4
Complex Number 167, probably signalling [550.1.167]	0.03291	ACT1	1 4
Complex Number 116, probably protein synthesis turnover [550.1.116]	0.03291	ARX1	1 4
Complex Number 5 [550.2.5]	0.03291	CYS3	1 4
Complex Number 111, probably protein synthesis turnover [550.1.111]	0.03401	PRE7 PGK1	2 35
Complex Number 212, probably transcription/DNA maintainance/chromatin structure [550.1.212]	0.03401	PGK1 HSC82	2 35
Complex Number 504 [550.2.504]	0.03767	PST2 STI1	2 37
Complex Number 130, probably RNA metabolism [550.1.130]	0.04097	TDH3	1 5
Complex Number 462 [550.2.462]	0.04097	STI1	1 5
Complex Number 94 [550.2.94]	0.04148	SEC53 ACO1	2 39
Complex Number 520 [550.2.520]	0.04148	SEC53 ACO1	2 39
Complex Number 396 [550.2.396]	0.04897	ACO1	1 6
Complex Number 52, probably intermediate and energy metabolism [550.1.52]	0.04897	ACT1	1 6
Complex Number 423 [550.2.423]	0.04897	AHP1	1 6
Complex Number 549 [550.2.549]	0.04897	ACO1	1 6
Complex Number 368 [550.2.368]	0.04897	PST2	1 6
Complex Number 256 [550.2.256]	0.04897	AHP1	1 6
Complex Number 352 [550.2.352]	0.04897	SEC53	1 6
Complex Number 410 [550.2.410]	0.04897	UBA1	1 6
Complex Number 38, Arx1 Complex (5) [550.3.38]	0.04897	ARX1	1 6
Complex Number 183 [550.2.183]	0.04897	AHP1	1 6
Complex Number 209, probably transcription/DNA maintainance/chromatin structure [550.1.209]	0.04949	PGK1 ADH1	2 43

MIPS Protein Classes (149 categories)

Category	p-value	In Category from Cluster	k	f
HSP90 family [101.31]	6.813e-05	HSC82 HSP82	2	2
other ATPases [41.61]	0.001389	HSP60 HSC82 HSP82	3	27
GroES-related proteins [101.11.21]	0.00833	HSP10	1	1
Actins [11]	0.00833	ACT1	1	1
GroEL-related proteins (HSP60 family) [101.11.11]	0.00833	HSP60	1	1
RHO-GDIs [91.51]	0.00833	RDI1	1	1
14-3-3 proteins [101.81]	0.01659	BMH2	1	2
Ubiquitin-activating enzymes (E1) [191.21]	0.04097	UBA1	1	5

GO Molecular Function (1533 categories)

Category	p-value	In Category from Cluster	k	f
catalytic activity [GO:0003824]	3.969e-08	CYS3 CDC19 GDH3 ADE1 SEC53 HXK2 YGR012W TDH3 INO1 AAT1 UBA1 TAL1 ILV5 ADE17 ZWF1 ADH1 ERG10 TKL1	18	492
unfolded protein binding [GO:0051082]	9.464e-05	HSP31 SSA4 HSP60 TSA1 HSC82 HSP10 HSP82	7	131
oxidoreductase activity [GO:0016491]	0.000134	GDH3 ARA1 PST2 HEM13 TDH3 GRE3 AHP1 ILV5 TSA1 ZWF1 ADH1 YPL088W	12	420
binding [GO:0005488]	0.001811	GDH3 TDH3 INO1 UBA1 ILV5 ZWF1 ADH1 STI1	8	275
peroxiredoxin activity [GO:0051920]	0.002362	AHP1 TSA1	2	9
isomerase activity [GO:0016853]	0.002494	PDI1 SEC53 INO1 PGM2	4	69
antioxidant activity [GO:0016209]	0.003571	AHP1 TSA1	2	11
ATPase activity, coupled [GO:0042623]	0.004262	HSC82 HSP82	2	12
pyridoxal phosphate binding [GO:0030170]	0.00499	CYS3 YGR012W AAT1	3	42
peroxidase activity [GO:0004601]	0.00501	AHP1 TSA1	2	13
aldehyde reductase activity [GO:0004032]	0.007586	ARA1 GRE3	2	16
ubiquitin activating enzyme activity [GO:0004839]	0.00833	UBA1	1	1
5'-3' DNA helicase activity [GO:0043139]	0.00833	ACT1	1	1
methylglyoxal reductase (NADH-dependent) activity [GO:0019170]	0.00833	ADH1	1	1
thioredoxin peroxidase activity [GO:0008379]	0.01064	AHP1 TSA1	2	19
single-stranded DNA binding [GO:0003697]	0.01414	HSP60 ACO1	2	22
chaperone binding [GO:0051087]	0.01414	HSP60 HSP10	2	22

actin lateral binding [GO:0003786]	0.01659	TPM2	1	2
acetyl-CoA C-acetyltransferase activity [GO:0003985]	0.01659	ERG10	1	2
glucose 1-dehydrogenase (NADP+) activity [GO:0047935]	0.01659	GRE3	1	2
Hsp70 protein binding [GO:0030544]	0.01659	STI1	1	2
Rho GDP-dissociation inhibitor activity [GO:0005094]	0.01659	RDI1	1	2
N-acyltransferase activity [GO:0016410]	0.01659	ACT1	1	2
actin monomer binding [GO:0003785]	0.01659	PFY1	1	2
ligase activity, forming carbon-nitrogen bonds [GO:0016879]	0.01659	ACT1	1	2
chaperone inhibitor activity [GO:0030190]	0.01659	STI1	1	2
phosphoglycerate kinase activity [GO:0004618]	0.02478	PGK1	1	3
coproporphyrinogen oxidase activity [GO:0004109]	0.02478	HEM13	1	3
protein domain specific binding [GO:0019904]	0.02478	BMH2	1	3
Hsp90 protein binding [GO:0051879]	0.02478	STI1	1	3
small protein activating enzyme activity [GO:0008641]	0.02478	UBA1	1	3
3,4-dihydroxy-2-butanone-4-phosphate synthase activity [GO:0008686]	0.02478	RIB3	1	3
glyceraldehyde-3-phosphate dehydrogenase activity [GO:0008943]	0.02478	TDH3	1	3
ketol-acid reductoisomerase activity [GO:0004455]	0.02478	ILV5	1	3
lysine N-acetyltransferase activity [GO:0004468]	0.02478	ACT1	1	3
phosphoribosylaminoimidazolesuccinocarboxamide synthase activity [GO:0004639]	0.02478	ADE1	1	3
phosphomannomutase activity [GO:0004615]	0.02478	SEC53	1	3
cystathionine gamma-lyase activity [GO:0004123]	0.02478	CYS3	1	3
transferase activity [GO:0016740]	0.02512	CDC19 RIB5 PGK1 HXK2 YGR012W AAT1 TAL1 ADE17 ERG10 TKL1	10	602
lyase activity [GO:0016829]	0.02681	CYS3 RIB3 ACO1	3	78
magnesium ion binding [GO:0000287]	0.03206	CDC19 RIB3 ILV5 PGM2	4	145
cysteine synthase activity [GO:0004124]	0.03291	YGR012W	1	4
transferase activity, transferring groups other than amino-acyl groups [GO:0016747]	0.03291	ACT1	1	4
transferase activity, transferring acyl groups [GO:0016746]	0.03291	ACT1	1	4
inositol-3-phosphate synthase activity [GO:0004512]	0.03291	INO1	1	4
D-arabinose 1-dehydrogenase [NAD(P)+] activity [GO:0045290]	0.03291	ARA1	1	4
ATP-dependent 5'-3' DNA helicase activity [GO:0043141]	0.04097	ACT1	1	5
riboflavin synthase activity [GO:0004746]	0.04097	RIB5	1	5
aspartate transaminase activity [GO:0004069]	0.04097	AAT1	1	5
ribosome binding [GO:0043022]	0.04097	TSA1	1	5
glucose-6-phosphate dehydrogenase activity				

[GO:0004345]	0.04097	ZWF1	1	5
glutamate dehydrogenase activity [GO:0004352]	0.04097	GDH3	1	5
DNA replication origin binding [GO:0003688]	0.04148	BMH2 HSP60	2	39
phosphoribosylaminoimidazolecarboxamide formyltransferase activity [GO:0004643]	0.04897	ADE17	1	6
IMP cyclohydrolase activity [GO:0003937]	0.04897	ADE17	1	6
aconitate hydratase activity [GO:0003994]	0.04897	ACO1	1	6
transaldolase activity [GO:0004801]	0.04897	TAL1	1	6
glutamate dehydrogenase (NADP+) activity [GO:0004354]	0.04897	GDH3	1	6

GO Biological Process (1695 categories)

