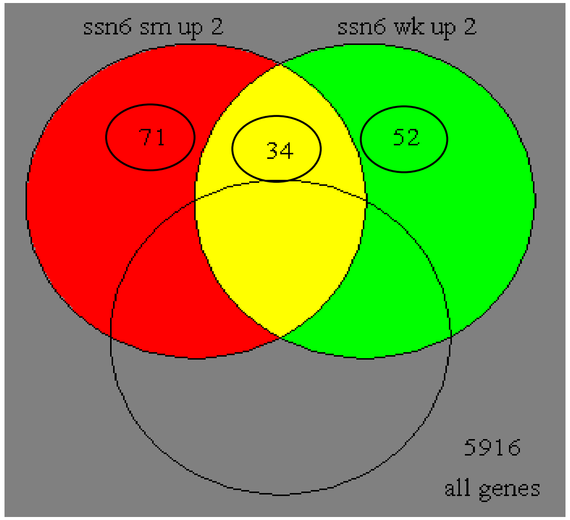
Supplementary Data for Garcia-Sanchez *et al.*

Transcript profiling data for *C. albicans ssn6, tup1* and *nrg1* cells are presented
Transcript levels are measured relative to wild type CAI4 cells
Using SAM, the False Discovery Rate was set at 10%

ssn6 sm = SGC123 cells from a large smooth white colony
ssn6 wr = SGC123 cells from a large wrinkly white colony
nrg1 = MMC4 cells
tup1 = BCA2-9 cells
wild type = CAI4
All were analysed in YPD at 30C in mid-exponential growth phase

Lists of regulated genes are presented
The full dataset is available at http://www.pasteur.fr/recherche/unites/Galar_Fungail/



Click on the circles to access data
sm=smooth
wk=wrinkly
Cut off at 2 with 10%FDR for SAM
Use of the one class SAM function
Triplicate

top

ssn6 sm, ssn6 wk, nrg1, tup1

Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA3909	0.71501833	2.0265765	0.47389245	0.933562	CIT1.exon2	Citrate synthase, exon 2
CA4713	0.982606	2.0223756	0.65169656	1.2884911	CCC1	Transmembrane Ca2+ transporter (by homology)
CA1977	2.571644	2.5064373	0.9424943	1.287123	RPL25.3	ribosomal protein L23a, 3-prime end (by homology)
CA1401	1.2640694	2.1029253	0.96631235	0.9902201	TOM22	mitochondrial outer membrane import receptor complex s
CA2973	2.230584	2.0958877	0.9802942	1.8178291	IPF14452.rep	F1-ATPase epsilon subunit (by homology)
CA5932	1.4232068	2.087321	0.98052955	1.2613094	UBI4	Polyubiquitin
CA4120	3.9250288	3.2938418	1.0075796	3.701131	SOD1.3	Cu,Zn-superoxide dismutase, 3-prime end
CA3363	1.119256	2.6253133	1.0102389	5.719718	FRE32	ferric reductase (by homology)
CA4263	2.275686	2.5600436	1.0112088	0.68797714	IPF2277	unknown function
CA3813	2.5727415	2.469728	1.0171987	4.2274	FRP1	member of the FRP family of proteins related to Yarrowia
CA1987	1.5072678	2.0171616	1.0241605	1.2035681	IPF14895	unknown function

CA5085	2.3990767	2.0990455	1.025553	1.3883607	RPS22.exon2	ribosomal protein S15a, exon 2 (by homology)
CA0046	2.0145977	2.4756584	1.043232	1.9489961	IPF14850	Hypothetical protein
CA2167	1.1306857	2.0678697	1.0671076	2.050551	IPF4553	unknown function
CA1637	2.0347762	2.0501392	1.0704397	1.2027845	RPL43A.3	ribosomal protein, 3-prime end (by homology)
CA1558	1.7093321	2.0312126	1.0819737	2.1582139	IPF15679	lipid transfer protein (by homology)
CA1928	1.26406	2.046597	1.0895609	1.2225615	MRPL37	Mitochondrial ribosomal protein YmL37 (by homology)
CA4894	1.0948482	2.4398894	1.0897282	1.2472212	IPF1617	unknown function
CA0519	0.87937164	3.7078621	1.0932541	0.944094	MRPL10.3	ribosomal protein, 3-prime end (by homology)
CA3604	1.4422477	2.6689525	1.107088	1.1118841	IPF12942	delta-12 fatty acid desaturase (by homology)
CA3861	1.0796819	2.335227	1.1080375	2.5657475	RIM8	regulator of PH response
CA0110	0.7870612	2.1520555	1.1143554	2.3942614	IPF17190	unknown function
CA2734	1.8066674	2.1366017	1.1294005	2.006265	RPL38	ribosomal protein L38 (by homology)
CA1441	1.6945947	2.149575	1.1327194	2.8305295	QCR8	ubiquinol-cytochrome-c reductase chain VIII (by homolog
CA5127	0.52784836	2.6184657	1.1456258	0.54232085	CYS3	cystathionine gamma-lyase by homology
CA4960	1.0996753	2.0112913	1.1497332	2.1191254	IPF3912	unknown function
CA0376	1.8473158	2.0310173	1.1582354	1.7043417	QCR9	ubiquinol--cytochrome-c reductase subunit 9(by homolog
CA3159	1.6857791	2.2814333	1.1686233	2.562769	PLC3	phosphatidylinositol phospholipase C
CA5354	1.4671774	2.729145	1.1688505	2.478678	FTR2	high affinity iron permease
CA1191	1.0742562	2.2203066	1.1718279	2.4142306	CAN2	amino acid permease (by homology)
CA5460	1.669829	2.2065947	1.1750168	1.2669102	IPF277	human IgE-dependent histamine-releasing factor homolo
CA3939	1.2130746	2.1954672	1.1784945	0.7486873	HNM1	Choline permease (by homology)
CA5811	1.1830173	2.1904144	1.1797328	1.6824212	IPF2690.5f	unknown function, 5-prime end
CA2587	1.7465401	2.3135412	1.1821876	3.39452	RPS30.3	40S ribosomal protein S30, 3-prime end (by homology)
CA1003	1.3355592	2.163818	1.1890621	1.5454962	ATP20	F1F0-ATPase complex, G subunit (by homology)
CA1907	1.4050182	2.2117507	1.1994566	1.6188326	ATP7	F1F0-ATPase complex, FO D subunit (by homology)
CA1024	1.7451615	2.6553879	1.24169	1.8992965	CAR1	arginase by homology
CA0781	1.5318766	2.3583264	1.2471559	2.0487628	CAR1.3eoc	arginase, 3-prime end (by homology)
CA1506	1.1440294	2.0003579	1.2607654	6.184525	HGT11	hexose transporter
CA0074	2.4741218	2.3165298	1.2859591	4.3034983	IFD7	Putative aryl-alcohol dehydrogenase (by homology)
CA5646	1.640702	3.1482902	1.2865974	1.8651897	RPS28B.3	Ribosomal protein S28B (S33B) (YS27), 3-prime end (by
CA6009	1.2267206	2.199051	1.2871764	2.5665615	IPF643	similar to Saccharomyces cerevisiae Ptp3p protein tyrosi
CA4667	2.2555993	2.2983606	1.3256712	1.8088285	GAP5	General amino acid permease (by homology)
CA5812	1.0944368	2.106876	1.3359967	1.5399506	IPF2690.3f	unknown function, 3-prime end
CA5039	4.943439	2.4793177	1.3393263	2.6330962	GAP2	general amino acid permease (by homology)
CA5940	1.3768561	4.7338495	1.357242	4.033005	IPF3485	aldo/keto reductase (by homology)
CA4225	2.49409	2.6793666	1.3701016	1.5889916	RPL39.3	ribosomal protein L39, 3-prime end

CA2023	2.238345	2.4160547	1.3762207	1.6030087	RPL42.3	ribosomal protein L36a, 3-prime end (by homology)
CA2862	1.2936786	2.1655772	1.384612	1.2258035	HHF21	histone H4
CA2937	2.025257	2.2761693	1.4024128	2.5987263	RPS21B.3	ribosomal protein S21, 3-prime end
CA4158	1.3624442	2.3023095	1.4580139	0.9719468	DLD3	D-lactate ferrycytochrome C oxidoreductase (by homolog
CA1716	1.2836169	2.1554434	1.4592322	2.3548872	IPF17237	unknown function
CA6092	1.7614974	2.370067	1.5062422	2.711128	RPL35.3	Ribosomal protein L35A, 3-prime end (by homology)
CA4127	2.572571	2.872415	1.5691296	2.8633184	IPF6629	unknown function
CA0763	1.9590598	2.131901	1.6045139	1.0726209	RPL11	60S ribosomal protein (by homology)
CA3689	2.5298672	2.353216	1.6226271	1.3270062	RPS22A	ribosomal protein S15a.e.c10 (by homology)
CA3305	1.918162	2.1581569	1.626187	1.9757177	RPL29	ribosomal protein, cytosolic(by homology)
CA1188	2.0218935	2.3438356	1.6616575	2.617158	RPL30.3	RNA binding, 3-prime end (by homology)
CA4534	2.1178093	2.5400507	1.6706233	2.2650256	RPS26A	ribosomal protein S26.e.A, cytosolic (by homology)
CA1902	1.668205	2.584995	1.6868098	1.7048866	OPT1	oligopeptide transporter
CA5645	1.8235648	2.3955984	1.6911954	0.9692316	CYB5	Cytochrome b5 (by homology)
CA2520	1.3019421	3.3499238	1.7118565	1.7886953	IPF20104	alcohol dehydrogenase (by homology)
CA0643	1.1448015	2.3831139	1.7443879	3.9895818	IDP2	isocitrate dehydrogenase, cytosolic (by homology)
CA2335	1.0304912	2.0233672	1.7832838	1.000126	LYS21	homocitrate synthase (by homology)
CA5807	1.408775	2.1268494	1.790088	1.4996694	RPS24	ribosomal protein S24.e
CA5650	2.0944498	2.0206504	1.8192797	3.2638543	IPF7109	unknown function
CA5203	2.054497	2.6309104	1.8216552	1.3385603	RPS18	Ribosomal protein S18 (by homology)
CA3372	1.4695072	2.1975799	1.8373599	1.0719833	HHF22	histone H4 (by homology)
CA5738	1.884387	2.3578064	1.8603568	1.0940509	LYS9	Lysine biosynthesis (by homology)
CA2579	1.8983214	2.1131756	1.8701817	1.4330214	RPL34B.3	Ribosomal protein L34.e, 3-prime end (by homology)
CA0472	1.1388903	2.3950908	1.9707843	1.3520784	STL1	sugar transporter (by homology)

ssn6 sm, ssn6 wk, nrg1, tup1

top

Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA3461	0.9191558	2.155338	27.964077	6.2765203	CFL2	ferric reductase (by homology)
CA5857	0.5617557	4.2111583	21.227001	4.3704286	PCK1	phosphoenolpyruvate carboxykinase
CA3923	1.3850785	2.8987198	12.216472	4.032031	ADH2	alcohol dehydrogenase I (by homology)
CA0828	5.367417	6.323738	8.866219	10.095109	IPF17186	unknown function
CA3011	1.486837	4.591529	7.786619	4.841869	CTA1	catalase A, peroxisomal(by homology)
CA5797	1.1279203	4.622469	6.8863077	4.710978	IPF4182	unknown function
CA3914	1.4589107	3.9490309	5.648925	13.761463	IPF3282	hexose transporter (by homology)
CA0586	1.620117	3.2617168	4.885278	4.70647	IPF13493	Unknown function

CA5345	1.3459353	4.181268	4.534462	4.7091246	FTR1	high affinity iron permease
CA4111	1.4873955	2.5618312	4.4083977	4.9373255	IPF3964	unknown function
CA0104	2.2168648	3.6346426	4.3207974	15.353998	RBT4	repressed by TUP1 protein
CA3957	1.1398981	2.6261272	4.0471034	6.3146377	RBT2	Repressed by TUP1 protein 2; Rbt2p, Ferric reductase (I
CA4159	0.90012336	2.549636	3.4320693	2.6647465	ALD5	aldehyde dehydrogenase (NAD+) (by homology)
CA3915	1.0695902	4.4134626	3.0571735	7.693217	IPF3277	unknown function
CA2644	2.901518	3.0142395	3.003237	4.4547634	GRP2	Reductase (by homology)
CA5259	0.9040627	2.315091	2.9111671	0.9709927	OSM2	Osmotic growth protein (by homology)
CA1929	1.0591209	2.9941583	2.6576035	9.547502	SAP7	secreted aspartyl proteinase 7
CA0380	3.0579672	2.1549833	2.6475146	2.3903513	IPF14109	unknown function
CA0185	1.066229	2.3378854	2.546466	2.2818184	PLB4.5f	Phospholipase, 5-prime end (by homology)
CA5798	1.4438856	4.171799	2.5277593	4.576299	IPF4181	putative permease (by homology)
CA5986	1.1172384	3.0652733	2.4884562	7.136552	INO1	myo-inositol-1-phosphate synthase
CA5316	1.2509731	2.4927685	2.4879956	0.8088036	MAM33	Mitochondrial acidic matrix protein (by homology)
CA0627	3.442861	2.464115	2.3805192	6.0799274	HSP12	Heat shock protein (by homology)
CA2565	1.2142556	2.2885797	2.356912	1.322487	MET15	O-acetylhomoserine O-acetylserine sulphydrylase
CA5344	0.72822946	2.1861043	2.3097293	0.8545483	PRY2	putative pathogen related proteins (by homology)
CA4038	1.4015005	2.259271	2.2398584	10.7495165	HGT12	hexose transporter
CA0186	1.2757971	2.3003912	2.2168145	2.001821	PLB4.3f	phospholipase, 3-prime end (by homology)
CA5418	1.2492762	2.0413504	2.1768246	1.1197813	IPF1580	unknown function
CA2240	1.7437482	4.060646	2.1156945	3.3611245	CRD2	Cu-binding metallothionein
CA0056	2.3410192	2.2703943	2.0854282	1.2863357	IPF15839	unknown function
CA2266	1.1235075	2.2259393	2.0447721	1.3999637	HEM1	5-aminolevulinic acid synthase
CA3901	0.6249911	2.9655433	2.0385473	9.069829	IPF3282.3eoc	hexose transporter, 3-prime end (by homology)
CA2082	2.0036108	2.2010849	2.0063972	1.772584	NTF2	nuclear transport factor (by homology)
CA4022	1.3693765	2.6349428	2.0014093	1.6286803	FRP6	member of the FRP family of proteins related to Yarrowia

