## Appendix files – Table of contents

**Appendix Figures:**

**Figure S1.** SAGA regulates differentiation gene expression independently of the cAMP/Pka1$^{PKA}$ pathway, the Sty1$^{p38}$ kinase, and the Ssp2$^{AMPK}$ kinase……. p2

**Figure S2.** SAGA, but not Gcn5, becomes phosphorylated upon nutrient starvation…… p4

**Figure S3.** Identification of Taf12 phosphorylated residues in *S. pombe*……. p5

**Figure S4.** Identification of Taf12 phosphorylated residues within SAGA…… p7

**Figure S5.** TFIID subunit composition and levels do not change in response to nutrient starvation……. p8

**Figure S6.** The cAMP/PKA pathway does not control Taf12 phosphorylation…… p9

**Figure S7.** The PP2A regulator Tap42 does not regulate Taf12 phosphorylation…….. p10

**Figure S8.** Epistasis analysis of sexual differentiation between Ppk18$^{Gwl}$-Igo1, PP2A-Pab1, and SAGA-Gcn5……. p11

**Figure S9.** Taf12 phosphorylation is epistatic to Gad8$^{AKT}$ for the inhibition of differentiation gene expression…….. p12

**Figure S10.** Taf12 phosphorylation does not affect SAGA or TFIID subunit composition. p13

**Figure S11.** Taf12 phosphorylation does not modulate SAGA HAT activity…… p14

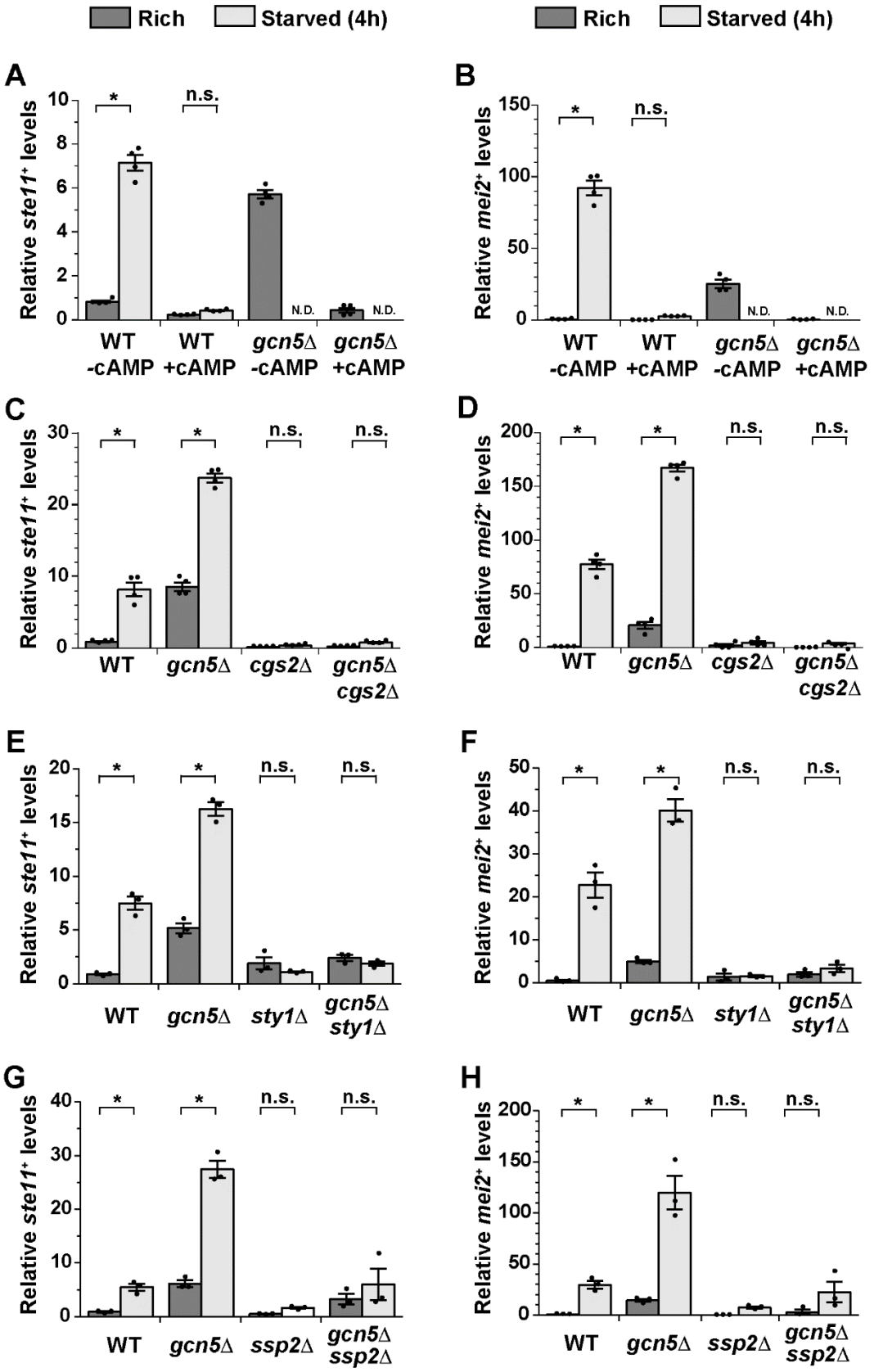
**Appendix Tables:**

**Table S1.** Quantitative mass spectrometry analysis of SAGA subunit composition in rich and starved conditions……. p15

**Table S2.** List of strains used in this study……... p16

**Table S3.** List of oligonucleotides used in this study…….. p18

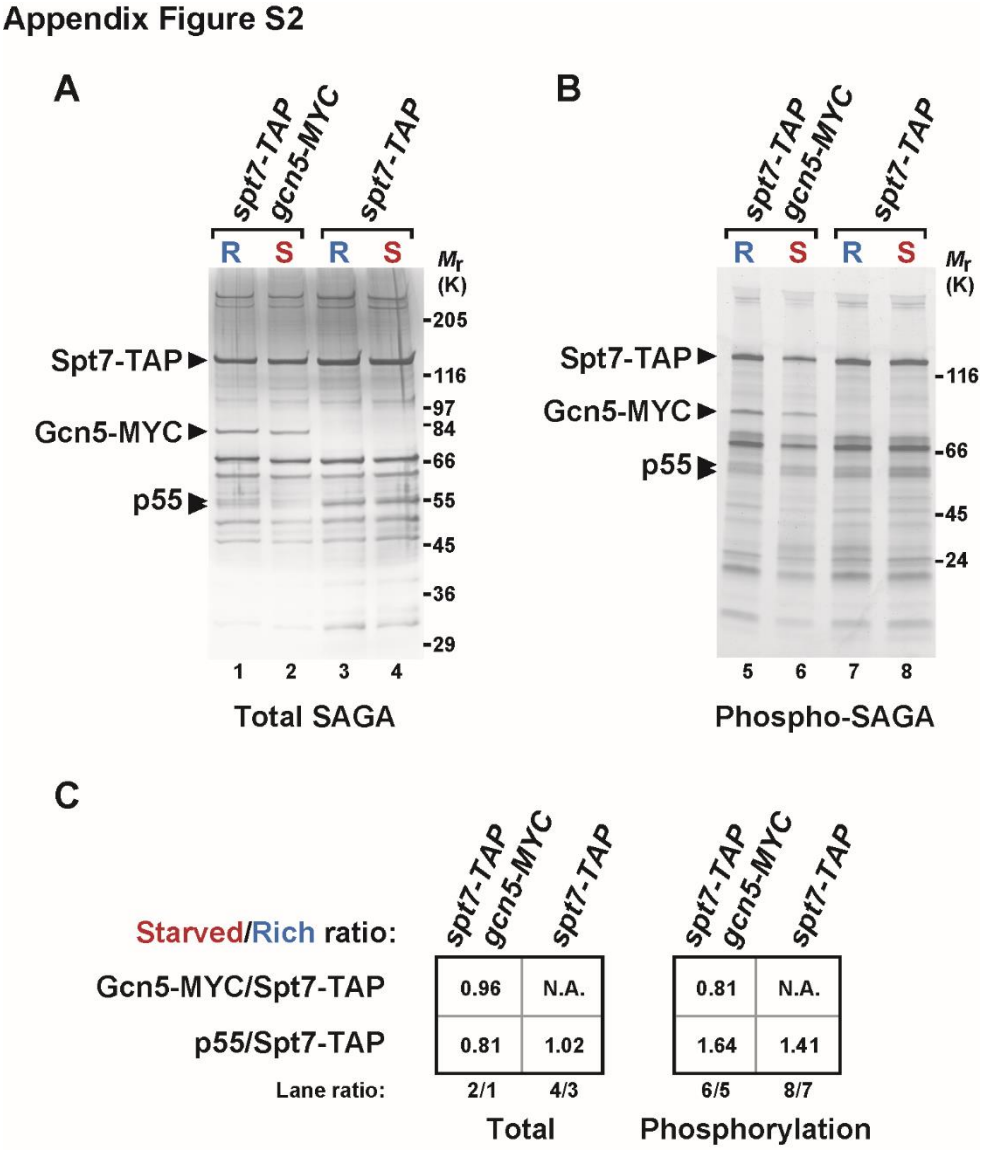
## Appendix Figure S1



**Appendix Figure S1.** SAGA regulates differentiation gene expression independently of the cAMP/Pka1$^{PKA}$ pathway, the Sty1$^{p38}$ kinase, and the Ssp2$^{AMPK}$ kinase.

(A-H) Expression of *ste11*$^{+}$ (A,C,E,G) and *mei2*$^{+}$ (B,D,F,H) using quantitative RT-PCR of RNA extracted from cells grown either in nutrient rich medium (dark gray) or shifted for 4 hours to starvation medium (light grey). (A,B) Wild-type isogenic controls (WT) and *gcn5*Δ cells were grown to mid-exponential phase in rich medium, with and without 5 mM cAMP, and then shifted to starvation medium for 4 hours. (C-H) Cells of the following genotypes were analyzed: WT, *gcn5*Δ, *cgs2*Δ, *gcn5*Δ *cgs2*Δ, *sty1*Δ, *gcn5*Δ *sty1*Δ. *ssp2*Δ, and *gcn5*Δ *ssp2*Δ. For all RT-qPCR, *act1*$^{+}$ served as a control for normalization across samples. Values from a WT strain grown in rich medium were set at 1 to allow comparisons across culture conditions and mutant strains. Each column represents the mean value of 4 (A-D) or 3 (E-H) independent experiments, overlaid with individual data points and standard error (SE) bars. Statistical significance was determined by 2-way ANOVA followed by Bonferroni's multiple comparison tests (n = 4 for A-D) (n = 3 for E-H). N.D., not determined.