Category	p-value	In Category from Cluster	k	f
biopolymer biosynthetic process [GO:0043284]	1.126e-08	CYS3 CDC19 PGK1 HEM13 ACT1 HXK2 TDH3 TAL1 HSC82 ADH1 ERG10	11	137
oxidation reduction [GO:0055114]	1.82e-06	GDH3 ARA1 HEM13 TDH3 GRE3 AHP1 ACO1 ILV5 TSA1 ZWF1 ADH1 YPL088W	12	274
protein refolding [GO:0042026]	9.464e-06	HSP60 HSC82 HSP10 HSP82	4	17
metabolic process [GO:0008152]	1.375e-05	GDH3 SEC53 YGR012W TDH3 INO1 UBA1 ACO1 TAL1 ILV5 ZWF1 ADH1 ERG10 TKL1	13	392
'de novo' protein folding [GO:0006458]	2.974e-05	HSP60 HSC82 HSP82	3	8
glucose metabolic process [GO:0006006]	5.623e-05	HXK2 TDH3 PGM2 ZWF1	4	26
protein folding [GO:0006457]	0.0001375	PDI1 SSA4 HSP60 HSC82 HSP10 STI1 HSP82	7	139
actin polymerization and/or depolymerization [GO:0008154]	0.0006704	TPM2 PFY1	2	5
response to stress [GO:0006950]	0.001106	HSP31 SSA4 GRE3 HSP60 HSC82 STI1 HSP82	7	196
budding cell isotropic bud growth [GO:0007119]	0.001847	ACT1 TPM2	2	8
amino acid metabolic process [GO:0006520]	0.002084	CYS3 GDH3 AAT1	3	31
glycolysis [GO:0006096]	0.003546	CDC19 PGK1 HXK2 TDH3	4	76
mitochondrial genome maintenance [GO:0000002]	0.004043	THI4 ACO1 ILV5	3	39
response to oxidative stress [GO:0006979]	0.005751	ACT1 GRE3 AHP1 TSA1	4	87
regulation of translation [GO:0006417]	0.006226	CYS3 CDC19 ADE1 HEM13 ACT1 HXK2 TDH3 ADE17 ADH1	9	410
cysteine biosynthetic process	0.006673	CYS3 YGR012W	2	15

[GO:0019344]				
protein maturation [GO:0051604]	0.00833	HSP60	1	1
transsulfuration [GO:0019346]	0.00833	CYS3	1	1
regulation of transcription by glucose [GO:0046015]	0.00833	HXK2	1	1
response to hydroperoxide [GO:0033194]	0.00833	TSA1	1	1
aspartate catabolic process [GO:0006533]	0.00833	AAT1	1	1
negative regulation of transcription by carbon catabolites [GO:0045013]	0.00833	ZWF1	1	1
asparagine biosynthetic process from oxaloacetate [GO:0019266]	0.00833	AAT1	1	1
mannose biosynthetic process [GO:0019307]	0.00833	SEC53	1	1
'de novo' IMP biosynthetic process [GO:0006189]	0.00957	ADE1 ADE17	2	18
riboflavin biosynthetic process [GO:0009231]	0.01064	RIB5 RIB3	2	19
glutamate biosynthetic process [GO:0006537]	0.01064	GDH3 ACO1	2	19
response to osmotic stress [GO:0006970]	0.01165	ACT1 PFY1 HSP82	3	57
pentose-phosphate shunt [GO:0006098]	0.01293	TAL1 TKL1	2	21
proteasome assembly [GO:0043248]	0.01541	HSC82 HSP82	2	23
vacuole inheritance [GO:0000011]	0.01541	ACT1 TPM2	2	23
fructose import [GO:0032445]	0.01659	HXK2	1	2
ethanol biosynthetic process during fermentation [GO:0043458]	0.01659	ADH1	1	2
cysteine biosynthetic process from serine [GO:0006535]	0.01659	YGR012W	1	2
cysteine metabolic process [GO:0006534]	0.01659	CYS3	1	2
aspartate biosynthetic process [GO:0006532]	0.01659	AAT1	1	2
IMP biosynthetic process [GO:0006188]	0.01659	ADE17	1	2
glucose 6-phosphate utilization [GO:0006010]	0.01659	PGM2	1	2
cell redox homeostasis [GO:0045454]	0.018	PDI1 AHP1 TSA1	3	67
vacuolar protein catabolic process [GO:0007039]	0.02092	GDH3 PDI1 AHP1 ACO1	4	127
gluconeogenesis [GO:0006094]	0.02093	PGK1 TDH3	2	27
glucose import [GO:0046323]	0.02478	HXK2	1	3
actin nucleation [GO:0045010]	0.02478	PFY1	1	3
inositol biosynthetic process [GO:0006021]	0.02478	INO1	1	3

carbohydrate metabolic process [GO:0005975]	0.02613	ARA1 TAL1 PGM2 ZWF1	4	136
intracellular transport [GO:0046907]	0.03291	PFY1	1	4
protein stabilization [GO:0050821]	0.03291	HSP60	1	4
citrate metabolic process [GO:0006101]	0.03291	ACO1	1	4
mannose metabolic process [GO:0006013]	0.03291	HXK2	1	4
NADPH regeneration [GO:0006740]	0.03291	ZWF1	1	4
purine nucleotide biosynthetic process [GO:0006164]	0.03956	ADE1 ADE17	2	38
vesicle transport along actin filament [GO:0030050]	0.04097	ACT1	1	5
actin cable formation [GO:0045011]	0.04097	TPM2	1	5
positive regulation of telomere maintenance via telomerase [GO:0032212]	0.04097	HSP82	1	5
chaperone-mediated protein complex assembly [GO:0051131]	0.04097	HSP60	1	5
UDP-glucose metabolic process [GO:0006011]	0.04097	PGM2	1	5
D-xylose catabolic process [GO:0042843]	0.04097	GRE3	1	5
sulfur amino acid metabolic process [GO:0000096]	0.04097	CYS3	1	5
thiamin biosynthetic process [GO:0009228]	0.04343	THI13 THI4	2	40
mitochondrion inheritance [GO:0000001]	0.04542	ACT1 TPM2	2	41
glucose 1-phosphate utilization [GO:0006008]	0.04897	PGM2	1	6
response to hydrogen peroxide [GO:0042542]	0.04897	ZWF1	1	6
galactose catabolic process [GO:0019388]	0.04897	PGM2	1	6
actin filament reorganization during cell cycle [GO:0030037]	0.04897	ACT1	1	6
oxygen and reactive oxygen species metabolic process [GO:0006800]	0.04897	TDH3	1	6
amino acid catabolic process to alcohol via Ehrlich pathway [GO:0000947]	0.04897	ADH1	1	6
contractile ring contraction involved in cytokinesis [GO:0000916]	0.04897	ACT1	1	6

GO Cellular Component (569 categories)

Category	p-value	In Category from Cluster	k	f
cytosol [GO:0005829]	1.944e-08	CDC19 PRE7 ARA1 RDI1 RIB3 SEC53 HXK2 THI4 ACO1 TSA1 ADE17 ADH1 ERG10	13	221
cellular bud neck contractile ring [GO:0000142]	0.0002837	ACT1 TPM2 PFY1	3	16
actin cable [GO:0030482]	0.001	ACT1 TPM2	2	6
mitochondrial nucleoid [GO:0042645]	0.001389	HSP60 ACO1 ILV5	3	27
small ribosomal subunit [GO:0015935]	0.006673	RPS0A RPS5	2	15
soluble fraction [GO:0005625]	0.007259	GDH3 RIB5 HSP31	3	48
cytosolic small ribosomal subunit [GO:0022627]	0.01463	RPS0A RPS5 RPS12	3	62
mitochondrial matrix [GO:0005759]	0.04031	AAT1 HSP60 ACO1 HSP10	4	156
actin cytoskeleton [GO:0015629]	0.04097	PFY1	1	5
mitochondrial proton-transporting ATP synthase, catalytic core [GO:0005754]	0.04097	ATP2	1	5
cytoskeleton [GO:0005856]	0.04538	ACT1 TPM2 PFY1	3	96
actin filament [GO:0005884]	0.04897	ACT1	1	6

SMART Domains (345 categories)

Category	p-value	In Category from Cluster	k	f
HATPase_c	0.002362	HSC82 HSP82	2	9
PROF	0.00833	PFY1	1	1
AICARFT_IMPCHas	0.01659	ADE17	1	2
14_3_3	0.01659	BMH2	1	2
Gp_dh_N	0.02478	TDH3	1	3
ELFV_dehydrog	0.02478	GDH3	1	3
STI1	0.04097	STI1	1	5
EFG_C	0.04897	EFT2	1	6

PFam-A Domains (2168 categories)

Category	p-value	In Category from Cluster	k	f
HSP90	6.813e-05	HSC82 HSP82	2	2
Aldo_ket_red	0.0001866	ARA1 GRE3 YPL088W	3	14
AhpC-TSA	0.0006704	AHP1 TSA1	2	5
Redoxin	0.0006704	AHP1 TSA1	2	5
HATPase_c	0.001393	HSC82 HSP82	2	7
DHBP_synthase	0.00833	RIB3	1	1
SAICAR_synt	0.00833	ADE1	1	1
G6PD_C	0.00833	ZWF1	1	1

