Table S1. Genes regulated by *pmt* mutations

Supplemental Table 1A

Transcript levels of genes in the *pmt1* mutant CAP1-312 relative to wild-type strain CAF2-1. The minimal FDR value calculated by the SAM program was 5.6 %. Only genes regulated at least by a factor 1.5 are shown. Functional assignments are according to http://mips.gsf.de/CYGD/db/index.html and http://www.candidagenome.org/

gene on array	**synonym**	**orf19 number**	**proposed function**	**q-value**	**fold regulation**	gene regulated in other mutants (*pmt* number)
Upregulation (59 genes)						
Unknown function or not classified						
IPF7109	*CA5650*	*orf19.7350*	unknown function	0.65	2.16	
IPF5217	*CA5382*	*orf19.7270*	unknown function	0.47	1.98	
IPF525	*CA5613*	*orf19.7085*	unknown function	0.93	1.98	
IPF9384	*CA4769*	*orf19.4001*	unknown function	0.65	1.91	
IPF14348.3f	*CA3231*	*orf19.6293.1*	unknown function, 3-prime end	4.91	1.89	
IPF8951	*CA2360*	*orf19.4897*	unknown function	0.47	1.84	↓: 4
IPF13577	*CA0434*	*orf19.1735*	unknown function	0.47	1.79	
IPF26	*CA6083*	*orf19.5976*	unknown function	3.98	1.79	
IPF1911	*CA5282*	*orf19.7139*	unknown function	3.98	1.71	
IPF19977	*CA3211*	*orf19.6192*	unknown function	3.98	1.70	↑: 5
IPF4129	*CA3647*	*orf19.2038*	unknown function	5.66	1.69	
IPF2233	*CA4580*	*orf19.6898.1*	unknown function	0.47	1.68	
IFF8	*CA2713*	*orf19.570*	unknown function	0.47	1.65	
IPF17380.2	*CA0078*	*orf19.381*	unknown function,5-prime end	0.79	1.57	
IPF1980	*CA5564*	*orf19.7328*	unknown function	4.14	1.54	↓: 6
IPF20054	*CA0262*	*orf19.6117*	unknown function	0.47	1.53	↓: 2
IPF2334	*CA5199*	*orf19.7013*	unknown function	5.66	1.53	
IPF9211.3f	*CA3141*	*orf19.3712*	unknown function, 3-prime end	3.98	1.51	
IPF8617	*CA0941*	*orf19.3705*	unknown function	3.26	1.51	
IPF4258	*CA4002*	*orf19.1634*	unknown function	4.63	1.51	
Cellular defense mechanisms, stress						
RTA2	*CA3607*	*orf19.24*	stress-associated protein	0.47	2.03	
AOX2.3f	*CA2189*	*orf19.4773*	alternative oxidase	0.47	1.92	
KAR2	*CA0915*	*orf19.2013*	DnaK-type molecular chaperone	0.47	1.89	↑: 5
RGD3	*CA3679*	*orf19.730*	Rho GTPase activating protein	0.47	1.87	
DDR48	*CA4336*	*orf19.4082*	stress protein	0.47	1.80	
SSR1	*CA5213*	*orf19.7030*	secretory stress response protein 1	0.47	1.70	
CDR1	*CA6066*	*orf19.6000*	multidrug resistance protein	0.47	1.64	
DEF1	*CA5968*	*orf19.7561*	induced by farnesol and high density	0.47	1.65	
GTT1	*CA4712*	*orf19.6947*	glutathione S-transferase	0.47	1.63	
HAC1	*CA0457*	*orf19.2432*	transcription factor (UPR pathway)	4.63	1.54	
SPR3	*CA0363*	*orf19.1524*	sporulation-specific septin	5.66	1.52	

Metabolism						
LPD1	*CA2998*	*orf19.6127*	dihydrolipoamide dehydrogenase	0.47	1.90	
RMT2.5eoc	*CA0119*	*orf19.920*	N-delta-arginine methyltransferase	0.47	1.78	
CFL1	*CA3460*	*orf19.1263*	ferric reductase	0.47	1.75	
KGD2	*CA2997*	*orf19.6126*	2-oxoglutarate dehydrogenase complex E2 component	0.47	1.66	
TFP3	*CA4937*	*orf19.6538*	H+-ATPase	0.65	1.60	
DPM1	*CA3899*	*orf19.5073*	dolichol phosphate mannose synthase	5.22	1.58	
ARD8	*CA3288*	*orf19.6322*	D-arabinitol dehydrogenase	1.50	1.58	
FGR28	*CA0296*	*orf19.1596*	adenylate cyclase	0.47	1.57	↓: 4; ↑: 5
IPF4293	*CA4249*	*orf19.538*	similar to *Saccharomyces cerevisiae* Gpi2p N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein	0.47	1.56	
IPF5673	*CA1103*	*orf19.4948*	similar to *Saccharomyces cerevisiae* Rex3p RNA exonuclease	5.66	1.53	
CHT1	*CA5859*	*orf19.7517*	endochitinase 1 precursor	4.14	1.52	
IPF15525	*CA2907*	*orf19.4520*	gluconokinase	0.47	1.50	
Transport						
IPF11059.2	*CA0993*	*orf19.1395*	phosphate transporter	0.47	2.27	
HGT16	*CA3414*	*orf19.6141*	glucose permease	3.98	1.70	
IPF6108	*CA3073*	*orf19.4811*	tricarboxylate carrier	1.50	1.67	↓: 4
HGT14	*CA0480*	*orf19.2633*	glucose permease	1.95	1.62	
YPT32	*CA0470*	*orf19.2622*	small GTP-binding protein essential for Golgi function	0.47	1.53	
Transcription						
CTA213.3	*CA5387*	*orf19.7276.1*	transcriptional activator, 3-prime end	0.47	1.71	
ZCF15	*CA1892*	*orf19.2753*	zinc finger transcription factor	0.47	1.64	
CTA21	*CA3851*	*orf19.6112*	transcriptional activator	3.98	1.55	
Protein fate						
MAP2	*CA1534*	*orf19.1214*	methionine aminopeptidase	0.79	1.56	
IPF11888	*CA4416*	*orf19.5180*	cystein peroxidase	4.91	1.56	↑: 2
IPF20016	*CA4514*	*orf19.491*	similar to *Saccharomyces cerevisiae* Sec63p ER protein-translocation complex subunit	0.47	1.52	
Interaction with environment						
PGA13	*CA5112*	*orf19.6420*	Similarity to mucin proteins	0.47	1.75	
ALS1	*CA0316*	*orf19.5741*	agglutinin-like protein	0.47	1.71	↓: 2
PGA36	*CA3827*	*orf19.5760*	GPI protein	0.47	1.54	
Protein biosynthesis						
MRPL8	*CA2999*		mitochondrial 60S ribosomal subunit	0.93	1.56	
Cell cycle and DNA processing						
HPR5	*CA5811*	*orf19.6614*	DNA helicase	3.26	1.84	↓: 2

