Table S8. List of the genes in Subgroup E

*** 369 genes**

Systematic	Gene name	Description (GeneDB)	Description (FunCat2)	Expression Ratio (gaf1Δ, +N) / (WT, +N)	(WT, -N) / (WT, +N)	(gaf1Δ, -N) / (gaf1Δ, +N)
SPMIT.09	*atp8*	F0-ATPase subunit 8		0.01	0.98	101.37
SPAC1093.06c	*dhc1*	dynein heavy chain		0.30	1.47	15.66
SPCC1020.01c	*pma2*	P-type proton ATPase Pma2		0.43	1.26	10.26
SPBC29A10.14	*rec8*	meiotic cohesin complex subunit Rec8		0.33	1.23	6.74
SPCC1235.13	*ght6*	hexose transporter Ght6	hexose transporter Ght6 (PMID 10735857)	0.68	1.32	4.81
SPAC212.08c		GPI anchored protein (predicted)	GPI anchored protein (predicted)	1.04	1.32	4.31
SPBC1718.02	*hop1*	linear element associated protein Hop1		0.90	1.17	4.26
SPBC1348.13		pseudogene	pseudogene	0.13	0.06	4.17
SPBC354.08c		DUF221 family protein	DUF221 family protein	0.36	0.92	4.07
SPAC5D6.10c	*mug116*	sequence orphan	sequence orphan	0.26	0.67	3.83
SPAC6C3.07	*mug68*	sequence orphan	sequence orphan	0.33	1.15	3.39
SPAPB18E9.04c		sequence orphan	sequence orphan	1.05	0.80	3.36
SPAC23D3.05c		alcohol dehydrogenase pseudogene	alcohol dehydrogenase pseudogene	0.51	0.44	3.30
SPBC14C8.05c	*meu17*	glucan-alpha-1,4-glucosidase		1.39	1.37	3.18
SPBP8B7.04	*mug45*	sequence orphan		0.74	1.19	3.14
SPCC1450.16c		triacylglycerol lipase	triacylglycerol lipase	0.67	1.13	3.12
SPBC1348.09		short chain dehydrogenase (predicted)		0.94	1.43	3.08
SPAC1786.04		sequence orphan	sequence orphan	0.36	0.87	3.06
SPAC13C5.03	*tht1*	nuclear membrane protein involved in karyogamy	nuclear membrane protein involved in karyogamy (PMID 9442101)	1.04	0.62	3.01
SPAC1786.01c		triacylglycerol lipase	triacylglycerol lipase	0.66	0.89	2.96
SPBC1685.13		non classical export pathway protein (predicted)	non classical export pathway protein (predicted)	0.71	1.43	2.93
SPBC32H8.11	*mei4*	meiotic forkhead transcription factor Mei4		0.83	1.24	2.88
SPBPB8B6.02c		urea transporter (predicted)	urea transporter (predicted)	0.34	0.68	2.88
SPAC1250.02	*mug95*	sequence orphan	sequence orphan	0.73	0.21	2.83
SPCC1902.01	*gaf1*	transcription factor Gaf1		0.01	1.45	1.71
SPBC6B1.03c		Pal1 family protein		0.77	1.03	2.77
SPAC4F8.13c	*rng2*	IQGAP	IQGAP	0.76	1.44	2.74
SPAC13A11.06		pyruvate decarboxylase (predicted)		1.27	1.14	2.69

SPBP4G3.02	*pho1*	acid phosphatase Pho1		1.41	1.48	2.59
SPCC4E9.01c	*rec11*	meiotic cohesin complex subunit Rec11		0.56	1.04	2.58
SPBC32H8.13c	*mok12*	alpha-1,3-glucan synthase Mok12		0.76	1.24	2.56
SPAC22F3.04	*mug62*	AMP binding enzyme (predicted)	AMP binding enzyme (predicted)	0.59	0.10	2.55
SPCC320.07c	*mde7*	RNA-binding protein Mde7	RNA-binding protein Mde7	0.34	0.95	2.45
SPBC16A3.13	*meu7*	alpha-amylase homolog Aah4		1.05	0.81	2.42
SPAPB2B4.03	*cig2*	cyclin Cig2	cyclin Cig2	0.80	1.09	2.39
SPAC4A8.10		lipase (predicted)	lipase (predicted)	0.83	1.12	2.38
SPCC736.09c		TRAX	TRAX (PMID 16043634)	0.51	0.95	2.37
SPCC338.17c	*rad21*	kleisin	kleisin	0.83	1.07	2.36
SPAC630.15	*mug177*	sequence orphan	sequence orphan	0.53	0.68	2.36
SPAC1687.08		sequence orphan	sequence orphan	0.93	1.45	2.32
SPAC13G6.12c	*chs1*	chitin synthase I		0.84	1.33	2.28
SPCC290.04	*ams2*	cell cycle regulated GATA-type transcription factor Ams2		1.11	1.21	2.28
SPCC1259.14c	*meu27*	S. pombe specific UPF0300 family protein 5	S. pombe specific UPF0300 family protein 5	0.68	0.84	2.25
SPAC17A5.18c	*rec25*	meiotic recombination protein Rec25	meiotic recombination protein Rec25	1.03	1.32	2.24
SPAC31G5.10	*eta2*	Myb family protein Eta2	Myb family transcriptional regulator Eta2	1.04	1.41	2.22
SPBC557.05		arrestin		0.86	0.60	2.21
SPAC22A12.02c	*mug103*	sequence orphan	sequence orphan	0.36	1.13	2.20
SPAC25B8.03		phosphatidylserine decarboxylase	phosphatidylserine decarboxylase	1.24	1.21	2.19
SPCC74.06	*mak3*	histidine kinase Mak3	histidine kinase Mak3 (PMID 11758939)	0.67	1.43	2.17