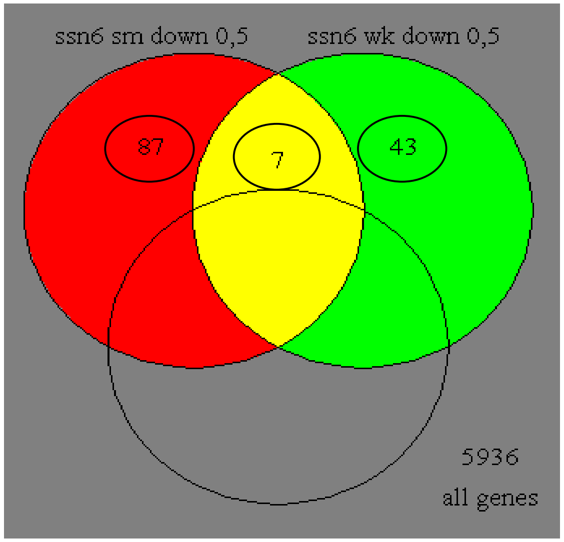
ssn6 sm, ssn6 wk, nrg1, tup1

top

Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA5263	1.0709612	1.8422302	7.3844094	2.2323203	CYB3	Lactate dehydrogenase cytochrome b2 (by homology)
CA2117	0.67601776	1.4641566	4.515525	1.5126379	SNG3	Drug transporter (by homology)
CA3757	0.6713223	1.1193647	4.2554307	0.6565525	MAE1	mitochondrial malic enzyme (by homology)
CA5788	1.0250741	0.8341547	4.0123334	1.0923829	RHR2	DL-glycerol phosphatase
CA1070	0.96906114	1.0269136	3.6495917	0.91971785	HXT61	sugar transporter
CA4748	1.6871184	1.7227279	3.4594636	2.291392	MLS1	malate synthase

CA3455	1.0097007	1.3929595	3.3119087	0.9850074	IPF10533.exc	unknown function, exon 2
CA3253			3.2309792		IPF4724	unknown Function
CA5467	1.2682608	0.4605216	3.084798	1.1939738	GSY1	UDP glucose--starch glucosyltransferase, glycogen synth
CA1067	0.7537103	0.5132388	3.0185628	0.8613476	HXT62	sugar transporter
CA2832	0.74387294	0.8101464	2.8907857	2.310107	CRD1	Cu-transporting P1-type ATPase
CA5076	1.3894492	1.4999741	2.8350651	2.1775382	IPF15301	unknown function
CA1230	1.2445732	0.5374674	2.8121736	2.1632292	SSA4	cahsp70 mRNA for heat shock
CA1069	0.7694129	0.9447703	2.802521	0.9428435	HXT5.3f	sugar transporter, 3-prime end
CA5505	0.80141205	0.2997947	2.7879558	0.7955833	TPS3.3	alpha,alpha-trehalose-phosphate synthase, regulatory su
CA4936	0.9666489	1.3585335	2.7488067	1.3451219	IPF8369	unknown function
CA3895	0.4086642	0.62261784	2.663101	0.8507365	CDR4	Multidrug resistance protein
CA2938	0.9903974	0.7906174	2.6326003	0.86663693	IPF8321	similar to Saccharomyces cerevisiae Glg2p self-glucosyla
CA2454	1.5908738	1.9831808	2.5490263	1.0554013	RPL23B.3	ribosomal protein L23.e, 3-prime end (by homology)
CA0706	1.06147	1.2686682	2.535071	3.0200193	IPF7715	unknown function
CA0848	0.8822334	0.6964547	2.5088112	0.7587808	ACS1	acetyl-coenzyme-A synthetase (by homology)
CA3587	0.5806266	1.2374868	2.467232	0.8765962	AAH1	adenosine deaminase (by homology)
CA1678	0.1294269	0.7701304	2.46304	0.43534693	IPF5185	putative cell wall protein (by homology)
CA2342	1.8097644	1.2375152	2.4548447	4.5908794	IPF13836	probable heat shock protein (by homology)
CA0824	1.1306429	0.84348667	2.4368386	0.9754854	GPD2	Glycerol 3-phosphate dehydrogenase (by homology)
CA0273	0.8964697	0.88623905	2.4266732	1.826639	IPF19066	unknown function
CA3771	1.1649503	1.1506609	2.4254627	1.1468565	SOU1	Sorbitol utilization protein Sou1p [Candida albicans]
CA3112	0.65498084	0.4895391	2.4110355	0.78812444	PFK2	6-phosphofructokinase, beta subunit
CA2386	2.0394626	1.7662947	2.4022403	3.0100074	ECM41.3	involved in cell wall biogenesis and architecture, 3-prime
CA0127	0.7621714	0.76690894	2.3493118	1.0044917	HXK2.3f	hexokinase II, 3-prime end (by homology)
CA0059	1.1695759	1.2272663	2.3475204	0.15128288	IPF17840	unknown function
CA2186	1.3934199	1.583391	2.3300998	2.6681	IPF6881	putative phosphatidyl synthase
CA3199	0.8564003	1.3591566	2.32001	1.5339363	FBP1	Fructose-1,6-bisphosphatase
CA4951	0.7047471	1.1957338	2.270079	1.34293	IPF13607	unknown function
CA4632	1.4924304	1.1261841	2.2635322	1.871973	IPF1531	unknown function
CA4765	0.87254	0.7417986	2.256763	0.8790859	ADH1	alcohol dehydrogenase (by homology)
CA1913	1.0920645	1.2169988	2.2218835	1.1222368	ARC35	subunit of the Arp2/3 complex involved in the control of a
CA4124	1.0475612	0.7981042	2.1901221	0.9098332	IPF20008	unknown function
CA0263	1.3523966	1.0709288	2.1742742	1.3647784	GLK1	aldohexose specific glucokinase (by homology)
CA2769	1.3423384	1.1317534	2.1693544	2.6604462	IPF15870	unknown function
CA2557	1.7839886	1.2083763	2.1475465	9.020808	IPF12101	mycelial surface antigen precursor (by homology to Cand
CA0171	1.4217516	0.97700435	2.1328912	1.8157859	IPF15957	unknown function

CA0853	1.004635	0.9035458	2.1320434	1.0140703	IPF19640	unknown function
CA1915	1.248644	1.2999505	2.1313896	1.3138317	IPF16565	unknown function
CA0748	1.5210046	0.8832197	2.1248333	1.6577989	TFS1	cdc25-dependent nutrient- and ammonia-response cell-cy
CA3161	1.3466454	1.3807156	2.1242871	1.159676	IPF13121.3	unknown function, 3-prime end
CA4492	0.6715204	0.22867817	2.1228752	0.8564172	RNR22	ribonucleoside-diphosphate reductase (by homology)
CA2758	1.2215174	0.78289187	2.0629117	1.7167068	GLC3	1,4-glucan branching enzyme (by homology)
CA2181	1.8364741	1.6051869	2.0615182	13.087005	ECM331	Involved in cell wall biogenesis and architecture (by homo
CA0163	1.8267837	1.1631643	2.0590353	1.9119525	AYR2	1-acyl dihydroxyacetone phosphate reductase (by homolo
CA2562	1.3367215	1.6323279	2.0285544	2.9947932	IPF19953	unknown function
CA3239	0.8544494	1.2713004	2.0215702	1.0086333	IPF10558	unknown function



Click on the circles to access data
sm=smooth
wk=wrinkly
Cut off at 0.5 with 10%FDR for SAM
Use of the one class SAM function
Triplicate

top

ssn6 sm, ssn6 wk, nrg1, tup1						
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA3186	0.6081999	0.49700895	0.7099897	0.50268906	ILS1	isoleucyl-tRNA synthetase (by homology)
CA0268	0.5938935	0.49661735	0.58634806	0.54560393	PUF2.exon2	RNA-binding protein, exon 2 (by homology
CA3880	0.9843044	0.49581632	0.62061465	0.50115174	CAF16	ABC ATPase (by homology)
CA4842	0.68245566	0.4936236	0.91463816	1.1848048	MTD1	methylenetetrahydrofolate dehydrogenase
CA2101	0.8932858	0.49288234	0.9238811	0.79842854	IPF9364	unknown function
CA0526	0.7633171	0.49265188	0.9559024	0.6802958	BUB3	cell cycle arrest protein (by homology)
CA0801	0.6373168	0.49201748	0.97858995	0.56205225	CHC1	clathrin heavy chain (by homology)
CA2216	0.750895	0.4917813	1.0109076	0.63576835	IPF6235	Candida albicans Tca2 retrotransposon
CA0503	0.74543554	0.49139115	1.1297462	0.4591729	PMT6	protein mannosyltransferase
CA3112	0.6549808	0.48953924	2.4110355	0.78812444	PFK2	6-phosphofructokinase, beta subunit
CA2368	0.3614167	0.48917997	0.78597325	0.26634574	RPA190	DNA-directed RNA polymerase I (by homo
CA4971	0.6463913	0.48519227	0.9948536	0.41684824	IPF4697	similar to Saccharomyces cerevisiae Scp1
CA0692	1.4805262	0.4845701	1.4216907	1.7086649	PGM2	Phosphoglucomutase (by homology)
CA1288	1.0265934	0.48015538	0.91380626	0.49950364	KSP1	SERINE/THREONINE-PROTEIN KINASE
CA4745	1.027954	0.47737783	1.1114794	0.69585544	URA1	dihydroorotate dehydrogenase

CA2989	0.44044363	0.47651947	0.76309067	0.49884483	SIN3.exon3	Histone deacetylase by homology
CA4155	1.233133	0.4751202	1.0712779	1.062116	RNR21	ribonucleoside-diphosphate reductase (by
CA4513	1.197583	0.47456592	0.5253022	0.7259848	ADE17	5-aminoimidazole-4-carboxamide ribotide t
CA5766	0.9059227	0.47272652	0.6473834	0.6405568	IPF1097	serine/threonine protein kinase (by homolo
CA0601	0.73988044	0.47260267	0.5343975	0.6950781	MSN5.3f	Importin-beta family member required for n
CA2353	0.92610854	0.47060362	1.0222856	0.886428	VPS13	involved in regulating membrane traffic (by
1615.2	0.7427659	0.47014374	1.0081333	0.69024813	IPF1615.3eoc	similar to Saccharomyces cerevisiae Vip1p
CA1496	0.6234988	0.46305433	0.6506361	0.23468634	CTR1	copper transport protein
CA2424	1.03733	0.46172813	0.9888149	0.9053555	IPF18468	unknown function
CA0160	0.67460746	0.4610834	0.9442282	0.40398553	GAP7.5eoc	general amino acid permease, 5-prime enc
CA5467	1.2682607	0.46052182	3.084798	1.1939739	GSY1	UDP glucose--starch glucosyltransferase,
CA1546	0.73336595	0.4546016	0.99400973	1.0486141	IPF6671	unknown function
CA1426	0.5923444	0.4523326	1.0708469	0.36999062	ALS11.3f	agglutinin-like protein, 3-prime end
CA1879	0.6573161	0.4514985	0.86369634	0.5106907	SMF12	manganese transporter (by homology)
CA0697	0.93038625	0.45087937	1.0025661	0.5474007	VTC4	putative polyphosphate synthetase (by hon
CA2803	0.655787	0.44526806	0.94236827	0.69011146	IPF11711	ubiquitin-protein ligase (by homology)
CA3809	0.6966613	0.44188002	0.9108536	0.501988	KAP123	karyopherin-beta protein (by homology)
CA0585	0.7910067	0.44020924	0.634516	0.92230433	ADE5,7	phosphoribosylamine-glycine ligase and ph
CA0015	0.4148603	0.44002897	0.9198669	0.4116917	PHO87.5eoc	Member of the phosphate permease family
CA6139	0.70615107	0.43697837	1.0450261	0.74776006	ADE2	phosphoribosylaminoimidazole carboxylas
CA0311	1.1633614	0.43469858	0.94942534	0.6024666	DAK2.3eoc	dihydroxyacetone kinase, 3-prime end (by
CA2217	1.1878972	0.4332179	1.1892797	0.48128355	POL0	pol polyprotein, reverse transcripase
CA1956	1.2101206	0.4244142	1.8456843	1.2625659	ERG3	C5,6 desaturase
CA6091	0.7467849	0.42256892	0.9073021	0.58770996	UFD2	Ubiquitin fusion degradation protein 2 (by h
CA4651	0.3288713	0.41995764	0.98083454	0.64427286	IPF3121	unknown function
2566.2	0.8057097	0.41352436	0.87461245	0.53757846	MHP1	Microtubule-associated protein (by homolo
CA4388	1.1142653	0.4082541	1.0221542	1.0422254	IPF12416.3	cytidine deaminase, 3-prime end (by homo
CA3165	0.35420853	0.4047533	0.7326944	0.25950727	FMI1	processing of pre-ribosomal RNA
CA0731	0.95295656	0.39914495	0.91917324	1.0235778	IPF7333	unknown function
CA2170	0.54035485	0.39808676	0.9153297	0.4999061	IPF4563.3f	similar to saccharomyces cerevisiae Tom1
CA2099	1.0346417	0.39489236	0.9151593	0.8894483	IPF11484	unknown function
CA0116	0.78393453	0.39466053	1.3582759	0.83549136	IPF17975	unknown function
CA5761	0.45576945	0.39377025	1.0163053	4.2494874	IFF11	unknown function
CA2169	0.5362729	0.39290926	0.9332083	0.32140818	IPF4563.5f	similar to saccharomyces cerevisiae Tom1
CA1775	0.30819935	0.39146242	1.0274577	0.39326876	GDH2	NAD-specific glutamate dehydrogenase (N
CA5735	0.55008703	0.3872182	0.97244906	0.6972627	IPF2878	unknown function
CA4059	1.1992267	0.38270757	0.7326146	0.7543772	PRD1	Proteinase (by homology)