Down-regulation (42 genes)						
Unknown function or not classified						
IPF6518	*CA2302*	*orf19.1691*	unknown function	4.63	0.48	↓: 2, 5
IPF6238	*CA2752*	*orf19.2374*	GAG protein of retrotransposon pCal (Tca2)	0.47	0.49	↓: 6
IPF6235	*CA2216*	*orf19.5372*	protein of retrotransposon pCal (Tca2)	0.47	0.52	↓: 2, 5, 6
IPF19568	*CA4870*	*orf19.6556*	unknown function	4.63	0.57	↓: 5
IPF5358	*CA3120*	*orf19.3007*	unknown function	3.98	0.58	
IPF10231.3f	*CA4052*	*orf19.427*	unkown function, 3-prime end	0.79	0.58	
IPF17119	*CA3934*	*orf19.2008*	unknown function	0.65	0.61	
IPF14802	*CA1184*	*orf19.3782.2*	unknown function	2.68	0.61	
IPF4459	*CA0523*	*orf19.3528*	unknown function	0.47	0.64	
IPF11854	*CA1412*	*orf19.1278*	unknown function	4.14	0.64	
IPF6237.2	*CA2217*	*orf19.5373*	protein of retrotransposon pCal (Tca2)	0.47	0.64	
IPF16143	*CA3581*	*orf19.2259*	unknown function	0.47	0.66	
IPF17055.3	*CA1692*	*orf19.5036*	unknown function, 3-prime end	4.63	0.66	
Protein fate						
PMT1	*CA4424*	*orf19.5171*	protein mannosyltransferase	0.47	0.19	
PRC1	*CA0430*	*orf19.1339*	carboxypeptidase Y precursor	0.65	0.48	
RPN5.3f	*CA4798*	*orf19.4032*	subunit of the regulatory particle of the proteasome, 3-prime end	1.50	0.53	
IPF1183	*CA4816*	*orf19.2082*	aspartyl protease	1.95	0.58	
TOM37	*CA0230*	*orf19.1532*	Mitochondrial outer membrane import receptor subunit	3.26	0.59	
CPS2.5f	*CA5172*	*orf19.4610*	carboxypeptidase YSCS precursor, 5-prime end	0.79	0.63	
SMP2	*CA4540*	*orf19.1462*	involved in plasmid maintenance, respiration and cell proliferation	4.14	0.65	
TOM6	*CA1043*	*orf19.1650*	mitochondrial outer membrane import receptor subunit	4.14	0.65	
ANP1	*CA0528*	*orf19.3622*	Golgi mannosyltransferase	4.91	0.65	
VPS27	*CA1585*	*orf19.6031*	vacuolar sorting	1.95	0.65	↓: 5
Transcription						
IPF19614.3f	*CA1859*	*orf19.1496*	transcription factor (zinc finger)	1.95	0.54	
ZNC1	*CA2539*	*orf19.3187*	transcription factor (zinc finger)	2.68	0.57	
SRB2.3f	*CA1292*	*orf19.2711.1*	DNA-directed RNA polymerase II holoenzyme and Kornberg s mediator (SRB) subcomplex subunit, 3-prime end	0.79	0.63	
SBP1	*CA2951*	*orf19.5854*	RNA binding protein	0.47	0.64	
IPF8362	*CA3384*	*orf19.325*	similar to *Saccharomyces cerevisiae* Cft2p cleavage and polyadenylation specificity factor	5.66	0.65	
IRO1	*CA2802*	*orf19.1715*	transcription factor for iron transport	3.26	0.65	↓: 5
Metabolism						
PLB1	*CA1975*	*orf19.689*	phospholipase B	0.93	0.54	↓: 2,5,6 ↑: 4
IFE1	*CA1958*	*orf19.769*	polyol dehydrogenase	3.98	0.58	
ERG11	*CA1387*	*orf19.922*	cytochrome P450 lanosterol 14a-demethylase	0.47	0.60	↓: 6
GPD1	*CA2263*	*orf19.1756*	glycerol-3-phosphate dehydrogenase	0.47	0.63	↓: 5, 6

Protein biosynthesis						
MRPL37	*CA1928*	*orf19.755*	mitochondrial ribosomal protein	0.65	0.57	
NEP1	*CA4099*	*orf19.665*	unknown function (ribosome biogenesis)	0.79	0.59	
MRP51	*CA1445*	*orf19.185*	mitochondrial ribosomal protein of the small subunit	4.14	0.62	
MRP10	*CA1724*	*orf19.2650.1*	mitochondrial ribosomal protein	4.63	0.65	
Interaction with environment						
PGA45	*CA0380*	*orf19.2451*	unknown function (GPI-linked protein)	0.47	0.47	
ALS9.3f	*CA1426*	*orf19.5745*	cell wall protein	5.66	0.62	
Cellular defense mechanisms						
HSP12	*CA0627*	*orf19.3160*	heat shock protein	0.47	0.64	↓: 5, 6
Cell cycle						
SPC19	*CA2420*	*orf19.4473*	spindle pole body protein	0.65	0.58	
Transport						
NIC96	*CA3940*	*orf19.2002*	nuclear pore protein	2.68	0.62	

Supplemental Table 1B

Transcript levels of genes in the *pmt2/PMT2* mutant P2-2 relative to wild-type strain CAF2-1. The minimal FDR value calculated by the SAM program was 2.3 %. Only genes regulated at least by a factor 1.5 are shown. Functional assignments are according to http://mips.gsf.de/CYGD/db/index.html and http://www.candidagenome.org/.

gene on array	**synonym**	**orf19 number**	**proposed function**	**q-value**	**fold regulation**	gene regulated in other mutants (*pmt* number)
Upregulation (10 genes)						
Metabolism						
GDH2	*CA1775*	*orf19.2192*	NAD-specific glutamate dehydrogenase (NAD)	1.79	1.69	
IPF15013	*CA2761*	*orf19.5626*	pyruvate decarboxylase regulatory protein (by homology)	1.79	1.69	
CIT1	*CA3909*	*orf19.4393*	citrate synthase	1.79	1.52	↑: 5
DBP9	*CA0715*	*orf19.3393*	DEAD box RNA helicase	2.36	1.52	
PYC2.3f	*CA1464*	*orf19.789*	pyruvate carboxylase 2, 3 prime end	1.07	1.51	↑: 6
Unknown function or not classified						
IPF1617	*CA4894*	*orf19.6586*	unknown function (induced by benomyl and diols)	1.07	1.99	
IPF538	*CA5609*	*orf19.7091*	unknown function	1.07	1.68	
IPF5330	*CA1339*	*orf19.3448*	unknown function	1.07	1.59	
Protein fate						

ALG2.5	*CA1530*	*orf19.1221*	mannosyltransferase, 5-prime end	2.36	1.72	
IPF11888	*CA4416*	*orf19.5180*	cystein peroxidase	1.79	1.52	↑: 1
Down-regulation (46 genes)						
Metabolism						
SOU2	*CA3770*	*orf19.2897*	sorbitol utilization protein	1.07	0.26	
RNR22	*CA4492*	*orf19.1868*	ribonucleoside-diphosphate reductase	1.07	0.30	↓: 6
DLD1	*CA4905*	*orf19.6043*	D-lactate ferricytochrome c oxidoreductase	2.36	0.35	
RHR2	*CA5788*	*orf19.5437*	DL-glycerol phosphatase	1.07	0.43	↓: 5, 6
PFK1	*CA1834*	*orf19.3967*	6-phosphofructokinase, alpha subunit	1.07	0.44	↓: 4, 5, 6
ADH5	*CA2391*	*orf19.2608*	alcohol dehydrogenase	1.07	0.48	↓: 5
GSY1	*CA5467*	*orf19.3278*	glycogen synthase	1.07	0.53	↓: 5
PLB1	*CA1975*	*orf19.689*	phospholipase B	1.07	0.54	↓: 1, 5, 6; ↑: 4
TPS3	*CA5505*	*orf19.5348*	alpha,alpha-trehalose-phosphate synthase, regulatory subunit	1.07	0.55	↓: 5, 6
GLK1	*CA0263*	*orf19.13*	aldohexose specific glucokinase	1.07	0.57	↓: 5, 6
CAF16	*CA3880*	*orf19.388*	ABC ATPase	2.10	0.59	↓: 5, 6
GPD2	*CA0824*	*orf19.691*	glycerol 3-phosphate dehydrogenase	1.07	0.59	↓: 5, 6
PFK2	*CA3112*	*orf19.6540*	6-phosphofructokinase, beta subunit	1.07	0.62	↓: 4, 6
PHO15	*CA4657*	*orf19.4444*	phosphatase	1.07	0.63	↓: 5
IPF1097	*CA5766*	*orf19.5408*	serine/threonine protein kinase	1.07	0.64	↓: 5
HXK2	*CA0127*	*orf19.542*	hexokinase II	1.07	0.65	↓: 6
IFE2	*CA2075*	*orf19.5288*	alcohol dehydrogenase	1.79	0.65	↓: 4, 5
IPF2471	*CA5728*	*orf19.7437*	maltose acetyltransferase	1.07	0.66	
IPF4959	*CA6057*	*orf19.7676*	D-xylulose reductase	1.07	0.66	↓: 5, 6
ERG1	*CA1353*	*orf19.406*	squalene epoxidase	1.07	0.66	↓: 5
FBA1	*CA5180*	*orf19.4618*	fructose-bisphosphate aldolase	1.07	0.66	↓: 5, 6
Unknown function or not classified						
IPF9000	*CA0732*	*orf19.4636*	unknown function	1.07	0.17	
IPF4976	*CA1739*	*orf19.2522*	unknown function	2.10	0.18	
IPF11273	*CA1108*	*orf19.5231*	unknown function	1.07	0.35	
NOP15	*CA5644*	*orf19.7050*	nucleolar ribosome biogenesis factor	1.07	0.44	
IPF7477	*CA1919*	*orf19.2442*	unknown function	2.10	0.57	
IPF20054	*CA0262*	*orf19.6117*	unknown function	1.07	0.63	↑: 1
IPF6518	*CA2302*	*orf19.1691*	unknown function	1.07	0.66	↓: 1, 5
IPF10493	*CA0831*	*orf19.247*	unknown function	1.07	0.67	↓: 5
IPF6235	*CA2216*	*orf19.5372*	protein of pCal (Tca2) retrotransposon	1.07	0.66	↓: 1, 5, 6
Interaction with environment						
CHS8	*CA5750*	*orf19.5384*	chitin synthase	1.07	0.08	
KRE1	*CA2589*	*orf19.4377*	ß-1,6-glucan synthesis	1.07	0.21	
ALS12.3f	*CA0413*	*orf19.2122*	agglutinin-like protein, 3-prime end	1.07	0.34	↓: 5
ALS4.3f	*CA1528*	*orf19.4556*	agglutinin-like protein, 3-prime end	1.07	0.44	↓: 5, 6
IRS4	*CA4717*	*orf19.6953*	cell wall integrity factor	1.07	0.55	
ALS1	*CA0316*	*orf19.5741*	agglutinin-like protein	1.07	0.57	↑: 1
Transport						
DAL52	*CA2478*	*orf19.3208*	allantoate permease	1.07	0.25	

