

## §S11 Genes Implicated In Sexual Reproduction in Fungi

Table §S11.1 provides a list of 215 genes that are implicated in sexual reproduction in fungi. In all cases, if a gene is present in *A. nidulans*, it is present in all three fungi.

Gene	Function	<i>A.nidulans</i>	<i>A.fumigatus</i>	<i>A.oryzae</i>
<b>Mating Process</b>				
MAT1 (matB)	Mating-type (alpha-box domain transcriptional activator)	AN2755.2	-	20164.m00251*
MAT2 (matA)	Mating-type (HMG-box transcriptional activator)	AN4734.2	59.m09249	-
ppgA (MFa1, MFa2)	Pheromone precursor (alpha-factor like)	AN5791.2	69.m14805	20086.m00080*
ppgB (MFa1, MFa2)	Pheromone precursor (for a-factor like)	Ambiguous	Ambiguous	Ambiguous
(KEX1)	Carboxypeptidase alpha-factor processing	AN1384.2	70.m14837	20080.m00038*
KexB (KEX2)	Endoprotease for alpha-factor processing	AN3583.2	58.m07381	20179.m00626
(STE13)	Dipeptidyl aminopeptidase alpha-factor processing	AN2946.2	59.m09093	20174.m00466*
(STE23)	Dipeptidyl aminopeptidase for a-factor processing	AN8044.2*	53.m03900*	20129.m0021*
(RCE1)	CAAX prenyl protease a-factor C-terminal processing	AN6528.2	62.m03116	20107.m00091*
(STE24)	CAAX prenyl protease	Yes**	58.m07859	20142.m00264*
(RAM1/STE16)	CAAX-farnesyltransferase beta subunit; a-factor modification	AN2002.2	58.m07610	20138.m00208*
(RAM2)	CAAX-farnesyltransferase alpha subunit	AN3867.2	58.m07839	20142.m00239*
(STE14)	CAAX-prenyl cysteine carboxymethyltransferase	AN6162.2	72.m19009	20177.m00422*
atrD (STE6)	ATP-dependent efflux pump for a-factor like pheromone	AN2300.2	58.m08958	20136.m00137*
<b>Mating Signalling</b>				
preB (STE 2)	Pheromone Receptor (for alpha-factor like pheromone)	AN2520.2	59.m08468	20123.m00180*
preA (STE 3)	Pheromone Receptor (for a-factor like pheromone)	AN7743.2	71.m15771	20162.m00356*
fadA (GPA1)	Alpha-subunit G protein	AN0651.2	70.m15256	20180.m01174
sfaD (STE 4)	Beta-subunit G protein	AN0081.2	71.m15359	20148.m002796*
(STE5)	Scaffold protein	-	-	-
(STE18)	Gamma-subunit G protein	AN2742.2 *	54.m06689	20175.m00541*
(STE20)	Serine/threonine protein kinase MKKKK	AN2067.2*	57.m05766	20178.m00629*
steC (STE11)	Serine/threonine protein kinase MKKK	AN2269.2	71.m15914	20132.m00123*
(STE7)	Serine/threonine protein kinase MKK	AN3422.2*	59.m09275	20164.m00222*
mpkB (FUS3)	Mitogen-activated protein kinase	AN3719.2	69.m15727	20178.m00764*
steA (Ste12)	Transcriptional Activator. Homeodomain DNA binding	AN2290.2	71.m15938*	20132.m00151*
(FAR1)	Cell cycle arrest in G1/various other roles	-	-	-

(STE50)	Pheromone adaptation feedback response	AN7252.2 *	72.m19797	20134.m00115*
(DIG1/RST1)	Transcription factor, interacts ste12 pheromone response	-	-	-
(DIG2/RST2)	Transcription factor, interacts ste12 pheromone response	-	-	-