G6PD_N	0.00833	ZWF1	1 1
NAD_binding_5	0.00833	INO1	1 1
Inos-1-P_synth	0.00833	INO1	1 1
IlvC	0.00833	ILV5	1 1
UBA_e1_C	0.00833	UBA1	1 1
Thi4	0.00833	THI4	1 1
Coprogen_oxidas	0.00833	HEM13	1 1
Cpn10	0.00833	HSP10	1 1
IlvN	0.00833	ILV5	1 1
PGK	0.00833	PGK1	1 1
Rho_GDI	0.00833	RDI1	1 1
Profilin	0.00833	PFY1	1 1
PMM	0.00833	SEC53	1 1
AICARFT_IMPCHas	0.01659	ADE17	1 2
14-3-3	0.01659	BMH2	1 2
Lum_binding	0.01659	RIB5	1 2
PGM_PMM_III	0.01659	PGM2	1 2
Ribosomal_S7	0.01659	RPS5	1 2
Thiolase_N	0.01659	ERG10	1 2
Transketolase_N	0.01659	TKL1	1 2
Ribosomal_L16	0.01659	RPL10	1 2
Thiolase_C	0.01659	ERG10	1 2
SBDS	0.01659	RTC3	1 2
ELFV_dehydrog_N	0.01659	GDH3	1 2
Hydrolase_3	0.01659	SEC53	1 2
PK_C	0.01659	CDC19	1 2
Transaldolase	0.01659	TAL1	1 2
PK	0.01659	CDC19	1 2
Gp_dh_N	0.02478	TDH3	1 3
Gp_dh_C	0.02478	TDH3	1 3
Ribosomal_S2	0.02478	RPS0A	1 3
PGM_PMM_IV	0.02478	PGM2	1 3
PGM_PMM_II	0.02478	PGM2	1 3
MGS	0.02478	ADE17	1 3
Transketolase_C	0.02478	TKL1	1 3
ELFV_dehydrog	0.02478	GDH3	1 3
PGM_PMM_I	0.03291	PGM2	1 4
DJ-1_PfpI	0.03291	HSP31	1 4
UBACT	0.03291	UBA1	1 4
EFG_IV	0.03291	EFT2	1 4
Aconitase_C	0.03291	ACO1	1 4
Aconitase	0.03291	ACO1	1 4
NMT1	0.03291	THI13	1 4
Hexokinase_2	0.03291	HXK2	1 4
Transket_nur			

	0.03291	TKL1	1 4
ATP-synt ab C	0.03291	ATP2	1 4
ATP-synt ab	0.03291	ATP2	1 4
ATP-synt ab N	0.03291	ATP2	1 4
Hexokinase 1	0.04097	HXK2	1 5
Ribosomal L7Ae	0.04897	RPS12	1 6

Yeast Two Hybrid - Uetz (509 categories)

Category	p-value	In Category from Cluster	k f
YCR004C (YCP4)	0.00833	PST2	1 1
YDR017C (KCS1)	0.00833	BMH2	1 1
YOR226C (ISU2)	0.00833	YPL088W	1 1
YDR077W (SED1)	0.00833	HEM13	1 1
YGR144W (THI4)	0.00833	THI4	1 1
YLL050C (COF1)	0.00833	ACT1	1 1
YLR335W (NUP2)	0.00833	HSP10	1 1
YBR052C	0.00833	PST2	1 1
YLR229C (CDC42)	0.01659	RDI1	1 2
YDR032C (PST2)	0.01659	PST2	1 2
YNR032W (PPG1)	0.02478	HSC82	1 3

Yeast Two Hybrid - Ito (core) (449 categories)

Category	p-value	In Category from Cluster	k f
YNL189W (SRP1)	5.351e-06	RIB3 HSP31 THI4 TDH3 HSP10 YPL088W	6 55
YLR267W (BOP2)	0.00833	GDH3	1 1
YOR020C (HSP10)	0.00833	HSP10	1 1
YPL088W	0.00833	YPL088W	1 1
YGR144W (THI4)	0.00833	THI4	1 1

Yeast Two Hybrid - Ito (full) (1532 categories)

Category	p-value	In Category from Cluster	k f
YNL189W (SRP1)	5.41e-07	GDH3 HEM13 RIB3 HSP31 SEC53 THI4 TDH3 HSP10 YPL088W	9 121
YJR091C (JSN1)	0.007951	CYS3 HSP31 THI4 RPS5 ZWF1 PFY1 YPL088W	7 279
YPR001W (CIT3)	0.00833	SSA4	1 1
YNL173C (MDG1)	0.00833	HSP10	1 1
YIL118W (RHO3)	0.00833	RTC3	1 1

YJL190C (RPS22A)	0.00833	INO1	1 1
YOR020C (HSP10)	0.00833	HSP10	1 1
YKR055W (RHO4)	0.00833	RDI1	1 1
YPL088W	0.00833	YPL088W	1 1
YLR343W	0.00833	SEC53	1 1
YMR010W	0.00833	HSP31	1 1
YMR101C (SRT1)	0.00833	CYS3	1 1
YOR226C (ISU2)	0.00833	CDC19	1 1
YLR267W (BOP2)	0.01659	GDH3	1 2
YNL176C	0.01659	RDI1	1 2
YGR144W (THI4)	0.01659	THI4	1 2
YCL043C (PDI1)	0.01659	TAL1	1 2
YOR110W (TFC7)	0.01659	PGK1	1 2
YBL066C (SEF1)	0.01659	BMH2	1 2
YBL056W (PTC3)	0.01659	HSP10	1 2
YNL116W	0.02478	THI4	1 3
YEL048C	0.03291	OM45	1 4

Synthetic Genetic Array Analysis (8 categories)

Category p-value In Category from Cluster k f

MDS Proteomics Complexes (493 categories)

Category	p-value	In Category from Cluster	k f
YBR055C (PRP6)	1.831e-06	CYS3 ARA1 UBA1 PGM2 ADE17 ERG10	6 46
YOR212W (STE4)	0.0001866	SEC53 PGM2 ADE17	3 14
YHR135C (YCK1)	0.0004568	PST2 UBA1 AHP1 ILV5	4 44
YBR136W (MEC1)	0.0006704	ACO1 STI1	2 5
YMR059W (SEN15)	0.001001	SEC53 UBA1 AHP1 ACO1	4 54
YBR109C (CMD1)	0.001105	PST2 UBA1 PGM2	3 25
YDL059C (RAD59)	0.001389	SEC53 UBA1 PGM2	3 27
YDR306C	0.001393	PGM2 STI1	2 7
YDR369C (XRS2)	0.001393	PST2 AHP1	2 7
YLR340W (RPP0)	0.002937	RTC3 AHP1	2 10
YGR223C	0.00833	ERG10	1 1
YIL007C	0.00833	ACO1	1 1
YOL062C (APM4)	0.00833	SEC53	1 1
YJL068C	0.00833	TAL1	1 1

YPL026C (SKS1)	0.00833	ERG10	1 1
YDL017W (CDC7)	0.008552	PST2 STI1	2 17
YJR035W (RAD26)	0.01293	SEC53 ACO1	2 21
YIL143C (SSL2)	0.01659	STI1	1 2
YGL058W (RAD6)	0.01659	UBA1	1 2
YPR178W (PRP4)	0.01659	STI1	1 2
YIR034C (LYS1)	0.02478	TAL1	1 3
YNL053W (MSG5)	0.02478	TAL1	1 3
YJL092W (HPR5)	0.02478	SEC53	1 3
YML112W (CTK3)	0.02478	UBA1	1 3
YKL210W (UBA1)	0.02478	STI1	1 3
YMR199W (CLN1)	0.02478	PGM2	1 3
YDR480W (DIG2)	0.02478	ACO1	1 3
YPL149W (APG5)	0.02478	CYS3	1 3
YBR155W (CNS1)	0.02478	ILV5	1 3
YGL090W (LIF1)	0.03291	AHP1	1 4
YER066C-A	0.03291	STI1	1 4
YMR049C (ERB1)	0.03956	SEC53 ACO1	2 38
YMR022W (QRI8)	0.04097	AHP1	1 5
YLR262C (YPT6)	0.04097	ACO1	1 5
YGL115W (SNF4)	0.04097	PST2	1 5
YOL006C (TOP1)	0.04097	ACO1	1 5
YDR227W (SIR4)	0.04097	SEC53	1 5
YDR092W (UBC13)	0.04097	UBA1	1 5
YAR007C (RFA1)	0.04097	ACO1	1 5
YML064C (TEM1)	0.04148	PST2 SEC53	2 39
YPR015C	0.04897	PGM2	1 6
YNL312W (RFA2)	0.04897	AHP1	1 6
YDR499W (LCD1)	0.04897	ILV5	1 6

Cellzome Complexes (459 categories)

Category	p-value	In Category from Cluster	k	f
YAL029C (MYO4)	2.03e-06	ARX1 ACT1 HSC82 ADH1	4	12
YGR123C (PPT1)	0.0002033	HSC82 HSP82	2	3
YDL042C (SIR2)	0.001393	TDH3 ADH1	2	7
YAL059W (ECM1)	0.001847	HSC82 ADH1	2	8
YOR244W (ESA1)	0.002937	ACT1 ADH1	2	10
YBR114W (RAD16)	0.003571	TDH3 ADH1	2	11
YNL127W	0.00501	HSC82 ADH1	2	13
YGL009C (LEU1)	0.01659	ADH1	1	2
YFR021W (AUT10)	0.01659	ADH1	1	2
YBR117C (TKL2)	0.01659	TKL1	1	2

YAR044W (OSH1)	0.01659	TDH3	1 2
YOL135C (MED7)	0.02093	PGK1 ADH1	2 27
YEL031W (SPF1)	0.02478	PGK1	1 3
YNL138W (SRV2)	0.02478	ACT1	1 3
YDR164C (SEC1)	0.02478	ADH1	1 3
YCR012W (PGK1)	0.02478	PGK1	1 3
YBR267W	0.02478	ARX1	1 3
YOR304W (ISW2)	0.02478	ADH1	1 3
YMR300C (ADE4)	0.02478	CYS3	1 3
YER036C (KRE30)	0.03291	ARX1	1 4
YJL005W (CYR1)	0.03291	ACT1	1 4
YDR075W (PPH3)	0.03291	TDH3	1 4
YBR058C (UBP14)	0.03291	ADH1	1 4
YPR180W (AOS1)	0.03291	ADH1	1 4
YHR170W (NMD3)	0.04097	ARX1	1 5
YPL106C (SSE1)	0.04097	TSA1	1 5
YGL240W (DOC1)	0.04097	ACT1	1 5
YOR056C (NOB1)	0.04097	ADH1	1 5
YBR031W (RPL4A)	0.04148	ARX1 RPL10	2 39
YOR014W (RTS1)	0.04897	TDH3	1 6
YML126C (ERG13)	0.04897	ACT1	1 6
YHR023W (MYO1)	0.04897	ACT1	1 6
YAL034C (FUN19)	0.04897	ADH1	1 6

