TABLE S1. Up- or down-regulated genes in non-sexual and sexual flocculation cells compared to non-flocculation cells

		WT	rpl32-1Δ			rpl32-2Δ			Haploid cells mixtures in YEPD	Diploid cells		
Gene Name	Annotation[a]	Mean	Mean	Fold Change[b]	P Value	Mean	Fold Change[b]	P Value	Mean	Mean	Fold Change[b]	P Value
ribosomal proteins												
rps1401[c]	40S ribosomal protein S14	5633.44	1248.06	**-4.52**	0.036	1326.02	**-4.25**	0.015	6315.58	2689.44	**-2.35**	0.026
rpl1603	60S ribosomal protein L13/L16	3300.57	2580.24	**-1.28**	0.033	2634.41	**-1.25**	0.034	3585.11	2675.73	**-1.34**	0.026
rpl1002	60S ribosomal protein L10	17886.71	14802.71	**-1.21**	0.034	14795.97	**-1.21**	0.011	16627.69	12594.82	**-1.31**	0.040
rpl3002[c]	60S ribosomal protein L30	4617.83	3830.89	**-1.21**	0.022	3837.77	**-1.20**	0.043	5565.13	4215.37	**-1.32**	0.017
rpl3201[c]	60S ribosomal protein L32	15052.34	18.00	**-836.11**	0.017	30959.65	**2.06**	0.018	14405.18	9593.92	**-1.50**	0.011
rps2401	40S ribosomal protein S24	14735.41	12052.33	**-1.22**	0.041	14409.47	-1.02	0.011	14220.65	11075.36	**-1.28**	0.045
rpl3202	60S ribosomal protein L32	17587.95	36239.27	**2.06**	0.027	152.37	**-115.42**	0.020	16567.86	11080.26	**-1.50**	0.030
rpl101	60S ribosomal protein L10a	18816.36	18969.15	1.01	0.026	18969.15	1.01	0.030	18094.96	11784.33	**-1.54**	0.042
rps1001[c]	40S ribosomal protein S10	10861.23	12052.49	1.11	0.041	11542.01	1.06	0.014	11121.78	7372.40	**-1.51**	0.009

rps1002[c]	40S ribosomal protein S10	14556.74	15476.00	1.06	0.032	15157.35	1.04	0.011	14060.89	9911.73	**-1.42**	0.011
rps2201	40S ribosomal protein S15a	14333.47	15542.50	1.08	0.032	14871.41	1.04	0.011	13948.28	11190.53	**-1.25**	0.045
rpl703	60S ribosomal protein L7	2739.70	6017.69	**2.20**	0.014	5063.29	**1.85**	0.032	2920.91	2377.35	**-1.23**	0.029
rps3001	40S ribosomal protein S30	13630.96	14623.43	1.07	0.036	14222.28	1.04	0.012	12263.64	9984.89	**-1.23**	0.011
rps1701	40S ribosomal protein S17	15215.98	16107.03	1.06	0.031	16565.03	1.09	0.034	14777.35	12035.24	**-1.23**	0.042
rps2601	40S ribosomal protein S26	13941.52	15681.42	1.12	0.032	15571.84	1.12	0.011	12662.72	10313.09	**-1.23**	0.011
rps002	40S ribosomal protein S0B	16414.69	16414.69	1.00	0.030	16414.69	1.00	0.034	15292.11	12486.72	**-1.22**	0.040
rps1901	40S ribosomal protein S19	19155.88	19207.22	1.00	0.026	19155.88	1.00	0.029	18104.99	14801.21	**-1.22**	0.034
rps401	40S ribosomal protein S4	13976.35	13976.35	1.00	0.036	13976.35	1.00	0.011	13624.35	11224.91	**-1.21**	0.045
rpl1801	60S ribosomal protein L18	14692.58	15140.85	1.03	0.033	15045.05	1.02	0.011	14273.98	11817.19	**-1.21**	0.042
rpl3001[c]	60S ribosomal protein L30	17511.32	18269.91	1.04	0.027	17742.12	1.01	0.032	16679.63	12456.60	**-1.34**	0.040
ribosomal biogenesis proteins												
urb2[c]	ribosome biogenesis protein Urb2 (predicted)	949.35	743.77	**-1.28**	0.013	759.67	**-1.25**	0.026	997.52	766.36	**-1.30**	0.033
SPBP16F5.06	ribosome biogenesis protein Nop6	692.14	552.76	**-1.25**	0.018	511.85	**-1.35**	0.039	305.91	199.86	**-1.53**	0.030