SPAC3C7.06c	*pit1*	serine/threonine protein kinase Pit1	serine/threonine protein kinase Pit1	0.93	1.44	2.17
SPBC354.09c		Tre1 family protein (predicted)	Tre1 family protein (predicted)	0.88	1.49	2.12
SPAC17A2.10c		sequence orphan	sequence orphan	0.74	1.29	2.11
SPBC336.07	*sfc3*	transcription factor TFIIIC complex subunit Sfc3		0.79	1.48	2.11
SPBC354.05c	*sre2*	membrane-tethered transcription factor (predicted)	membrane-tethered transcription factor (predicted) (PMID 11790253)	0.99	1.28	2.11
SPBC1703.04	*mlh1*	MutL family protein Mlh1 (predicted)		0.77	1.14	2.10
SPAC27E2.09	*mak2*	histidine kinase Mak2	histidine kinase Mak2 (PMID 11758939)	0.82	1.44	2.09
SPBC119.04	*mei3*	meiosis inducing protein Mei3		1.12	1.33	2.08
SPBP4H10.11c	*lcf2*	long-chain-fatty-acid-CoA ligase		0.75	1.02	2.08

SPBC2G2.06c	*apl1*	AP-2 adaptor complex subunit Apl1 (predicted)		0.78	1.46	2.06
SPAC18G6.10		chromosome segregation protein Heh1 (predicted)	chromosome segregation protein (predicted)	0.80	1.29	2.06
SPAC7D4.04	*taf1*	Taz1 interacting factor 1	Taz1 interacting factor 1	0.86	1.48	2.06
SPBC1E8.02		ubiquitin family protein, unknown		0.66	1.11	2.05
SPAPB1E7.05	*gde1*	glycerophosphoryl diester phosphodiesterase Gde1	glycerophosphoryl diester phosphodiesterase	0.84	1.33	2.05
SPAC56F8.13		dubious	dubious	0.49	0.44	2.05
SPBC21.05c	*ral2*	Ras guanyl-nucleotide exchange factor Ral2 (predicted)		0.74	1.41	2.05
SPBC12D12.02c	*cdm1*	DNA polymerase delta subunit Cdm1		1.05	0.99	2.04
SPAC57A10.02	*cdr2*	GIN4 family protein kinase Cdr2	GIN4 family protein kinase Cdr2	0.90	1.26	2.04
SPBC2A9.07c		zf-PARP type zinc finger protein		0.89	1.03	2.03
SPBC3B8.07c	*dsd1*	dihydroceramide delta-4 desaturase		1.06	1.49	2.03
SPAC15A10.13	*ppk3*	serine/threonine protein kinase Ppk3	serine/threonine protein kinase Ppk3	0.97	1.35	2.03
SPBC29A3.08	*pof4*	elongin-A, F-box protein Pof4		0.86	1.19	2.00
SPAC1F3.08c		dubious	dubious	0.57	0.20	2.00
SPAC2F3.10		GARP complex subunit Vps54 (predicted)	GARP complex subunit Vps54 (predicted)	0.82	1.43	1.99
SPAC3H8.06	*aur1*	inositol phosphorylceramide synthase (predicted)	inositol phosphorylceramide synthase (predicted)	0.94	1.08	1.99
SPAC24B11.12c		P-type ATPase	P-type ATPase (PMID 12707717)	0.81	1.47	1.99
SPCC4F11.05		dubious	dubious	0.98	0.69	1.98
SPAC22E12.11c	*set3*	histone lysine methyltransferase Set3	histone lysine methyltransferase Set3	0.92	1.30	1.98
SPAC13G7.03		up-frameshift suppressor3 family	up-frameshift suppressor3 family	0.55	0.99	1.97
SPBC530.04	*mod5*	Tea1 anchoring protein Mod5		0.96	1.16	1.97
SPAC18B11.09c		N-acetyltransferase (predicted)	N-acetyltransferase (predicted)	0.69	1.39	1.97
SPAPB1A10.13		sequence orphan	sequence orphan	0.89	1.18	1.96
SPCC16C4.01	*sif2*	Sad1 interacting factor 2		0.57	0.98	1.96
SPAC56F8.16	*esc1*	transcription factor Esc1 (predicted)	transcription factor Esc1 (predicted)	1.01	1.39	1.96
SPAC3A11.11c		pyridoxal reductase (predicted)	pyridoxal reductase (predicted)	0.88	1.41	1.96
SPAC8F11.10c	*pvg1*	pyruvyltransferase		1.27	1.39	1.96
SPAC30D11.11		Haemolysin-III family protein	Haemolysin-III family protein	0.74	0.53	1.96
SPCC11E10.03	*mug1*	dynactin complex subunit (predicted)	dynactin complex subunit (predicted)	0.61	0.84	1.95
SPAPB1A10.08		sequence orphan	sequence orphan	1.03	1.36	1.95
SPAC31A2.05c	*mis4*	cohesin loading factor Mis4	cohesin loading factor Mis4	0.81	1.44	1.95

SPBC1718.04		glycerol-3-phosphate O-acyltransferase (predicted)		0.83	1.38	1.94
SPAC1687.14c		EF hand family protein, unknown role	EF hand family protein, unknown role	0.96	1.43	1.94
SPAC1565.01		conserved fungal protein	conserved fungal protein	0.97	0.89	1.93
SPAC13G7.02c	*ssa1*	heat shock protein Ssa1 (predicted)	heat shock protein Ssa1	0.82	1.43	1.93
SPBC27B12.11c		transcription factor (predicted)		1.21	1.25	1.93
SPBC3B8.02	*php5*	CCAAT-binding factor complex subunit Php5		0.94	1.42	1.92