CA1834	0.87139934	0.38243124	1.2254146	0.82726055	PFK1	6-phosphofructokinase, alpha subunit
CA1515	0.51679784	0.3822427	1.056212	0.57873964	ECM21.3	Involved in cell wall biogenesis and archite
CA0199	0.6587875	0.38214025	0.6546916	0.6465464	KAP104	karyopherin-beta protein (by homology)
CA3679	0.5843978	0.38152388	0.8378414	0.32617658	IPF20142	unknown function
CA3954	1.0979444	0.37872055	1.0661243	0.7882072	YFH1	Regulates mitochondrial iron accumulation
CA4611	0.32794163	0.37541455	0.8534489	0.5793506	IPF10727	unknown function
CA4084	1.0147239	0.37141675	1.1045116	1.4679205	TPS1	TREHALOSE-6-PHOSPHATE SYNTHAS
CA5824	0.49086165	0.37073305	1.094585	1.1358209	NTH1	Neutral trehalase
CA1969	0.8007181	0.3679687	0.9931417	1.0845354	IPF18579.3f	unknown function, 3-prime end
CA0895	1.1418684	0.3658803	1.0457716	1.2903042	SHM2	Serine hydroxymethyltransferase precurso
CA1123	0.6903943	0.36325777	1.0691116	0.610103	IPF19723	similar to Saccharomyces cerevisiae Bph1
CA0081	0.6622879	0.36273474	1.0159655	0.7016431	IPF11379	unknown function
CA0755	1.2802929	0.35869122	0.9530587	1.2077786	IPF14861	unknown function
CA3878	0.7552454	0.3466167	0.95280343	0.44408342	IPF7289	similar to Saccharomyces cerevisiae Upc2
CA3756	0.668603	0.34368914	1.0953072	0.6743285	IPF8884	unknown function
CA5753	0.52954596	0.33493346	0.99468285	0.55374795	FKH1	Fork head protein type transcription factor
CA5069	0.75843257	0.32819358	0.9918228	0.7745762	IPF3593	unknown function
CA4220	1.2355016	0.32415846	0.59379977	0.23984526	IPF8762	unknown function
CA1564	1.091001	0.3038365	0.77486366	1.3606873	GAD1	Glutamate decarboxylase (by homology)
CA5505	0.80141205	0.29979482	2.7879558	0.7955834	TPS3.3	alpha,alpha-trehalose-phosphate synthase
CA1353	0.91306156	0.2882663	1.16852	1.1209449	ERG1	squalene epoxidase
CA5907	0.45082903	0.2866156	0.6298484	0.74455947	SSN6	transcriptional repressor (by homology)
CA2263	1.2686032	0.28645417	0.85477287	0.8459036	GPD1	Glycerol-3-phosphate dehydrogenase (by
CA2250	0.8835184	0.28405827	0.88830304	0.68011856	MIS11	mitochondrial C1-tetrahydrofolate synthas
11759.2	0.44725293	0.27365333	1.3684672	0.74908495	IPF11759	unknown function
5124.1	0.7549973	0.26917723	1.019544	0.58947587	IPF5124	unknown function
CA4570	0.89375454	0.26625213	0.8034064	1.0170966	IPF9550	similar to Saccharomyces cerevisiae Osm
CA4827	0.6163688	0.24950121	0.8789946	0.78778726	SMF2	Manganese transporter (by homology)
CA3284	0.68132454	0.22912966	0.61785406	0.28287748	ADE6	5 -phosphoribosylformyl glycinamidine syn
CA4492	0.6715204	0.22867827	2.1228752	0.85641724	RNR22	ribonucleoside-diphosphate reductase (by
CA2225	0.8125856	0.21328557	0.87933135	0.74740976	SUR2	Hydroxylation of C-4 of the sphingoid moie
CA5066	0.6630318	0.19937016	1.453793	0.53623444	TPS2	Threalose-6-phosphate phosphatase (by h
CA3883	1.0876632	0.17827564	0.52161294	0.6356464	GCV2	Glycine decarboxylase P subunit
CA0413	0.43578106	0.07917202	1.1710278	0.10707929	ALS12.3f	agglutinin-like protein, 3-prime end
CA1528	0.44184864	0.07401408	1.1540561	0.10354521	ALS4.3f	agglutinin-like protein, 3-prime end

ssn6 sm, ssn6 wk, nrg1, tup1

top

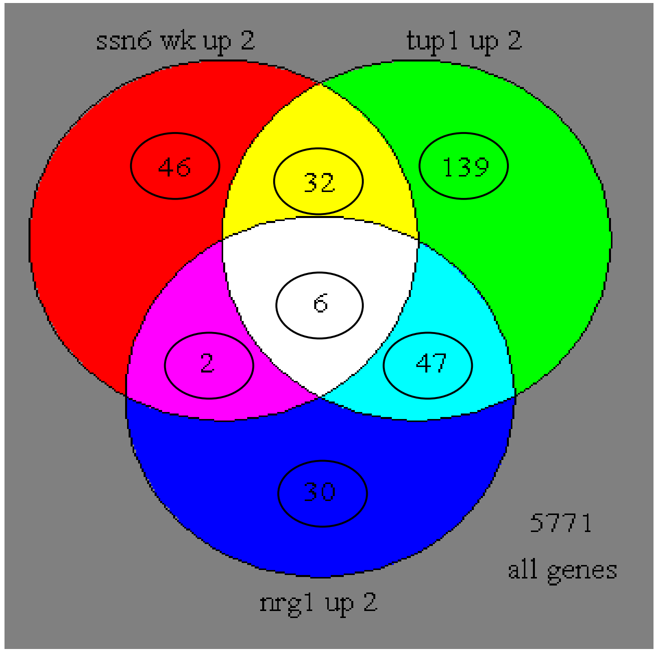
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA0653	0.92095226	0.3157931	0.46173912	1.3093486	MET6	BY HOMOLOGY TO S.CEREV.: 5-methylt
CA0083	1.8878063	0.46970806	0.4433222	0.7651498	PHO84	high-affinity inorganic phosphate/H+ symp
CA6066	0.2756082	0.21324588	0.43937033	0.50057906	CDR1	multidrug resistance protein (by homology)
CA1579	3.0532446	0.27840567	0.4141629	0.66349393	GDH3	NADP-glutamate dehydrogenase (by hom
CA5828	0.48055813	0.4496822	0.3937094	0.40234515	CRM1	Nuclear export factor
CA1377	0.46097752	0.45716923	0.37908378	0.5118704	IPF18690	unknown function
CA2001	0.8880252	0.44158286	0.374392	0.92580074	IPF17074	unknown function

ssn6 sm, ssn6 wk, nrg1, tup1

top

Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA3892	0.7320831	0.8717249	0.49808657	0.5399062	PSE1	karyopherin-beta protein (by homology)
CA0302	1.4312928	0.60017616	0.49564344	1.1052151	MEP3	low affinity high capacity ammonium perme
CA1539	1.1325097	0.9327139	0.49367118	0.7867963	BFR1	Similar to Saccharomyces cerevisiae Bfr1p
CA3539	1.114242	1.1518888	0.49316552	0.6253989	RPS22	ribosomal protein by homology
CA0043	0.69655514	0.5256571	0.48903778	0.50478786	HRD1	Involved in degradation of Hmg2p
CA2675	1.0673984	1.3273641	0.48582745	1.2203592	GSP1	GTP-binding protein (by homology)
CA3007	0.9026484	1.0446184	0.48307714	0.89284307	IPF12148	Unknown function
CA3224	0.59184295	0.7856163	0.48197582	0.57563645	GLC7	Ser/thr phosphoprotein phosphatase 1 (by
CA0665	0.6110582	0.9648186	0.4816036	0.67853725	INT1	integrin-like protein alpha chain
CA4804	1.1480575	0.5302769	0.47602662	0.6073508	ARO8	aromatic amino acid aminotransferase I (b
CA3909	0.7150184	2.0265765	0.47389245	0.93356204	CIT1.exon2	Citrate synthase, exon 2
CA1766	0.64189893	1.0449106	0.4728319	0.68188864	NOP4	Nucleolar protein
CA2414	0.5446939	1.1660302	0.47169626	0.86803114	IPF13756.3f	unknown function, 3-prime end
CA2035	0.814408	1.0349655	0.46225557	0.89487475	SGD1.5f	Involved in HOG pathway, 5-prime end
CA4808	0.7973123	0.810279	0.45786926	0.6684908	RFA1	DNA replication factor A, 69 KD subunit (b
CA0030	0.7121348	0.59942967	0.45609546	0.4531875	IPF17790	unknown function
CA2028	0.5525037	0.5416357	0.45320758	0.44371805	IPF18561.3	unknown function, , 3-prime end
CA5173	1.1428531	0.89248776	0.45095378	0.8930719	CPS2.3f	Carboxypeptidase YSCS precursor, 3-prim
CA1793	0.87292606	1.0613143	0.44669357	0.9582537	IPF18608.5f	unknown function, 5-prime end
CA0139	1.1260798	1.1976418	0.44559065	0.988463	RUD3	Suppressor of uso1-1 transport defect (by
CA3416	0.5188829	0.5243892	0.44521728	0.46014127	FRE30.3	Strong similarity to ferric reductase Fre2p,
CA3754	0.54134244	0.82164145	0.43855596	0.365095	TIF3	translation initiation factor eIF4B (by homol

CA6159	0.88144547	1.2162875	0.4352636	0.6087905	IPF1837	unknown function
CA3174	0.95340437	1.0081936	0.42252243	1.1097429	CCT2	chaperonin of the TCP1 ring complex,cytos
CA0914	0.97161067	0.89863837	0.42095095	0.8200896	SRA1	cAMP dependent protein kinase, regulator
CA5957	0.94075817	1.2099376	0.4194908	0.8182007	RRP3.3eoc	RNA-dependent ATPase, helicase,require
CA1414	0.83614117	1.2205139	0.41598073	0.55285937	CHO2	phosphatidylethanolamine N-methyltransfe
CA0003	0.86268884	0.97825825	0.409795	0.9532794	IPF19484	putative zinc amino peptidase (by homolog
CA5025	0.5697571	0.65936327	0.40712798	0.8072937	AMI3	protein required for normal mitochondrial s
CA0265	1.0842717	1.2903576	0.40542522	0.6215726	STI1	stress-induced protein (by homology)
CA0259	0.8539704	1.0686314	0.40508157	0.5594266	SOL1	multicopy suppressor of los1-1
CA2696	1.0724192	0.9914263	0.3979617	0.70940787	IPF9169	similar to Saccharomyces cerevisiae Bur6
CA0667	0.9570241	1.2278978	0.39655852	0.61488044	TIF5	Translation initiation factor eIF5 (by homol
CA3495	0.9033116	1.136247	0.39149672	1.0083956	RIB7	HTP reductase (By homology)
CA1291	0.8979681	0.9613264	0.37835678	0.7957567	IPF16752	unknown function
CA1315	0.63373715	0.5040496	0.35919425	0.51913226	URA2.5eoc	multifunctional pyrimidine biosynthesis pro
CA1782	1.7958919	0.5511176	0.3343826	1.0157186	PHO84.3eoc	Inorganic phosphate transport protein, 3-pr
CA4039	0.4788499	1.4146252	0.33216083	0.5567332	SKS1	serine/threonine kinase by homology
CA0670	0.7322035	0.8379864	0.32175526	0.63341033	IPF5915	phosphatidyl synthase (by homology)
CA3707	0.63161993	0.9134564	0.31369206	0.5310238	TYE7	Basic helix-loop-helix transcription factor b
CA1639	0.72113913	0.9588295	0.30233496	0.8292303	IPF18641.exo	unknown function, exon 1
CA3828	1.0954584	0.9651476	0.27345043	0.7015281	SNQ2	multidrug resistance protein (by homology)
CA0098	0.7406667	1.2689064	0.24955483	0.73681784	IPF16479	unknown function



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wk=wrinkly
Cut off at 2 with 10%FDR for SAM
Use of the one class SAM function
Triplicate

ssn6 sm, ssn6 wk, nrg1, tup1						
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA2117	0.67601776	1.4641567	4.515525	1.5126377	SNG3	Drug transporter (by homology)
CA3757	0.6713223	1.1193646	4.2554307	0.65655255	MAE1	mitochondrial malic enzyme (by homology)
CA5788	1.0250741	0.834155	4.0123334	1.092383	RHR2	DL-glycerol phosphatase
CA1070	0.96906114	1.026914	3.6495917	0.9197179	HXT61	sugar transporter
CA3455	1.0097007	1.3929595	3.3119087	0.9850074	IPF10533.exc	unknown function, exon 2
CA3253			3.2309792		IPF4724	unknown Function
CA5467	1.2682607	0.46052182	3.084798	1.1939739	GSY1	UDP glucose--starch glucosyltransferase, glycogen synth
CA1067	0.75371027	0.51323897	3.0185628	0.8613477	HXT62	sugar transporter
CA5259	0.9040627	2.315091	2.9111671	0.9709926	OSM2	Osmotic growth protein (by homology)
CA1069	0.7694129	0.9447705	2.802521	0.9428436	HXT5.3f	sugar transporter, 3-prime end
CA5505	0.80141205	0.29979482	2.7879558	0.7955834	TPS3.3	alpha,alpha-trehalose-phosphate synthase, regulatory su
CA4936	0.9666489	1.3585336	2.7488067	1.3451219	IPF8369	unknown function