SPAC890.05	ribosome biogenesis protein (predicted)	1984.28	1705.68	-1.16	0.050	1912.93	-1.04	0.046	739.57	376.74	**-1.96**	0.016
SPAC1952.02	ribosome biogenesis protein (predicted)	795.50	767.77	-1.04	0.013	830.70	1.04	0.024	550.99	380.96	**-1.45**	0.016
brx1	ribosome biogenesis protein Brx1	4530.33	5137.57	1.13	0.017	5062.42	1.12	0.032	1661.42	1264.63	**-1.31**	0.020
SPAC3F10.17	ribosome biogenesis protein Ltv1 (predicted)	3782.44	3822.04	1.01	0.022	3835.39	1.01	0.043	680.65	527.71	**-1.29**	0.047
SPAC1486.09	ribosome biogenesis protein Nob1 (predicted)	4274.68	4374.11	1.02	0.034	4182.13	-1.02	0.039	816.10	540.52	**-1.51**	0.046
SPAC4F10.09c	ribosome biogenesis protein Noc1 (predicted)	2001.83	1963.71	-1.02	0.044	1732.39	-1.16	0.033	768.91	544.89	**-1.41**	0.046
SPBC83.15	ribosome biogenesis protein Nsa1	1474.80	1577.87	1.07	0.028	1541.46	1.04	0.029	390.84	307.90	**-1.27**	0.019
SPCP1E11.08	ribosome biogenesis protein Nsa2 (predicted)	10258.98	12704.83	**1.24**	0.020	11230.71	1.09	0.031	1928.82	1586.63	**-1.22**	0.016
SPCC4G3.18	ribosome biogenesis protein Rix1 (predicted)	1298.11	1261.07	-1.03	0.036	1258.13	-1.03	0.016	772.62	604.75	**-1.28**	0.041
SPAPB8E5.07c	ribosome biogenesis protein Rrp12	1721.44	1724.28	1.00	0.049	1711.17	1.00	0.026	571.62	467.30	**-1.22**	0.013
SPBC947.07	ribosome biogenesis protein Rrp14-C	669.62	609.37	-1.10	0.016	669.62	1.00	0.030	250.67	199.59	**-1.26**	0.030
rrs1	ribosome biogenesis protein Rrs1 (predicted)	1426.83	1659.62	1.16	0.052	1619.73	1.14	0.028	643.13	454.87	**-1.41**	0.013
SPAC23H4.15	ribosome biogenesis protein Tsr1 (predicted)	2057.68	2192.25	1.07	0.039	2214.59	1.08	0.040	1091.81	796.05	**-1.37**	0.031

SPCC14G10.02	ribosome biogenesis protein Urb1	841.91	981.51	1.17	0.046	871.25	1.03	0.023	441.51	330.81	**-1.33**	0.018
nop16	ribosome biogenesis protein Nop16 (predicted)	2373.50	2420.21	1.02	0.036	2385.87	1.01	0.037	441.10	177.15	**-2.49**	0.034
ribosome synthesis-regulating transcription factors												
SFP1[c]	Transcription factor that controls expression of ribosome biogenesis genes in repression	9.11	9.11	1.00	0.011	9.11	1.00	0.022	11.49	13.97	**1.22**	0.021
CRF1	Transcriptional co-repressor involved in repression of ribosomal protein (RP) gene	7.93	7.93	1.00	0.013	7.93	1.00	0.025	10.46	12.60	**1.21**	0.024
Pheromone response pathway (MAPK signal pathway)												
STE11[c]	Signal transducing MEK kinase involved in pheromone response	15.14	26.85	**1.77**	0.019	26.01	**1.72**	0.038	171.39	20.36	**8.41**	0.035
pmk1[c]	MAP kinase Pmk1	1001.53	1233.16	**1.23**	0.036	1064.71	**1.26**	0.019	1269.90	1788.71	**1.41**	0.014
cmk2	MAPK-activated protein kinase Cmk2	245.11	426.14	**1.74**	0.012	329.03	**1.34**	0.024	268.40	379.48	**1.41**	0.016
byr1	MAP kinase kinase Byr1	2198.95	2772.39	**1.26**	0.031	3110.40	**1.41**	0.029	2364.80	3050.59	**1.29**	0.023
srk1	MAPK-activated protein kinase Srk1	1332.67	824.57	**-1.62**	0.012	817.19	**-1.63**	0.024	1497.67	4191.64	**2.80**	0.017
STE12	Transcription factor that is activated by a MAP kinase signaling cascade	28.89	29.72	1.03	0.017	29.72	1.03	0.034	40.36	53.18	**1.32**	0.027