## Fruiting Body Development

veA	Velvet activator induces sexual reproduction <i>A.nidulans</i>	AN1052.2	70.m15191*	20173.m00346*
NsdD	GATA-transcription factor	AN3152.2	59.m08512*	20010.m00003*
CsnD	Signalosome subunit 4, regulation of sexual development	AN1539.2	55.m03058*	20171.m00527*
CsnE	Signalosome subunit 5, regulation of sexual development	AN2129.2	72.m19712*	20115.m00100*
rosA	Binuclear zinc transcription factor	AN5170.2	69.m14866	20084.m00028
mutA	Mutanase, cell wall turnover during sexual development	AN7349.2	57.m05694*	20150.m00367*
stuA	APSES-transcription factor	AN5836.2	72.m19916*	20177.m00377*
medA	Transcription factor	AN6230.2	72.m19977*	20141.m00193*
prot1 <sup>††</sup>	Cys6-Zn2 transcriptional activator	AN1848.2*	58.m07662*	20129.m00151*
Nc mat A-2	mating type TF; conserved amphipathic helix	No	No	No
Nc mat A-3	mating type HMG box TF	No	No	No
Nc asd-1	ascus development; rhamnogalacturonase B	AN7135.2	89.m02015	20153.m00219
Nc asd-4	ascus development; GATA-Zn finger transcription factor	areB	72.m19434	20141.m00163
Nc mei-3 (Sc RAD52)	meiosis defective;	uvsC	uvsC	uvsC
Um rum1	repressor of b mating type regulated genes	AN8211.2	53.m03763	20147.m00252
Um umc1	MADS-box TF, modulator of pheromone-inducible gene expression	AN8676.2	62.m03394	20152.m00250
Pa cro1 (Sc SHE4)	regulator of myosin function;required for syncytial to cellular transition	AN0135.2	71.m15419	20158.m00313

## Budding and Fission Yeast Genes Involved in Mating, Karyogamy and Meiosis

Sc BIM1	microtubule-binding protein	AN2862.2	59.m08708	20175.m00472
Sc BNI1	formin	AN6523.2	62.m03112	20107.m00085
Sc CDC31	spindle pole body component	AN5618.2*	58.m07543*	20138.m00126*
Sc CSM1	mediates accurate chromosome segregation during Meiosis I	No	No	No
Sc CSM3	mediates accurate chromosome segregation during meiosis	No	No	No
Sc DIT1	sporulation-specific enzyme required for spore wall maturation	AN2705.2	67.m02885	20137.m00125
Sc HO	endonuclease, mating type switching	No	No	No
Sc IDS2	modulator of lme2 activity	No	No	No
Sc IME1	master transcriptional regulator of meiosis	No	No	No
Sc IME2	inducer of meiosis, S/T kinase	AN6243.2	72.m19414	20141.m00207
Sc IME4	mRNA N6-adenosine methyltransferase, IME1 regulation	No	No	No
Sc KAR1	required for karyogamy	No	No	No
Sc KAR3	kinesin-like motor required for karyogamy	AN6340.2	72.m19518	20135.m00123
Sc KAR4	TF required for mating and meiosis	No	No	No
Sc KAR5	nuclear membrane fusion during karyogamy	ambiguous	ambiguous	No