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CA3895	0.4086642	0.6226179	2.663101	0.8507366	CDR4	Multidrug resistance protein
CA2938	0.9903974	0.7906174	2.6326003	0.8666372	IPF8321	similar to Saccharomyces cerevisiae Glg2p self-glucosyla
CA2454	1.5908737	1.9831818	2.5490263	1.0554014	RPL23B.3	ribosomal protein L23.e, 3-prime end (by homology)
CA0848	0.88223326	0.6964547	2.5088112	0.75878084	ACS1	acetyl-coenzyme-A synthetase (by homology)
CA5316	1.2509731	2.4927685	2.4879956	0.8088036	MAM33	Mitochondrial acidic matrix protein (by homology)
CA3587	0.5806266	1.2374868	2.467232	0.8765962	AAH1	adenosine deaminase (by homology)
CA1678	0.1294269	0.7701305	2.46304	0.43534696	IPF5185	putative cell wall protein (by homology)
CA0824	1.1306429	0.8434867	2.4368386	0.97548544	GPD2	Glycerol 3-phosphate dehydrogenase (by homology)
CA0273	0.8964697	0.88623905	2.4266732	1.826639	IPF19066	unknown function
CA3771	1.1649503	1.150661	2.4254627	1.1468565	SOU1	Sorbitol utilization protein Sou1p [Candida albicans]
CA3112	0.6549808	0.48953924	2.4110355	0.78812444	PFK2	6-phosphofructokinase, beta subunit
CA2565	1.2142557	2.2885797	2.356912	1.322487	MET15	O-acetylhomoserine O-acetylserine sulphydrylase
CA0127	0.7621714	0.7669092	2.3493118	1.0044918	HXK2.3f	hexokinase II, 3-prime end (by homology)
CA0059	1.1695759	1.2272666	2.3475204	0.15128288	IPF17840	unknown function
CA3199	0.8564003	1.3591567	2.32001	1.5339364	FBP1	Fructose-1,6-bisphosphatase
CA5344	0.72822946	2.1861045	2.3097293	0.8545483	PRY2	putative pathogen related proteins (by homology)
CA4951	0.7047471	1.1957339	2.270079	1.34293	IPF13607	unknown function
CA4632	1.4924304	1.1261841	2.2635322	1.8719734	IPF1531	unknown function
CA4765	0.87254	0.7417987	2.2567632	0.8790861	ADH1	alcohol dehydrogenase (by homology)
CA1913	1.0920645	1.2169988	2.2218838	1.1222368	ARC35	subunit of the Arp2/3 complex involved in the control of a
CA4124	1.047561	0.79810447	2.1901221	0.90983325	IPF20008	unknown function
CA5418	1.2492762	2.0413506	2.1768246	1.1197813	IPF1580	unknown function
CA0263	1.3523966	1.070929	2.1742742	1.3647785	GLK1	aldohexose specific glucokinase (by homology)
CA0171	1.4217516	0.9770047	2.1328912	1.8157861	IPF15957	unknown function
CA0853	1.004635	0.9035459	2.1320434	1.0140703	IPF19640	unknown function
CA1915	1.248644	1.2999505	2.1313896	1.3138317	IPF16565	unknown function
CA0748	1.5210046	0.8832197	2.1248333	1.6577989	TFS1	cdc25-dependent nutrient- and ammonia-response cell-cy
CA3161	1.3466454	1.3807155	2.1242871	1.159676	IPF13121.3	unknown function, 3-prime end
CA4492	0.6715204	0.22867827	2.1228752	0.85641724	RNR22	ribonucleoside-diphosphate reductase (by homology)
CA2758	1.2215174	0.7828918	2.0629117	1.7167069	GLC3	1,4-glucan branching enzyme (by homology)
CA0163	1.8267837	1.1631643	2.0590353	1.9119525	AYR2	1-acyl dihydroxyacetone phosphate reductase (by homolo
CA2266	1.1235076	2.22594	2.0447721	1.3999637	HEM1	5-aminolevulinic acid synthase
CA3239	0.8544494	1.2713006	2.0215702	1.0086335	IPF10558	unknown function
CA4022	1.3693765	2.6349428	2.0014093	1.6286803	FRP6	member of the FRP family of proteins related to Yarrowia

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ssn6 sm, ssn6 wk, nrg1, tup1

Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA2156	0.93707937	1.9046867	1.0755863	35.58791	IPF8535	unknown function
CA4246	0.8817579	1.3440794	1.2775601	30.602057	IPF4299	unknown function
CA1430	1.121607	0.9366603	0.9062953	13.592975	IPF14331	Probable extracellular alpha-1,4-glucan glucosidase (by h
CA2873	0.3460081	0.87713015	1.6337901	7.204591	AQY1	similarity to plasma membrane and water channel protein
CA5077	1.4280769	1.0686829	0.9806278	7.081324	YPT1	GTP-binding protein of the rab family (by homology)
CA0855	1.1118358	1.1305091	1.0649861	6.959184	AMYG1	glucoamylase
CA0338	1.426206	1.1594986	0.9412954	6.1948996	IPF13252	unknown function
CA1506	1.1440294	2.0003579	1.2607654	6.184525	HGT11	hexose transporter
CA3698	0.90883064	0.9671255	1.0562403	5.882345	IPF4861	unknown function
CA3363	1.119256	2.625313	1.0102389	5.719717	FRE32	ferric reductase (by homology)
CA1925	1.3540152	1.0691543	0.7103349	5.5688343	IPF18587	putative methyltransferase (by homology)
CA2452	1.4756068	0.96050227	1.1187155	5.3525333	IPF9955	unknown function
CA4041	0.506573	1.1099801	1.4193443	5.2124157	GAL10	UDP-glucose 4-epimerase by homology
CA1673	1.9409207	1.491286	1.0533519	5.1577044	PST2	1,4-benzoquinone reductase by homology
CA0397	1.2654754	0.9325934	0.9793737	5.004847	FRE31	Ferric reductase (by homology)
CA3844	1.5835769	1.3955228	0.94805735	4.9740725	IPF7945	unknown function
CA1812	1.4552541	1.3531796	1.8826249	4.823428	IPF13879	unknown function
CA5846	1.5936763	1.6503083	0.9663101	4.711614	IPF409	unknown function
CA2750	1.1107813	1.1455185	0.9981972	4.3904037	ATX1	antioxidant protein and metal homeostasis factor (by hom
CA2348	1.2133582	1.1849015	0.9856341	4.3699794	IPF12811	putative serine/threonine kinase
CA2975	1.7123929	1.2774011	0.9989052	4.3354983	ARO9	aromatic amino acid aminotransferase II(by homology)
CA3025	1.0238668	0.7958827	1.102575	4.2506757	IPF11503	unknown function
CA5761	0.45576945	0.39377025	1.0163053	4.2494874	IFF11	unknown function
CA1120	1.6780479	0.8929449	1.0625345	4.2470155	IPF7666	unknown function
CA5940	1.3768561	4.7338505	1.357242	4.033005	IPF3485	aldo/keto reductase (by homology)
CA0643	1.1448015	2.3831139	1.7443879	3.9895818	IDP2	isocitrate dehydrogenase, cytosolic (by homology)
CA1582	1.6486925	0.8766049	0.9703049	3.9516695	CLN21	G1 cyclin (by homology)
CA4394	1.4818205	1.0380043	1.0758375	3.826845	IPF12297	mycelial surface antigen (by homology)
CA4040	0.53552616	1.2830417	1.4251996	3.822235	GAL1	galactokinase
CA2710	1.6557212	1.3496311	1.3773891	3.80341	IPF7403	unknown function
CA3560	1.5023335	1.339813	1.0977607	3.73006	CZF1	canal zinc finger protein
CA2146	1.8254917	1.3953968	1.4829316	3.7166219	IPF12799	unknown function
CA3685	1.4420836	1.5705159	1.5565554	3.710774	IPF19540	unknown function

CA2874	1.1020402	1.242972	1.0570265	3.5885992	IPF4999	unknown function
CA5476	0.82784635	1.3792549	0.7810688	3.5779438	IPF8527	unknown function
CA4643	0.90304977	1.3375517	0.9328309	3.468684	PRE9	20S proteasome subunit Y13 (alpha3) (by homology)
CA1359	0.8858521	0.7543184	0.98836154	3.4196002	IPF11842	unknown function
CA2587	1.7465401	2.3135407	1.1821876	3.3945208	RPS30.3	40S ribosomal protein S30, 3-prime end (by homology)
CA5409	1.4129195	1.6824512	1.7148428	3.3188236	COF1	cofilin (by homology)
CA2334	1.0153939	0.97214574	1.6573447	3.266433	ADH3	probable alcohol dehydrogenase (by homology)
CA3518	1.2014109	1.1080836	1.0259897	3.2371402	AMYG2	glucoamylase
CA2895	1.095114	1.5117751	1.3131399	3.230313	IFS1	Unknown function
CA0045	1.9616092	0.8919018	1.1738267	3.1649795	IPF8985.5eoc	unknown function, 5-prime end
CA5826	0.9075098	1.5233709	1.4111558	3.1563241	MDH11	Malate dehydrogenase (by homology)
CA2625	0.67307156	0.60872793	0.97822815	3.1151218	IPF10919	Similar to Flo1p (by homology)
CA2885	0.8285418	1.2847298	1.1740668	3.0292382	IPF7204	unknown function
CA1411	0.68425894	0.86478394	0.9964702	3.0138562	IPF11858	unknown function
CA1504	1.4670051	1.113843	0.7750263	3.007524	ARF3	GTP-binding protein of the ARF family (by homology)
CA2923	0.8887414	1.4704963	1.1309491	3.0045657	FET32	cell surface ferroxidase (by homology)
CA2738	1.5668098	1.362679	1.1376697	2.9863448	STF2	ATP synthase regulatory factor (by homology)
CA1720	1.4283448	1.6525797	1.9779757	2.9491408	IPF15581	unknown function
CA0188	1.31483	1.1831979	1.4165792	2.9357865	IPF15442	unknown function
CA1042	1.92103	1.0780216	0.9893728	2.881497	IPF18784	unknown function
CA1975	1.7405664	0.87372315	0.9851637	2.87766	PLB1	phospholipase B
CA5029	1.0620981	1.387423	1.0080951	2.8743668	IPF2997	unknown function
CA2805	1.2495564	0.7150684	0.85145473	2.8638618	RNR1	ribonucleoside-diphosphate reductase (by homology)
CA1441	1.6945947	2.149575	1.1327194	2.8305295	QCR8	ubiquinol-cytochrome-c reductase chain VIII (by homolog
CA1330	1.630795	0.9559174	1.9511675	2.8154626	IPF11713	unknown function
CA4835	0.6189626	1.9580905	0.97585255	2.8087666	IPF1218	Similar to superoxide dismutase (by homology)
CA3259	0.916457	0.87983906	1.0549903	2.7491286	IPF7970	unknown function
CA3399	0.87516606	1.4520133	1.8202541	2.7120662	PUT2	1-pyrroline-5-carboxylate dehydrogenase (by homology)
CA6092	1.7614974	2.370067	1.5062422	2.711128	RPL35.3	Ribosomal protein L35A, 3-prime end (by homology)
CA0182	1.6391579	1.6081406	1.087905	2.7059708	IFI1	unknown function
CA1148	1.3215305	1.6714123	1.0950737	2.6864161	CAN1	amino acid permease (by homology)
CA2556	1.3885095	1.1866448	1.4582903	2.6773126	FRE5	ferric reductase transmembrane component (by homolog
CA0924	1.7801275	1.9722455	1.0495723	2.6408675	IFD5	Putative aryl-alcohol dehydrogenase (by homology)
CA1333	1.1319624	0.97179776	0.9980682	2.6369653	MRF1	mitochondrial respiratory function protein (by homology)
CA2561	1.472224	1.6485437	1.8439491	2.6307886	CAR2	ornithine aminotransferase (by homology)
CA4358	1.8293415	1.41177	0.9681645	2.6242387	IPF6067	putative transcription factor (by homology)

CA2135	1.767419	1.6559265	1.1634734	2.6036215	COX9	CYTOCHROME C OXIDASE (by homology)
CA6009	1.2267206	2.199051	1.2871764	2.5665615	IPF643	similar to Saccharomyces cerevisiae Ptp3p protein tyrosi
CA5535	0.65980303	1.3147572	1.1977866	2.566055	IPF2839	unknown function
CA3861	1.0796819	2.335227	1.1080375	2.5657475	RIM8	regulator of PH response
CA1035	1.6708269	1.3532606	1.226917	2.5641327	IFI2.3f	unknown function, 3-prime end
CA3159	1.6857792	2.281433	1.1686233	2.562769	PLC3	phosphatidylinositol phospholipase C
CA1988	1.1504802	1.2371029	1.3180344	2.5585341	IPF19749	unknown function
CA5227	1.1919271	1.5155208	1.1693813	2.556849	IPF3087	unknown function
CA2349	1.4080982	0.83502275	1.0532329	2.518871	IFC3	Unknown function
CA2836	1.3253506	1.2107891	1.0376202	2.507565	ARG5,6	acetylglutamate kinase and acetylglutamyl-phosphate re
CA5354	1.4671774	2.7291458	1.1688505	2.478678	FTR2	high affinity iron permease
CA3138	0.79152715	0.86885697	0.9357028	2.4763734	SAP2	aspartic protease
CA0822	1.1251569	1.489867	1.3999678	2.4540892	EXG1	glucan 1,3-beta-glucosidase
CA5968	1.7008127	1.1909053	0.91206527	2.4414642	IPF946	unknown function
CA1191	1.0742562	2.2203066	1.1718279	2.4142306	CAN2	amino acid permease (by homology)
CA5657	0.86622655	1.53892	1.0964137	2.396912	IPF14682	putative transcription factor (by homology)
CA0249	1.4010953	1.4276389	1.8074641	2.3948653	IPF19617	unknown function
CA0110	0.7870612	2.1520555	1.1143554	2.3942616	IPF17190	unknown function
CA2016	1.1598413	1.8612256	0.9747418	2.3813913	IPF3415	similar to Saccharomyces cerevisiae Yim1p mitochondria
CA4044	0.40820667	1.0387884	0.8548418	2.3776064	GAL7	UDP-glucose-hexose-1-phosphate uridylyltransferase (by
CA1180	1.2686343	1.166214	0.89841056	2.37181	UGA12.3f	4-aminobutyrate aminotransferase (GABA transaminase
CA1716	1.2836169	2.1554434	1.4592322	2.3548872	IPF17237	unknown function
CA4437	1.6897347	1.2540637	1.5626258	2.3335454	IPF13867	unknown function
CA1181	1.1485479	1.6323491	1.2694662	2.3311193	UGA12.5f	4-aminobutyrate aminotransferase (GABA transaminase)
CA2020	1.8769021	1.4876107	1.0740172	2.3290741	IPF16901	unknown function
CA0558	1.8071791	1.5565999	1.001311	2.3199694	GPX2	glutathione peroxidase (by homology)
CA4601	1.5736405	1.9505366	1.5090197	2.31851	IPF2195	unknown function
CA1139	0.87846184	1.1383502	1.6137038	2.3074026	IPF9466	unknown function
CA2950	1.2783546	1.0180178	1.0598516	2.302296	CLN2	G1/S-SPECIFIC CYCLIN CLN2
CA2677	1.6224748	1.9388672	1.1491288	2.301596	ATP14.exon2	F1F0-ATPase complex, subunit h, exon 2 (by homology)
CA1576	1.1928915	0.83395284	1.013336	2.2852287	HYR1	hyphally regulated protein
CA1786	1.7504206	1.4084052	1.0076236	2.270509	IPF7629	unknown function
CA4870	1.6501518	1.0057378	1.463253	2.2682388	IPF19568	unknown function
CA0687	0.8201559	1.5575262	1.1296221	2.264347	CPA2	arginine-specific carbamoylphosphate (by homology)
CA5116	1.6801977	1.4030699	1.1468993	2.2587504	TPM2.3	Tropomyosin, 3-prime end
CA4250	1.2547482	0.96106756	0.98560417	2.219426	IPF4292	bleomycin Hydrolase