CAN2	*CA1191*	*orf19.111*	amino acid permease	1.07	0.37	
SNC2	*CA5256*	*orf19.5006.1*	v-SNARE	1.07	0.65	↓: 5, 6
Transcription						
HOS1	*CA1453*	*orf19.4411*	histon deacetylase	1.07	0.39	
IPF9347	*CA1643*	*orf19.1729*	transcription factor (zinc finger)	1.07	0.34	
IPF1674	*CA4874*	*orf19.6559*	transcription initiation factor	1.07	0.59	
Cellular defense mechanisms						
OSM1	*CA4570*	*orf19.6882*	similar to *Saccharomyces cerevisiae* Osm1p osmotic growth protein	1.07	0.47	↓: 4, 5, 6
IPF4065	*CA0386*	*orf19.1862*	stress-related protein	1.07	0.64	↓: 5
Cell cycle and DNA processing						
HRP5	*CA5811*	*orf19.6614*	DNA helicase	1.07	0.64	↑: 1
Protein fate						
STF2	*CA2738*	*orf19.2107.1*	ATP synthase regulatory factor	1.07	0.53	↓: 4, 5, 6

Supplemental Table 1C

Transcript levels of genes in the *pmt4* mutant CAP4-216 relative to wild-type strain CAF2-1. The minimal FDR value calculated by the SAM program was 4.79 %. Only genes regulated at least by a factor 1.5 are shown. Functional assignments are according to http://mips.gsf.de/CYGD/db/index.html and http://www.candidagenome.org/.

gene on array	**synonym**	**orf19 number**	**proposed function**	**q-value**	**fold regulation**	gene regulated in other mutants (*pmt* number)
Upregulation (67 genes)						
Protein biosynthesis						
SMD3	*CA3087*	*orf19.4146*	core snRNP protein	4.79	6.50	
MRPL36	*CA2481*	*orf19.3205*	ribosomal protein YmL36 precursor, mitochondrial	3.73	2.35	
IPF5446	*CA2613*	*orf19.5698*	putative ribosomal protein	1.52	2.24	
VAS1	*CA0223*	*orf19.1295*	valyl-tRNA synthetase	1.52	2.16	
IPF3361	*CA4785*	*orf19.4018*	putative mitochondrial ribosomal protein S7	1.52	1.91	
IPF10027	*CA3016*	*orf19.3914*	unknown function	1.52	1.86	
TRM1	*CA5457*	*orf19.3265*	tRNA methyltransferase	1.52	1.81	
IPF6893	*CA3324*	*orf19.2675*	RNA splicing factor	3.98	1.70	
NOP1	*CA3570*	*orf19.3138*	fibrillarin	1.52	1.70	
MRPL16	*CA0910*	*orf19.2019*	ribosomal protein	1.52	1.74	
IPF13717	*CA0712*	*orf19.2167*	pre-rRNA processing	1.52	1.66	
MAK21	*CA6134*	*orf19.5912*	ribosome biogenesis protein	1.52	1.60	
IPF4776	*CA1443*	*orf19.4492*	nucleolar protein	3.22	1.57	
TIF5	*CA0667*	*orf19.4261*	translation initiation factor eIF5	1.52	1.54	
IMG1	*CA2945*	*orf19.1967*	ribosomal protein, mitochondrial	3.73	1.53	
IPF10301	*CA1876*	*orf19.2275*	putative 60S ribosomal protein L7/L12 homolog, mitochondrial precursor	3.98	1.52	

LPA4	*CA5198*	*orf19.7012*	similar to ribosomal protein S16, mitochondrial	3.98	1.51	
Unknown and not classified						
IPF20137	*CA3583*	*orf19.2257*	unknown function	1.52	7.78	
JIP5	*CA1950*	*orf19.4746*	unknown function	1.52	2.28	
IPF2988	*CA5030*	*orf19.6984*	unknown function (membrane protein)	3.22	2.12	
IPF6328	*CA1807*	*orf19.1114*	unknown function	4.79	2.05	
IPF8275	*CA3993*	*orf19.1569*	unknown function	3.98	1.88	
IPF18109	*CA5391*	*orf19.934*	unknown function	3.98	1.85	
IPF19617	*CA0249*	*orf19.1350*	unknown function	3.98	1.85	
IPF14797.5f	*CA1082*	*orf19.4818*	unknown function	3.98	1.80	
IPF14013	*CA3012*	*orf19.6227*	unknown function	1.52	1.66	
IPF3618	*CA4339*	*orf19.6710*	unknown function	1.52	1.66	
IPF15664	*CA2160*	*orf19.5296*	unknown function	3.73	1.64	
IPF6754	*CA3389*	*orf19.319*	unknown function	3.98	1.59	
SOL1	*CA0259*	*orf19.1355*	unknown function	3.98	1.54	
IPF9130	*CA1923*	*orf19.5539*	unknown function	1.52	1.51	
Metabolism						
PLB1	*CA1975*	*orf19.689*	phospholipase B	3.73	30.47	↓: 1, 2, 5, 6
IPF2861	*CA5524*	*orf19.7281*	pyruvate dehydrogenase kinase	3.98	3.35	
PEL1	*CA5625*	*orf19.7072*	CDP-diacylglycerol-serine-O-phosphatidyltransfer	1.52	2.20	
IMH3	*CA1246*	*orf19.18*	IMP dehydrogenase	1.52	2.09	
CYS3	*CA5127*	*orf19.6402*	cystathionine gamma-lyase	1.52	1.94	
IMH3	*CA1246*	*orf19.19*	IMP dehydrogenase	1.52	1.89	
CYB5	*CA5645*	*orf19.7049*	cytochrome b5	1.52	1.69	
HPT1	*CA3787*	*orf19.5832*	hypoxanthine guanine phosphoribosyl- transferase	1.52	1.63	
ACS2	*CA2858*	*orf19.1064*	acetyl-coenzyme-A synthetase	1.52	1.63	
PRS3	*CA3168*	*orf19.1575*	ribosephosphate pyrophosphokinase	4.79	1.59	
ERG6	*CA4005*	*orf19.1631*	sterol transmethylase	3.98	1.54	
IPP1	*CA0870*	*orf19.3590*	inorganic pyrophosphatase	3.98	1.52	
Protein fate						
IMP1	*CA5084*	*orf19.3061*	protease, mitochondrial	4.79	4.54	
SLA2	*CA5327*	*orf19.7201*	cytoskeleton assembly control protein	1.52	2.16	
YTA7	*CA1092*	*orf19.3949*	26S proteasome subunit	1.52	1.78	
VAN1	*CA5956*	*orf19.6738*	vanadate resistance protein	2.54	1.75	
UBP12	*CA1124*	*orf19.6260*	ubiquitin C-terminal hydrolase	3.22	1.63	
FAA4	*CA5992*	*orf19.7592*	long-chain fatty acid--CoA ligase and synthetase 4	1.52	1.63	
TOM72	*CA1397*	*orf19.3700*	mitochondrial import receptor	3.98	1.53	
IPF2973	*CA3064*	*orf19.4283*	subunit of proteasome regulatory particle	3.98	1.53	
Transport						
IPF9224	*CA3806*	*orf19.2485*	similar to *Saccharomyces cerevisiae* Nup170p nuclear pore protein	1.52	2.25	
PSE1	*CA3892*	*orf19.5085*	karyopherin-beta protein	1.52	1.95	