Sc KAR9	cytoplasmic microtubule orientation during karyogamy	No	No	No
Sc MUM2	essential for meiotic DNA replication	No	No	No
Sc MUS81	Holliday junction resolvase	AN3118.2	59.m08619	20140.m00135
Sc NAM8/MRE2	RNA binding protein required for meiotic recombination	AN9090.2	66.m04770	20169.m00407
Sc NDT80	meiosis-specific transcriptional activator	AN6015.2*	72.m19128*	20177.m00637*
Sc REC102	chromosome synapsis during meiotic recombination	No	No	No
Sc RIM4	RNA-binding protein, early and middle sporulation gene expression	No	No	No
Sc RME1	Zn finger transcriptional repressor of IME1	No	No	No
Sc STE6	ABC transporter required for a-factor transport	AN2300.2	58.m08958	20136.m00137
Sc SPO1	meiosis-specific phospholipase B	No	No	No
Sc SPO11	required for synaptonemal complex formation	AN8259.2	53.m03702	20147.m00194
Sc SPO13	meiosis specific protein required for Meiosis I and II	No	No	No
Sc SST2	RGS protein, regulates desensitization to alpha-factor	fibA	72.m19237	20082.m00044
Sc SPO22	meiosis-specific phospholipase A2	No	No	No
Sc SUM1	transcriptional repressor of middle sporulation-specific genes	No	No	No
Sc UME3/SSN8	C-type cyclin	AN2172.2	72.m19668	20180.m00841
Sc UME6	C6 Zn finger regulator of early meiotic genes	No	No	No
Sp atf21	bZip TF, involved in regulation of meiosis	AN6849.2*	59.m09396*	20175.m00406*
Sp bgs1	1,3-beta-glucan synthase subunit, Sp Mei4 target gene	AN3729.2	69.m15386	20179.m00743
Sp byr1	homologue of Sc STE7			
Sp byr2	homologue of Sc STE11			
Sp dhc1	dynein heavy chain, homologue of Sc DYN1	nudA	71.m15397	10004.m0006
Sp fus1	homologue of Sc BNI1			
Sp gpa1	GTP binding (alpha-1 subunit) involved in conjugation	AN3090.2	59.m08656	20171.m00394
Sp hsk1	homologue of Sc CDC7, Dbf4-dependent kinase	AN3450.2	59.m09313	20102.m00075
Sp isp5	amino acid permease involved in sexual differentiation	AN5678.2	65.m07404	20146.m00246
Sp isp6	serine protease involved in sexual differentiation	AN0238.2	71.m15644	20121.m00147
Sp lid2	homologue of Um rum1, Sc ECM5			
Sp ume3	homologue of Sc UME3			
Sp mam1	abc transporter for m-factor pheromone, homologue of Sc STE6			
Sp mam2	pheromone p-factor receptor, homologue of Sc STE2			
Sp mam4	M-factor farnesyl cysteine carboxyl methyltransferase	AN6162.2	72.m19009	20177.m00422
Sp map1	MADS-box domain TF, pheromone receptor activator	AN8676.2*	62.m03394*	20152.m00250*
Sp map2	P-factor pheromone	No	No	No
Sp map3	pheromone M-factor receptor, homologue of Sc STE3			
Sp mat1-Mc	mating-type M-specific polypeptide Mc, HMG-box TF	AN1962.2*	58.m09001*	20138.m00150*
Sp mat1-Mi	mating-type M-specific polypeptide Mi	No	No	No
Sp mat1-Pc	mating-type P-specific polypeptide Pc, HMG-box TF	No	No	No
Sp mat1-Pi	mating-type P-specific polypeptide Pi, homeodomain TF	No	No	No
Sp mde3	homologue of Sc IME2, Sp Mei4 target gene	AN6243.2	72.m19414	20141.m00207