**Appendix Figure S2**

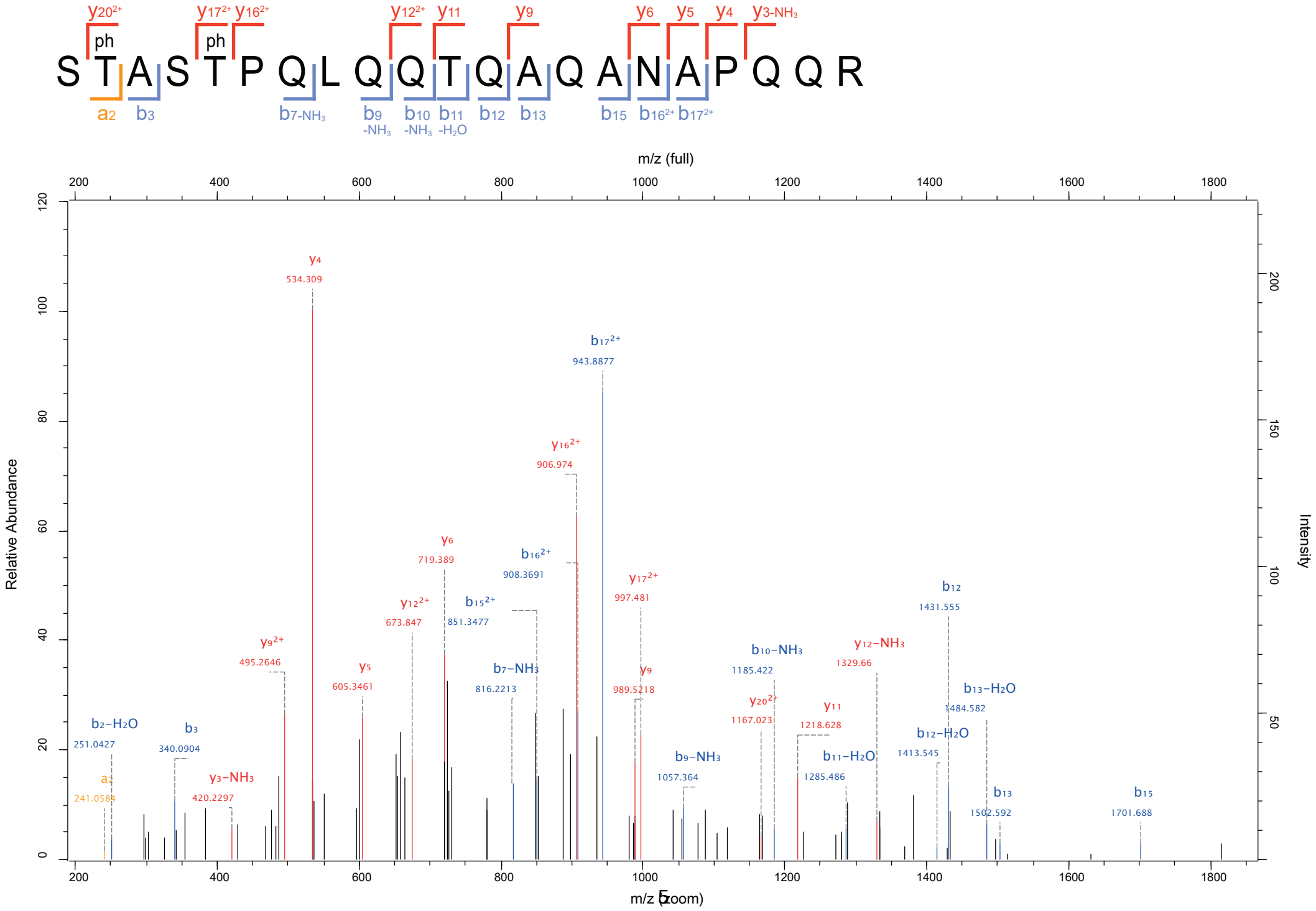



**Appendix Figure S2.** SAGA, but not Gcn5, becomes phosphorylated upon nutrient starvation.

(A,B) 4-20% gradient SDS-polyacrylamide gel electrophoresis analysis of SAGA purified from cells grown either in rich medium (R) or starved for 45 minutes (S). SAGA was purified using endogenously TAP-tagged Spt7, from strains in which Gcn5 was either endogenously MYC-tagged or not. Purification eluates were loaded and stained either with silver (A) or with Pro-Q® Diamond (B).

(C) Relative signal intensities of total (left) or phosphorylated Spt7, Gcn5, and p55 (right), measured and averaged from four independent experiments, using ImageJ. Shown are starved-to-rich ratios for Gcn5-MYC (top rows) and p55 (bottom rows), normalized to the starved-to-rich ratio of the bait, Spt7-TAP.