SPAC1093.03		inositol polyphosphate phosphatase (predicted)	polyphosphoinositide phosphatase (predicted)	0.87	1.46	1.92
SPBC25H2.13c	*cdc20*	DNA polymerase epsilon catalytic subunit a Pol2		0.97	1.17	1.92
SPBC409.09c	*mis13*	kinetochore protein Mis13	kinetochore protein Mis13	0.58	1.27	1.91
SPMIT.11	*cox2*	cytochrome c oxidase 2	cytochrome c oxidase 2; similar to S. cerevisiae Q0250	0.95	1.47	1.91
SPBC3H7.05c		sequence orphan		1.13	1.20	1.91
SPAC227.11c		sensor for misfolded ER glycoproteins Yos9 (predicted)	sensor for misfolded ER glycoproteins Yos9 (predicted)	0.93	1.48	1.90
SPAC9E9.12c	*ybt1*	ABC transporter Ybt1	ABC transporter Ybt1	0.75	1.27	1.90
SPAC25G10.09c		actin cortical patch component, with EF hand and WH2 motif (predicted)		1.00	1.44	1.90
SPBC1105.15c	*htd2*	3-hydroxyacyl-ACP dehydratase Htd2 (predicted)		0.84	1.34	1.89
SPAC10F6.09c	*psm3*	mitotic cohesin complex subunit Psm3	mitotic cohesin complex subunit Psm3	1.24	1.16	1.89
SPAC1006.03c		human CCDC131 homolog	human CCDC131 homolog	0.84	1.17	1.88
SPBC2D10.13	*est1*	telomerase regulator Est1		0.79	0.90	1.87
SPAC19G12.01c	*cut20*	anaphase-promoting complex subunit Apc4	anaphase-promoting complex subunit Apc4	0.85	1.15	1.87
SPAC17A5.04c	*mde10*	spore wall assembly peptidase Mde10	spore wall assembly peptidase Mde10	0.89	0.83	1.87
SPBC12C2.09c		Haemolysin-III family protein		0.89	1.13	1.87
SPBC106.20	*exo70*	exocyst complex subunit Exo70 (predicted)		0.82	1.44	1.87
SPAC11E3.08c	*nse6*	Smc5-6 complex non-SMC subunit Nse6	Smc5-6 complex non-SMC subunit Nse6	0.77	1.32	1.87
SPAC4F10.08	*mug126*	sequence orphan	sequence orphan	0.65	1.29	1.86
SPBC25H2.08c	*mrs2*	magnesium ion transporter Mrs2	magnesium ion transporter Mrs2	0.78	1.27	1.86
SPCC1742.01		sequence orphan		0.44	0.51	1.86
SPCC550.08		N-acetyltransferase (predicted)	N-acetyltransferase (predicted)	0.87	1.31	1.86
SPBC216.07c	*tor2*	phosphatidylinositol kinase Tor2		0.88	1.42	1.86

SPBC24C6.08c		vesicle coat protein		0.78	1.12	1.85
SPBC8E4.02c		sequence orphan		0.72	1.35	1.85
SPAC11D3.18c		nicotinic acid plasma membrane transporter (predicted)	nicotinic acid plasma membrane transporter (predicted)	0.61	1.42	1.85
SPBC691.03c	*apl3*	AP-2 adaptor complex subunit Alp3 (predicted)		0.84	0.91	1.84
SPAC1556.06b			sequence orphan	1.29	0.91	1.84
SPAC12G12.09		sequence orphan	sequence orphan	0.82	1.40	1.84
SPAC19G12.08		fatty acid hydroxylase (predicted)	fatty acid hydroxylase (predicted)	0.87	0.68	1.84
SPBC29A3.14c	*trt1*	telomerase reverse transcriptase 1 protein Trt1		0.79	1.08	1.84
SPCC645.06c	*rgf3*	RhoGEF Rgf3	RhoGEF Rgf3	0.98	1.12	1.84
SPBC30D10.10c	*tor1*	phosphatidylinositol kinase Tor1		0.85	1.41	1.83
SPCC663.06c		short chain dehydrogenase (predicted)	short chain dehydrogenase (predicted)	0.55	0.75	1.83
SPCC970.06		cargo receptor for soluble proteins (predicted)	cargo receptor for soluble proteins (predicted)	0.94	1.49	1.83
SPAC12B10.08c		mitochondrial tRNA(Ile)-lysidine synthetase family (predicted)	tRNA(Ile)-lysidine synthetase family	0.98	1.33	1.83
SPCC970.04c	*mob2*	protein kinase activator Mob2	protein kinase activator Mob2	0.91	1.15	1.82
SPCPJ732.01	*vps5*	retromer complex subunit Vps5	retromer complex subunit Vps5	0.83	1.48	1.82
SPAC589.02c	*med13*	mediator complex subunit Srb9	mediator complex subunit Srb9	0.93	1.21	1.81
SPCC550.03c		Ski complex RNA helicase Ski2 (predicted)	RNA helicase involved in mRNA catabolism	0.83	1.44	1.81
SPAPYUG7.02c	*sin1*	stress activated MAP kinase interacting protein Sin1	stress activated MAP kinase interacting protein Sin1	0.88	1.41	1.80
SPBC3D6.10	*apn2*	AP-endonuclease Apn2		0.89	1.43	1.80
SPCC23B6.03c	*tel1*	ATM checkpoint kinase	ATM checkpoint kinase	1.06	1.50	1.80
SPCC320.14		threo-3-hydroxyaspartate ammonia-lyase (predicted)	threo-3-hydroxyaspartate ammonia-lyase (predicted)	0.89	1.17	1.80
SPAC1565.06c	*spg1*	GTPase Spg1	GTPase Spg1	0.96	1.30	1.80