sin1	stress activated MAP kinase interacting protein Sin1	894.37	651.98	**-1.37**	0.015	685.41	**-1.30**	0.029	976.55	1185.04	**1.21**	0.021
pka1[c]	cAMP-dependent protein kinase catalytic subunit Pka1	2378.11	976.17	**-2.44**	0.046	1110.66	**-2.14**	0.018	4026.47	3056.57	**-1.24**	0.023
Sexual reproduction												
mug57[c]	meiotically upregulated gene Mug57	102.77	200.03	**1.95**	0.012	202.70	**1.97**	0.040	177.45	288.68	**1.63**	0.021
mug97	meiotically upregulated gene Mug97	34.19	59.33	**1.73**	0.019	72.82	**2.13**	0.041	45.17	65.89	**1.46**	0.024
mei4	meiotic forkhead transcription factor Mei4	46.01	59.61	**1.30**	0.009	80.37	**1.75**	0.037	69.59	104.19	**1.50**	0.015
SPCC1442.04c	meiotic recombination protein (predicted)	116.70	127.57	**1.29**	0.020	152.69	**1.31**	0.020	122.67	204.18	**1.66**	0.029
SPAC11D3.03c	meiotic chromosome segregation protein	83.70	246.14	**2.94**	0.010	281.44	**3.36**	0.028	95.17	65.60	**-1.45**	0.024
rec15	meiotic recombination protein Rec15	15.13	24.02	**1.59**	0.021	27.87	**1.84**	0.036	20.72	17.52	-1.18	0.040
mug146	meiotically upregulated gene Mug46	102.70	133.03	**1.30**	0.019	153.47	**1.49**	0.020	129.40	109.27	-1.18	0.015
mug5	meiotically upregulated gene Mug5	30.17	51.37	**1.70**	0.010	49.18	**1.63**	0.020	19.85	14.63	**-1.36**	0.021
tht2	meiotically upregulated gene Mug22	28.44	41.34	**1.45**	0.012	40.84	**1.45**	0.034	30.65	21.01	**-1.46**	0.033
rec8	meiotic cohesin complex subunit Rec8	33.54	33.54	1.00	0.015	33.54	1.00	0.030	49.66	71.05	**1.43**	0.023

rec10	meiotic recombination protein Rec10	112.85	67.03	**-1.68**	0.016	80.12	**-1.41**	0.037	131.28	164.18	**1.25**	0.037
rec25	meiotic recombination protein Rec25	46.27	51.37	1.11	0.010	51.37	1.11	0.019	56.53	72.65	**1.29**	0.022
mug184	meiotically upregulated gene Mug184	84.70	41.27	**-2.05**	0.012	65.03	**-1.30**	0.015	117.20	158.59	**1.35**	0.038
mug66	meiotically upregulated gene Mug66	143.83	158.70	1.10	0.016	158.70	1.10	0.019	181.76	454.43	**2.50**	0.013
MEI5	Meiosis specific protein involved in DMC1-dependent meiotic recombination	6.67	6.67	1.00	0.015	6.67	1.00	0.030	7.58	9.48	**1.25**	0.032
REC8	Meiosis-specific component of sister chromatid cohesion complex	29.72	29.72	1.00	0.017	29.72	1.00	0.034	49.66	71.05	**1.43**	0.023
SMA2	Meiosis-specific prospore membrane protein	20.33	21.26	1.05	0.014	21.26	1.05	0.047	27.36	37.02	**1.35**	0.019
Sporulation and spore formation												
mde10[c]	spore wall assembly peptidase Mde10	596.03	746.70	**1.25**	0.013	789.27	**1.32**	0.025	671.15	776.10	**1.26**	0.032
meu14	sporulation protein Meu14	76.17	102.70	**1.35**	0.024	102.70	**1.35**	0.029	86.43	115.46	**1.34**	0.052
ADY3	Protein required for spore wall formation	9.99	12.14	**1.21**	0.016	10.68	**1.27**	0.019	11.99	14.09	**1.28**	0.021