Proteome Localization--Observed (11 categories)

Category	p-value	In Category from Cluster	k	f
cyto	5.501e-05	CYS3 CDC19 GDH3 ADE1 RIB5 PGK1 HEM13 SSA4 TDH3 GRE3 INO1 RPS5 RPL10 AHP1 TAL1 TSA1 PGM2 ADE17 HSC82 ZWF1 ADH1 YPL088W HSP82 TKL1	24	1321
mixed	0.01659	TPM2	1	2
mixed (cyto / ER)	0.02862	PRE7 PST2 HSP31	3	80

Proteome Localization--Predicted+Observed (4 categories)

Category	p-value	In Category from Cluster	k	f
cyt	1.968e-05	CYS3 CDC19 GDH3 ADE1 PRE7 ARA1 RIB5 PGK1 RDI1 THI13 HEM13 BMH2 EFT2 RIB3 SSA4 ACT1 SEC53 HXK2 TDH3 RPS0A RTC3 GRE3 TPM2 INO1 RPS5 UBA1 RPL10 AHP1 TAL1 TSA1 PGM2 ADE17 HSC82 ZWF1 ADH1 STI1 PFY1 RPS12 ERG10 YPL088W HSP82 TKL1	42	3195

Deletions Consortium (Essentiality, Morphology) (11 categories)

Category	p-value	In Category from Cluster	k	f
essential	0.006312	CDC19 PRE7 RIB5 PDI1 PGK1 HEM13 RIB3 ACT1 SEC53 RPS5 UBA1 RPL10 HSP60 ILV5 HSP10 PFY1 ERG10	17	1099

Yeast Fitness Data (1 category)

Category p-value In Category from Cluster k f

Published Complexes (7 categories)

Category	p-value	In Category from Cluster	k	f
Andersen et al. (2002) - Curr Bio 12:1-	0.000396	PDI1 ACT1 RPS0A ATP2 RPS5 HSP60 RPS12	7	165
Harnicharnpai et al. (2001) - Mol Cell 8:505-	0.03224	TDH3 RPL10	2	34

A tab-delimited version of the results can be downloaded [here](#). Note: This link will expire in 3 hours.

FunSpec was created by Jorg Grigull, Naveed Mohammad and Mark Robinson.

Table S5. CGD Gene Ontology Term Finder analysis of *C. albicans* yeast-to-hypha differentially abundant proteins identified: a) analysis of processes and b) analysis of functions.

Results in Table Form. Genes in the table below are listed for GO terms to which they are directly annotated as well as parents of those GO terms.

Background gene set: Default

6435 genes based on the following filtering criteria:

Annotations: Default

Annotation Source(s) included: CGD, AWG

Annotation Method(s) included: computational, high-throughput, manually curated

Evidence Code(s) included: IGC, RCA, ND, ISM, NAS, ISO, TAS, IGI, ISA, IC, IDA, ISS, IEP, IPI, IEA, IMP

Results with a corrected P-value <0.1 are listed.

Table S5.a) CGD Gene Ontology Term Finder analysis of processes: a.1) results from the analysis of *C. albicans* proteins detected as more abundant in hyphal cells

Results in Table Form for top 25 hits

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
hexose catabolic process AmiGO	5 out of 30 genes, 16.7%	35 out of 6435 background genes, 0.5%	0.00010	0.00%	ADH1 , GRE3 , HXK2 , PGM2 , TAL1
protein folding AmiGO	6 out of 30 genes, 20.0%	67 out of 6435 background genes, 1.0%	0.00011	0.00%	HSP60 , HSP70 , HSP90 , PDI1 , STI1 , orf19.7215.3

alcohol metabolic process AmiGO	8 out of 30 genes, 26.7%	171 out of 6435 background genes, 2.7%	0.00016	0.00%	ADH1 , BMH1 , ERG10 , GRE3 , HXK2 , INO1 , PGM2 , TAL1
protein refolding AmiGO	4 out of 30 genes, 13.3%	18 out of 6435 background genes, 0.3%	0.00025	0.00%	HSP60 , HSP70 , HSP90 , orf19.7215.3
monosaccharide catabolic process AmiGO	5 out of 30 genes, 16.7%	43 out of 6435 background genes, 0.7%	0.00029	0.00%	ADH1 , GRE3 , HXK2 , PGM2 , TAL1
alcohol catabolic process AmiGO	5 out of 30 genes, 16.7%	46 out of 6435 background genes, 0.7%	0.00041	0.00%	ADH1 , GRE3 , HXK2 , PGM2 , TAL1
monosaccharide metabolic process AmiGO	6 out of 30 genes, 20.0%	88 out of 6435 background genes, 1.4%	0.00056	0.00%	ADH1 , BMH1 , GRE3 , HXK2 , PGM2 , TAL1
metabolic process AmiGO	25 out of 30 genes, 83.3%	2679 out of 6435 background genes, 41.6%	0.00074	0.00%	AAT1 , ACT1 , ADH1 , BMH1 , CYS3 , ERG10 , GRE3 , HEM13 , HSP60 , HSP70 , HSP90 , HXK2 , INO1 , PDI1 , PGM2 , RIB5 , RPL10 , RPS5 , STI1 , TAL1 , TSA1 , UBA1 , YST1 , orf19.1862 , orf19.7215.3
carbohydrate catabolic process AmiGO	5 out of 30 genes, 16.7%	54 out of 6435 background genes, 0.8%	0.00093	0.00%	ADH1 , GRE3 , HXK2 , PGM2 , TAL1
anatomical structure formation AmiGO	10 out of 30 genes, 33.3%	388 out of 6435 background genes, 6.0%	0.00128	0.00%	ACT1 , BMH1 , HSP60 , HSP70 , HSP90 , RPL10 , STI1 , TPM2 , YST1 , orf19.7215.3
hexose metabolic process AmiGO	5 out of 30 genes, 16.7%	61 out of 6435 background genes, 0.9%	0.00172	0.00%	ADH1 , GRE3 , HXK2 , PGM2 , TAL1

cellular component assembly AmiGO	9 out of 30 genes, 30.0%	341 out of 6435 background genes, 5.3%	0.00354	0.00%	ACT1 , HSP60 , HSP70 , HSP90 , RPL10 , STI1 , TPM2 , YST1 , orf19.7215.3
macromolecular complex subunit organization AmiGO	9 out of 30 genes, 30.0%	341 out of 6435 background genes, 5.3%	0.00354	0.00%	HSP60 , HSP70 , HSP90 , PFY1 , RPL10 , STI1 , TPM2 , YST1 , orf19.7215.3
cellular metabolic process AmiGO	23 out of 30 genes, 76.7%	2547 out of 6435 background genes, 39.6%	0.00888	0.14%	AAT1 , ACT1 , ADH1 , BMH1 , CYS3 , ERG10 , HEM13 , HSP60 , HSP70 , HSP90 , HXK2 , PDI1 , PGM2 , RIB5 , RPL10 , RPS5 , STI1 , TAL1 , TSA1 , UBA1 , YST1 , orf19.1862 , orf19.7215.3
glucose metabolic process AmiGO	4 out of 30 genes, 13.3%	43 out of 6435 background genes, 0.7%	0.00935	0.13%	ADH1 , HXK2 , PGM2 , TAL1
cellular component biogenesis AmiGO	11 out of 30 genes, 36.7%	605 out of 6435 background genes, 9.4%	0.01078	0.12%	ACT1 , BMH1 , HSP60 , HSP70 , HSP90 , RPL10 , RPS5 , STI1 , TPM2 , YST1 , orf19.7215.3
cellular process AmiGO	27 out of 30 genes, 90.0%	3639 out of 6435 background genes, 56.6%	0.01767	0.24%	AAT1 , ACT1 , ADH1 , BMH1 , CYS3 , ERG10 , HEM13 , HSP60 , HSP70 , HSP90 , HXK2 , PDI1 , PFY1 , PGM2 , PMM1 , RDI1 , RIB5 , RPL10 , RPS5 , STI1 , TAL1 , TPM2 , TSA1 , UBA1 , YST1 , orf19.1862 , orf19.7215.3
macromolecular complex assembly AmiGO	7 out of 30 genes, 23.3%	260 out of 6435 background genes, 4.0%	0.03335	0.44%	HSP60 , HSP70 , HSP90 , RPL10 , STI1 , YST1 , orf19.7215.3
regulation of biological quality AmiGO	7 out of 30 genes, 23.3%	274 out of 6435 background genes, 4.3%	0.04622	0.42%	ADH1 , BMH1 , HSP60 , HSP70 , HXK2 , PGM2 , TPM2
galactose catabolic process AmiGO	2 out of 30 genes, 6.7%	5 out of 6435 background genes,	0.04656	0.40%	GRE3 , PGM2