SPAC1687.02		CAAX prenyl protease (predicted)	CAAX prenyl protease (predicted)	1.01	1.49	1.80
SPAC29B12.08		sequence orphan	sequence orphan	0.80	0.45	1.80
SPCC188.10c		pseudo		1.22	0.52	1.80
SPAC17H9.20	*psc3*	mitotic cohesin complex, non-SMC subunit Psc3		1.10	1.11	1.80
SPAC1250.01	*snf21*	ATP-dependent DNA helicase Snf21	ATP-dependent DNA helicase Snf21	0.91	1.22	1.79
SPAC23C11.16	*plo1*	Polo kinase Plo1	Polo kinase Plo1	0.94	1.29	1.79
SPBC16G5.09		serine carboxypeptidase (predicted)		0.92	1.28	1.78

SPAC26H5.11		spore wall assembly protein (predicted)	spore wall assembly protein (predicted)	0.67	1.08	1.78
SPAC11E3.10		VanZ-like family protein	VanZ-like family protein	0.87	1.23	1.78
SPBC16A3.10		membrane bound O-acyltransferase, MBOAT (predicted)		0.86	1.40	1.78
SPAC23G3.09	*taf4*	transcription factor TFIID complex subunit Taf4 (predicted)	transcription factor TFIID complex subunit Taf4	0.75	1.36	1.77
SPAC57A10.04	*mug10*	sequence orphan	sequence orphan	0.87	0.74	1.77
SPBC1105.08		EMP70 family		0.82	1.17	1.76
SPBC4C3.04c		guanyl-nucleotide exchange factor (predicted)		0.99	1.28	1.76
SPBC651.03c	*gyp10*	GTPase activating protein Gyp10		1.04	1.48	1.76
SPCC16C4.09	*sts5*	RNB-like protein	RNB-like protein	0.94	1.32	1.76
SPBC582.04c		sequence orphan	sequence orphan	0.90	1.35	1.75
SPAC144.05		ATP-dependent DNA helicase (predicted)	ATP-dependent DNA helicase	0.85	1.15	1.75
SPAC4A8.09c	*cwf21*	complexed with Cdc5 protein Cwf21	complexed with Cdc5 protein Cwf21 (PMID 11884590)	0.83	0.88	1.75
SPAC12B10.03		WD repeat protein, human WDR20 family	WD repeat protein, human WDR20 family	0.91	1.24	1.75
SPBC1709.12	*rid1*	GTPase binding protein Rid1		1.02	0.69	1.75
SPCC4B3.15	*mid1*	medial ring protein Mid1	medial ring protein Mid1	0.88	1.42	1.75
SPBC8E4.01c		inorganic phosphate transporter (predicted)		1.22	0.96	1.75
SPBC776.10c	*cog6*	Golgi transport complex peripheral subunit Cog6 (predicted)		0.84	1.37	1.74
SPAC3C7.09	*set8*	lysine methyltransferase Set8 (predicted)	lysine methyltransferase Set8 (predicted)	0.78	1.30	1.74
SPCC777.11		sequence orphan	sequence orphan	0.78	0.92	1.74
SPCC417.02	*dad5*	DASH complex subunit Dad5	DASH complex subunit Dad5	0.49	0.11	1.74
SPCC126.07c		human CTD-binding SR-like protein rA9 homolog	ubiquitin-protein ligase E3 (predicted)	0.73	1.21	1.73
SPAC22E12.14c	*sck2*	serine/threonine protein kinase Sck2	serine/threonine protein kinase Sck2	0.76	0.89	1.73
SPBC27B12.12c		CorA family magnesium ion transporter (predicted)		0.86	1.42	1.73
SPCC548.05c		ubiquitin-protein ligase E3 (predicted)	ubiquitin-protein ligase E3 (predicted)	0.78	1.30	1.73
SPCC132.05c		trichothecene 3-O-acetyltransferase pseudogene		1.31	1.16	1.73

SPBC660.13c	*ssb1*	DNA replication factor A subunit Ssb1	DNA replication factor A subunit Ssb1 (PMID 9111307) (PMID 8702843)	0.96	1.13	1.73
SPCC18.01c	*adg3*	beta-glucosidase Adg3 (predicted)	beta-glucosidase Adg3 (predicted)	1.23	0.89	1.72
SPAC17D4.03c	*cis4*	cation diffusion family zinc membrane transporter Cis4	membrane transporter (predicted)	0.88	1.36	1.72
SPAC2G11.14	*taf111*	transcription factor TFIID complex subunit Taf111	transcription factor TFIID complex subunit Taf111	0.79	1.35	1.72
SPBC21H7.03c		acid phosphatase (predicted)		0.82	1.28	1.72
SPAC23C4.11	*atp18*	F0-ATPase subunit J (predicted)	F-0 ATPase subunit J (predicted)	0.76	1.47	1.72
SPAC343.12	*rds1*	conserved fungal protein	conserved fungal protein	0.71	1.30	1.72
SPAC926.03	*rlc1*	myosin II regulatory light chain	myosin II regulatory light chain (PMID 11056543)	0.86	1.46	1.72
SPAC19G12.07c	*rsd1*	RNA-binding protein Rsd1	RNA-binding protein Rsd1	1.15	0.91	1.72
SPAC343.19		phosphatidylinositol 4-kinase Lsb6 (predicted)		0.94	1.49	1.71
SPBC23G7.08c	*rga7*	GTPase activating protein Rga7		0.85	0.97	1.71
SPBC17F3.01c	*rga5*	GTPase activating protein Rga5		1.31	1.38	1.71
SPAC630.09c	*mug58*	glycerate kinase (predicted)	glycerate kinase (predicted)	0.80	1.16	1.71