SPO75	Meiosis-specific protein of unknown function, required for spore wall formation	15.79	15.79	1.00	0.019	15.79	1.00	0.032	14.65	17.95	**1.23**	0.039
ISC10	Protein required for sporulation, transcript is induced 7.5 hours after induction	13.30	13.30	1.00	0.015	13.30	1.00	0.015	12.54	15.12	**1.21**	0.020
SSP2	Sporulation specific protein that localizes to the spore wall; required for sporulation	8.72	9.11	1.04	0.011	9.11	1.04	0.022	9.87	11.94	**1.21**	0.025
CRR1	Putative glycoside hydrolase of the spore wall envelope; required for normal sporulation	15.18	15.18	1.00	0.020	15.49	1.02	0.013	19.46	24.15	**1.24**	0.029
Potential agglutination proteins												
SPBC947.04[c]	cell surface glycoprotein (predicted), DIPSY family, 47.5% homology with S. pombe adhesin Mam3	672.03	2843.93	**4.23**	0.030	1803.99	**2.68**	0.025	768.69	2624.16	**3.41**	0.027
SPBPJ4664.02	cell surface glycoprotein (predicted), 55.1% homologue with S. cerevisiae adhesin FLO11	656.27	1992.06	**3.04**	0.043	1303.66	**1.99**	0.015	99.37	245.91	2.47	0.014
SPAC186.01	cell surface glycoprotein (predicted), DIPSY family, 53.1% homology with S. pombe adhesin Mam3	238.95	538.90	**2.26**	0.019	624.70	**2.61**	0.032	249.55	500.35	**2.01**	0.039

Mug2	cell surface glycoprotein (predicted), DUF1773 family protein 1	141.85	224.85	**1.59**	0.011	171.37	**1.21**	0.0.18	76.99	111.07	**1.44**	0.025
SPCC569.01c	cell surface glycoprotein (predicted), DUF1773 family protein 5 /// cell surface	984.54	1433.52	**1.46**	0.043	1413.70	**1.44**	0.020	1080.74	1561.71	**1.45**	0.016
SPBC359.04c	cell surface glycoprotein (predicted), DIPSY family, 50.4% homology with S. pombe adhesin Map4	343.03	433.63	**1.26**	0.012	454.69	**1.33**	0.044	384.72	604.61	**1.57**	0.041
ecm33	cell wall protein Ecm33	4615.59	5854.92	**1.27**	0.022	5468.09	**1.28**	0.030	7788.34	8409.62	1.08	0.048
SPAC977.07c	cell surface glycoprotein (predicted) /// cell surface glycoprotein (predicted), 50.6% homology with S. pombe adhesin Map4	116.36	148.23	**1.27**	0.017	198.03	**1.70**	0.040	177.89	107.05	**-1.66**	0.015
Mam3	cell agglutination protein Mam3	726.13	490.05	**-1.48**	0.013	404.37	**-1.80**	0.049	637.44	820.46	**1.29**	0.030
Map4	cell surface agglutination protein Map4	645.40	603.04	-1.07	0.017	580.32	-1.11	0.034	688.65	903.50	**1.31**	0.028
Dan1	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p	24.60	22.35	-1.10	0.013	22.35	-1.10	0.0.45	21.01	26.98	**1.28**	0.026
Dan4	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p	27.99	27.99	1.00	0.018	26.97	-1.04	0.037	33.05	48.25	**1.46**	0.033

pau24	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p	19.45	20.09	1.03	0.015	19.45	1.00	0.051	32.76	43.41	**1.33**	0.037
ccw12	Cell wall mannoprotein, mutants are defective in mating and agglutination	62.03	62.03	1.00	0.018	62.03	1.00	0.016	100.66	122.61	**1.22**	0.049

[a]: Annotations are from Gene DB (http://www.genedb.org/genedb/pombe/index.jsp).

[b]: Bold numbers indicated ＞1.2 fold change (P<0.05).

[c]: Changes in transcripts level were confirmed by QPCR.