		0.1%			
glucose catabolic process AmiGO	3 out of 30 genes, 10.0%	28 out of 6435 background genes, 0.4%	0.06198	0.57%	ADH1 , HXK2 , TAL1
protein complex assembly AmiGO	5 out of 30 genes, 16.7%	131 out of 6435 background genes, 2.0%	0.06876	0.55%	HSP60 , HSP70 , HSP90 , STI1 , orf19.7215.3
protein complex biogenesis AmiGO	5 out of 30 genes, 16.7%	131 out of 6435 background genes, 2.0%	0.06876	0.52%	HSP60 , HSP70 , HSP90 , STI1 , orf19.7215.3
actin polymerization or depolymerization AmiGO	2 out of 30 genes, 6.7%	6 out of 6435 background genes, 0.1%	0.06964	0.50%	PFY1 , TPM2
primary metabolic process AmiGO	21 out of 30 genes, 70.0%	2419 out of 6435 background genes, 37.6%	0.07083	0.48%	AAT1 , ACT1 , ADH1 , BMH1 , CYS3 , ERG10 , GRE3 , HSP60 , HSP70 , HSP90 , HXK2 , PDI1 , PGM2 , RPL10 , RPS5 , STI1 , TAL1 , UBA1 , YST1 , orf19.1862 , orf19.7215.3

Results in Table Form for hitsNo. 26

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
cellular carbohydrate catabolic process AmiGO	3 out of 30 genes, 10.0%	30 out of 6435 background genes, 0.5%	0.07633	0.85%	ADH1, TAL1, HXK2

Table S5.a) CGD Gene Ontology Term Finder analysis of processes: a.2) results from the analysis of *C. albicans* proteins detected as less abundant in hyphal cells

Results in Table Form for top 25 hits

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
hexose catabolic process AmiGO	6 out of 30 genes, 20.0%	35 out of 6435 background genes, 0.5%	1.50e-06	0.00%	CDC19 , PGK1 , SOU1 , TDH3 , TKL1 , ZWF1
monosaccharide catabolic process AmiGO	6 out of 30 genes, 20.0%	43 out of 6435 background genes, 0.7%	5.49e-06	0.00%	CDC19 , PGK1 , SOU1 , TDH3 , TKL1 , ZWF1
alcohol catabolic process AmiGO	6 out of 30 genes, 20.0%	46 out of 6435 background genes, 0.7%	8.36e-06	0.00%	CDC19 , PGK1 , SOU1 , TDH3 , TKL1 , ZWF1
carbohydrate catabolic process AmiGO	6 out of 30 genes, 20.0%	54 out of 6435 background genes, 0.8%	2.24e-05	0.00%	CDC19 , PGK1 , SOU1 , TDH3 , TKL1 , ZWF1
glucose catabolic process AmiGO	5 out of 30 genes, 16.7%	28 out of 6435 background genes, 0.4%	2.37e-05	0.00%	CDC19 , PGK1 , TDH3 , TKL1 , ZWF1
cellular carbohydrate catabolic process AmiGO	5 out of 30 genes, 16.7%	30 out of 6435 background genes, 0.5%	3.42e-05	0.00%	CDC19 , PGK1 , TDH3 , TKL1 , ZWF1

hexose metabolic process AmiGO	6 out of 30 genes, 20.0%	61 out of 6435 background genes, 0.9%	4.72e-05	0.00%	CDC19 , PGK1 , SOU1 , TDH3 , TKL1 , ZWF1
glucose metabolic process AmiGO	5 out of 30 genes, 16.7%	43 out of 6435 background genes, 0.7%	0.00022	0.00%	CDC19 , PGK1 , TDH3 , TKL1 , ZWF1
positive regulation of defense response AmiGO	4 out of 30 genes, 13.3%	20 out of 6435 background genes, 0.3%	0.00029	0.00%	ACO1 , CDC19 , PGK1 , TDH3
induction by symbiont of host defense response AmiGO	4 out of 30 genes, 13.3%	20 out of 6435 background genes, 0.3%	0.00029	0.00%	ACO1 , CDC19 , PGK1 , TDH3
induction by organism of defense response of other organism during symbiotic interaction AmiGO	4 out of 30 genes, 13.3%	20 out of 6435 background genes, 0.3%	0.00029	0.00%	ACO1 , CDC19 , PGK1 , TDH3
positive regulation by symbiont of host defense response AmiGO	4 out of 30 genes, 13.3%	20 out of 6435 background genes, 0.3%	0.00029	0.00%	ACO1 , CDC19 , PGK1 , TDH3
positive regulation by organism of defense response of other organism during symbiotic interaction AmiGO	4 out of 30 genes, 13.3%	20 out of 6435 background genes, 0.3%	0.00029	0.00%	ACO1 , CDC19 , PGK1 , TDH3
monosaccharide metabolic process AmiGO	6 out of 30 genes, 20.0%	88 out of 6435 background genes, 1.4%	0.00042	0.00%	CDC19 , PGK1 , SOU1 , TDH3 , TKL1 , ZWF1
regulation of defense response AmiGO	4 out of 30 genes, 13.3%	23 out of 6435 background genes, 0.4%	0.00053	0.00%	ACO1 , CDC19 , PGK1 , TDH3

positive regulation of response to stimulus AmiGO	4 out of 30 genes, 13.3%	23 out of 6435 background genes, 0.4%	0.00053	0.00%	ACO1 , CDC19 , PGK1 , TDH3
modulation by symbiont of host defense response AmiGO	4 out of 30 genes, 13.3%	23 out of 6435 background genes, 0.4%	0.00053	0.00%	ACO1 , CDC19 , PGK1 , TDH3
modulation by organism of defense response of other organism during symbiotic interaction AmiGO	4 out of 30 genes, 13.3%	23 out of 6435 background genes, 0.4%	0.00053	0.00%	ACO1 , CDC19 , PGK1 , TDH3
modification by symbiont of host morphology or physiology AmiGO	4 out of 30 genes, 13.3%	25 out of 6435 background genes, 0.4%	0.00076	0.00%	ACO1 , CDC19 , PGK1 , TDH3
modification of morphology or physiology of other organism during symbiotic interaction AmiGO	4 out of 30 genes, 13.3%	25 out of 6435 background genes, 0.4%	0.00076	0.00%	ACO1 , CDC19 , PGK1 , TDH3
cellular metabolic process AmiGO	24 out of 30 genes, 80.0%	2547 out of 6435 background genes, 39.6%	0.00121	0.00%	ACO1 , ADE1 , ADE17 , ARA1 , ATP2 , CDC19 , CSH1 , EFT2 , GDH3 , ILV5 , PDI1 , PGK1 , RIB3 , RPL10 , RPS12 , SOU1 , TDH3 , THI13 , THI4 , TKL1 , YST1 , ZWF1 , orf19.1862 , orf19.2755
regulation of response to stress AmiGO	4 out of 30 genes, 13.3%	30 out of 6435 background genes, 0.5%	0.00162	0.00%	ACO1 , CDC19 , PGK1 , TDH3
regulation of response to stimulus AmiGO	4 out of 30 genes, 13.3%	35 out of 6435 background genes, 0.5%	0.00305	0.00%	ACO1 , CDC19 , PGK1 , TDH3

vitamin metabolic process AmiGO	5 out of 30 genes, 16.7%	74 out of 6435 background genes, 1.1%	0.00335	0.00%	RIB3 , THI13 , THI4 , TKL1 , ZWF1
water-soluble vitamin metabolic process AmiGO	5 out of 30 genes, 16.7%	74 out of 6435 background genes, 1.1%	0.00335	0.00%	RIB3 , THI13 , THI4 , TKL1 , ZWF1

Results in Table Form for hits No. 26 - 50

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
metabolic process AmiGO	24 out of 30 genes, 80.0%	2679 out of 6435 background genes, 41.6%	0.00339	0.00%	orf19.1862, ARA1, orf19.2755, SOU1, RPL10, CDC19, PGK1, CSH1, GDH3, ZWF1, ADE17, TKL1, PDI1, RIB3, ATP2, EFT2, THI4, ACO1, RPS12, TDH3, YST1, THI13, ADE1, ILV5
response to host defenses AmiGO	4 out of 30 genes, 13.3%	36 out of 6435 background genes, 0.6%	0.00342	0.00%	CDC19, PGK1, ACO1, TDH3
response to host AmiGO	4 out of 30 genes, 13.3%	36 out of 6435 background genes, 0.6%	0.00342	0.00%	CDC19, PGK1, ACO1, TDH3
response to defenses of other organism during symbiotic interaction AmiGO	4 out of 30 genes, 13.3%	39 out of 6435 background genes, 0.6%	0.00473	0.00%	CDC19, PGK1, ACO1, TDH3
response to other organism	4 out of 30	40 out of 6435	0.00523	0.00%	CDC19, PGK1, ACO1, TDH3