SPBC3D6.13c		protein disulfide isomerase (predicted)		0.91	1.43	1.71
SPAC1296.01c		phosphoacetylglucosamine mutase (predicted)	phosphoacetylglucosamine mutase (predicted)	0.89	1.46	1.71
SPAC29B12.07	*sec16*	multidomain vesicle coat component Sec16	multidomain vesicle coat component Sec16	0.82	1.46	1.71
SPAC12G12.03	*cip2*	RNA-binding protein Cip2	RNA-binding protein Cip2	1.03	1.24	1.71
SPAC9G1.07		sequence orphan	sequence orphan	0.90	1.36	1.71
SPCC4E9.02	*cig1*	cyclin Cig1		0.88	0.65	1.71
SPAC1A6.08c	*mug125*	sequence orphan	sequence orphan	0.83	0.66	1.71
SPBP23A10.13	*orc4*	origin recognition complex subunit Orc4		0.85	1.36	1.70
SPCC1494.10		transcription factor (predicted)		0.91	1.18	1.70
SPAC3A12.17c	*cys12*	cysteine synthase Cys12	cysteine synthase Cys12	1.02	1.16	1.70
SPCC1183.01	*sec15*	exocyst complex subunit Sec15 (predicted)	exocyst complex subunit Sec15 (predicted)	0.78	0.99	1.70
SPAC821.13c		P-type ATPase		1.07	1.30	1.70
SPAC5H10.01		DUF1445 family protein	DUF1445 family protein	0.87	1.14	1.70
SPAC688.10	*rev3*	DNA polymerase zeta catalytic subunit Rev3	DNA polymerase zeta catalytic subunit Rev3	0.79	1.47	1.70
SPBC1347.10	*cdc23*	MCM-associated protein Mcm10		0.89	1.47	1.70

SPAC3G9.12	*peg1*	CLASP family microtubule-associated protein	CLASP family microtubule-associated protein	0.88	1.14	1.69
SPAC22F3.02	*atf31*	transcription factor Atf31	transcription factor Atf31	1.22	1.35	1.69
SPAC6F6.13c		DUF726 family protein	DUF726 family protein	0.97	1.25	1.69
SPBC23E6.02		ATP-dependent DNA helicase (predicted)		0.80	1.35	1.69
SPAC29B12.01	*ino80*	SNF2 family helicase Ino80	SNF2 family helicase Ino80	0.83	1.43	1.69
SPBC32F12.07c		ubiquitin-protein ligase E3 (predicted)		0.86	1.43	1.69
SPCC970.08		inositol polyphosphate kinase (predicted)	inositol polyphosphate kinase (predicted)	0.84	1.14	1.69
SPAC26A3.09c	*rga2*	GTPase activating protein Rga2	GTPase activating protein Rga2	0.97	1.20	1.68
SPAC1639.02c	*trk2*	potassium ion transporter Trk2		0.98	1.18	1.68
SPCC1620.13		phosphoglycerate mutase family	phosphoglycerate mutase family	0.93	1.14	1.68
SPCC550.12	*arp6*	actin-like protein Arp6	actin-like protein Arp6	0.78	0.98	1.68
SPBC29A3.17	*gef3*	RhoGEF Gef3		0.76	0.96	1.68
SPBC3B8.04c		membrane transporter		1.01	1.33	1.68
SPBC317.01	*mbx2*	MADS-box transcription factor Pvg4		0.39	1.16	1.67
SPCC417.03		sequence orphan	sequence orphan	0.73	0.82	1.67
SPBC1826.01c	*mot1*	TATA-binding protein associated factor Mot1	TATA-binding protein associated factor Mot1	0.88	1.20	1.67
SPCC338.08	*ctp1*	CtIP-related endonuclease	sequence orphan	0.94	1.19	1.67
SPAC16A10.03c		zinc finger protein Pep5/Vps11 (predicted)	zinc finger protein Pep5/Vps11 (predicted)	1.02	1.43	1.66
SPBC28F2.12	*rpb1*	DNA-directed RNA polymerase II large subunit		0.79	0.96	1.66
SPBC428.20c	*alp6*	gamma tubulin complex Spc98/GCP3 subunit Alp6		0.95	1.12	1.66
SPAC6C3.06c		P-type ATPase, calcium transporting	P-type ATPase, calcium transporting (PMID 12707717)	0.92	1.34	1.65
SPBC29A3.01		heavy metal ATPase		0.97	1.45	1.65
SPBC649.05	*cut12*	spindle pole body protein Cut12	spindle pole body protein Cut12 (PMID 9531532)	0.96	1.37	1.65
SPAC1A6.07		sequence orphan	sequence orphan	0.82	1.46	1.65
SPAC4G9.05	*mpf1*	meiotic PUF family protein 1	meiotic PUF family protein 1	0.67	0.84	1.65
SPAC27E2.01		alpha-amylase homolog (predicted)	alpha-amylase homolog (predicted)	0.86	1.46	1.65
SPAC17A5.05c		conserved fungal protein	conserved fungal protein	0.67	0.78	1.65
SPAC14C4.04	*B22918-2*	hypothetical protein	hypothetical protein	0.88	1.42	1.65

SPBC26H8.02c	*sec9*	SNAP-25 homologue, t-SNARE component Sec9		0.85	1.01	1.65
SPAC1952.10c		conserved fungal protein	conserved fungal protein (predicted)	0.89	1.26	1.64
SPBC342.05	*crb2*	DNA repair protein RAD9 homolog, Rhp9		0.89	1.40	1.64
SPAC1783.02c	*vps66*	acyltransferase (predicted)	acyltransferase (predicted)	0.95	1.33	1.64