Sp mde5	kelch repeat protein, Sp Mei4 target gene	No	No	No
Sp mde6	kelch repeat protein, Sp Mei4 target gene	No	No	No
Sp mde7	RNA-binding protein involved in meiosis, Sp Mei4 target	AN7700.2	71.m15729	20162.m00295
Sp mfm1,mfm2,mfm3	M-factor pheromone precursor	No	No	No
Sp mei2	RNA-binding protein involved in meiosis	AN6494.2*	62.m03081*	20059.m00031*
Sp mei3	meiosis inducing protein, inactivates Sp Ran1	No	No	No
Sp mei4	fork head domain TF, meiotic regulator	AN8858.2*	71.m15996*	20108.m00079*
Sp mes1	meiosis II protein, Sp Mei4 target gene	No	No	No
Sp meu1	Sp Mei4 target gene	apsB	62.m03168	20174.m00436
Sp meu14	involved in Meiosis II nuclear division, Sp Mei4 target gene	AN3931.2	69.m14916	20174.m00532
Sp mus81	homologue of Sc MUS81			
Sp pk1	homologue of Sc KAR3			
Sp rad22	DNA repair protein	radC	58.m08972	20110.m00135
Sp ran1/pat1	serine/threonine protein kinase, negative regulator of meiosis	AN4935.2	59.m08839	20175.m00321
Sp rec6	meiotic recombination protein	No	No	No
Sp rec8	cohesin complex (meiotic), homologue of Sc REC8	No	No	No
Sp rec10	sister chromatid cohesion	No	No	No
Sp rec11	sister chromatid cohesion	No	No	No
Sp rec12	homologue of Sc SPO11			
Sp rec15	meiotic recombination protein	No	No	No
Sp rem1	meiotic B-type cyclin	AN2137.2	72.m19703	20180.m00780
Sp rep1	regulator of pre-meiotic DNA replication	No	No	No
Sp rgs1	homologue of Sc SST2			
Sp rhp51	homologue of Sc RAD51//52, Nc mei-3	uvsC	uvsC	uvsC
Sp spk1	homologue of Sc FUS3	mpkB	69.m15727	20178.m00764
Sp spo6	homologue of Sc DBF4, required for origin of replication firing	nimO	69.m15647	20161.m00192
Sp ssm4	dynactin complex, homologue of Sc NIP100	AN6323.2	72.m19441	20141.m00154
Sp ste4	SAM domain, similar to Sc STE50	AN7252.2	72.m19797	20134.m00115
Sp ste6	GEF involved in conjugation; related to Sc CDC25	AN2130.2	72.m19711	20115.m00099
Sp ste7	meiotic suppressor protein	No	No	No
Sp ste11	HMG-box TF, target of pheromone signaling	AN3667.2*	58.m07428*	20179.m00464*
Sp spn5	septin, Sp Mei4 target gene	sepB	65.m07502	20176.m00407
Sp spn7	septin, Sp Mei4 target gene	AN4667.2	71.m15708	20176.m00407
Sp sx2	serine carboxypeptidase, degrades extracellular P-factor	AN2555.2	57.m05650	20156.m00343
Sp tht1	homologue of Sc KAR5			

## Core Meiotic Transcriptome Conserved in *S. cerevisiae* and *S. pombe*

### Anaphase-promoting complex

Sc CDC27/ Sp nuc2	APC component	bimA	72.m19026	20177.m00440
Sc APC4/ Sp cut20	APC component	AN0905.2	70.m15514	ambiguous