CA6052	0.9335715	1.6462101	1.5762196	2.2091236	IPF4942	similar to Saccharomyces cerevisiae Mal32p alpha-gluco
CA5078	1.6504283	1.3916051	1.4074807	2.1918566	IPF15297	unknown function
CA0423	1.1430146	0.90983796	1.0307826	2.1893675	IPF15273	unknown function
CA4576	0.8216055	0.8187995	1.0166503	2.1824996	IPF9425.3	unknown function, 3-prime end
CA1796	0.9684104	1.1740807	1.0352509	2.1803782	IPF11259	unknown function
CA5395	1.2723452	0.8742633	1.0934798	2.176391	IPF9401	unknown function
CA0277	1.8618749	0.5430632	0.8490001	2.1666985	RNH1	ribonuclease H (by homology)
CA1558	1.7093321	2.0312126	1.0819737	2.1582139	IPF15679	lipid transfer protein (by homology)
CA3169	1.5544146	1.3892643	1.2777077	2.149949	IPF7686	putative mitochondrial phosphate carrier protein (by hom
CA4676	1.6922565	1.1324661	1.2403471	2.1474698	HK1	Histidine kinase
CA4369	1.538085	1.8917364	0.970554	2.123584	TIM11	subunit e of mitochondrial F1F0-ATPase by homology
CA5394	1.0109538	1.0466908	1.0720427	2.1195364	IPF9400	unknown function
CA4960	1.0996753	2.0112913	1.1497332	2.119125	IPF3912	unknown function
CA3293	1.5840162	1.5182256	1.4311227	2.1114845	IPF5726	unknown function
CA2764	1.3692231	1.6123226	1.5508863	2.103819	QCR7	ubiquinol--cytochrome-c reductase subunit 7 (by homolo
CA6058	1.4472523	1.6887851	0.9242023	2.0916889	ATP16	F1F0-ATPase complex, F1 delta subunit
CA2361	1.428093	0.8239875	0.9822871	2.0880837	IPF8950	unknown function
CA1234	1.4185753	1.1253909	1.2049983	2.0819113	IPF18732	histidine-rich glycoprotein precursor (by homology)
CA0993	1.290152	1.1998464	0.9997718	2.0817363	IPF11059	unknown function
CA1514	0.776968	0.8082268	1.0241075	2.079199	IPF7539	unknown function
CA2333	1.0447099	1.363893	1.1331989	2.0787	ADH4	probable alcohol dehydrogenase (by homology)
CA0782	1.2389414	1.0942552	0.9988451	2.0580425	IPF16253	unknown function
CA1512	0.8432716	0.96456826	1.1183132	2.0573971	IPF15255	unknown function
CA5206	1.5302649	1.4252263	1.5916325	2.0554078	GPH1	Glycogen phosphorylase (by homology)
CA2167	1.1306857	2.0678694	1.0671076	2.050551	IPF4553	unknown function
CA0781	1.5318766	2.3583264	1.2471559	2.0487628	CAR1.3eoc	arginase, 3-prime end (by homology)
CA5546	1.0247416	0.7243924	1.0751281	2.0481713	TUB1.3	Alpha-1 tubulin, 3-prime end
CA1352	1.1376429	1.2494477	1.1672965	2.032796	VCX1	Ca2+-transport by homology
CA2891	0.9426824	1.0300412	0.9338703	2.0203207	IFS4	Pirin protein (by homology)
CA3657	1.1272943	0.9565689	0.8871651	2.0171237	IPF7459	unknown function
CA0169	1.0875338	0.84915227	1.2362443	2.0144787	RBT7	repressed by TUP1
CA5906	0.9227177	0.9331219	1.2237093	2.0143692	IPF5949	unknown function
CA2734	1.8066674	2.1366017	1.1294005	2.006265	RPL38	ribosomal protein L38 (by homology)
CA1701	1.2797304	1.1348684	1.040224	2.0026462	CFL11	Ferric reductase (by homology)

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA4836	7.3015494	1.3058554	1.0261139	0.8466616	IPF1222	Similar to superoxide dismutase (by homology)
CA0579	6.246421	1.6503984	0.97548753	0.84199625	IPF3184.exon	unknown function, exon 1
CA0442	3.3153994	1.1931956	0.9272733	0.9592888	IFC4	unknown function
CA1579	3.0532446	0.27840567	0.4141629	0.66349393	GDH3	NADP-glutamate dehydrogenase (by homology)
CA4184	2.8317466	0.93735427	1.0098432	1.1914663	SNZ1	stationary phase protein by homology
CA1977	2.5716438	2.5064375	0.9424943	1.2871228	RPL25.3	ribosomal protein L23a, 3-prime end (by homology)
CA2416	2.5711226	1.7659807	1.7912257	1.3070298	IFD4	Putative aryl-alcohol dehydrogenase (by homology)
CA4618	2.549496	0.9613474	1.1081053	1.4480075	IPF5757	unknown function
CA3689	2.529867	2.3532162	1.6226271	1.3270062	RPS22A	ribosomal protein S15a.e.c10 (by homology)
CA4225	2.4940896	2.6793664	1.3701016	1.5889915	RPL39.3	ribosomal protein L39, 3-prime end
CA5085	2.3990767	2.0990455	1.025553	1.3883607	RPS22.exon2	ribosomal protein S15a, exon 2 (by homology)
CA4122	2.3805692	1.2998719	1.0388371	1.6713512	PBI2	proteinase B inhibitor 2 (by homology)
CA4263	2.275686	2.560043	1.0112088	0.68797714	IPF2277	unknown function
CA4667	2.2555993	2.2983603	1.3256712	1.8088285	GAP5	General amino acid permease (by homology)
CA2023	2.238345	2.4160554	1.3762207	1.6030087	RPL42.3	ribosomal protein L36a, 3-prime end (by homology)
CA2973	2.230584	2.0958874	0.9802942	1.8178291	IPF14452.rep	F1-ATPase epsilon subunit (by homology)
CA2756	2.2130468	0.9050904	0.8421485	1.3104248	IPF18418	unknown function
CA2273	2.211046	1.0534452	0.92087036	1.13324	BIO2	biotin synthetase (by homology)
CA4919	2.193566	1.512973	1.0445107	1.7285776	TTR1	Glutaredoxin (by homology)
CA4510	2.141999	1.1261832	0.85096115	1.0882769	IPF8970	similar to Saccharomyces cerevisiae Msh1p DNA mismat
CA2578	2.1286657	1.6557801	1.0415792	1.6189591	MMD1.3	Maintenance of mitochondrial DNA, 3-prime end (by hom
CA1431	2.1025243	0.8912944	0.99597675	1.3610572	FET34.3eoc	iron transport multicopper oxidase, 3-prime end (by homc
CA1285	2.0746424	1.6020696	1.2484511	1.9638261	SKP1	kinetochore protein complex CBF3 by homology
CA4133	2.0556855	1.4944489	1.2018776	1.1226512	IPF7010.3	unknown function, 3-prime end
CA5203	2.054497	2.6309114	1.8216552	1.3385603	RPS18	Ribosomal protein S18 (by homology)
CA0375	2.0428348	1.7896218	1.2611014	1.6390727	CRH11	Probable membrane protein (by homology)
CA1637	2.0347762	2.0501392	1.0704397	1.2027845	RPL43A.3	ribosomal protein, 3-prime end (by homology)
CA0046	2.0145977	2.475658	1.043232	1.9489961	IPF14850	Hypothetical protein
CA5848	2.0082552	0.9512017	0.9866937	1.2487504	IPF407	unknown function
CA3244	2.00409	1.9068376	1.4260414	0.8485978	AGP2	amino-acid permease (by homology)

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()* Systematic	nrg1 Normalized	ssn6 sm Normalized	ssn6 wk Normalized	tup1 Normalized	Common	EC
CA3461	0.9191558	2.1553383	27.964077	6.2765207	CFL2	ferric reductase (by homology)
CA5857	0.5617557	4.21116	21.227001	4.3704286	PCK1	phosphoenolpyruvate carboxykinase
CA3923	1.3850785	2.8987205	12.216472	4.0320315	ADH2	alcohol dehydrogenase I (by homology)
CA3011	1.486837	4.591529	7.786619	4.841869	CTA1	catalase A, peroxisomal(by homology)
CA5263	1.0709612	1.8422302	7.3844094	2.2323205	CYB3	Lactate dehydrogenase cytochrome b2 (by homology)
CA5797	1.1279203	4.622469	6.8863077	4.7109785	IPF4182	unknown function
CA3914	1.4589107	3.9490309	5.648925	13.761463	IPF3282	hexose transporter (by homology)
CA0586	1.620117	3.2617168	4.885278	4.70647	IPF13493	Unknown function
CA5345	1.3459355	4.1812706	4.534462	4.709125	FTR1	high affinity iron permease
CA4111	1.4873955	2.561831	4.4083977	4.9373255	IPF3964	unknown function
CA3957	1.1398981	2.6261272	4.0471034	6.3146377	RBT2	Repressed by TUP1 protein 2; Rbt2p, Ferric reductase (I
CA4748	1.6871184	1.7227278	3.4594636	2.291392	MLS1	malate synthase
CA4159	0.9001233	2.5496364	3.4320693	2.6647475	ALD5	aldehyde dehydrogenase (NAD+) (by homology)
CA3915	1.0695902	4.4134617	3.0571735	7.693217	IPF3277	unknown function
CA2832	0.7438729	0.8101467	2.8907857	2.3101075	CRD1	Cu-transporting P1-type ATPase
CA5076	1.3894492	1.4999741	2.8350651	2.1775384	IPF15301	unknown function
CA1230	1.2445731	0.5374674	2.8121736	2.1632297	SSA4	cahsp70 mRNA for heat shock
CA1929	1.0591209	2.9941578	2.6576035	9.547502	SAP7	secreted aspartyl proteinase 7
CA0185	1.066229	2.3378854	2.546466	2.2818186	PLB4.5f	Phospholipase, 5-prime end (by homology)
CA0706	1.0614699	1.2686682	2.535071	3.0200193	IPF7715	unknown function
CA5798	1.4438856	4.171799	2.5277593	4.576299	IPF4181	putative permease (by homology)
CA5986	1.1172384	3.0652733	2.4884562	7.136552	INO1	myo-inositol-1-phosphate synthase
CA2342	1.8097645	1.2375152	2.4548447	4.5908794	IPF13836	probable heat shock protein (by homology)
CA2186	1.3934199	1.583391	2.3300998	2.6681	IPF6881	putative phosphatidyl synthase
CA4038	1.4015005	2.259271	2.2398584	10.7495165	HGT12	hexose transporter
CA0186	1.2757971	2.3003912	2.2168145	2.001821	PLB4.3f	phospholipase, 3-prime end (by homology)
CA2769	1.3423383	1.1317534	2.1693544	2.6604466	IPF15870	unknown function
CA2557	1.7839886	1.2083763	2.1475465	9.020808	IPF12101	mycelial surface antigen precursor (by homology to Cand
CA2240	1.7437482	4.060647	2.1156945	3.3611245	CRD2	Cu-binding metallothionein
CA2181	1.8364741	1.6051868	2.0615182	13.087005	ECM331	Involved in cell wall biogenesis and architecture (by homo
CA3901	0.6249911	2.9655428	2.0385473	9.069829	IPF3282.3eoc	hexose transporter, 3-prime end (by homology)
CA2562	1.3367215	1.6323279	2.0285544	2.9947932	IPF19953	unknown function