SPBC16A3.19		histone acetyltransferase complex subunit Eaf7 (predicted)		0.72	1.08	1.64
SPAPB2C8.01		glycoprotein (predicted)	glycoprotein (predicted)	0.84	1.31	1.64
SPAC22H10.03c	*kap114*	karyopherin Kap14	karyopherin Kap14	0.87	1.49	1.64
SPBP26C9.03c	*fet4*	iron/zinc ion transporter (predicted)	iron ion transporter (predicted)	0.88	1.46	1.63
SPBC21B10.13c		transcription factor, homeobox type (predicted)		0.86	0.96	1.63
SPAC2F3.14c		conserved fungal protein	conserved fungal protein	0.70	0.91	1.63
SPAC30D11.09	*cwf19*	complexed with Cdc5 protein Cwf19	complexed with Cdc5 protein Cwf19 (PMID 11884590)	0.84	0.84	1.63
SPCC1183.04c	*pet127*	mitochondrial membrane protein Pet127	mitochondrial membrane protein Pet127	0.88	1.15	1.63
SPAC57A7.11	*mip1*	WD repeat protein Mip1	WD repeat protein Mip1	0.72	1.08	1.63
SPCC622.10c		exocyst complex subunit Sec5 (predicted)	exocyst complex subunit Sec5 (predicted)	0.78	1.05	1.63
SPAC222.11	*hem13*	coproporphyrinogen III oxidase (predicted)	coproporphyrinogen III oxidase (predicted)	0.72	0.42	1.62
SPBC1921.06c	*pvg3*	beta-1,3-galactosyltransferase		1.03	1.46	1.62
SPAC1327.01c		transcription factor, zf-fungal binuclear cluster type (predicted)	transcription factor (predicted)	1.03	1.28	1.62
SPCC736.04c	*gma12*	alpha-1,2-galactosyltransferase Gma12	alpha-1,2-galactosyltransferase Gma12 (PMID 95003210)	0.76	0.93	1.62
SPCC1919.02		pig-X	pig-X	1.07	1.48	1.62
SPBC31F10.13c	*hip1*	hira protein Hip1		0.82	1.44	1.62
SPBC25B2.11	*pof2*	F-box protein Pof2		0.85	1.38	1.62
SPCC1620.07c		lunapark homolog	lunapark homolog	1.21	1.46	1.62
SPAC110.01	*ppk1*	serine/threonine protein kinase Ppk1 (predicted)	serine/threonine protein kinase Ppk1 (predicted)	0.99	1.46	1.62
SPBC215.01		GTPase activating protein		0.70	1.25	1.62
SPMIT.10	*atp9*	F0-ATPase subunit 9	F0-ATPase subunit 9; similar to S. cerevisiae Q0130	0.53	0.84	1.61
SPBC18E5.14c		sequence orphan		0.86	1.20	1.61
SPAC26H5.05		IPT/TIG ankyrin repeat protein	IPT/TIG ankyrin repeat protein	0.90	1.31	1.61
SPCC4G3.07c	*phf1*	PHD finger containing protein Phf1	PHD finger containing protein Phf1	0.91	1.22	1.61

SPAC823.05c	*tlg2*	SNARE Tlg2 (predicted)	SNARE Tlg2	0.84	1.24	1.61
SPBC2D10.04		arrestin Aly1 related		0.87	1.25	1.61
SPAC30D11.13	*hus5*	SUMO conjugating enzyme Hus5	SUMO conjugating enzyme Hus5	0.86	1.11	1.61
SPAC1687.15	*gsk3*	serine/threonine protein kinase Gsk3	serine/threonine protein kinase Gsk3	0.90	1.38	1.61
SPAC12G12.15	*sif3*	Sad1 interacting factor 3	Sad1 interacting factor 3	0.88	1.44	1.61
SPBC2F12.08c	*ceg1*	mRNA guanylyltransferase Ceg1		0.84	1.25	1.61
SPAC15E1.04		thymidylate synthase (predicted)	thymidylate synthase (predicted)	0.88	1.40	1.61
SPBC1198.10c		asparagine-tRNA ligase Slm5	asparagine-tRNA ligase Slm5	0.90	1.26	1.61
SPAC1296.05c		cyclin L family cyclin	cyclin L family cyclin	0.87	0.91	1.61
SPAC1556.08c	*cbs2*	protein kinase activator (predicted)		0.91	1.37	1.61
SPAC57A7.13		RNA-binding protein	RNA-binding protein	0.94	1.47	1.60
SPBC19C7.02	*ubr1*	N-end-recognizing protein Ubr1		0.77	1.28	1.60
SPBC11B10.06	*sws1*	SWIM domain containing-Srs2 interacting protein 1		1.00	1.25	1.60
SPAC3H1.12c	*snt2*	Lid2 complex subunit Snt2	Lid2 complex subunit Snt2 (PMID 12488447)	0.91	1.15	1.60
SPBC21C3.19		DUF1960 family protein		0.66	1.41	1.60
SPBC19C7.11		ClC chloride channel (predicted)		0.87	1.41	1.60
SPBC428.08c	*clr4*	histone H3 methyltransferase Clr4	histone H3 methyltransferase Clr4	0.88	1.41	1.60
SPCC162.07	*ent1*	epsin	epsin	0.91	1.33	1.59
SPAC3H5.09c		conserved fungal protein	conserved fungal protein	0.74	1.15	1.59
SPBC3E7.12c	*chr1*	chitin synthase regulatory factor (putative) Chr1		1.01	0.97	1.59
SPBC685.02		conserved eukaryotic protein		1.08	1.43	1.59
SPBC15D4.08c		dubious		0.61	0.93	1.59
SPCP1E11.05c		sterol O-acyltransferase (predicted)	sterol O-acyltransferase (predicted)	0.95	1.32	1.59