IPF7706	*CA4115*	*orf19.680*	mitochondrial phosphatase	1.52	1.75	
IPF15660	*CA1226*	*orf19.4159*	mitochondrial carrier	3.22	1.63	
IPF11224	*CA3781*	*orf19.5839*	similar to *Saccharomyces cerevisiae* Pdr16p protein involved in lipid biosynthesis and multidrug resistance	1.52	1.60	
Transcription						
CUP1	*CA4960*	*orf19.6514*	transcription factor	1.52	3.01	
ZCF37	*CA5678*	*orf19.7381*	transcription factor (zinc-finger)	3.98	1.87	
BDF1	*CA5425*	*orf19.978*	transcription factor	1.52	1.87	
ARC1	*CA3042*	*orf19.2422*	RNA binding protein	3.98	1.84	↑: 5
RPB5	*CA3494*	*orf19.6340*	DNA-directed RNA polymerase I, II, III	1.52	1.60	
MCM1	*CA5209*	*orf19.7025*	transcription factor (MADS box)	1.52	1.56	
Cellular defense and stress						
SNZ1	*CA4184*	*orf19.2947*	stationary phase protein	1.52	3.87	↑: 6; ↓: 5
SSE1	*CA1911*	*orf19.2435*	heat shock protein of HSP70 family	3.98	1.63	
Cellular organization and differentiation						
IPF7423.3f	*CA0400*	*orf19.6223*	similar to *Saccharomyces cerevisiae* Spo22 involved in sporulation, 3-prime end	1.52	1.97	
CBF5	*CA2373*	*orf19.1833*	centromere/ microtubule binding protein	1.52	1.74	↑: 5
CDC42	*CA3879*	*orf19.390*	small GTPase	1.52	1.69	
Down-regulation (61 genes)						
Unknown and not classified						
IPF4696	*CA4970*	*orf19.5282*	unknown function	3.73	0.28	
IPF4859	*CA3700*	*orf19.6276*	unknown function	3.73	0.34	↓: 5
IPF13080	*CA0589*	*orf19.1162.1*	unknown function	3.98	0.35	
IPF3857	*CA3608*	*orf19.25*	unknown function	3.98	0.37	↓: 5
IPF8951	*CA2360*	*orf19.4897*	unknown function	3.73	0.37	↓: 1
IPF20134	*CA3522*	*orf19.994*	unknown function	3.73	0.38	↓: 5
IPF10424	*CA5230*	*orf19.5034*	unknown function	4.79	0.38	↓: 5
IFR1	*CA2258*	*orf19.1763*	unknown function	1.52	0.39	
IPF1631	*CA4888*	*orf19.6580*	unknown function	4.79	0.43	
IPF13868	*CA4436*	*orf19.5159*	unknown function	3.73	0.43	
IPF11995	*CA0427*	*orf19.2761*	unknown function (membrane protein)	4.79	0.43	↓: 5
IPF20056	*CA0495*	*orf19.2659*	unknown function	1.52	0.44	↓: 5
IPF13621	*CA3398*	*orf19.3973*	unknown function	2.54	0.46	↓: 5
IPF10032.3f	*CA2237*	*orf19.3917*	unknown function, 3-prime end	2.54	0.48	
IPF2106	*CA4318*	*orf19.4104*	unknown function	3.73	0.49	↓: 5
IPF16267	*CA0634*	*orf19.1772*	unknown function	3.22	0.50	
IPF14219.2	*CA0564*	*orf19.2928*	unknown function	3.73	0.55	↓: 5
IPF8114	*CA2200*	*orf19.2939*	unknown function	3.73	0.55	
IPF7353	*CA2716*	*orf19.577*	unknown function	2.54	0.56	

IPF19936	*CA1935*	*orf19.4185*	unknown function	3.98	0.56	
IPF8990	*CA3135*	*orf19.1366*	unknown function	3.98	0.57	
IPF9162	*CA4486*	*orf19.1877*	unknown function	2.54	0.57	
IPF3866	*CA1248*	*orf19.21*	unknown function	3.73	0.58	
SDS24	*CA3920*	*orf19.5118*	unknown function	3.22	0.59	
IPF14825	*CA0799*	*orf19.1610*	unknown function	3.73	0.61	
IPF11858	*CA1411*	*orf19.1277*	unknown function	4.79	0.62	
IPF11299	*CA4378*	*orf19.5671*	unknown function	4.79	0.62	
IPF3964	*CA4111*	*orf19.675*	unknown function	3.98	0.63	
IPF4949	*CA6053*	*orf19.7670*	unknown function	4.79	0.63	
IPF7403	*CA2710*	*orf19.4664*	unknown function	4.79	0.64	
IPF3257.2	*CA4850*	*orf19.3820*	unknown function	3.98	0.65	
IPF9483	*CA2435*	*orf19.3395*	unknown function (membrane protein)	3.73	0.64	
Metabolism						
ISN1	*CA1020*	*orf19.3355*	inosine 5'-monophosphate 5'-nucleotidase	2.54	0.31	
AMYG2.5f	*CA3518*	*orf19.999*	glucoamylase, 5-prime end	4.79	0.39	
PCK1	*CA5857*	*orf19.7514*	phosphoenolpyruvate carboxykinase	3.73	0.42	
BNA1	*CA0804*	*orf19.3515*	3-hydroxyanthranilic acid dioxygenase	1.52	0.46	
FGR28	*CA0296*	*orf19.1596*	adenylate cyclase	1.52	0.50	↑: 1, 5
IFE2	*CA2075*	*orf19.5288*	alcohol dehydrogenase	1.52	0.55	↓: 2, 5
IPF1912	*CA5283*	*orf19.7140*	catechol o-methyltransferase	3.98	0.55	
TPS2	*CA5066*	*orf19.3038*	trehalose-6-phosphate phosphatase	2.54	0.55	
PFK2	*CA3112*	*orf19.6540*	6-phosphofructokinase, beta subunit	3.73	0.59	↓: 2, 6
PFK1	*CA1834*	*orf19.3967*	6-phosphofructokinase, alpha subunit	4.79	0.61	↓: 2, 5, 6
IPF12210	*CA1742*	*orf19.5054*	quinolinate phosphoribosyltransferase	4.79	0.62	
IPF4942	*CA6052*	*orf19.7668*	similar to *Saccharomyces cerevisiae* Mal32p alpha-glucosidase	4.79	0.64	↓: 5
GPH1	*CA5206*	*orf19.7021*	glycogen phosphorylase	3.73	0.65	
Transport						
SFT1	*CA5433*	*orf19.3234*	SNARE-like protein	2.54	0.27	↓: 5
SEC10	*CA2012*	*orf19.3086*	exocyst component	3.73	0.40	
HGT7	*CA1067*	*orf19.2023*	glucose transporter	3.98	0.63	
IPF6108	*CA3073*	*orf19.4811*	tricarboxylate carrier	4.79	0.64	↑: 1
IPF1022	*CA5142*	*orf19.4579*	similar to *Saccharomyces cerevisiae* Erv29p ER-Golgi transport vesicle protein	3.73	0.65	
Transcription						
EST3	*CA5778*	*orf19.5423*	telomerase subunit	4.79	0.42	
HDA1	*CA1899*	*orf19.2606*	histone deacetylase	1.52	0.52	
IPF12537	*CA5577*	*orf19.7344*	subunit of histone deacetylase complex	3.73	0.58	
IPF7646	*CA1865*	*orf19.861*	transcription factor (bZIP)	4.79	0.65	
Cellular defense						
YHB1	*CA0943*	*orf19.3707*	nitric oxide dioxygenase	1.52	0.46	
OSM1	*CA4570*	*orf19.6882*	similar to *Saccharomyces cerevisiae* Osm1p osmotic growth protein	3.73	0.61	↓: 2, 5, 6