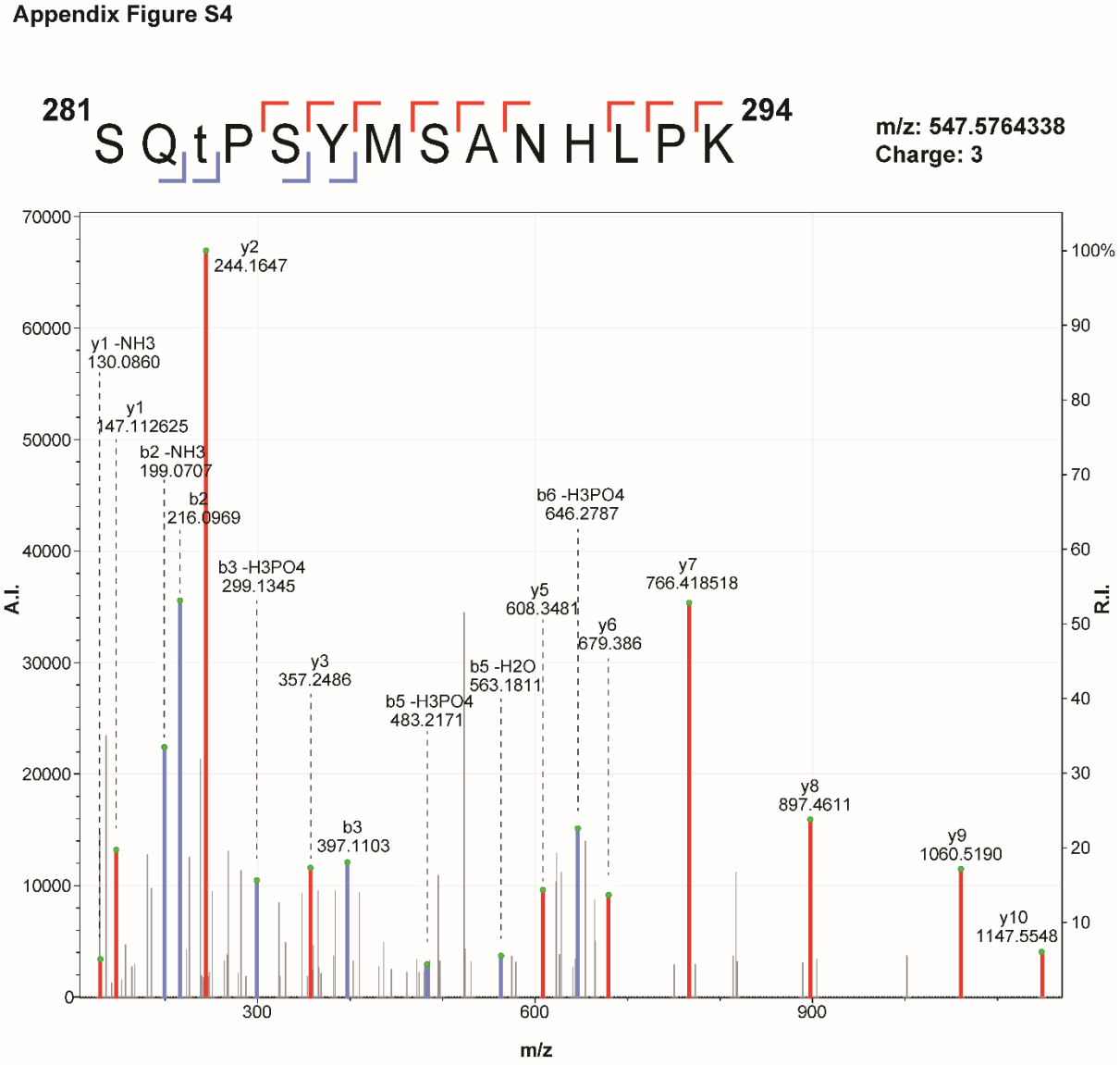
**Appendix Figure S3**



**Appendix Figure S3.** Identification of phosphorylated Taf12 residues in *S. pombe*.

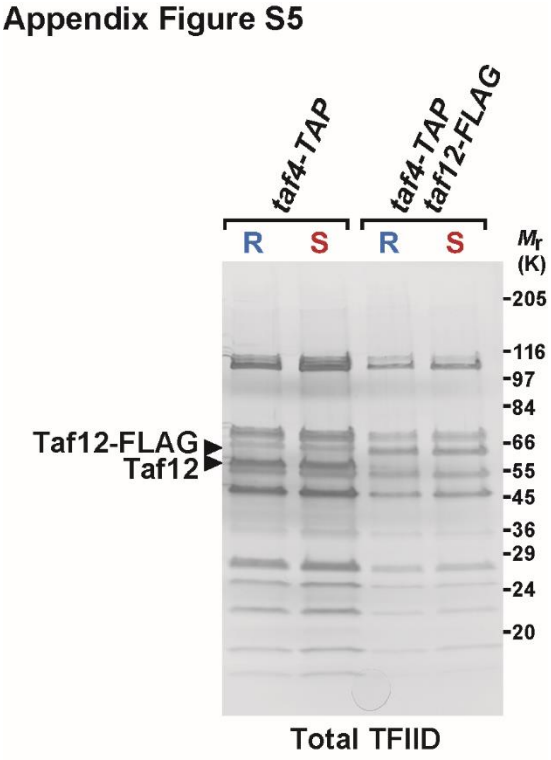
Phospho-peptides were enriched from total protein extracts of cells labelled using a SILAC procedure (Figure 3A) and identified by liquid chromatography coupled to tandem mass spectrometry analysis (LC-MS/MS). The ST*AST*PQLQQTQAQANAPQQR peptide of Taf12 is phosphorylated (*) on Thr218 and Thr221. See Materials and methods for details.