Sc CDC16/ Sp cut9	APC component	AN8002.2	53.m03844	20159.m00191
Sc APC1/ Sp cut4	APC component	AN2772.2	59.m09271	20164.m00226
Sc APC5/ Sp apc5	APC component	AN4735.2	59.m09246	20164.m00254
Sc CDC23/ Sp cut23	APC component	AN8013.2	53.m03861	20159.m00208
Sc CDC26/ Sp hcn1	APC component	No	No	No
Sc HCT1/ Sp ste9	APC regulator	AN2965.2	59.m09050	20174.m00432
Sc CDC20/ Sp mfr1	APC regulator	AN2965.2	59.m09050	20174.m00432
Sc AMA1/ Sp slp1	APC regulator	AN0814.2	70.m15414	20125.m00181
<b>Septins</b>				
Sc CDC10/ Sp spn2	septin	AN1394.2	70.m14828	20070.m00026
Sc CDC3/ Sp spn5	septin	sepB	65.m07502	20176.m00407
Sc SPR3/ Sp spn6	sporulation regulated septin	AN8182.2	53.m03797	20147.m00293
Sc SPR28/ Sp spn7	sporulation regulated septin	AN4667.2	71.m15708	20148.m00144
<b>Cell cycle regulators</b>				
Sc CDC14/ Sp clp1	protein phosphatase	AN5057.2	59.m08669	20175.m00513
Sc CDC5/ Sp plo1	polo kinase	AN1560.2	55.m03076	20176.m00605
Sc CLB1/ Sp cig2	B-type cyclin	nimE	58.m07451	20165.m00281
Sc CLB3/ Sp cdc13	B-type cyclin	AN2137.2	72.m19703	20180.m00780
Sc CLB4/ Sp cig1	B-type cyclin			
Sc CLB5	B-type cyclin			
Sc CLB6	B-type cyclin			
<b>Recombination/chromosome cohesion</b>				
Sc REC114/ Sp rec7	meiotic recombination protein	No	No	No
Sc DMC1/ Sp dmc1	DNA-binding helix-hairpin-helix protein, DNA strand exchange	AN9092.2	66.m04768	20169.m00401
Sc MND1/ Sp mcp7	recombinatino and meioic nuclear division, interacts with Hop2	AN1843.2	58.m07668	20129.m00169
Sc HOP2/ Sp meu13	prevents synapsis between nonhomologous chromosomes	No	No	No
Sc SMC3/ Sp smc3	cohesin	AN6364.2	72.m19496	20116.m00127
Sc REC8/ Sp rec8	cohesin complex (meiotic)	No	No	No
<b>Chromosome segregation</b>				
Sc STU1/ Sp dis1	spindle pole body component	AN5521.2	69.m15719	20178.m00784
Sc TID3/ Sp ncd10	chromosome segregation, kinetochore-associated Ndc80 complex	AN4969.2	59.m08873	20125.m00127
Sc UBC11/ Sp ubc11	ubiquitin-conjugating enzyme, chromosome segregation in Sp	AN5495.2	69.m15458	20178.m00805
<b>DNA repair</b>				
Sc RAD23/ Sp rhp23	DNA excision-repair, NEF2 subunit	AN2304.2	71.m15953	20108.m00125
Sc EXO1/ Sp exo1	DNA repair, recombination	AN3035.2	59.m08982	20174.m00347
Sc HRR25/ Sp hhp1	casein kinase involved in DNA repair and chromsome segregation	AN4563.2	57.m05554	20158.m00387
<b>Other genes in the conserved meiotic core program</b>				
Sc HUL4/ SPBP87.27	hect domain E3 ubiquitin-protein ligase	AN0444.2	54.m06635	20175.m00618
Sc LEE1/ Sp scp3	Zn finger transcription factor, unknown function	AN3447.2	59.m09478	20102.m00073
Sc ENA2/ Sp cta3	P-type ATPase sodium pump	AN6642.2, AN1628.2	62.m03239, 58.m07687	20132.m00104, 20136.m00211