MUM2	*CA2490*	*orf19.4044*	ubiquitin C-terminal hydrolase	4.79	0.66	
Interaction with environment						
SMK1	*CA5334*	*orf19.7208*	MAP kinase	2.54	0.43	↓: 5
PRA1	*CA4399*	*orf19.3111*	pH-regulated cell surface protein	2.54	0.50	
GPR1	*CA3354*	*orf19.9499*	G-protein-coupled receptor of plasma membrane	4.79	0.60	
Protein fate						
STF2	*CA2738*	*orf19.2107.1*	ATP synthase regulatory factor	1.52	0.43	↓: 2, 5, 6

Supplemental Table 1D

Transcript levels of genes in the *pmt5* mutant P5-571 relative to wild-type strain CAF2-1. The minimal FDR value calculated by the SAM program was 5.4 %. Only genes regulated at least by a factor 1.5 are shown. Functional assignments are according to http://mips.gsf.de/CYGD/db/index.html and http://www.candidagenome.org/.

gene on array	synonym	orf19 number	proposed function	q-value	fold regulation	gene regulated in other mutants (*pmt* number)
Upregulation (31 genes)						
Unknown function or not classified						
IPF10138	*CA1356*	*orf19.409*	unknown function (membrane protein)	3.42	1.62	
IPF3709	*CA5051*	*orf19.3015*	unknown function	2.18	1.58	
IPF16479	*CA0098*	*orf19.2319*	unknown function	5.49	1.57	
IPF17283	*CA2021*	*orf19.4907*	unknown function	2.18	1.54	
IPF19977	*CA3211*	*orf19.6192*	unknown function	2.18	1.54	↑: 1
IPF18447	*CA2592*	*orf19.59*	unknown functin (zinc-finger)	3.42	1.52	
NOG2	*CA2847*	*orf19.5733*	unknown function (nuclear/nucleolar GTP-binding protein)	2.96	1.50	
Interaction with environment						
CCC2	*CA1655*	*orf19.4328*	putative copper-transporting ATPase	2.18	2.13	
FET35	*CA1431*	*orf19.1206*	multicopper ferroxidase	2.18	1.57	
SUN42	*CA5232*	*orf19.5032*	cell wall beta-glucosidase	3.74	1.55	
IHD1	*CA3827*	*orf19.5760*	GPI protein	2.18	1.55	
PHR1	*CA4857*	*orf19.3829*	GPI-anchored pH responsive glycosyl transferase	3.74	1.54	
FET34	*CA2920*	*orf19.4215*	multicopper ferroxidase	2.18	1.51	
Protein fate						
KAR2	*CA0915*	*orf19.2013*	dnaK-type molecular chaperone	2.96	2.14	↑: 1
MNT1	*CA3469*	*orf19.1665*	mannosyltransferase involved in n-linked and o-linked glycosylation	2.96	1.66	
NPI46	*CA1629*	*orf19.1030*	proline cis-trans isomerase	2.96	1.56	
MNT2	*CA3467*	*orf19.1663*	alpha-1,2-mannosyltransferase	3.29	1.51	
Protein biosynthesis						

EFT3	*CA3081*	*orf19.4152*	translation elongation factor 3	3.29	1.73	
RPS21	*CA1715*	*orf19.3334*	ribosomal protein	3.42	1.56	
GCD11	*CA1322*	*orf19.4223*	translation initiation factor eIF2	3.29	1.52	
SQT1	*CA4794*	*orf19.4029*	suppresses dominant-negative mutants of the ribosomal protein QSR1	2.18	1.52	
Metabolism						
URA7	*CA1635*	*orf19.3941*	CTP synthase 1	2.18	1.63	
IPF6105	*CA3075*	*orf19.4813*	GMP synthase	2.18	1.57	
CIT1	*CA3909*	*orf19.4393*	citrate synthase	3.42	1.55	↑: 2
FGR28	*CA0296*	*orf19.1596*	adenylate cyclase	3.29	1.55	↑: 1; ↓: 4
Transcription						
ARC1	*CA3042*	*orf19.2422*	G4 nucleic acid binding protein	3.42	7.82	↑: 4
TYE7	*CA3707*	*orf19.4941*	bHLH transcription factor	3.74	1.65	
IPF16752	*CA1291*	*orf19.2711*	RNA polymerase II elongator subunit	4.68	1.62	
Cellular organisation						
CBF5	*CA2373*	*orf19.1833*	centromere/ microtubule binding protein	3.29	9.78	↑: 4
PHR1	*CA4857*	*orf19.3829*	GPI-anchored pH responsive glycosyl transferase	3.74	1.54	
NSR1	*CA3862*	*orf19.6090*	nuclear localization sequence binding protein	3.29	1.52	
Downregulation (41 genes)						
Unknown function or not classified						
IFU5	*CA2679*	*orf19.2568*	unknown function (membrane protein)	0.46	0.06	
IPF9398	*CA5393*	*orf19.936*	unknown function	3.42	0.35	
IPF6156	*CA1625*	*orf19.1034*	unknown function	0.46	0.44	
IPF6518	*CA2302*	*orf19.1691*	unknown function	0.46	0.50	↓: 1, 2
IPF8878	*CA3614*	*orf19.31*	unknown function	0.46	0.50	
IPF1382	*CA5097*	*orf19.6444*	unknown function	0.46	0.51	
IPF11480	*CA4755*	*orf19.4824*	unknown function	0.46	0.51	
IPF15822	*CA1869*	*orf19.2457*	unknown function	0.46	0.51	
IPF1820	*CA5254*	*orf19.5008.1*	unknown function	0.46	0.51	
IPF8024	*CA2118*	*orf19.1334*	unknown function	0.46	0.53	
IPF3790	*CA2883*	*orf19.5852*	unknown function	0.46	0.53	
IPF19377	*CA0036*	*orf19.3336*	unknown function	0.46	0.54	
IPF373	*CA5861*	*orf19.7519*	unknown function	0.46	0.54	
IPF3105	*CA4652*	*orf19.4439*	unknown function	2.18	0.54	
IPF9972.3eoc	*CA1511*	*orf19.4522*	unknown function, 3-prime end	0.46	0.54	
IPF9069	*CA3617*	*orf19.199*	unknown function (membrane protein)	2.71	0.55	
IPF2234	*CA4579*	*orf19.6898*	unknown function	0.46	0.55	
IPF10424	*CA5230*	*orf19.5034*	unknown function	0.46	0.55	↓: 4
IPF13972	*CA0513*	*orf19.4955*	unknown function	0.46	0.58	
IPF900.3f	*CA5332*	*orf19.7206*	unknown function, 3-prime end	3.29	0.56	
IPF20134	*CA3522*	*orf19.994*	unknown function	0.46	0.56	↓: 4
IPF8856.5f	*CA0595*	*orf19.4901*	unknown function, 5-prime end	0.46	0.57	