AmiGO	genes, 13.3%	background genes, 0.6%			
glycolysis AmiGO	3 out of 30 genes, 10.0%	14 out of 6435 background genes, 0.2%	0.00539	0.00%	CDC19, PGK1, TDH3
nucleoside phosphate metabolic process AmiGO	5 out of 30 genes, 16.7%	93 out of 6435 background genes, 1.4%	0.01017	0.00%	ZWF1, ADE17, TKL1, ATP2, ADE1
nucleotide metabolic process AmiGO	5 out of 30 genes, 16.7%	93 out of 6435 background genes, 1.4%	0.01017	0.00%	ZWF1, ADE17, TKL1, ATP2, ADE1
carbohydrate metabolic process AmiGO	7 out of 30 genes, 23.3%	228 out of 6435 background genes, 3.5%	0.01090	0.00%	ARA1, SOU1, CDC19, PGK1, ZWF1, TKL1, TDH3
cellular nitrogen compound metabolic process AmiGO	7 out of 30 genes, 23.3%	236 out of 6435 background genes, 3.7%	0.01357	0.00%	GDH3, ZWF1, TKL1, RIB3, ACO1, ADE1, ILV5
carboxylic acid metabolic process AmiGO	8 out of 30 genes, 26.7%	327 out of 6435 background genes, 5.1%	0.01504	0.00%	ARA1, SOU1, CDC19, PGK1, GDH3, ACO1, TDH3, ILV5
oxoacid metabolic process AmiGO	8 out of 30 genes, 26.7%	327 out of 6435 background genes, 5.1%	0.01504	0.00%	ARA1, SOU1, CDC19, PGK1, GDH3, ACO1, TDH3, ILV5
organic acid metabolic process AmiGO	8 out of 30 genes, 26.7%	327 out of 6435 background genes, 5.1%	0.01504	0.00%	ARA1, SOU1, CDC19, PGK1, GDH3, ACO1, TDH3, ILV5
generation of precursor metabolites and energy AmiGO	6 out of 30 genes, 20.0%	168 out of 6435 background genes,	0.01717	0.00%	CDC19, PGK1, RIB3, ATP2, ACO1, TDH3

		2.6%			
alcohol metabolic process AmiGO	6 out of 30 genes, 20.0%	171 out of 6435 background genes, 2.7%	0.01894	0.00%	SOU1, CDC19, PGK1, ZWF1, TKL1, TDH3
cellular ketone metabolic process AmiGO	8 out of 30 genes, 26.7%	339 out of 6435 background genes, 5.3%	0.01938	0.00%	ARA1, SOU1, CDC19, PGK1, GDH3, ACO1, TDH3, ILV5
pyruvate metabolic process AmiGO	3 out of 30 genes, 10.0%	22 out of 6435 background genes, 0.3%	0.02223	0.00%	CDC19, PGK1, TDH3
cellular biosynthetic process AmiGO	15 out of 30 genes, 50.0%	1240 out of 6435 background genes, 19.3%	0.02438	0.00%	RPL10, PGK1, GDH3, ADE17, RIB3, ATP2, EFT2, THI4, ACO1, RPS12, TDH3, YST1, THI13, ADE1, ILV5
biosynthetic process AmiGO	15 out of 30 genes, 50.0%	1254 out of 6435 background genes, 19.5%	0.02783	0.00%	RPL10, PGK1, GDH3, ADE17, RIB3, ATP2, EFT2, THI4, ACO1, RPS12, TDH3, YST1, THI13, ADE1, ILV5
response to biotic stimulus AmiGO	4 out of 30 genes, 13.3%	61 out of 6435 background genes, 0.9%	0.02795	0.00%	CDC19, PGK1, ACO1, TDH3
monocarboxylic acid metabolic process AmiGO	5 out of 30 genes, 16.7%	120 out of 6435 background genes, 1.9%	0.03418	0.00%	SOU1, CDC19, PGK1, ACO1, TDH3
cell-matrix adhesion AmiGO	2 out of 30 genes, 6.7%	5 out of 6435 background genes, 0.1%	0.03487	0.09%	CSH1, TDH3
nucleobase, nucleoside and nucleotide metabolic process AmiGO	5 out of 30 genes, 16.7%	122 out of 6435 background genes, 1.9%	0.03693	0.08%	ZWF1, ADE17, TKL1, ATP2, ADE1

purine ribonucleotide biosynthetic process AmiGO	3 out of 30 genes, 10.0%	28 out of 6435 background genes, 0.4%	0.04641	0.08%	ADE17, ATP2, ADE1
thiamin and derivative biosynthetic process AmiGO	2 out of 30 genes, 6.7%	6 out of 6435 background genes, 0.1%	0.05215	0.12%	THI4, THI13

Results in Table Form for hits No. 51 - 67

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
thiamin biosynthetic process	2 out of 30 genes, 6.7%	6 out of 6435 background genes, 0.1%	0.05215	0.12%	THI4:THI13
primary metabolic process	21 out of 30 genes, 70.0%	2419 out of 6435 background genes, 37.6%	0.05304	0.12%	orf19.1862, ARA1, orf19.2755, SOU1, RPL10, CDC19, PGK1, GDH3, ZWF1, ADE17, TKL1, PDI1, ATP2, EFT2, THI4, ACO1, RPS12, TDH3, YST1, ADE1, ILV5
ribonucleotide biosynthetic process	3 out of 30 genes, 10.0%	31 out of 6435 background genes, 0.5%	0.06308	0.11%	ADE17, ATP2, ADE1
mitochondrial genome maintenance	3 out of 30 genes, 10.0%	32 out of 6435 background genes, 0.5%	0.06939	0.11%	THI4, ACO1, ILV5
purine nucleotide biosynthetic process	3 out of 30 genes, 10.0%	32 out of 6435 background genes, 0.5%	0.06939	0.11%	ADE17, ATP2, ADE1

purine ribonucleotide metabolic process	3 out of 30 genes, 10.0%	32 out of 6435 background genes, 0.5%	0.06939	0.11%	ADE17, ATP2, ADE1
heterocycle metabolic process	5 out of 30 genes, 16.7%	141 out of 6435 background genes, 2.2%	0.07240	0.11%	ADE17, ATP2, THI4, THI13, ADE1
cell-substrate adhesion	2 out of 30 genes, 6.7%	7 out of 6435 background genes, 0.1%	0.07281	0.14%	CSH1, TDH3
thiamin and derivative metabolic process	2 out of 30 genes, 6.7%	7 out of 6435 background genes, 0.1%	0.07281	0.14%	THI4, THI13
pentose-phosphate shunt	2 out of 30 genes, 6.7%	7 out of 6435 background genes, 0.1%	0.07281	0.13%	ZWF1:TKL1
thiamin metabolic process	2 out of 30 genes, 6.7%	7 out of 6435 background genes, 0.1%	0.07281	0.13%	THI4, THI13
purine nucleotide metabolic process	3 out of 30 genes, 10.0%	35 out of 6435 background genes, 0.5%	0.09071	0.13%	ADE17, ATP2, ADE1
ribonucleotide metabolic process	3 out of 30 genes, 10.0%	35 out of 6435 background genes, 0.5%	0.09071	0.13%	ADE17, ATP2, ADE1
cellular catabolic process	8 out of 30 genes, 26.7%	428 out of 6435 background genes, 6.7%	0.09608	0.12%	orf19.2755, SOU1, CDC19, PGK1, ZWF1, TKL1, ACO1, TDH3
IMP biosynthetic process	2 out of 30	8 out of 6435	0.09679	0.15%	ADE17, ADE1

	genes, 6.7%	background genes, 0.1%			
‘de novo’ IMP biosynthetic process	2 out of 30 genes, 6.7%	8 out of 6435 background genes, 0.1%	0.09679	0.15%	ADE17, ADE1
NADPH regeneration	2 out of 30 genes, 6.7%	8 out of 6435 background genes, 0.1%	0.09679	0.15%	ZWF1, TKL1

Table S5.a) CGD Gene Ontology Term Finder analysis of processes: a.3) results from the analysis of all *C. albicans* differentially abundant proteins identified

Results in Table Form for top 25 hits

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
hexose catabolic process AmiGO	11 out of 56 genes, 19.6%	35 out of 6435 background genes, 0.5%	8.59e-13	0.00%	ADH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
monosaccharide catabolic process AmiGO	11 out of 56 genes, 19.6%	43 out of 6435 background genes, 0.7%	1.12e-11	0.00%	ADH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1

alcohol catabolic process AmiGO	11 out of 56 genes, 19.6%	46 out of 6435 background genes, 0.7%	2.55e-11	0.00%	ADH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
carbohydrate catabolic process AmiGO	11 out of 56 genes, 19.6%	54 out of 6435 background genes, 0.8%	1.74e-10	0.00%	ADH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
hexose metabolic process AmiGO	11 out of 56 genes, 19.6%	61 out of 6435 background genes, 0.9%	7.27e-10	0.00%	ADH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
monosaccharide metabolic process AmiGO	12 out of 56 genes, 21.4%	88 out of 6435 background genes, 1.4%	2.13e-09	0.00%	ADH1 , BMH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
glucose catabolic process AmiGO	8 out of 56 genes, 14.3%	28 out of 6435 background genes, 0.4%	1.66e-08	0.00%	ADH1 , CDC19 , HXK2 , PGK1 , TAL1 , TDH3 , TKL1 , ZWF1
glucose metabolic process AmiGO	9 out of 56 genes, 16.1%	43 out of 6435 background genes, 0.7%	2.06e-08	0.00%	ADH1 , CDC19 , HXK2 , PGK1 , PGM2 , TAL1 , TDH3 , TKL1 , ZWF1
cellular carbohydrate catabolic process AmiGO	8 out of 56 genes, 14.3%	30 out of 6435 background genes, 0.5%	3.09e-08	0.00%	ADH1 , CDC19 , HXK2 , PGK1 , TAL1 , TDH3 , TKL1 , ZWF1
alcohol metabolic process AmiGO	14 out of 56 genes, 25.0%	171 out of 6435 background genes, 2.7%	3.56e-08	0.00%	ADH1 , BMH1 , CDC19 , ERG10 , GRE3 , HXK2 , INO1 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
metabolic process AmiGO	45 out of 56 genes, 80.4%	2679 out of 6435 background genes, 41.6%	1.00e-06	0.00%	AAT1 , ACO1 , ACT1 , ADE1 , ADE17 , ADH1 , ARA1 , ATP2 , BMH1 , CDC19 , CSH1 , CYS3 , EFT2 , ERG10 , GDH3 , GRE3 , HEM13 , HSP60 , HSP70 , HSP90 , HXK2 , ILV5 , INO1 , PDI1 , PGK1 , PGM2 , RIB3 , RIB5 , RPL10 ,