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA0056	2.3410192	2.2703943	2.0854282	1.2863357	IPF15839	unknown function
CA2082	2.0036108	2.2010849	2.006397	1.772584	NTF2	nuclear transport factor (by homology)

ssn6 sm, ssn6 wk, nrg1, tup1

top

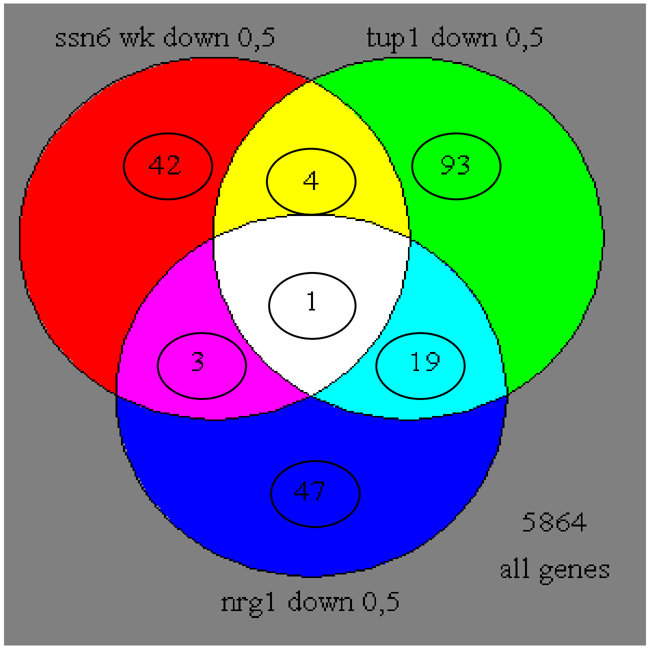
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA4336	13.640597	1.3442764	0.9917073	22.084005	DDR48	stress protein (by homology)
CA2825	11.773237	0.99795735	1.0410674	15.420576	HWP1	Hyphal wall protein
CA2830	9.570067	0.97253275	1.010064	27.946674	RBT1	repressed by TUP1 protein 1
CA1402	8.6961775	1.0107222	1.0451641	20.007708	ECE1	Cell Elongation Protein
CA0448	8.547307	1.263211	1.078776	4.713121	ALS10	agglutinin like protein
CA3827	6.3104124	1.7445797	1.2224324	3.3461185	IPF10662	unknown function
CA5112	5.8777804	1.4241582	1.7140766	9.977981	IPF1341	Similarity to mucin proteins (by homology)
CA3173	5.8752313	1.0358634	1.0469145	2.943858	IPF14145	unknown function
CA5039	4.943439	2.4793177	1.3393263	2.6330962	GAP2	general amino acid permease (by homology)
CA4120	3.9250288	3.2938416	1.0075796	3.7011306	SOD1.3	Cu,Zn-superoxide dismutase, 3-prime end
CA1238	3.9134505	1.1990708	1.0688771	3.8135488	IPF15781	unknown function
CA4985	3.5967207	1.2505891	1.118247	3.904794	IPF2050	similar to Saccharomyces cerevisiae Kip1p kinesin-relate
CA0316	3.4127862	0.6673134	0.7818457	3.5220606	ALS1.3eoc	agglutinin-like protein, 3-prime end
CA2405	3.3973367	1.2555462	1.1068544	7.365009	IPF3844	unknown function
CA4857	3.1618156	1.5521454	1.145309	4.1768346	PHR1	GPI-anchored pH responsive glycosyl transferase
CA0716	3.0390272	1.3393632	1.1128057	2.050822	DOG2	2-deoxyglucose-6-phosphate phosphatase (by homology
CA4189	3.0244727	0.8819732	0.9500586	3.0304832	IPF7527	unknown function
CA4381	2.797829	0.87941444	1.1245539	5.9735136	IPF20169	unknown function
CA5339	2.780447	1.3778378	1.1530452	2.5130787	IPF885	glucan 1,3-beta-glucosidase (by homology)
CA2391	2.7043796	0.6822699	1.2386014	2.7423737	ADH5	probable alcohol dehydrogenase (by homology)
CA2558	2.6978226	1.1447924	1.2035651	13.303168	RBT5	repressed by TUP1 protein 5
CA5641	2.686706	1.7521985	1.0409926	4.2963924	GAC1	ser/thr phosphoprotein phosphatase 1, regulatory chain (
CA3766	2.5815728	0.9393187	1.0688289	2.2669718	IPF18298.3	unknown function, 3-prime end

CA3813	2.5727415	2.469728	1.0171987	4.2273993	FRP1	member of the FRP family of proteins related to Yarrowia
CA4127	2.5725708	2.8724167	1.5691296	2.8633187	IPF6629	unknown function
CA2291	2.5134842	1.5488219	1.6535249	2.56207	IPF9740	oligo-1,4 -1,4-glucantransferase / amylo-1,6-glucosidase
CA3897	2.4854796	1.7225853	1.0551167	2.2171042	PFY1	BINDS TO ACTIN
CA0074	2.4741218	2.3165298	1.2859591	4.3034987	IFD7	Putative aryl-alcohol dehydrogenase (by homology)
CA2947	2.4368606	1.4302539	1.193811	2.003023	IPF6298	unknown function
CA4174	2.4253197	1.1748303	1.0812684	4.552148	IPF4119.5	unknown function, 5-prime end
CA2589	2.4198985	1.8685176	0.9460411	2.4267209	KRE1	secretory pathway protein
CA0722	2.3497472	1.4831182	1.1888087	3.8240552	ERK1	mitogen-activated protein kinase (FUS3 homolog)
CA3260	2.3405476	1.4959646	1.0134637	3.294753	IPF7968	unknown function
CA2302	2.272454	0.5523043	1.4300466	2.794472	IPF6518	unknown function
CA4113	2.2511413	1.1545577	1.1420785	2.2473197	CHO1	Phosphatidylserine synthase
CA5225	2.2480514	1.7640431	1.5226145	2.461204	ACB1.exon2	acyl-coenzyme-A-binding protein, exon 2 (by homology)
CA0671	2.226716	1.2596254	1.0367024	3.6464832	GRP4	putative reductase (by homology)
CA5953	2.2063828	1.0075856	1.0324726	2.479758	IPF3506	unknown function
CA3842	2.1383529	1.3665289	1.4356192	3.3067837	YKE2.3	Gim complex component, 3-prime end (by homology)
CA0840	2.1272256	1.8633741	1.0821114	3.4814103	IFD1	Putative aryl-alcohol dehydrogenase (by homology)
CA4534	2.117809	2.5400507	1.6706233	2.2650256	RPS26A	ribosomal protein S26.e.A, cytosolic (by homology)
CA5650	2.0944498	2.0206501	1.8192797	3.263855	IPF7109	unknown function
CA3154	2.0747607	1.9784498	1.8141639	4.4362288	FUN34.5eoc	unknown function, 5-prime end
CA0386	2.0520227	1.6131731	1.141796	5.433375	IPF4065	unknown function
CA0559	2.0301747	1.6449019	1.2723858	2.478721	GPX1	glutathione peroxidase (by homology)
CA2937	2.025257	2.2761693	1.4024128	2.5987263	RPS21B.3	ribosomal protein S21, 3-prime end
CA1188	2.0218935	2.3438356	1.6616575	2.617158	RPL30.3	RNA binding, 3-prime end (by homology)

ssn6 sm, ssn6 wk, nrg1, tup1

top

Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA0828	5.367417	6.3237405	8.866219	10.095109	IPF17186	unknown function
CA0104	2.2168648	3.6346426	4.3207974	15.353998	RBT4	repressed by TUP1 protein
CA2644	2.9015176	3.0142403	3.003237	4.454764	GRP2	Reductase (by homology)
CA0380	3.0579672	2.1549833	2.6475146	2.3903515	IPF14109	unknown function
CA2386	2.0394626	1.7662947	2.4022403	3.0100074	ECM41.3	involved in cell wall biogenesis and architecture, 3-prime
CA0627	3.442861	2.464115	2.3805192	6.079929	HSP12	Heat shock protein (by homology)



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wk=wrinkly
Cut off at 0.5 with 10%FDR for SAM
Use of the one class SAM function
Triplicate

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA3892	0.7320831	0.8717249	0.49808657	0.5399062	PSE1	karyopherin-beta protein (by homology)
CA0302	1.4312928	0.60017616	0.49564344	1.1052151	MEP3	low affinity high capacity ammonium perme
CA1539	1.1325097	0.9327139	0.49367118	0.7867963	BFR1	Similar to Saccharomyces cerevisiae Bfr1p
CA3539	1.114242	1.1518888	0.49316552	0.6253989	RPS22	ribosomal protein by homology
CA0043	0.69655514	0.5256571	0.48903778	0.50478786	HRD1	Involved in degradation of Hmg2p
CA2675	1.0673984	1.3273641	0.48582745	1.2203592	GSP1	GTP-binding protein (by homology)
CA3007	0.9026484	1.0446184	0.48307714	0.89284307	IPF12148	Unknown function
CA3224	0.59184295	0.7856163	0.48197582	0.57563645	GLC7	Ser/thr phosphoprotein phosphatase 1 (by
CA0665	0.6110582	0.9648186	0.4816036	0.67853725	INT1	integrin-like protein alpha chain
CA4804	1.1480575	0.5302769	0.47602662	0.6073508	ARO8	aromatic amino acid aminotransferase I (by
CA3909	0.7150184	2.0265765	0.47389245	0.93356204	CIT1.exon2	Citrate synthase, exon 2
CA1766	0.64189893	1.0449106	0.4728319	0.68188864	NOP4	Nucleolar protein
CA2414	0.5446939	1.1660302	0.47169626	0.86803114	IPF13756.3f	unknown function, 3-prime end

CA2035	0.814408	1.0349655	0.46225557	0.89487475	SGD1.5f	Involved in HOG pathway, 5-prime end
CA0653	0.92095226	0.3157931	0.46173912	1.3093486	MET6	BY HOMOLOGY TO S.CEREV.: 5-methylt
CA4808	0.7973123	0.810279	0.45786926	0.6684908	RFA1	DNA replication factor A, 69 KD subunit (b
CA5173	1.1428531	0.89248776	0.45095378	0.8930719	CPS2.3f	Carboxypeptidase YSCS precursor, 3-prim
CA1793	0.87292606	1.0613143	0.44669357	0.9582537	IPF18608.5f	unknown function, 5-prime end
CA0139	1.1260798	1.1976418	0.44559065	0.988463	RUD3	Suppressor of uso1-1 transport defect (by
CA0083	1.8878063	0.46970806	0.4433222	0.7651498	PHO84	high-affinity inorganic phosphate/H+ symp
CA6159	0.88144547	1.2162875	0.4352636	0.6087905	IPF1837	unknown function
CA3174	0.95340437	1.0081936	0.42252243	1.1097429	CCT2	chaperonin of the TCP1 ring complex,cyto
CA0914	0.97161067	0.89863837	0.42095095	0.8200896	SRA1	cAMP dependent protein kinase, regulator
CA5957	0.94075817	1.2099376	0.4194908	0.8182007	RRP3.3eoc	RNA-dependent ATPase, helicase,require
CA1414	0.83614117	1.2205139	0.41598073	0.55285937	CHO2	phosphatidylethanolamine N-methyltransfe
CA1579	3.0532446	0.27840567	0.4141629	0.66349393	GDH3	NADP-glutamate dehydrogenase (by hom
CA0003	0.86268884	0.97825825	0.409795	0.9532794	IPF19484	putative zinc amino peptidase (by homolog
CA5025	0.5697571	0.65936327	0.40712798	0.8072937	AMI3	protein required for normal mitochondrial s
CA0265	1.0842717	1.2903576	0.40542522	0.6215726	STI1	stress-induced protein (by homology)
CA0259	0.8539704	1.0686314	0.40508157	0.5594266	SOL1	multicopy suppressor of los1-1
CA2696	1.0724192	0.9914263	0.3979617	0.70940787	IPF9169	similar to Saccharomyces cerevisiae Bur6
CA0667	0.9570241	1.2278978	0.39655852	0.61488044	TIF5	Translation initiation factor eIF5 (by homol
CA3495	0.9033116	1.136247	0.39149672	1.0083956	RIB7	HTP reductase (By homology)
CA1291	0.8979681	0.9613264	0.37835678	0.7957567	IPF16752	unknown function
CA2001	0.8880252	0.44158286	0.374392	0.92580074	IPF17074	unknown function
CA1315	0.63373715	0.5040496	0.35919425	0.51913226	URA2.5eoc	multifunctional pyrimidine biosynthesis pro
CA1782	1.7958919	0.5511176	0.3343826	1.0157186	PHO84.3eoc	Inorganic phosphate transport protein, 3-pr
CA0670	0.7322035	0.8379864	0.32175526	0.63341033	IPF5915	phosphatidyl synthase (by homology)
CA3707	0.63161993	0.9134564	0.31369206	0.5310238	TYE7	Basic helix-loop-helix transcription factor b
CA1639	0.72113913	0.9588295	0.30233496	0.8292303	IPF18641.exc	unknown function, exon 1
CA3828	1.0954584	0.9651476	0.27345043	0.7015281	SNQ2	multidrug resistance protein (by homology)
CA0098	0.7406667	1.2689064	0.24955483	0.73681784	IPF16479	unknown function

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA2170	0.54035485	0.39808676	0.9153297	0.4999061	IPF4563.3f	similar to saccharomyces cerevisiae Tom1
CA2951	0.94027823	0.570971	0.8096161	0.49974906	SBP1	RNA binding protein-like (by homology)
CA1288	1.0265934	0.48015538	0.91380626	0.49950364	KSP1	SERINE/THREONINE-PROTEIN KINASE