SPAC1486.02c	*ucp14*	UBA domain protein Ucp14	UBA domain protein Ucp14	0.84	1.32	1.59
SPAC23H3.02c	*ini1*	RING finger-like protein Ini1	RING finger-like protein Ini1	0.71	1.01	1.58
SPCC663.15c		conserved fungal protein	conserved fungal protein	0.94	1.46	1.58
SPAC2H10.01		transcription factor, zf-fungal binuclear cluster type (predicted)	transcription factor	0.55	1.28	1.58
SPCC1020.12c		xap-5-like protein	xap-5-like protein	0.90	1.49	1.58
SPCC777.03c		nifs homolog	nifs homolog	0.72	0.95	1.58
SPAPB24D3.03		agmatinase (predicted)	agmatinase (predicted)	0.88	1.26	1.58
SPCC1235.07	*fta7*	Sim4 and Mal2 associated (4 and 2 associated) protein 7	Sim4 and Mal2 associated (4 and 2 associated) protein 7 (PMID 16079914)	0.99	0.88	1.58
SPBC8D2.03c	*hhf2*	histone H4 h4.2		1.00	0.87	1.58
SPAC17A2.05	*osm1*	fumerate reductase	fumerate reductase	0.83	0.84	1.58

SPBC56F2.01	*pof12*	F-box protein Pof12		0.97	1.45	1.58
SPBP35G2.09	*usp103*	U1 snRNP-associated protein Usp103 (predicted)		0.92	1.02	1.58
SPCC23B6.04c		sec14 cytosolic factor family	sec14 cytosolic factor family	1.01	1.35	1.58
SPAC25B8.11		transcription factor (predicted)	transcription factor	0.97	1.46	1.58
SPAC7D4.03c		conserved fungal family	conserved fungal family	0.88	1.27	1.58
SPBP23A10.12		FRG1 family protein		0.68	1.09	1.57
SPAC589.11	*mug82*	mitochondrial translation release factor (predicted)	translation release factor (predicted)	0.75	1.13	1.57
SPAC3C7.07c		arginine-tRNA protein transferase (predicted)	arginine-tRNA protein transferase (predicted)	0.99	1.49	1.57
SPCC794.11c		ENTH domain protein Ent3	ENTH domain protein Ent3	0.99	1.32	1.57
SPBC800.03	*clr3*	histone deacetylase (class II) Clr3	histone deacetylase (class II) Clr3	1.01	1.39	1.57
SPBC4C3.06		actin cytoskeletal protein Syp1		0.97	1.37	1.57
SPAC20H4.10	*ufd2*	ubiquitin-protein ligase E4 (predicted)	ubiquitin-protein ligase E4 (predicted)	0.98	1.49	1.57
SPAC24H6.06	*sld3*	DNA replication pre-initiation complex subunit Sld3	pre-initiation complex subunit Sld3 (PMID 12006645)	0.91	1.33	1.57
SPAC29E6.10c		kinetochore protein (predicted)	kinetochore protein (predicted)	0.81	1.14	1.57
SPCC895.04c	*ufe1*	SNARE Ufe1	SNARE Ufe1	0.90	1.42	1.57
SPBC3F6.05	*rga1*	GTPase activating protein Rga1		1.19	1.37	1.56
SPAC22E12.19		histone deacetylase complex subunit (predicted)	histone deacetylase complex subunit (predicted)	0.93	0.89	1.56
SPAC4F8.11		WD repeat protein, human WDR24 family	WD repeat protein, human WDR24 family	0.82	1.43	1.56
SPCC1827.08c	*pof7*	F-box protein Pof7	F-box protein Pof7	0.79	1.28	1.56
SPCC24B10.16c		sequence orphan	sequence orphan	0.85	1.50	1.56
SPAC664.07c	*rad9*	checkpoint clamp complex protein Rad9	checkpoint clamp complex protein Rad9	1.19	1.27	1.56
SPAC1002.18	*urg3*	DUF1688 family protein	DUF1688 family protein	0.79	1.19	1.56
SPBC1861.09	*ppk22*	serine/threonine protein kinase Ppk22 (predicted)		0.83	1.21	1.56
SPBC83.09c		GYF domain		0.81	1.10	1.56
SPAC3G9.07c	*hos2*	histone deacetylase (class I) Hos2	histone deacetylase (class I) Hos2	0.82	0.97	1.56
SPCC576.05		nucear export factor	nucear export factor	0.77	1.26	1.56
SPBC887.09c		leucine-rich repeat protein Sog2 (predicted)		0.94	1.26	1.56
SPAC57A10.09c		High-mobility group non-histone chromatin protein	High-mobility group non-histone chromatin protein	0.98	1.40	1.56

SPAC110.02	*pds5*	cohesin-associated protein Pds5	cohesin-associated protein Pds5	0.86	1.30	1.56
SPBC1348.11		membrane transporter	membrane transporter	0.42	0.48	1.55
SPCC4B3.04c	*nte1*	lysophospholipase	lysophospholipase	0.99	1.30	1.55
SPAC10F6.05c	*ubc6*	ubiquitin conjugating enzyme Ubc6	ubiquitin conjugating enzyme Ubc6	0.88	1.22	1.55
SPBC1215.01	*shy1*	SURF-family protein Shy1	SURF-family protein Shy1	0.87	1.37	1.55
SPAC22H10.11c				0.92	1.27	1.55
SPCC594.07c		sequence orphan	sequence orphan	0.97	1.30	1.54
SPAC24H6.09	*gef1*	RhoGEF Gef1	RhoGEF Gef1	0.90	1.16	1.54