IPF7647	*CA1866*	*orf19.860*	unknown function	0.46	0.57	
IPF11995	*CA0427*	*orf19.2761*	unknown function (membrane protein)	0.46	0.57	↓: 4
IPF8856.5f	*CA0595*	*orf19.4901*	unknown function, 5-prime end	0.46	0.57	
IPF13839	*CA0477*	*orf19.6017*	unknown function	0.46	0.58	
IPF1306	*CA5123*	*orf19.6405*	unknown function	0.46	0.58	
IPF12900	*CA3592*	*orf19.2246*	unknown function	0.46	0.59	
IPF18234.3f	*CA4254*	*orf19.542.2*	unknown function, 3-prime end	0.46	0.59	
IPF5279	*CA4370*	*orf19.5661*	unknown function	0.46	0.59	
SKI3	*CA4737*	*orf19.4848*	unknown function	0.46	0.59	
IPF6235	*CA2216*	*orf19.5372*	protein of pCal (Tca2) retrotransposon	0.46	0.61	↓: 1, 2, 6
IPF10493	*CA0831*	*orf19.247*	unknown function	0.46	0.62	↓: 2
IPF4859	*CA3700*	*orf19.6276*	unknown function	1.59	0.62	↓: 4
IPF16024	*CA0226*	*orf19.1297*	unknown function	0.46	0.62	
IPF8953	*CA2358*	*orf19.4895*	unknown function	1.59	0.62	
IPF2125	*CA4310*	*orf19.4116*	unknown function	0.46	0.63	
IPF2106	*CA4318*	*orf19.4104*	unknown function	0.46	0.63	↓: 4
IPF7385	*CA3748*	*orf19.3430*	unknown function	1.59	0.63	
IPF19154	*CA0172*	*orf19.1126*	unknown function	0.46	0.63	
IPF15297	*CA5078*	*orf19.3053*	unknown function	0.46	0.63	
IPF4405	*CA0905*	*orf19.1482*	unknown function	0.46	0.64	
IPF14219.2	*CA0564*	*orf19.2928*	unknown function	1.59	0.64	↓: 4
IPF11093	*CA5182*	*orf19.4621*	unknown function	2.18	0.64	
IPF1437	*CA4910*	*orf19.6048*	unknown function	1.59	0.65	
IPF19568	*CA4870*	*orf19.6556*	unknown function	1.59	0.65	↓: 1
IPF20163	*CA4135*	*orf19.4239*	unknown function	2.18	0.65	
IPF7999	*CA1940*	*orf19.4190*	unknown function	2.18	0.66	
IPF3857	*CA3608*	*orf19.25*	unknown function	2.71	0.66	↓: 4
IPF2878	*CA5735*	*orf19.7445*	unknown function	0.46	0.66	
IPF4497	*CA4740*	*orf19.4844*	unknown function	2.18	0.64	
IPF8810	*CA3312*	*orf19.2305*	unknown function	0.46	0.63	
IPF630	*CA6016*	*orf19.7618*	unknown function	1.59	0.62	
IPF16024	*CA0226*	*orf19.1297*	unknown function	0.46	0.62	
IPF13621	*CA3398*	*orf19.3973*	unknown function	0.46	0.63	↓: 4
Metabolism						
STF2	*CA2738*	*orf19.2107.1*	ATP synthase regulatory factor	0.46	0.29	↓: 2, 4, 6
IFE2	*CA2075*	*orf19.5288*	alcohol dehydrogenase	0.46	0.31	↓: 2, 4
DAK2	*CA0776*	*orf19.4777*	dihydroxyacetone kinase	0.46	0.34	↓: 6
RHR2	*CA5788*	*orf19.5437*	DL-glycerol phosphatase	0.46	0.37	↓: 2, 6
GPD1	*CA2263*	*orf19.1756*	glycerol-3-phosphate dehydrogenase	0.46	0.41	↓: 1, 6
IPF4959	*CA6057*	*orf19.7676*	D-xylulose reductase	0.46	0.42	↓: 2, 6
PHO15	*CA4657*	*orf19.4444*	phosphatase	0.46	0.42	↓: 5
GPD2	*CA0824*	*orf19.691*	glycerol 3-phosphate dehydrogenase	0.46	0.44	↓: 2, 6
GSY1	*CA5467*	*orf19.3278*	glycogen synthase	0.46	0.46	↓: 2
PLB1	*CA1975*	*orf19.689*	phospholipase B	0.46	0.46	↓: 1, 2, 6; ↑: 4
IFP3	*CA1840*	*orf19.4707*	secreted acid sphingomyelin phosphodiesterase	0.46	0.47	
CAF16	*CA3880*	*orf19.388*	ABC ATPase	0.46	0.53	↓: 2, 6
IPF6439.3	*CA2404*	*orf19.3545*	protein kinase in cytokinesis	0.46	0.53	
COQ4	*CA3118*	*orf19.3008*	ubiquinone biosynthesis	0.46	0.54	
CDC21	*CA2665*	*orf19.3549*	thymidylate synthase	0.46	0.54	

IPF4905	*CA0899*	*orf19.411*	GTPase regulator	0.46	0.54	
PFK1	*CA1834*	*orf19.3967*	6-phosphofructokinase, alpha subunit	0.46	0.55	↓: 2, 4, 6
IPF4942	*CA6052*	*orf19.7668*	similar to *Saccharomyces cerevisiae* Mal32p alpha-glucosidase	0.46	0.56	↓: 4
ADH5	*CA2391*	*orf19.2608*	alcohol dehydrogenase	0.46	0.57	↓: 2
PDC11	*CA2474*	*orf19.2877*	pyruvate decarboxylase	0.46	0.57	↓: 6
ERG1	*CA1353*	*orf19.406*	squalene epoxidase	0.46	0.57	↓: 2
TRP3	*CA5004*	*orf19.5243*	anthranilate synthase	0.46	0.58	
RIB3.5f	*CA1111*	*orf19.5228*	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime end	0.46	0.58	
IPF8321	*CA2938*	*orf19.3325*	similar to *Saccharomyces cerevisiae* Glg2p self-glucosylating initiator of glycogen synthesis	0.46	0.59	
TPS3	*CA5505*	*orf19.5348*	alpha,alpha-trehalose-phosphate synthase, regulatory subunit	0.46	0.60	↓: 2, 6
IPF1097	*CA5766*	*orf19.5408*	serine/threonine protein kinase	0.46	0.60	↓: 2
CNA1	*CA4137*	*orf19.4235*	cyclic nucleotide phosphodiesterase	1.59	0.61	
MET7	*CA2911*	*orf19.4516*	tetrahydrofolylpolyglutamate synthase	0.46	0.62	
SDH41	*CA2423*	*orf19.4468*	succinate dehydrogenase membrane anchor subunit for Sdh2p	0.46	0.62	
SUR2	*CA2225*	*orf19.5818*	sphinganine C4-hydroxylase	0.46	0.62	↓: 6
LYS12	*CA1737*	*orf19.2525*	homo-isocitrate dehydrogenase	0.46	0.62	
AMYG1	*CA0855*	*orf19.4899*	glucoamylase	1.59	0.63	
IDI1	*CA4116*	*orf19.2775*	isopentenyl diphosphate isomerase	1.59	0.63	
PDX3	*CA4261*	*orf19.550*	pyridoxamine-phosphate oxidase	0.46	0.64	
FBA1	*CA5180*	*orf19.4618*	fructose-bisphosphate aldolase	1.59	0.64	↓: 2, 6
GLK1	*CA0263*	*orf19.13*	aldohexose specific glucokinase	0.46	0.64	↓: 2, 6
GPM2	*CA2855*	*orf19.1067*	phosphoglycerate mutase	0.46	0.65	
HEM14	*CA1951*	*orf19.4747*	mitochondrial protoporphyrinogen oxidase	0.46	0.65	
Protein fate						
ESA1	*CA5772*	*orf19.5416*	histone acetyltransferase	0.46	0.54	
MAK3	*CA5179*	*orf19.4617*	N-acetyltransferase	0.46	0.54	
IPF7862	*CA4548*	*orf19.1450*	ubiquitin conjugating factor	0.46	0.56	
IPF4500	*CA4738*	*orf19.4846*	GTP-binding protein	0.46	0.57	
SEC2	*CA3598*	*orf19.4928*	GDP/GTP exchange factor	0.46	0.64	
IPF13316	*CA1880*	*orf19.2269*	phosphoserine phosphatase	0.46	0.65	
Cellular defense and stress						
HSP12	*CA0627*	*orf19.3160*	heat shock protein	0.46	0.44	↓: 1, 6
OSM1	*CA4570*	*orf19.6882*	similar to *Saccharomyces cerevisiae* Osm1p osmotic growth protein	0.46	0.46	↓: 2, 4, 6
SSA1	*CA2857*	*orf19.1065*	heat shock protein of Hsp70 family	0.46	0.49	
IPF4065	*CA0386*	*orf19.1862*	stress-related protein	0.46	0.53	↓: 2
CHK1	*CA4676*	*orf19.896*	histidine kinase	0.46	0.55	
OGG1	*CA5318*	*orf19.7190*	8-oxoguanine DNA glycosylase	2.96	0.56	
SNZ1	*CA4184*	*orf19.2947*	stationary phase protein	0.46	0.58	↑: 4, 6
CRD1	*CA2832*	*orf19.4784*	Cu-transporting P1-type ATPase	0.46	0.60	
PXA2	*CA4993*	*orf19.5255*	ABC transporter, peroxisomal	0.46	0.61	
DAP1	*CA4516*	*orf19.489*	stress response protein	0.46	0.63	
Transcription						