CA1356	0.78378	1.3543868	0.82764447	0.4994215	IPF10138.5f	unknown function, 5-prime end
CA1289	0.6796964	0.79526776	0.9145032	0.49826434	ZUO1	Zuotin, a putative Z-DNA binding (by homo
CA4940	0.7057173	0.82555896	0.874954	0.49622437	CRN1.3f	actin-binding protein, 3-prime end (by hom
CA1137	0.94744986	0.8380903	1.2552012	0.49556485	IFN1	glycerophosphoinositol transporter (by hom
CA3183	0.62362796	0.7379941	0.9330307	0.49213746	TSM1.3f	component of TFIID complex, 3-prime end
CA1477	0.5261544	0.6292459	0.89673096	0.4903781	YME1	family of ATPases
CA3338	0.65735203	0.98489803	0.9508548	0.48822284	IPF13582	unknown function
CA2752	1.091652	0.5445118	0.95736563	0.48714483	IPF6238	GAG protein of retrotransposon pCal
CA4546	0.6726313	0.90336615	1.0526284	0.4870959	SPT5	Transcription elongation protein
CA4441	0.6912858	0.98615307	0.9541937	0.485712	IPF2268.3	unknown function, 3-prime end
CA0916	0.74010646	0.6125852	0.8615584	0.48435426	LYS2	L-aminoadipate-semialdehyde dehydrogen
CA4909	0.7841839	1.2827908	1.2098278	0.48417613	TUF1	Translation elongation factor TU (by homol
CA1751	0.97474414	1.6660373	1.1656854	0.4815161	ARO3.exon2	3-deoxy-D-arabinoheptulosonate-7-phosph
CA2217	1.1878972	0.4332179	1.1892797	0.48128355	POL0	pol polyprotein, reverse transcripase
CA0048	0.73724324	0.7168912	0.94664437	0.47900295	TIF4631	mRNA cap-binding protein (by homology)
CA1261	0.84248865	0.5402304	1.0775748	0.47819033	IPF9887.3eoc	unknown function, 3-prime end
CA2322	0.5610166	0.7509004	0.7474091	0.47639164	YSH1	component of pre-mRNA polyadenylation f
CA3748	0.72627264	0.9793976	1.1237389	0.47522885	IPF7385	unknown function
CA1761	1.3061224	1.8455215	0.90374184	0.475036	IPF7602	oxidoreductase (by homology)
CA1138	1.1089131	1.0303773	0.95138913	0.47471002	IFN3	glycerophosphoinositol transporter (by hom
CA2602	0.6429375	0.6181026	0.9494533	0.47431487	IPF5473	unknown function
CA5794	1.0164795	0.574166	0.9152684	0.47139013	IPF4191	unknown function
CA4878	1.0026505	1.8396767	1.088957	0.46907842	OXA1	Cytochrome oxidase biogenesis protein (by
CA4435	0.52346355	0.866102	0.87970597	0.46801633	SAP190	phosphatase associated protein by homolo
CA1322	0.6019785	0.80761945	0.6862465	0.46572834	GCD11	Translation initiation factor eIF2 (by homolo
CA2021	0.67786473	0.87718534	1.1326855	0.46385026	IPF17283	unknown function
CA4844	0.6324843	0.72634315	0.5664689	0.4629442	PDR13	Drug resistance
CA4838	0.78981024	0.8771084	0.9194768	0.46131617	YTA12	Protease of the SEC18/CDC48/PAS1 famil
CA5281	0.56531537	0.71164614	1.2542604	0.46088728	SPT6	Transcription elongation protein (by homolo
CA5183	0.7019542	1.0865934	0.88101935	0.4608416	IPF11090.exo	weak similarity to glutenin, exon 1
CA0503	0.74543554	0.49139115	1.1297462	0.4591729	PMT6	protein mannosyltransferase
CA2061	0.5494191	0.5456036	0.6655783	0.45794752	CDC61.5f	Cytosolic leucyl-tRNA synthetase, 5-prime
CA0733	0.7518321	0.9382508	0.9264726	0.4567755	NIP1	translation initiation factor subunit
CA2720	0.74870664	0.7963097	0.63774323	0.45330656	IPF7366	Arginyl-tRNA synthetase
CA4505	0.6325306	0.89618576	0.5255419	0.45262635	NOP2	nucleolar protein (by homology)
CA2400	0.7240947	1.2308354	0.8467719	0.4492017	SUP45	Translational release factor (by homology)
CA3878	0.7552454	0.3466167	0.95280343	0.44408342	IPF7289	similar to Saccharomyces cerevisiae Upc2

CA0005	0.81474173	0.7020485	0.84100604	0.4427753	IPF14994	unknown function
CA0811	0.76165015	0.7673407	0.97632605	0.44114566	IPF17625	putative cell wall protein of the PIR family
CA4407	0.65475523	0.59335905	0.9740644	0.43796524	RPO31	DNA-directed RNA polymerase III (by hom
CA3737	0.7444124	0.5253111	0.7878262	0.4358704	BLM3	bleomycin resistance (by homology)
CA1464	0.8214814	1.066422	0.7559761	0.42447707	PYC2.exon2	Pyruvate carboxylase 2 (by homology)
CA1158	0.72135437	0.70032597	1.0434151	0.42446586	IPF13275	unknown function
CA1842	0.89108604	0.59082305	1.1322373	0.42361253	ARO1	arom pentafunctional enzyme (by homolog
CA4971	0.6463913	0.48519227	0.9948536	0.41684824	IPF4697	similar to Saccharomyces cerevisiae Scp1
CA1335	0.604975	0.6951941	0.99841815	0.41347542	TRA1	phosphatidylinositol kinase by homology
CA1245	0.90624774	0.93089205	0.6037	0.4083994	IMH3.exon2	IMP dehydrogenase, exon 2
CA4733	0.8252296	1.1128346	0.9443182	0.40712586	IPF7732	similar to Saccharomyces cerevisiae Hcm1
CA5184	0.78381914	1.0187548	0.9164875	0.40573275	IPF11090.exo	weak similarity to glutenin, exon 2
CA0160	0.67460746	0.4610834	0.9442282	0.40398553	GAP7.5eoc	general amino acid permease, 5-prime en
CA3918	0.8410699	0.5780004	0.6025553	0.4013518	VTC2	putative polyphosphate synthetase (by ho
CA4238	0.8171843	1.022838	1.0729917	0.39964873	PIM1	mitochondrial ATP-dependent protease (by
CA2559	0.94258416	0.6351582	0.7594819	0.3964493	HIS4	Histidine biosynthesis trifunctional protein (
CA3862	0.6553081	1.0768602	0.91227424	0.39365718	NSR1	nuclear localization sequence binding prot
CA1911	0.68904203	0.83731705	0.53733534	0.39303294	SSE1	heat shock protein of HSP70 family (by ho
CA0223	0.68948543	0.7408472	0.68477386	0.39263594	VAS1	valyl-tRNA synthetase (by homology)
CA2638	0.5021449	0.57794803	1.2012389	0.3899196	GAP3	General amino acid permease (by homolog
CA4954	0.69367987	1.3096464	1.4949121	0.38652647	TOM40	mitochondrial import receptor chain TOM4
CA3882	1.3296115	1.1660234	1.0076841	0.38536468	IPF7279	putative cobalamin-dependent homocystei
CA4474	0.66872096	0.9459434	0.99668854	0.38145226	SSC1	Mitochondrial heat shock protein 70-relate
CA4326	0.5551662	0.8866429	0.71690935	0.38138226	IPF2093	nuclear protein of unknown function (by ho
CA1438	0.52958524	0.9958789	0.62209076	0.37478083	NOP58	nucleolar protein required for pre-18S rRN
CA1426	0.5923444	0.4523326	1.0708469	0.36999062	ALS11.3f	agglutinin-like protein, 3-prime end
CA0984	1.1482829	0.55417514	0.9796729	0.3696116	IPF7400	unknown function
CA3367	1.4569646	0.81452346	0.7506637	0.36943808	IPF4667	unknown Function
CA1635	0.5171813	0.83239126	0.7156555	0.36891335	URA7	CTP synthase 1 (by homology)
CA1239	0.863782	1.210531	1.2397562	0.33573526	HSP60	Heat Shock Protein 60 (HSP60)
CA5264	0.5246615	0.69454116	1.0425613	0.33501107	IPF1798	unknown function
CA5065	0.5149588	0.6130842	0.95874935	0.33333713	IPF3584	similar to Saccharomyces cerevisiae Pab1
CA5633	0.6094896	0.9317831	0.8473107	0.32718655	RPA135	DNA-directed RNA polymerase I, 135 KD
CA3679	0.5843978	0.38152388	0.8378414	0.32617658	IPF20142	unknown function
CA2169	0.5362729	0.39290926	0.9332083	0.32140818	IPF4563.5f	similar to saccharomyces cerevisiae Tom1
CA1397	0.82997626	1.1842616	0.93895	0.31788075	TOM72	mitochondrial import receptor (by homolog
CA1246	0.92612255	0.90479875	0.9547839	0.31560743	IMH3.exon1	IMP dehydrogenase, exon 1

CA3852	1.1346581	1.3999875	1.039178	0.30946097	TUP1	general transcription repressor
CA2745	0.64279836	0.69207066	0.9133087	0.2973055	HIR1	Histone transcription regulator (by homolo
CA0757	0.6087561	0.59607106	1.0054668	0.28897804	GAP7.3eoc	general amino-acid permease, 3-prime en
CA3284	0.68132454	0.22912966	0.61785406	0.28287748	ADE6	5 -phosphoribosylformyl glycinamidine syn
2262.1	0.54208946	0.84047556	0.9942541	0.27682376		
CA2143	1.0876033	1.1107912	0.98388815	0.24551576	IPF12803	unknown function
CA1217	1.0870517	0.9336576	1.0883621	0.24151221	IPF13909	Unknown function
CA4220	1.2355016	0.32415846	0.59379977	0.23984526	IPF8762	unknown function
CA1496	0.6234988	0.46305433	0.6506361	0.23468634	CTR1	copper transport protein
CA1889	1.0936544	0.96056366	1.0694333	0.22090693	CBP6	Apo-cytochrome B pre-mRNA processing
CA0429	1.2024812	1.0069321	1.0115669	0.21452841	IPF14827	unknown function
CA3736	0.5958576	0.7946159	0.71106416	0.21161598	IPF5533	ABC transporter (by homology)
CA4747	0.9220374	0.86052674	0.93911475	0.20890827	IPF4484	unknown function
CA2746	1.5667993	0.7457264	1.9680161	0.20145041	IPF19766	unknown function
CA3065	0.7253646	0.85921866	0.90476495	0.17920294	IPF19775	unknown function
CA0059	1.1695759	1.2272666	2.3475204	0.15128288	IPF17840	unknown function

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA1898	0.49927837	0.66680324	1.0002426	0.62015957	IPF11998	unknown function
CA3450	0.49883884	0.96614784	0.96720564	0.7590585	PDE2	Nucleotide phosphodiesterase
CA2033	0.4985764	0.58856875	0.68924415	0.70971346	SEC27	coatomer complex beta chain (beta -cop)
CA3566	0.49854973	0.9777746	1.6732558	0.9545082	GUT2	Glycerol-3-phosphate dehydrogenase, mit
CA2997	0.4947529	0.89179075	0.8228981	0.9691978	KGD2	2-oxoglutarate dehydrogenase complex E
CA4983	0.49452442	1.2842313	1.4053522	1.8294376	IPF2053	unknown function
CA2881	0.49213377	0.9854028	0.7424612	0.54307234	RAD4	Excision repair protein (by homology)
CA5824	0.49086165	0.37073305	1.094585	1.1358209	NTH1	Neutral trehalase
CA1388	0.48195693	0.5487432	0.78279364	0.5498245	IPF16514	unknown function
CA6103	0.47860003	0.7413363	0.9819425	0.55320746	SFP1	zinc finger protein (by homology)
CA2554	0.47027013	0.55877143	1.0097193	0.8800412	Cirt4b	probable transposase (by homology)
CA1053	0.4698554	1.3028947	1.0428787	0.70950735	SCW11.3eoc	glucanase gene family member, 3-prime e
CA3894	0.46564916	0.6728294	0.7934281	0.74685484	YIF2	general translation factor eIF2 homolog (b
CA4633	0.4610291	0.5491547	0.5217232	0.5224445	NDH1	Mitochondrial NADH dehydrogenase
CA2489	0.46050152	1.2170624	1.6693558	1.0973338	IPF7217	unknown function
CA5051	0.4577804	0.9839287	0.72049075	0.919806	IPF3709	unknown function

CA5761	0.45576945	0.39377025	1.0163053	4.2494874	IFF11	unknown function
CA3938	0.45498157	0.7215254	1.0904795	0.56770945	IPF4764	unknown Function
CA5091	0.45402858	0.9234426	1.2411503	0.723086	ACF3	endo-1,3-beta-glucanase
CA0691	0.45135504	0.8027978	0.97662103	0.5618089	Cirt4a	Transposase (by homology)
CA5907	0.45082903	0.2866156	0.6298484	0.74455947	SSN6	transcriptional repressor (by homology)
11759.2	0.44725293	0.27365333	1.3684672	0.74908495	IPF11759	unknown function
CA0276	0.4407509	1.4035714	1.0405375	0.6887696	IPF15015	unknown function
CA4501	0.43716732	0.5800426	1.5253515	0.5780762	QDR1	putative antibiotic resistance proteins (by h
CA4266	0.42945743	0.68776846	1.1801203	0.8861926	IPF2283	unknown function
CA2024	0.42731136	1.3012024	0.95648324	0.823296	IPF9616	unknown function
CA3014	0.4217209	0.7359381	0.9930128	0.628826	IPF11915	similar to Saccharomyces cerevisiae Pcl7p
CA5842	0.40917304	0.589206	0.8377528	0.61644095	LEU1	3-isopropylmalate dehydratase (by homolo
CA3895	0.4086642	0.6226179	2.663101	0.8507366	CDR4	Multidrug resistance protein
CA4044	0.40820667	1.0387884	0.8548418	2.3776064	GAL7	UDP-glucose-hexose-1-phosphate uridylyl
CA0007	0.40777332	0.8433255	1.003466	0.62314796	IPF12061	unknown function
CA2802	0.40377903	0.80467814	0.9584478	0.5633022	IPF11363	unknown function
CA0752	0.40181622	0.66349477	0.79403996	0.56788146	MNN22	Golgi alpha-1,2-mannosyltransferase (by h
CA6099	0.3969762	0.66821516	0.7813819	0.65231526	CDR2	Candida albicans drug resistance protein 2
CA0641	0.39498708	0.55851066	1.0098311	0.5954394	IPF15977	unknown function
CA2597	0.39403892	0.9020174	0.6995971	0.6111112	IFQ3	unknown function
CA5353	0.3848065	0.5470999	1.009824	0.8135146	IML2	unknown function
CA4564	0.37470195	0.8836821	1.3184923	0.91581494	IPF6572	unknown function
CA1593	0.368085	0.92002314	1.0342151	0.53762704	MIG1	transcriptional regulator
NAD2	0.3679233	1.1441481	1.062795	0.72768503	mito	
CA2761	0.36538061	0.5845315	0.7105247	0.6109348	IPF15013	pyruvate decarboxylase regulatory protein
CA1278	0.3498125	0.7448376	0.9642458	0.68421465	IPF10835	unknown function
CA2873	0.3460081	0.87713015	1.6337901	7.204591	AQY1	similarity to plasma membrane and water c
CA4651	0.3288713	0.41995764	0.98083454	0.64427286	IPF3121	unknown function
CA4611	0.32794163	0.37541455	0.8534489	0.5793506	IPF10727	unknown function
CA4970	0.31555858	0.62293386	0.943888	0.9134028	IPF4696	unknown Function
CA5987	0.2754111	1.0588659	1.597967	0.7755917	CHT3	chitinase 3 precursor

ssn6 sm, ssn6 wk, nrg1, tup1

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Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC

CA0030	0.7121348	0.59942967	0.45609546	0.4531875	IPF17790	unknown function
CA2028	0.5525037	0.5416357	0.45320758	0.44371805	IPF18561.3	unknown function, , 3-prime end
CA3416	0.5188829	0.5243892	0.44521728	0.46014127	FRE30.3	Strong similarity to ferric reductase Fre2p,
CA3754	0.54134244	0.82164145	0.43855596	0.365095	TIF3	translation initiation factor eIF4B (by homol

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ssn6 sm, ssn6 wk, nrg1, tup1						
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA6066	0.2756082	0.21324588	0.43937033	0.50057906	CDR1	multidrug resistance protein (by homology)
CA1377	0.46097752	0.45716923	0.37908378	0.5118704	IPF18690	unknown function
CA4039	0.4788499	1.4146252	0.33216083	0.5567332	SKS1	serine/threonine kinase by homology

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ssn6 sm, ssn6 wk, nrg1, tup1						
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA5975	0.49538872	1.0894604	0.8883422	0.38698378	SIK1	nucleolar protein involved in pre-rRNA proc
CA1620	0.48152986	1.2509152	1.3659838	0.47730064	MET10	Sulfite reductase flavin-binding subunit (by
CA0554	0.47187597	0.98914194	0.944882	0.49281675	HAS1	ATP-DEPENDENT RNA HELICASE (by hc
CA5197	0.46699682	0.77298504	0.76463056	0.45018378	IPF2342	unknown function
CA5327	0.44437858	1.1756715	0.8949112	0.39147043	SLA2	Cytoskeleton assembly control protein
CA1528	0.44184864	0.07401408	1.1540561	0.10354521	ALS4.3f	agglutinin-like protein, 3-prime end
CA2989	0.44044363	0.47651947	0.76309067	0.49884483	SIN3.exon3	Histone deacetylase by homology
CA0413	0.43578106	0.07917202	1.1710278	0.10707929	ALS12.3f	agglutinin-like protein, 3-prime end
CA4320	0.42459178	1.0397458	1.3011088	0.34516054	ECM17	Putative sulfite reductase (by homology)
CA0015	0.4148603	0.44002897	0.9198669	0.4116917	PHO87.5eoc	Member of the phosphate permease family
CA2649	0.39538333	0.6491122	1.0254694	0.43685696	IPF9057	unknown function
CA4498	0.37529862	0.7647061	0.80859286	0.45298538	IPF11315	unknown function
CA2368	0.3614167	0.48917997	0.78597325	0.26634574	RPA190	DNA-directed RNA polymerase I (by homo
CA3165	0.35420853	0.4047533	0.7326944	0.25950727	FMI1	processing of pre-ribosomal RNA
CA4229	0.34645438	0.6715892	0.89855236	0.3855621	IPF12480.5	unknown function, 5-prime end
CA1775	0.30819935	0.39146242	1.0274577	0.39326876	GDH2	NAD-specific glutamate dehydrogenase (N
CA5890	0.2815831	0.67346156	1.3719516	0.41763717	FCR1	Zinc cluster transcription factor
CA5289	0.13175318	1.6146661	0.8621155	0.47087875	NRG1	similar to transcriptional repressor Nrg1p/N

CA1678	0.1294269	0.7701305	2.46304	0.43534696	IPF5185	putative cell wall protein (by homology)

ssn6 sm, ssn6 wk, nrg1, tup1

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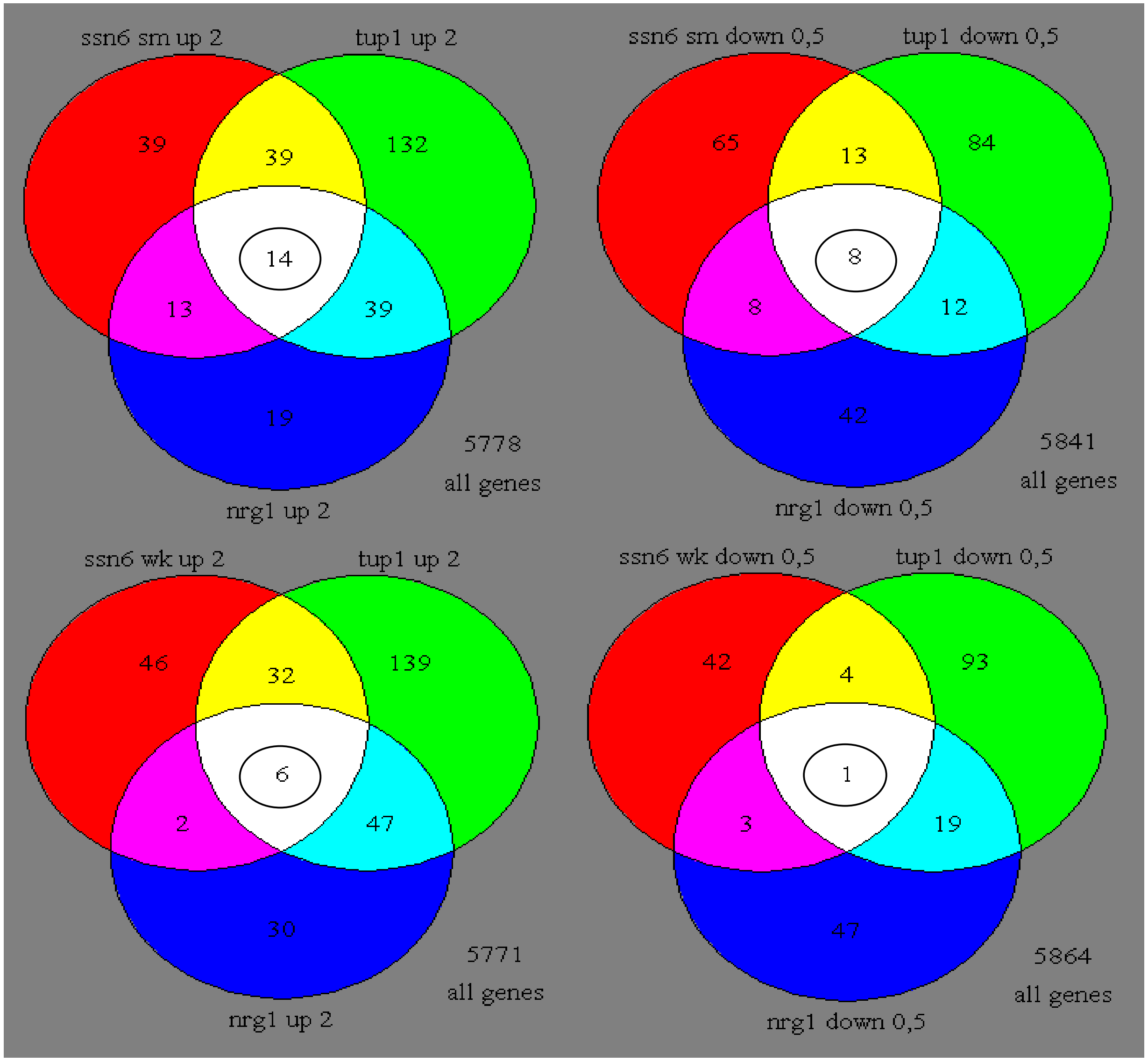
Strain ()*	nrg1	ssn6 sm	ssn6 wk	tup1		
Systematic	Normalized	Normalized	Normalized	Normalized	Common	EC
CA5828	0.48055813	0.4496822	0.3937094	0.40234515	CRM1	Nuclear export factor



Click here for comparison wk-sm

up ssn6 sm, ssn6 wk, nrg1, tup

Strain ()*	nrg1
Systematic	Normalized
CA0828	5.367417
CA0104	2.2168648
CA2644	2.9015176
CA0380	3.0579672
CA2386	2.0394626
CA0627	3.442861

up ssn6 sm, ssn6 wk, nrg1, tup

Strain ()*	nrg1
Systematic	Normalized
CA0828	5.367417
CA0104	2.2168648
CA4120	3.9250288
CA2644	2.9015176
CA4127	2.5725708
CA4534	2.117809
CA5039	4.943439
CA3813	2.5727415
CA0627	3.442861
CA1188	2.0218935
CA0074	2.4741218
CA2937	2.025257
CA0380	3.0579672
CA5650	2.0944498

Down ssn6 sm, ssn6 wk, nrg1, tup

Strain ()*	nrg1
Systematic	Normalized
CA5828	0.48055813

Down ssn6 sm, ssn6 wk, nrg1, tup

Strain ()*	nrg1
Systematic	Normalized
CA2368	0.3614167
CA2989	0.44044363
CA5828	0.48055813
CA0015	0.4148603
CA3165	0.35420853
CA1775	0.30819935
CA0413	0.43578106
CA1528	0.44184864

ssn6 sm, ssn6 wk, nrg1, tup1							
Strain ()*		nrg1	tup1	ssn6 sm	ssn6 wk		
Systematic	Common	Normalized	Normalized	Normalized	Normalized	dif log2 wk-sm	EC
CA1528	ALS4.3f	0.44	0.10	0.07	1.15	3.96	agglutinin-like protein, 3-prime end
CA0413	ALS12.3f	0.44	0.11	0.08	1.17	3.89	agglutinin-like protein, 3-prime end
CA3461	CFL2	0.92	6.28	2.16	27.96	3.70	ferric reductase (by homology)
CA5505	TPS3.3	0.80	0.80	0.30	2.79	3.22	alpha,alpha-trehalose-phosphate synthase
CA4492	RNR22	0.67	0.86	0.23	2.12	3.21	ribonucleoside-diphosphate reductase (by
CA5066	TPS2	0.66	0.54	0.20	1.45	2.87	Threalose-6-phosphate phosphatase (by h
CA0310	PEX11	1.00	0.82	0.23	1.64	2.81	peroxisomal membrane protein - peroxin b
CA5467	GSY1	1.27	1.19	0.46	3.08	2.74	UDP glucose--starch glucosyltransferase,
CA1067	HXT62	0.75	0.86	0.51	3.02	2.56	sugar transporter
CA1230	SSA4	1.24	2.16	0.54	2.81	2.39	cahsp70 mRNA for heat shock
CA5857	PCK1	0.56	4.37	4.21	21.23	2.33	phosphoenolpyruvate carboxykinase
11759.2	IPF11759	0.45	0.75	0.27	1.37	2.32	unknown function
CA3112	PFK2	0.65	0.79	0.49	2.41	2.30	6-phosphofructokinase, beta subunit
CA5788	RHR2	1.03	1.09	0.83	4.01	2.27	DL-glycerol phosphatase
CA1956	ERG3	1.21	1.26	0.42	1.85	2.12	C5,6 desaturase
CA3895	CDR4	0.41	0.85	0.62	2.66	2.10	Multidrug resistance protein
CA3923	ADH2	1.39	4.03	2.90	12.22	2.08	alcohol dehydrogenase I (by homology)
CA2225	SUR2	0.81	0.75	0.21	0.88	2.04	Hydroxylation of C-4 of the sphingoid moie
CA1353	ERG1	0.91	1.12	0.29	1.17	2.02	squalene epoxidase

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ssn6 sm	ssn6 wk	tup1		
Normalized	Normalized	Normalized	Common	EC
6.3237405	8.866219	10.095109	**IPF17186**	unknown function
3.6346426	4.3207974	15.353998	**RBT4**	repressed by TUP1 protein
3.0142403	3.003237	4.454764	**GRP2**	Reductase (by homology)
2.1549833	2.6475146	2.3903515	**IPF14109**	unknown function
1.7662947	2.4022403	3.0100074	ECM41.3	involved in cell wall biogenesis and architecture, 3-prime end (by homology)
2.464115	2.3805192	6.079929	**HSP12**	Heat shock protein (by homology)

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ssn6 sm	ssn6 wk	tup1		
Normalized	Normalized	Normalized	Common	EC
6.3237405	8.866219	10.095109	**IPF17186**	unknown function
3.6346426	4.3207974	15.353998	**RBT4**	repressed by TUP1 protein
3.2938416	1.0075796	3.7011306	SOD1.3	Cu,Zn-superoxide dismutase, 3-prime end
3.0142403	3.003237	4.454764	**GRP2**	Reductase (by homology)
2.8724167	1.5691296	2.8633187	IPF6629	unknown function
2.5400507	1.6706233	2.2650256	RPS26A	ribosomal protein S26.e.A, cytosolic (by homology)
2.4793177	1.3393263	2.6330962	GAP2	general amino acid permease (by homology)
2.469728	1.0171987	4.2273993	FRP1	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway
2.464115	2.3805192	6.079929	**HSP12**	Heat shock protein (by homology)
2.3438356	1.6616575	2.617158	RPL30.3	RNA binding, 3-prime end (by homology)
2.3165298	1.2859591	4.3034987	IFD7	Putative aryl-alcohol dehydrogenase (by homology)
2.2761693	1.4024128	2.5987263	RPS21B.3	ribosomal protein S21, 3-prime end
2.1549833	2.6475146	2.3903515	**IPF14109**	unknown function
2.0206501	1.8192797	3.263855	IPF7109	unknown function

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ssn6 sm	ssn6 wk	tup1		
Normalized	Normalized	Normalized	Common	EC
0.4496822	0.3937094	0.40234515	**CRM1**	Nuclear export factor

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ssn6 sm Normalized	ssn6 wk Normalized	tup1 Normalized	Common	EC
0.48917997	0.78597325	0.26634574	RPA190	DNA-directed RNA polymerase I (by homology)
0.47651947	0.76309067	0.49884483	SIN3.exon3	Histone deacetylase by homology
0.4496822	0.3937094	0.40234515	**CRM1**	Nuclear export factor
0.44002897	0.9198669	0.4116917	PHO87.5eoc	Member of the phosphate permease family, 5-prime end (by homology)
0.4047533	0.7326944	0.25950727	FMI1	processing of pre-ribosomal RNA
0.39146242	1.0274577	0.39326876	GDH2	NAD-specific glutamate dehydrogenase (NAD) (by homology)
0.07917202	1.1710278	0.10707929	ALS12.3f	agglutinin-like protein, 3-prime end
0.07401408	1.1540561	0.10354521	ALS4.3f	agglutinin-like protein, 3-prime end

, regulatory subunit, 3-prime end (by homology)
homology)
omology)
y homology
glycogen synthase (by homology)

ty of ceramide by homology