					RPS12 , RPS5 , SOU1 , STI1 , TAL1 , TDH3 , THI13 , THI4 , TKL1 , TSA1 , UBA1 , YST1 , ZWF1 , orf19.1862 , orf19.2755 , orf19.7215.3
positive regulation of defense response AmiGO	6 out of 56 genes, 10.7%	20 out of 6435 background genes, 0.3%	3.63e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
induction by symbiont of host defense response AmiGO	6 out of 56 genes, 10.7%	20 out of 6435 background genes, 0.3%	3.63e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
induction by organism of defense response of other organism during symbiotic interaction AmiGO	6 out of 56 genes, 10.7%	20 out of 6435 background genes, 0.3%	3.63e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
positive regulation by symbiont of host defense response AmiGO	6 out of 56 genes, 10.7%	20 out of 6435 background genes, 0.3%	3.63e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
positive regulation by organism of defense response of other organism during symbiotic interaction AmiGO	6 out of 56 genes, 10.7%	20 out of 6435 background genes, 0.3%	3.63e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
cellular metabolic process AmiGO	43 out of 56 genes, 76.8%	2547 out of 6435 background genes, 39.6%	4.61e-06	0.00%	AAT1 , ACO1 , ACT1 , ADE1 , ADE17 , ADH1 , ARA1 , ATP2 , BMH1 , CDC19 , CSH1 , CYS3 , EFT2 , ERG10 , GDH3 , HEM13 , HSP60 , HSP70 , HSP90 , HXK2 , ILV5 , PDI1 , PGK1 , PGM2 , RIB3 , RIB5 , RPL10 , RPS12 , RPS5 , SOU1 , STI1 , TAL1 , TDH3 , THI13 , THI4 , TKL1 , TSA1 , UBA1 , YST1 , ZWF1 , orf19.1862 , orf19.2755 , orf19.7215.3

regulation of defense response AmiGO	6 out of 56 genes, 10.7%	23 out of 6435 background genes, 0.4%	9.28e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
positive regulation of response to stimulus AmiGO	6 out of 56 genes, 10.7%	23 out of 6435 background genes, 0.4%	9.28e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
modulation by symbiont of host defense response AmiGO	6 out of 56 genes, 10.7%	23 out of 6435 background genes, 0.4%	9.28e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
modulation by organism of defense response of other organism during symbiotic interaction AmiGO	6 out of 56 genes, 10.7%	23 out of 6435 background genes, 0.4%	9.28e-06	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
carbohydrate metabolic process AmiGO	13 out of 56 genes, 23.2%	228 out of 6435 background genes, 3.5%	1.51e-05	0.00%	ADH1 , ARA1 , BMH1 , CDC19 , GRE3 , HXK2 , PGK1 , PGM2 , SOU1 , TAL1 , TDH3 , TKL1 , ZWF1
modification by symbiont of host morphology or physiology AmiGO	6 out of 56 genes, 10.7%	25 out of 6435 background genes, 0.4%	1.60e-05	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
modification of morphology or physiology of other organism during symbiotic interaction AmiGO	6 out of 56 genes, 10.7%	25 out of 6435 background genes, 0.4%	1.60e-05	0.00%	ACO1 , ADH1 , CDC19 , HSP70 , PGK1 , TDH3
glycolysis AmiGO	5 out of 56 genes, 8.9%	14 out of 6435 background genes, 0.2%	2.44e-05	0.00%	ADH1 , CDC19 , HXK2 , PGK1 , TDH3

Results in Table Form for hits No. 26 - 50

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
regulation of response to stress AmiGO	6 out of 56 genes, 10.7%	30 out of 6435 background genes, 0.5%	5.21e-05	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3
regulation of response to stimulus AmiGO	6 out of 56 genes, 10.7%	35 out of 6435 background genes, 0.5%	0.00013	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3
response to host defenses AmiGO	6 out of 56 genes, 10.7%	36 out of 6435 background genes, 0.6%	0.00016	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3
response to host AmiGO	6 out of 56 genes, 10.7%	36 out of 6435 background genes, 0.6%	0.00016	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3
cellular nitrogen compound metabolic process AmiGO	12 out of 56 genes, 21.4%	236 out of 6435 background genes, 3.7%	0.00018	0.00%	HEM13, AAT1, RIB5, TAL1, GDH3, ZWF1, TKL1, RIB3, ACO1, CYS3, ADE1, ILV5
response to defenses of other organism during symbiotic interaction AmiGO	6 out of 56 genes, 10.7%	39 out of 6435 background genes, 0.6%	0.00026	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3
response to other organism AmiGO	6 out of 56 genes, 10.7%	40 out of 6435 background genes, 0.6%	0.00031	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3

generation of precursor metabolites and energy AmiGO	10 out of 56 genes, 17.9%	168 out of 6435 background genes, 2.6%	0.00044	0.00%	PGM2, BMH1, CDC19, PGK1, ADH1, RIB3, HXK2, ATP2, ACO1, TDH3
cellular carbohydrate metabolic process AmiGO	10 out of 56 genes, 17.9%	175 out of 6435 background genes, 2.7%	0.00064	0.00%	PGM2, BMH1, CDC19, PGK1, ADH1, TAL1, ZWF1, TKL1, HXK2, TDH3
cellular process AmiGO	48 out of 56 genes, 85.7%	3639 out of 6435 background genes, 56.6%	0.00088	0.00%	ERG10, orf19.1862, ARA1, orf19.2755, AHP1, HEM13, PGM2, SOU1, RPL10, PMM1, BMH1, STI1, AAT1, CDC19, PGK1, ADH1, RIB5, RPS5, TAL1, CSH1, GDH3, ZWF1, ADE17, HSP70, ACT1, PFY1, TKL1, PDI1, RIB3, HXK2, ATP2, EFT2, RDI1, THI4, ACO1, CYS3, TPM2, HSP90, RPS12, TDH3, YST1, HSP60, orf19.7215.3, THI13, TSA1, UBA1, ADE1, ILV5
regulation of biological quality AmiGO	12 out of 56 genes, 21.4%	274 out of 6435 background genes, 4.3%	0.00091	0.00%	AHP1, PGM2, BMH1, CDC19, PGK1, ADH1, HSP70, HXK2, ACO1, TPM2, TDH3, HSP60
vitamin metabolic process AmiGO	7 out of 56 genes, 12.5%	74 out of 6435 background genes, 1.1%	0.00092	0.00%	RIB5, TAL1, ZWF1, TKL1, RIB3, THI4, THI13
water-soluble vitamin metabolic process AmiGO	7 out of 56 genes, 12.5%	74 out of 6435 background genes, 1.1%	0.00092	0.00%	RIB5, TAL1, ZWF1, TKL1, RIB3, THI4, THI13
primary metabolic process AmiGO	38 out of 56 genes, 67.9%	2419 out of 6435 background genes, 37.6%	0.00125	0.00%	ERG10, orf19.1862, ARA1, orf19.2755, PGM2, SOU1, RPL10, BMH1, STI1, AAT1, CDC19, PGK1, ADH1, GRE3, RPS5, TAL1, GDH3, ZWF1, ADE17, HSP70, ACT1, TKL1, PDI1, HXK2, ATP2, EFT2, THI4, ACO1, CYS3, HSP90, RPS12, TDH3, YST1, HSP60, orf19.7215.3, UBA1, ADE1, ILV5

interaction with host AmiGO	7 out of 56 genes, 12.5%	85 out of 6435 background genes, 1.3%	0.00234	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3, TSA1
catabolic process AmiGO	15 out of 56 genes, 26.8%	486 out of 6435 background genes, 7.6%	0.00337	0.00%	orf19.2755, PGM2, SOU1, AAT1, CDC19, PGK1, ADH1, GRE3, TAL1, ZWF1, TKL1, HXK2, ACO1, TDH3, TSA1
response to biotic stimulus AmiGO	6 out of 56 genes, 10.7%	61 out of 6435 background genes, 0.9%	0.00395	0.00%	CDC19, PGK1, ADH1, HSP70, ACO1, TDH3
protein refolding AmiGO	4 out of 56 genes, 7.1%	18 out of 6435 background genes, 0.3%	0.00447	0.00%	HSP70, HSP90, HSP60, orf19.7215.3
symbiosis, encompassing mutualism through parasitism AmiGO	10 out of 56 genes, 17.9%	225 out of 6435 background genes, 3.5%	0.00607	0.00%	BMH1, CDC19, PGK1, ADH1, CSH1, HSP70, ACO1, HSP90, TDH3, TSA1
interspecies interaction between organisms AmiGO	10 out of 56 genes, 17.9%	226 out of 6435 background genes, 3.5%	0.00631	0.00%	BMH1, CDC19, PGK1, ADH1, CSH1, HSP70, ACO1, HSP90, TDH3, TSA1
pentose-phosphate shunt AmiGO	3 out of 56 genes, 5.4%	7 out of 6435 background genes, 0.1%	0.00663	0.00%	TAL1, ZWF1, TKL1
protein folding AmiGO	6 out of 56 genes, 10.7%	67 out of 6435 background genes, 1.0%	0.00683	0.04%	STI1, HSP70, PDI1, HSP90, HSP60, orf19.7215.3
NADPH regeneration AmiGO	3 out of 56 genes, 5.4%	8 out of 6435 background genes, 0.1%	0.01054	0.04%	TAL1, ZWF1, TKL1

response to stimulus AmiGO	20 out of 56 genes, 35.7%	919 out of 6435 background genes, 14.3%	0.01526	0.20%	CIP1, AHP1, BMH1, CDC19, PGK1, ADH1, GRE3, ZWF1, HSP70, ACT1, PFY1, HXK2, EFT2, THI4, ACO1, CYS3, HSP90, TDH3, TSA1, ADE1
cellular catabolic process AmiGO	13 out of 56 genes, 23.2%	428 out of 6435 background genes, 6.7%	0.01763	0.24%	orf19.2755, SOU1, AAT1, CDC19, PGK1, ADH1, TAL1, ZWF1, TKL1, HXK2, ACO1, TDH3, TSA1