HSH49	*CA3579*	*orf19.2261*	spliceosome-associated protein	0.46	0.36	
SWI1	*CA4366*	*orf19.5657*	transcription regulation	0.46	0.42	
POP7	*CA3718*	*orf19.4168*	nuclear RNase P subunit	0.46	0.43	
IRO1	*CA2802*	*orf19.1715*	transcription factor in iron transport	0.46	0.46	↓: 1
ZCF21	*CA3716*	*orf19.4166*	transcription factor (zinc finger)	0.46	0.58	
TEA1	*CA5031*	*orf19.6985*	trancription factor (zinc finger)	0.46	0.59	
GTS1	*CA5132*	*orf19.6393*	transcription factor	0.46	0.61	
CRZ2	*CA0424*	*orf19.2356*	transcription factor (zinc finger)	0.46	0.62	
IPF8044	*CA4556*	*orf19.6866*	similar to *Saccharomyces cerevisiae* Snp1p U1 small nuclear ribonucleoprotein	1.59	0.63	
IPF1598	*CA5424*	*orf19.976*	transcription factor (zinc finger)	2.71	0.65	
Biosynthesis of cellular components						
MSM1	*CA1093*	*orf19.3950*	mitochondrial methionyl-tRNA synthetase	1.59	0.12	
KAR3.3	*CA4321*	*orf19.4100*	kinesin-related protein, 3-prime end	0.46	0.56	
APL6	*CA2826*	*orf19.1323*	AP-3 complex subunit, beta3-adaptin	0.46	0.56	
ARP6	*CA0593*	*orf19.4904*	actin-related protein	0.46	0.57	
BMH2	*CA5050*	*orf19.3014*	similar to *Saccharomyces cerevisae* Bmh2p suppressor of clathrin deficency	0.46	0.58	
SAC6.5f	*CA0408*	*orf19.5544*	actin filament bundling protein, fimbrin, 5-prime end	0.46	0.60	
SCW11.3eoc	*CA1053*	*orf19.3893*	glucanase gene family member, 3-prime end	1.59	0.63	
DNM1	*CA5033*	*orf19.6987*	dynamin-related protein	0.46	0.64	
UTR2	*CA0605*	*orf19.1671*	beta-glucanase	2.71	0.66	
CSL4	*CA0142*	*orf19.1026*	involved in kinetochore-related function	2.18	0.66	
Interaction with environment						
ALS4.3f	*CA1528*	*orf19.4556*	agglutinin-like protein, 3-prime end	0.46	0.39	↓: 2, 6
FGR14	*CA0930*	*orf19.559*	filamentous growth	0.46	0.43	
ALS12.3f	*CA0413*	*orf19.2122*	agglutinin-like protein, 3-prime end	0.46	0.40	↓: 2
SMK1	*CA5334*	*orf19.7208*	MAP kinase	0.46	0.54	↓: 4
MTLA1	*CA0760*	*orf19.3201*	repression of switching and mating	0.46	0.57	
SYG1	*CA1957*	*orf19.768*	similar to *Saccharomyces cerevisiae* Syg1p plasma membrane protein	0.46	0.65	
PGA50	*CA1777*	*orf19.1824*	GPI-anchor protein	2.18	0.66	
Transport						
VPS27	*CA1585*	*orf19.6031*	vacuolar protein sorting	0.46	0.54	↓: 1
SFT1	*CA5433*	*orf19.3234.1*	SNARE-like protein	0.46	0.58	↓: 4
SNC2	*CA5256*	*orf19.5006.1*	v-SNARE	0.46	0.64	↓: 2, 6
RAV2	*CA1653*	*orf19.5561*	acidification of the vacuole	0.46	0.64	
IPF4632	*CA3859*	*orf19.6094*	similar to *Saccharomyces cerevisiae* Vps53p subunit of VP52-54 complex, required for protein sorting at the yeast late Golgi	2.18	0.65	

Supplemental Table 1E

Transcript levels of genes in the *pmt6* mutant CAP2-239 relative to wild-type strain CAF2-1. The minimal FDR value calculated by the SAM program was 5.4 %. Only genes regulated at least by a factor 1.5 are shown. Functional assignments are according to http://mips.gsf.de/CYGD/db/index.html and http://www.candidagenome.org/.

gene on array	**synonym**	**orf19 number**	**proposed function**	**q-value**	**fold regulation**	gene regulated in other mutants (*pmt* number)
Upregulation (5 genes)						
Metabolism						
HIS7	*CA2447*	*orf19.5505*	histidine biosynthesis	0.92	1.69	
IPF7602	*CA1761*	*orf19.5193*	oxidoreductase	2.69	1.49	
PYC2.3f	*CA1464*	*orf19.789*	pyruvate carboxylase 2, 3 prime end	5.55	1.47	↑: 2
URA2	*CA1315*	*orf19.2360*	pyrimidine biosynthesis	5.55	1.46	
Cellular defense						
SNZ1	*CA4184*	*orf19.2947*	stationary phase protein	5.55	1.80	↑: 4; ↓: 5
Downregulation (46 genes)						
Metabolism						
RHR2	*CA5788*	*orf19.5437*	DL-glycerol phosphatase	0.92	0.44	↓: 2, 5
TPS3	*CA5505*	*orf19.5348*	alpha,alpha-trehalose-phosphate synthase, regulatory subunit	0.92	0.44	↓: 2, 5
PFK1	*CA1834*	*orf19.3967*	6-phosphofructokinase, alpha subunit	0.92	0.45	↓: 2, 4, 5
IPF4959	*CA6057*	*orf19.7676*	D-xylulose reductase	0.92	0.46	↓: 2, 5
TPI1	*CA5950*	*orf19.6745*	triose phosphate isomerase	0.92	0.46	
GPM1	*CA4671*	*orf19.903*	phosphoglycerate mutase	0.92	0.46	
PFK2	*CA3112*	*orf19.6540*	6-phosphofructokinase, beta subunit	0.92	0.47	↓: 2, 4
PGK1	*CA1691*	*orf19.3651*	phosphoglycerate kinase	0.92	0.47	
FBA1	*CA5180*	*orf19.4618*	fructose-bisphosphate aldolase	0.92	0.49	↓: 2, 5
ERG11	*CA1387*	*orf19.922*	cytochrome P450 lanosterol 14a-demethylase	0.92	0.49	↓: 1
COX8	*CA2134*	*orf19.5213.*	cytochrome c oxidase	0.92	0.49	
RNR22	*CA4492*	*orf19.1868*	ribonucleoside-diphosphate reductase	3.50	0.49	↓: 2
PDC11	*CA2474*	*orf19.2877*	pyruvate decarboxylase	0.92	0.50	↓: 5
ADH1	*CA4765*	*orf19.3997*	alcohol dehydrogenase	0.92	0.53	
URA1	*CA4745*	*orf19.4836*	dihydroorotate dehydrogenase	0.92	0.55	
GPD2	*CA0824*	*orf19.691*	glycerol 3-phosphate dehydrogenase	0.92	0.55	↓: 2, 5
PLB1	*CA1975*	*orf19.689*	phospholipase B	0.92	0.56	↓: 1, 2, 5; ↑: 4
GLK1	*CA0263*	*orf19.13*	aldohexose specific glucokinase	0.92	0.57	↓: 2, 5
HXK2	*CA0127*	*orf19.542*	hexokinase II	0.92	0.58	↓: 2
PGI1	*CA3559*	*orf19.3888*	glucose-6-phosphate isomerase	0.92	0.59	
GAP1	*CA5892*	*orf19.6814*	glyceraldehyde-3-phosphate dehydrogenase	0.92	0.61	
GPD1	*CA2263*	*orf19.1756*	glycerol-3-phosphate dehydrogenase	0.92	0.62	↓: 1, 5
DAK2	*CA0776*	*orf19.4777*	dihydroxyacetone kinase	0.92	0.62	↓: 5
ADH2	*CA3923*	*orf19.5113*	alcohol dehydrogenase I	0.92	0.63	
CAR2	*CA2561*	*orf19.5641*	ornithine aminotransferase	0.92	0.65	