Sc PMC1/ SPBC839.06	vacuolar ATPase Ca <sup>2+</sup> pump	AN1189.2	70.m15033	20168.m00440
Sc CMK2/ Sp cmk1	calmodulin-dependent protein kinase	AN3065.2,	59.m08933,	20174.m00277,
		AN2412.2	72.m19463	20073.m00030
Sc CHS1/ Sp chs1	chitin synthase, pheromone inducible	AN4566.2	57.m05488	20153.m00320
Sc ISA1/ SPCC645.03	mitochondrial matrix protein, iron metabolism	AN1974.2	58.m07579	20138.m00166
Sc HTZ1/ Sp pht1	histone H2AZ variant	AN8039.2	53.m03907	20167.m00250
Sc AUT7/ SPBP8B7.24	required for autophagic vesicle delivery to vacuole in Sc	AN5131.2	54.m06897	20128.m00130
Sc BAG7/ SPBC557.01	Rho-GAP	AN7650.2	57.m05408	20105.m00070
Sc ROM2/ SPAC1006.0	Rho-GEF	AN4719.2	71.m15707	10080.m00170
Sc RAS2/ Sp ras1	Ras	AN0182.2	71.m16065	20158.m00254
Sc GNA1/ Sp gna1	glucosamine acetyl transferase involved in cell cycle progression	AN8706.2	62.m03363	20152.m00287
Sc SGA1/ Sp meu17	sporulation-specific glucosamylase, Sp Mei4 target gene	AN8904.2	57.m05372	20130.m00115,
				20178.m00683
Sc CLG1/ SPBC1D7.03	cyclin-like protein interacts with Sc Pho85	AN4984.2	59.m08886	20125.m00144
Sc CYB2/ SPAB1A11.0	cytochrome-c oxidoreductase	AN3901.2	89.m01949	20115.m00086
Sc ECM4/ SPCC1281.0	glutathione-S-transferase domain, unknown function	AN5831.2	72.m19666	20097.m00066
Sc TOS7/ SPCC1739.1	unknown function in yeasts, putative membrane component of signal transduction pathways for pH regulation in <i>A. nidulans</i>	pal	59.m09122	20164.m00305
Sc ARN2/ SPCC61.01	ARN family of transporters for siderophore-iron chelates	AN5378.2	65.m07225	20176.m00502
Sc GTT1/ SPAC688.04	ER associated glutathione S-transferase	AN0629.2	70.m15652	20155.m00295
Sc RIB5/ SPCC1450.13	riboflavin synthase, alpha subunit	AN4231.2	54.m06785	20071.m00045
Sc CHO1/ SPCC1442.1	phosphatidylserine synthase	AN5661.2	58.m08891	20179.m00714
Sc XKS1/ SPCPJ732.0	xylose kinase	AN8790.2	71.m15584	20113.m00155
Sc PCT1/ SPCC1827.0	CTP:phosphocholine cytidyltransferase	AN1357.2	70.m14873	20074.m00033
Sc ELC1/ SPBC1861.0	transcription elongation factor	No	69.m15210	20101.m00073
Sc SYF2/ SPBC3E7.13	spliceosome component	AN1861.2	58.m07654	20129.m00143
Sc PGM2/ SPBC32F.12	phosphoglucomutase	AN2867.2	59.m08711	20175.m00469
Sc RKI1/ Sp ppi	ribose-5-phosphate isomerase	AN2440.2	69.m15218	20101.m00084
Sc SUR4/ SPAC1B2.03	long chain fatty acid elongation enzyme	AN8117.2	53.m03827	20159.m00172
Sc PIB1/ SPBC36B7.06	RING-type ubiquitin ligase, FYVE finger domain	AN0627.2*	70.m15658*	20174.m00539*, 20093.m00096*
Sc PIN3/ Sp csh3	SH3-domain protein	AN2995.2	59.m09437	20174.m00392
Sc SSO2/ Sp sso1	syntaxin	AN3416.2	66.m04618	20041.m00017
Sc FBP1/ Sp fbp1	fructose-1,6-biphosphatase	AN5604.2	58.m07528	20138.m00109
Sc GLG1/ SPBC4C3.08	self-glucosylating initiator of glycogen synthesis	AN4082.2	54.m06723	No
Sc ARE2/ SPAC13G7.0	acyl-CoA:sterol acyltransferase	AN4208.2	54.m06767	20068.m00041
Sc GDI1/ Sp gdi1	secretory pathway regulator	AN5895.2	72.m19235	20082.m00039
Sc PDC1/ SPAC3H8.01	pyruvate decarboxylase	AN4888.2	59.m08784	20175.m00382
Sc OXR1/ SPAC8C9.16	unknown function	AN3004.2	59.m09010	20174.m00378
Sc KGD1// SPBC3H7.0	mitochondrial alpha-ketoglutarate dehydrogenase complex	AN5571.2	58.m07497	20165.m00219
Sc DAP1/ SPAC26H5.1	Sc damage response, related to mammalian membrane progesterone	AN4939.2	59.m08843	20175.m00316

\* homology limited to functional domain

\*\*present but missing in official annotation

Sc=*Saccharomyces cerevisiae*; Sp=*Schizosaccharomyces pombe*; Nc=*Neurospora crassa*; Um=*Ustilago maydis*; Pa=*Podospora anserina*