**Appendix Figure S4**




**Appendix Figure S4.** Identification of phosphorylated Taf12 residues within SAGA.

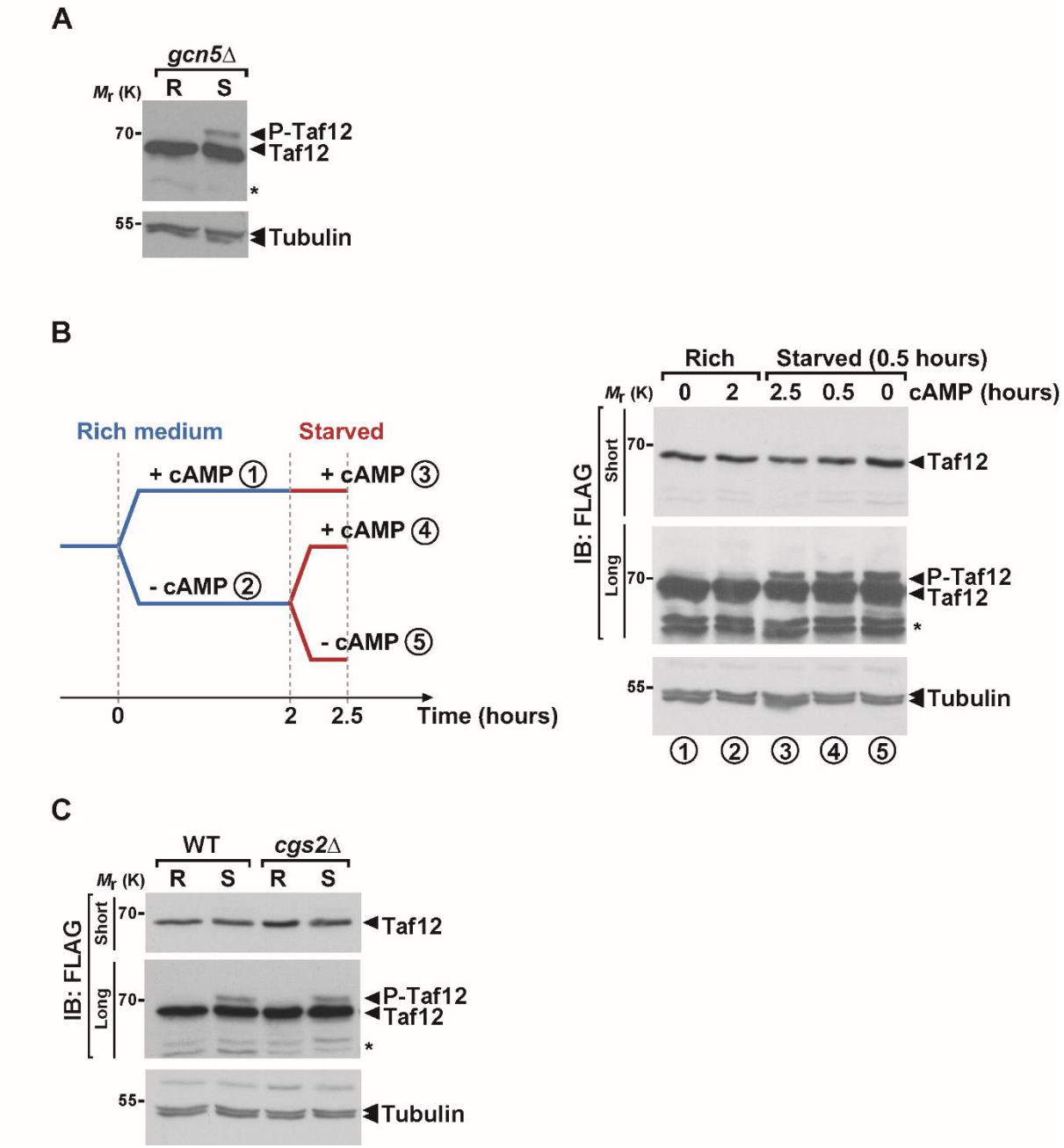
Phospho-peptides were enriched from SAGA complexes that were purified from cells labelled using a SILAC procedure (Figure 3A) and identified by LC-MS/MS. The SQT*PSYMSANHLPK peptide of Taf12 is phosphorylated (*) on Thr283. See Materials and methods for details.