SPCC584.05	*sec1*	SNARE binding protein Sec1	SNARE binding protein Sec1	0.83	1.40	1.54
SPAC13C5.07	*rad32*	Rad32 nuclease	Rad32 nuclease	0.96	1.13	1.54
SPCC16C4.05		RNase P and RNase MRP subunit (predicted)	RNase P and RNase MRP subunit (predicted)	0.74	0.83	1.54
SPCC1827.02c		cholinephosphate cytidylyltransferase (predicted)	cholinephosphate cytidylyltransferase (predicted)	1.01	1.30	1.54
SPCC1235.03		SMR and CUE domain protein	SMR and CUE domain protein	0.65	1.31	1.54
SPAC9G1.02	*wis4*	MAP kinase kinase kinase Wis4	MAP kinase kinase kinase Wis4	0.77	1.23	1.53
SPAC17H9.18c		dubious	dubious	0.81	0.76	1.53
SPAC6G9.15c		sequence orphan	sequence orphan	0.76	1.06	1.53
SPCC645.13		transcription elongation regulator	transcription elongation regulator	0.93	1.37	1.53
SPAC2G11.12	*rqh1*	RecQ type DNA helicase Rqh1	RecQ type DNA helicase Rqh1	0.92	1.34	1.53
SPAC630.11	*vps55*	vacuolar sorting protein Vps55 (predicted)	vacuolar sorting protein Vps55 (predicted)	0.85	1.24	1.52
SPAC2F3.15	*lsk1*	latrunculin sensitive kinase Lsk1	latrunculin sensitive kinase Lsk1 (PMID 15537703)	0.92	0.96	1.52
SPCC162.08c	*nup211*	nuclear pore complex associated protein	nuclear pore complex associated protein	0.87	1.38	1.52
SPCC1235.10c	*sec6*	exocyst complex subunit Sec6	exocyst complex subunit Sec6	1.07	1.44	1.52
SPBC1685.07c		amino acid transporter (predicted)	amino acid transporter (predicted)	0.89	1.44	1.52
SPAC1002.02	*mug31*	nucleoporin Pom34 (predicted)	nucleoporin Pom34 (predicted)	0.94	0.86	1.52
SPCC1840.01c	*mog1*	Ran GTPase binding protein Mog1		0.78	1.48	1.52
SPBC14F5.13c		alkaline phosphatase (predicted)		0.95	1.31	1.52
SPCC1442.17c		DUF292 family protein	DUF292 family protein	0.95	1.03	1.52
SPAC20H4.06c		RNA-binding protein	RNA-binding protein	0.79	1.34	1.52
SPBC530.11c		transcription factor (predicted)		0.81	1.23	1.52
SPAC1565.02c		GTPase activating protein	GTPase activating protein	0.86	1.47	1.52
SPBC582.06c	*mcp6*	horsetail movement protein Hrs1/Mcp6	meiosis specific coiled-coil protein Mcp6	1.01	0.86	1.52

SPAC1A6.01c		human thyroid receptor interacting protein homolog	human thyroid receptor interacting protein homolog	0.89	1.23	1.51
SPBC2A9.02		NAD dependent epimerase/dehydratase family protein		0.95	1.19	1.51
SPAP27G11.14c		sequence orphan	sequence orphan	0.81	1.16	1.51
SPCC830.05c	*epl1*	histone acetyltransferase complex subunit Epl1 (predicted)	histone acetyltransferase complex subunit Epl1 (predicted)	0.77	1.17	1.51
SPCC553.01c		meiotic chromosome segregation protein		0.86	1.29	1.51
SPBC1734.07c		TRAPP complex subunit Trs85 (predicted)		0.74	0.93	1.51
SPCC1020.13c		phospholipase (predicted)	phospholipase (predicted)	0.96	1.29	1.51
SPBC56F2.11	*met6*	homoserine O-acetyltransferase		0.88	1.22	1.51
SPBC409.03	*swi5*	Swi5 protein		0.75	1.02	1.51
SPBC16A3.01	*spn3*	septin Spn3		0.89	1.20	1.51
SPBC530.14c	*dsk1*	SR protein-specific kinase Dsk1		0.91	1.06	1.51
SPCC663.01c	*ekc1*	protein phosphatase regulatory subunit Ekc1 (predicted)	protein phosphatase regulatory subunit Ekc1 (predicted)	1.03	1.44	1.51
SPBC11C11.11c		mitochondrial ATP-dependent DNA helicase Irc3 (predicted)		0.92	1.37	1.51
SPBC3B9.15c	*scp1*	sterol regulatory element binding protein Scp1		0.98	1.09	1.51
SPAC1805.01c	*ppk6*	serine/threonine protein kinase Ppk6	serine/threonine protein kinase Ppk6	0.89	1.08	1.50
SPBC29A10.13	*atp7*	F0-ATPase subunit D		0.83	1.41	1.50
SPBC146.11c	*mug97*	meiotically upregulated gene Mug97		0.66	0.96	1.50
SPAC16C9.07	*ppk5*	serine/threonine protein kinase Ppk5 (predicted)		0.87	1.43	1.50
SPBC577.06c		phosphatidylinositol kinase (predicted)		0.84	0.97	1.50
SPAC31A2.11c	*cuf1*	Cu metalloregulatory transcription factor Cuf1	Cu metalloregulatory transcription factor Cuf1 (PMID 10593913)	0.92	1.24	1.50
SPBP35G2.02		DUF1000 family protein		0.87	1.32	1.50
SPBC2D10.14c	*myo51*	myosin type V		0.96	1.15	1.50