Results in Table Form for hits No. 51 –58

Terms from the Process Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
nitrogen compound biosynthetic process	8 out of 56 genes, 14.3%	161 out of 6435 background genes, 2.5%	0.02063	0.31%	HEM13, RIB5, GDH3, RIB3, ACO1, CYS3, ADE1, ILV5
NADP metabolic process	3 out of 56 genes, 5.4%	10 out of 6435 background genes, 0.2%	0.02232	0.35%	TAL1, ZW1, TKL1
nucleoside phosphate metabolic process	6 out of 56 genes, 10.7%	93 out of 6435 background genes, 1.4%	0.04388	0.60%	TAL1, ZWF1, ADE17, TKL1, TP2, ADE1
nucleotide metabolic process	6 out of 56 genes, 10.7%	93 out of 6435 background genes, 1.4%	0.04388	0.59%	TAL1, ZWF1, ADE17, TKL1, TP2, ADE1
biosynthetic process	23 out of 56 genes, 41.1%	1254 out of 6435 background genes, 19.5%	0.04973	0.58%	ERG10, HEM13, PGM2, RPL10, BMH1, PGK1, RIB5, RPS5, GDH3, ADE17, RIB3, ATP2, EFT2, THI4, ACO1, CYS3, RPS12, TDH3, YST1, THI13, ADE1, INO1, ILV5

response to oxidative stress	6 out of 56 genes, 10.7%	100 out of 6435 background genes, 1.6%	0.06548	0.93%	CIP1, AHP1, GRE3, ZWF1, ACT1, TSA1
water-soluble vitamin biosynthetic process	4 out of 56 genes, 7.1%	38 out of 6435 background genes, 0.6%	0.09492	0.98%	RIB5, RIB3, THI4, THI13
vitamin biosynthetic process	4 out of 56 genes, 7.1%	38 out of 6435 background genes, 0.6%	0.09492	0.97%	RIB5, RIB3, THI4, THI13

Table S5.b) CGD Gene Ontology Term Finder analysis of functions: b.1) results from the analysis of *C. albicans* proteins detected as more abundant in hyphal cells

Terms from the Function Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
protein binding AmiGO	9 out of 30 genes, 30.0%	395 out of 6435 background genes, 6.1%	0.00163	2.00%	ADH1 , HSP60 , HSP70 , HSP90 , PFY1 , STI1 , TPM2 , TSA1 , orf19.7215.3
unfolded protein binding AmiGO	4 out of 30 genes, 13.3%	46 out of 6435 background genes, 0.7%	0.00175	1.00%	HSP60 , HSP70 , HSP90 , orf19.7215.3
isomerase activity AmiGO	4 out of 30 genes, 13.3%	53 out of 6435 background genes, 0.8%	0.00307	0.67%	INO1 , PDI1 , PGM2 , PMM1

intramolecular transferase activity, phosphotransferases AmiGO	2 out of 30 genes, 6.7%	6 out of 6435 background genes, 0.1%	0.00997	0.50%	PGM2 , PMM1
catalytic activity AmiGO	18 out of 30 genes, 60.0%	1848 out of 6435 background genes, 28.7%	0.01084	0.40%	AAT1 , ACT1 , ADH1 , CYS3 , ERG10 , GRE3 , HEM13 , HSP60 , HSP90 , HXK2 , INO1 , PDI1 , PGM2 , PMM1 , RIB5 , TAL1 , TSA1 , UBA1
intramolecular transferase activity AmiGO	2 out of 30 genes, 6.7%	15 out of 6435 background genes, 0.2%	0.06805	6.00%	PGM2 , PMM1
chaperone binding AmiGO	2 out of 30 genes, 6.7%	17 out of 6435 background genes, 0.3%	0.08763	6.00%	HSP60 , orf19.7215.3

Table S5.b) CGD Gene Ontology Term Finder analysis of functions: b.2) results from the analysis of *C. albicans* proteins detected as less abundant in hyphal cells

Terms from the Function Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
oxidoreductase activity AmiGO	9 out of 30 genes, 30.0%	298 out of 6435 background genes, 4.6%	0.00011	0.00%	AHP1 , ARA1 , CSH1 , GDH3 , ILV5 , PDI1 , SOU1 , TDH3 , ZWF1
oxidoreductase activity, acting on the CH-OH group of donors, NAD	5 out of 30 genes, 16.7%	59 out of 6435 background genes,	0.00013	0.00%	ARA1 , CSH1 , ILV5 , SOU1 , ZWF1

or NADP as acceptor AmiGO		0.9%			
oxidoreductase activity, acting on CH-OH group of donors AmiGO	5 out of 30 genes, 16.7%	69 out of 6435 background genes, 1.1%	0.00029	0.00%	ARA1 , CSH1 , ILV5 , SOU1 , ZWF1
catalytic activity AmiGO	20 out of 30 genes, 66.7%	1848 out of 6435 background genes, 28.7%	0.00036	0.00%	ACO1 , ADE1 , ADE17 , AHP1 , ARA1 , ATP2 , CDC19 , CSH1 , EFT2 , GDH3 , ILV5 , PDI1 , PGK1 , RIB3 , SOU1 , TDH3 , TKL1 , ZWF1 , orf19.2755 , orf19.7152

Table S5.b) CGD Gene Ontology Term Finder analysis of functions: b.3) results from the analysis of all *C. albicans* differentially abundant proteins identified

Terms from the Function Ontology					
Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
catalytic activity AmiGO	37 out of 56 genes, 66.1%	1831 out of 6435 background genes, 28.5%	3.03e-07	0.00%	AAT1 , ACO1 , ACT1 , ADE1 , ADE17 , ADH1 , AHP1 , ARA1 , ATP2 , CDC19 , CSH1 , CYS3 , EFT2 , ERG10 , GDH3 , GRE3 , HEM13 , HSP60 , HSP90 , HXK2 , ILV5 , INO1 , PDI1 , PGK1 , PGM2 , PMM1 , RIB3 , RIB5 , SOU1 , TAL1 , TDH3 , TKL1 , TSA1 , UBA1 , ZWF1 , orf19.2755 , orf19.7152
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor AmiGO	7 out of 56 genes, 12.5%	59 out of 6435 background genes, 0.9%	3.78e-05	0.00%	ADH1 , ARA1 , CSH1 , GRE3 , ILV5 , SOU1 , ZWF1

oxidoreductase activity AmiGO	13 out of 56 genes, 23.2%	300 out of 6435 background genes, 4.7%	7.18e-05	0.00%	ADH1 , AHP1 , ARA1 , CSH1 , GDH3 , GRE3 , HEM13 , ILV5 , PDI1 , SOU1 , TDH3 , TSA1 , ZWF1
oxidoreductase activity, acting on CH-OH group of donors AmiGO	7 out of 56 genes, 12.5%	69 out of 6435 background genes, 1.1%	0.00011	0.00%	ADH1 , ARA1 , CSH1 , GRE3 , ILV5 , SOU1 , ZWF1
transferase activity, transferring aldehyde or ketonic groups AmiGO	2 out of 56 genes, 3.6%	4 out of 6435 background genes, 0.1%	0.02694	4.80%	TAL1 , TKL1
protein binding AmiGO	11 out of 56 genes, 19.6%	398 out of 6435 background genes, 6.2%	0.03203	4.67%	ADH1 , HSP60 , HSP70 , HSP90 , PFY1 , PGK1 , STI1 , TDH3 , TPM2 , TSA1 , orf19.7215.3
unfolded protein binding AmiGO	4 out of 56 genes, 7.1%	45 out of 6435 background genes, 0.7%	0.03593	4.00%	HSP60 , HSP70 , HSP90 , orf19.7215.3
intramolecular transferase activity, phosphotransferases AmiGO	2 out of 56 genes, 3.6%	6 out of 6435 background genes, 0.1%	0.06661	6.50%	PGM2 , PMM1
isomerase activity AmiGO	4 out of 56 genes, 7.1%	53 out of 6435 background genes, 0.8%	0.06706	5.78%	INO1 , PDI1 , PGM2 , PMM1
peroxiredoxin activity AmiGO	2 out of 56 genes, 3.6%	7 out of 6435 background genes, 0.1%	0.09274	7.20%	AHP1 , TSA1
thioredoxin peroxidase activity AmiGO	2 out of 56 genes, 3.6%	7 out of 6435 background genes, 0.1%	0.09274	6.55%	AHP1 , TSA1