Table 2. Ste11p target genes expressed in both cell types

Common name	Systematic name	Sexual diff. function	Known Ste11p target	Description
Regulation of meiosis				
mei2	*SPAC27D7.03c*	Meiotic defect	Yes	RNA-binding protein that regulates meiosis progression
sme2	*SPNCRNA.103*	Meiotic defect	Yes	Noncoding RNA that binds to mei2
ran1;pat1	*SPBC19C2.05*	Meiotic defect	Not studied	Protein kinase that negatively regulates meiosis
Regulation of mating/pheromone response				
spk1	*SPAC31G5.09c*	Abnormal mating	Predicted	MAP kinase of the pheromone pathway
pmp1;dsp1	*SPBC1685.01*	Not studied	Not studied	Protein phosphatase, may dephosphorylate spk1
pyp2	*SPAC19D5.01*	Not studied	Not studied	Protein phosphatase, may dephosphorylate spk1
gap1;src1;sar1	*SPBC646.12c*	Abnormal mating	Reported not regulated by starvation or pheromone	GTPase-activating protein, negative regulator of mating
rgs1	*SPAC22F3.12c*	Abnormal mating	Yes	Regulator of G protein signalling (RGS) family member
ste6	*SPCC1442.01*	Abnormal mating	Yes	Guanyl-nucleotide exchange factor, regulates conjugation
ste7	*SPAC23E2.03c*	Abnormal mating	Yes	Regulator of mating
gpa1	*SPBC24C6.06*	Abnormal mating	Induced by starvation, Ste11p-dependency not tested	G-alpha family
ste11;steX;aff1	*SPBC32C12.02*	Abnormal mating	Yes	Transcription factor, contains an HMG box
map1	*SPAC11E3.06*	Abnormal mating	Yes	MADS box transcription factor, regulates of mating-type specific genes
ste4	*SPAC1565.04c*	Abnormal mating	Yes	Contains SAM and RAS association domains, regulates mating
Nuclear movement				
dhc1	*SPAC1093.06c*	Meiotic defect	Induced by starvation, Ste11p-dependency not tested	Cytoplasmic dynein heavy chain, required for nuclear movement
Cell fusion				
fus1	*SPAC20G4.02c*	Abnormal cell fusion	Yes	Required for cell fusion
	SPAP7G5.03	Not studied	Not studied	Similar to *Sa. cerevisiae* Prm1p, which is required for mating
	SPAC31G5.07	Not studied	Not studied	Similar to *Sa. cerevisiae* Fig1p, which is required for mating
Nuclear fusion				
tht1	*SPAC13C5.03*		Not studied	Required for nuclear fusion after mating

Cell cycle regulators				
cig2;cyc17	*SPAPB2B4.03*	No	Not studied	G_1/S-phase cyclin
rum1	*SPBC32F12.09*	Abnormal mating	Not studied	cdk inhibitor
cdc10	*SPBC336.12c*	No	Not studied	Subunit of the MBF transcription factor complex, required for S phase
apc2	*SPBP23A10.04*	Not studied	Not studied	Component of the Anaphase Promoting Complex (APC)
Others				
ubp11	*SPBC19C2.04c*	Not studied	Not studied	Ubiquitin C-terminal hydrolase activity
shk2;pak2	*SPAC1F5.09c*	Normal mating	Not studied	PAK-related serine/threonine protein kinase
	SPCC162.10	Not studied	Not studied	Serine/threonine protein kinase
ehs1;yam8	*SPAC1F5.08c*	Abnormal mating	Not studied	Predicted glycoprotein, required for cell wall integrity
itr2	*SPAC20G8.03*	Abnormal mating	No, induced by glucose starvation	Myo-inositol transporter, essential gene
	SPBP4H10.11c	Not studied	Not studied	Long-chain-fatty-acid-CoA ligase activity (predicted)
cpp1	*SPAC17G6.04c*	Abnormal mating	Not studied	Beta subunit of farnesyltransferase (FTase)
rlc1	*SPAC926.03*	Not studied	Not studied	Myosin II regulatory light chain, involved in cytokinesis
rad54;rhp54	*SPAC15A10.03c*	Not studied	Not studied	DEAD/DEAH box helicase involved in DNA repair
	SPBC3F6.01c	Not studied	Not studied	Serine/threonine protein phosphatase
rep1;rec16	*SPBC2D10.06*	Normal mating	Yes	Transcription factor regulator of pre-meiotic DNA synthesis
	SPBC3D6.13c	Not studied	Not studied	Member of the protein disulfide isomerase oxidoreductase family
	SPAC4G9.14	Not studied	Not studied	Member of the Mpv17/PMP22 family of peroxisomal membrane proteins
etr1	*SPAC26F1.04c*	Not studied	Not studied	Enoyl-[acyl-carrier protein] reductase (predicted)
mcp5	*SPBC216.02*	Not studied	Not studied	Similarity to nuclear migration protein 1 (*Sa. cerevisiae* Num1p),
	SPAC7D4.09c	Not studied	Not studied	Member of the 3-oxo-5-alpha-steroid 4-dehydrogenase family
	SPBC13G1.02	Not studied	Not studied	Mannose-1-phosphate guanyltransferase (predicted)
rad17	*SPAC14C4.13*	Not studied	Not studied	Involved in DNA repair and replication checkpoint control
	SPBC4.01	Not studied	Not studied	Sequence orphan, unknown function
	SPBC146.02	Not studied	Not studied	Sequence orphan, unknown function
	SPCC338.18	Not studied	Not studied	Sequence orphan, unknown function
	SPAC29B12.11c	Not studied	Not studied	Orthologue of human WW domain binding protein-2, unknown function
	SPAC18G6.01c	Not studied	Not studied	Conserved hypothetical protein, unknown function
	SPAC8C9.16c	Not studied	Not studied	Unknown function, contains TLD domain
	SPAP27G11.14c	Not studied	Not studied	Sequence orphan, unknown function
	SPBC1604.01	Not studied	Not studied	Contains a domain of unknown function (DUF323)
	SPBC359.06	Not studied	Not studied	Contains a Class II aldolase domain and adducin N terminal domain
	SPBC902.06	Not studied	Not studied	Sequence orphan, predicted coiled-coil, localised to spindle pole body

	SPCC1393.07c	Not studied	Not studied	Sequence orphan, unknown function
eta2	*SPAC31G5.10*	Not studied	Not studied	Contains two Myb DNA-binding domains
	SPAC22A12.06c	Not studied	Not studied	Contains a domain of unknown function (DUF341)
	SPAC2C4.17c	Not studied	Not studied	Possible ion channel
	SPAC32A11.01	Not studied	Not studied	Conserved hypothetical protein, unknown function
pvg2	*SPAC27E2.07*	Normal mating	Not studied	Involved in cell wall biosynthesis
	SPBC19G7.14c	Not studied	Not studied	Sequence orphan, unknown function
elg1	*SPBC947.11c*	Not studied	Not studied	Replication factor C complex
omt2	*SPAC27D7.04*	Abnormal sporulation	Not studied	Required for spore wall formation
	SPBC354.08c	Not studied	Not studied	Contains a domain of unknown function (DUF221)
	SPAC227.06	Not studied	Not studied	Member of the YIP1 family, predicted to be involved in vesicle traffic

Ste11p targets were identified as described in the text. Column three indicates whether the genes are known to have a function in sexual differentiation and column four indicates whether their Ste11p-dependency has been studied. Mutant phenotypes and descriptions were compiled by using information from GeneDB (www.genedb.org), PombePD (www.proteome.com), and our own literature searches.