TABLE S2. PCR primers* used in this study

Primer	Sequence
Primers for target gene deletion	
rpl32-1 deletion	
RPL32-1D1	5'-gtgctgtattggtttcatattttaataaag-3'
RPL32-1D2	5'-gcaagctaaacagatctgttttcgaccgttgc-3'
RPL32-1D3	5'-cgccatccagtttaaaatttaaaaagctattc-3'
RPL32-1D4	5'-gttcgtttaaataacattgaagctcaag-3'
rpl32-2 deletion	
RPL32-2D1	5'-cagcgagagcggtagtcgcttgac-3'
RPL32-2D2	5'-gcaagctaaacagatctttctgttgtgtgggtg-3'
RPL32-2D3	5'-aaaaatatacaatgtaaccaaggatg-3'
RPL32-2D4	5'-cgccatccagtttaaaattagaatcacgacttag-3'
rpl21-2 deletion	
RPL21-2D1	5'-tagttctgaaataagcgcaacataa-3'
RPL21-2D2	5'-gctaaacagatcttgctgttcctg-3'
RPL21-2D3	5'-catccagtttaaattttaaaaaagaatg-3'
RPL21-2D4	5'-ttttgcagccttcacgaatgt-3'
rpl9-2 deletion	
RPL9-2D1	5'-cactttttccatcggtccagaa-3'
RPL9-2D2	5'-gctaaacagatctgttgatgttgtt-3'
RPL9-2D3	5'-catccagtttaaaatgtatcacatgc-3'
RPL9-2D4	5'-catcctcgatacattattgtaatttttg-3'
mpg deletion	
Mpg-D1	5'-caatcttccagcgtagtgcgtgaag-3'
Mpg-D2	5'-gctaaacagatctaatagcaatttaatac-3'
Mpg-D3	5'-ccatccagtttaaagatactacatttaac-3'
Mpg-D4	5'-agcaaattaagaaatctcaagaagaag-3'
fbp deletion	
Fbp-D1	5'-cttgagatcacttaatgtagcttacgg-3'
Fbp-D2	5'-gctaaacagatctgttcgatcttaatg-3'
Fbp-D3	5'-ccatccagtttaaaaagaaaattcttt-3'
Fbp-D4	5'-cgctattttgtgagtttttcgatatc-3'
Primers for gene expression in *S. pombe*	
RPL32-1 expression	
upL32-1	5'-atcccatatgatggctgcaatcaacattgtc-3' (*Nde* I)
doL32-1	5'-gcagggatccctaagcgtccaagatgtc-3' (*Bam*H I)

RPL32-2 expression	
upL32-2	5'-atcccatatgatggctgctgtcaatatcatc-3' (*Nde* I)
doL32-2	5'-gcagggatccttactcctgagagcgaatt-3' (*Bam*H I)
KanMX6 expression	
upMX6	5'-atcccatatgatggggtaaggaaaag-3' (*Nde* I)
doMX6	5'-gcagggatccgattagaaaaactcatcgag-3' (*Bam*H I)
Primers for QPCR	
rpl32-1	
SP3201F	5'-ggctgcaatcaacattgtcaaaaagcg-3'
SP3201R	5'-gttcgacatcagagacattgcgaacaag-3'
rpl32-2	
SP3202F	5'-ggctgctgtcaatatcatcaagaagcg-3'
SP3202R	5'-gctcaacatctgaaacgttacggactag-3'
beta-actin	
SPACTF	5'-ggattcctacgttggtgaagctc-3'
SPACTR	5'-gggttcaaaggagcctcaaac-3'
rpl30-1	
SP3001F	5'-ctgtggttaccaagaagtctaaaaagagc-3'
SP3001R	5'-cagcgtaatggtgaacatttgcc-3'
rpl30-2	
SP3002F	5'-gctgcacctaccactgcacc-3'
SP3002R	5'-ctgtagtggtgtacagagcagcg-3'
rps10-1	
SP1001F	5'-gcaaagctattcatcaagcccttttttc-3'
SP1001R	5'-ggtaaccagcatcagcagaagc-3'
rps10-2	
SP1002F	5'-ggccattcatcaagctttgttcc-3'
SP1002R	5'-ccagcatcagcagcagagc-3'
Primers for gene expression in *E. coli*	
RPL32-2 expression	
upL32-2	5'-cagtgaattcatggctgctgtcaatatc-3' (*Eco*R I)
doL32-2	5'-gcagctcgagttactcctgagagcgaatt-3' (*Xho* I)
Primers for determination of haploid and diploid yeast cells	
MT1	5'-agaagagagagtagttgaag-3'
MP	5'-acggtagtcatcggtcttcc-3'
MM	5'-tacgttcagtatacgtagtg-3'

*, all the oligonucleotide primers were synthesized by Sangon Corporation (Shanghai, China).