CAF16	*CA3880*	*orf19.388*	ABC ATPase	0.92	0.66	↓: 2, 5
SUR2	*CA2225*	*orf19.5818*	sphinganine C4-hydroxylase	0.92	0.67	↓: 5
Cellular defense and stress						
OSM1	*CA4570*	*orf19.6882*	similar to *Saccharomyces cerevisiae* Osm1p osmotic growth protein	0.92	0.43	↓: 2, 4, 5
HSP12	*CA0627*	*orf19.3160*	heat shock protein	0.92	0.45	↓: 1, 5
SSA4	*CA1230*	*orf19.4980*	Hsp70 heat shock protein	0.92	0.59	
IPF284	*CA5463*	*orf19.3272*	heat shock protein	0.92	0.60	
IPF6629	*CA4127*	*orf19.2762*	alkyl hydroperoxide reductase	0.92	0.65	
Unknown and not classified						
IPF6235	*CA2216*	*orf19.5372*	Protein of pCal (Tca2) retrotransposon	0.92	0.48	↓: 1, 2, 5
IPF1980	*CA5564*	*orf19.7328*	unknown function	0.92	0.64	↑: 4
IPF15540	*CA0486*	*orf19.258*	unknown function	5.55	0.65	
IPF6238	*CA2752*	*orf19.2374*	GAG protein of retrotransposon pCal (Tca2)	1.90	0.66	↓: 1
IPF1217	*CA4834*	*orf19.2063*	unknown function	1.90	0.56	
IPF7033	*CA1212*	*orf19.131*	unknown function	3.50	0.67	
Protein fate and transport						
STF2	*CA2738*	*orf19.2107.*	ATP synthase regulatory factor	0.92	0.58	↓: 2, 4, 5
CDC48	*CA3333*	*orf19.2340*	microsomal ATPase	0.92	0.65	
SNC2	*CA5256*	*orf19.5006.*	v-SNARE	3.50	0.66	↓: 2, 5
PRD1	*CA4059*	*orf19.434*	proteinase	0.92	0.66	
Transcription, protein biosynthesis						
MRPS5.5f	*CA3526*	*orf19.989*	Probable ribosomal protein S5, mitochondrial	5.55	0.03	
IPF7289	*CA3878*	*orf19.391*	similar to *Saccharomyces cerevisiae* Upc2p RNA polymerase II transcription factor	0.92	0.63	
IPF4276	*CA4260*	*orf19.549*	similar to *Saccharomyces cerevisiae* Mrpl32p putative mitochondrial ribosomal protein	5.55	0.66	
Interaction with environment						
ALS4.3f	*CA1528*	*orf19.4556*	agglutinin-like protein, 3-prime end	0.92	0.32	↓: 2, 5

Table S2. Genes regulated by *O*-glycosylation inhibitor

Transcript levels of genes in the wild-type strain CAF2-1 treated with inhibitor OGT2599 (5 µM) relative to untreated wild-type strain CAF2-1 during growth of a culture at 30 °C from OD_{600}= 0.1 to OD_{600}= 0.5. The minimal FDR value calculated by the SAM program was 5.1 %. Only genes regulated at least by a factor 1.5 are shown.

gene on array	**synonym**	**orf19 number**	**proposed function**	**q-value**	**fold regulation**	gene regulated in *pmt* mutants (*pmt* number)
Upregulation (27 genes)						
IPF7109	*CA5650*	*orf19.7350*	unknown function	0.00	2.67	↑: 1
KAR2	*CA0915*	*orf19.2013*	DnaK-type molecular chaperone	0.00	2.02	↑: 1, 5
SCJ1	*CA4025*	*orf19.3438*	mitochondrial and ER import protein	0.00	1.88	
GFA1	*CA4016*	*orf19.1618*	glutamine:fructose-6-phosphateamidotransferase	0.00	1.82	
IPF12676	*CA1681*	*orf19.4914*	unknown function	0.00	1.80	
TPM2	*CA5116*	*orf19.6414.3*	tropomyosin	0.00	1.79	
SPC3	*CA3600*	*orf19.4930*	signal peptidase subunit	1.20	1.78	
RNR22	*CA4492*	*orf19.1868*	ribonucleoside-diphosphate reductase	0.00	1.77	↓: 2, 6
CEK1	*CA0722*	*orf19.2886*	ERK-family protein kinase	0.00	1.75	
DPM1	*CA3899*	*orf19.5073*	dolichol-phosphate (beta-D) mannosyltransferase 1	0.00	1.72	
YSY6	*CA1267*	*orf19.242.2*	protein involved in the secretory pathway	0.00	1.72	
SEC23	*CA3453*	*orf19.1254*	component of COPII coat	0.00	1.69	
HOS3	*CA4118*	*orf19.2772*	histone deacetylase	5.10	1.69	
HAC1	*CA0457*	*orf19.2432*	transcription factor	0.00	1.68	↑: 1
IPF2532	*CA0356*	*orf19.6630*	unknown function	0.00	1.67	
IPF11101	*CA5177*	*orf19.4615*	unknown function	2.08	1.66	
PDI1	*CA1755*	*orf19.5130*	protein disulfide-isomerase	0.00	1.62	
PMM1	*CA2198*	*orf19.2937*	phosphomannomutase	4.22	1.57	
ASG1	*CA0465*	*orf19.166*	transcription factor	4.22	1.56	
CLC1	*CA5156*	*orf19.4594*	clathrin light chain	0.00	1.54	
SOD5	*CA4836*	*orf19.2060*	superoxide dismutase	0.00	1.53	
PHO100	*CA1363*	*orf19.4424*	acid phosphatase	5.10	1.53	
ALS10	*CA0448*	*orf19.2355*	agglutinin like protein	4.22	1.53	
IPF1461	*CA4898*	*orf19.6035*	NADH dehydrogenase	5.10	1.52	
IFD4	*CA2416*	*orf19.4477*	aryl-alcohol dehydrogenase	4.22	1.51	
IPF10901	*CA0538*	*orf19.2819*	unknown function	1.20	1.50	
RTA2	*CA3607*	*orf19.24*	stress-associated protein	0.00	1.50	↑: 1
Downregulation (13 genes)						
FTR2	*CA5354*	*orf19.7231*	high affinity iron permease	0.00	0.52	
YWP1	*CA1678*	*orf19.3618*	cell wall protein	0.00	0.54	
CHT2	*CA1051*	*orf19.3895*	chitinase 2 precursor	0.00	0.59	
FRP1	*CA3813*	*orf19.2496*	unknown function	2.08	0.61	
IPF17283	*CA2021*	*orf19.4907*	unknown function	4.22	0.61	
FTR1	*CA5345*	*orf19.7219*	high affinity iron permease	1.33	0.63	↑: 5
CHT3	*CA5987*	*orf19.7586*	chitinase 3 precursor	0.00	0.63	
ERG5	*CA4418*	*orf19.5178*	C-22 sterol desaturase	0.00	0.64	
PGA59	*CA4124*	*orf19.2767*	GPI anchored protein	0.00	0.65	
PHO84	*CA0083*	*orf19.655*	high-affinity inorganic phosphate/H+ symporter	0.00	0.65	
IPF13782	*CA3301*	*orf19.2314*	unknown function	0.00	0.66	
UBR12	*CA3263*	*orf19.2697*	ubiquitin-protein ligase by homology	2.79	0.66	
IMH3	*CA1246*	*orf19.19*	IMP dehydrogenase	0.00	0.66	↑: 4