**Appendix Figure S5.** TFIID subunit composition and levels do not change in response to nutrient starvation.

4-20% gradient SDS-polyacrylamide gel electrophoresis analysis of TFIID purified from cells grown either in rich medium (R) or starved for 45 minutes (S). TFIID was purified using endogenously TAP-tagged Taf4, from strains in which Taf12 was either endogenously MYC-tagged or not. Purification eluates were loaded and stained with silver.

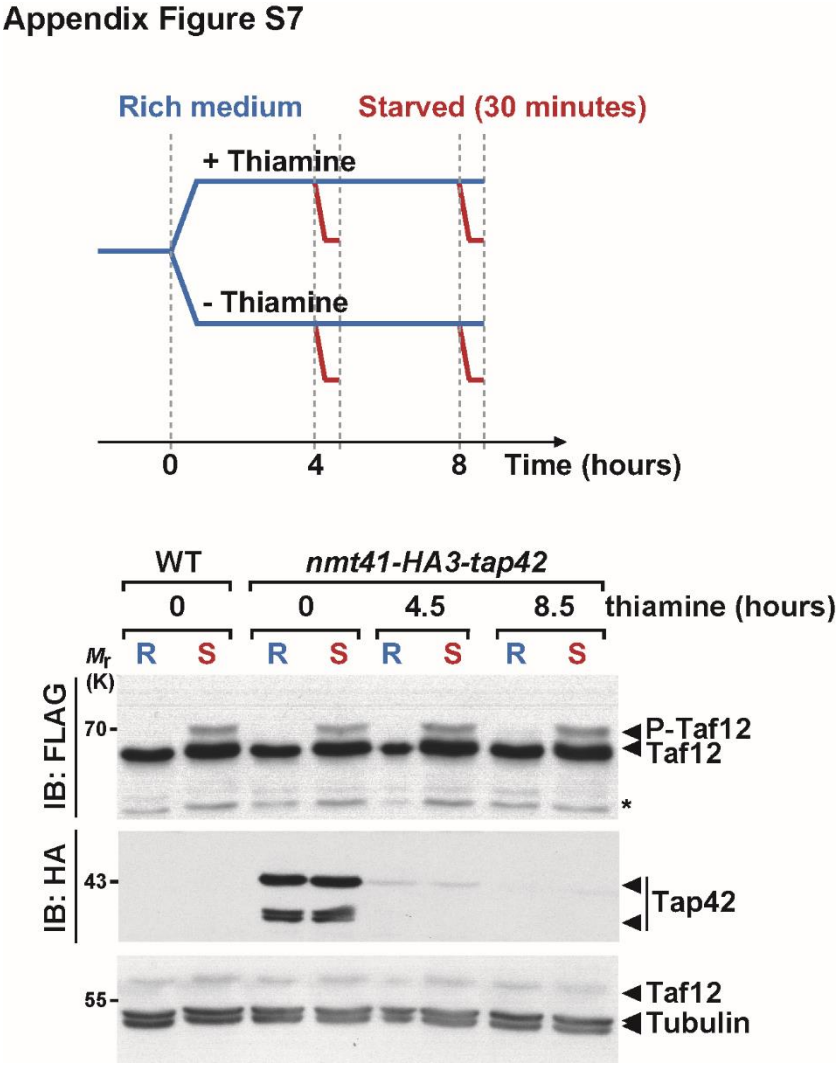
**Appendix Figure S6**




**Appendix Figure S6.** The cAMP/PKA pathway does not control Taf12 phosphorylation.

(A-C) P-Taf12 was followed by anti-FLAG IBs of protein extracts from different strains and growth conditions. (A) WT and *gcn5*Δ cells were grown in rich medium (R) or starved for 45 minutes (S). (B) WT cells were treated with 5 mM cAMP, which was added for various times either to rich or starved media, as described on the experimental scheme. (C) WT and *cgs2*Δ cells were grown in rich medium (R) or starved for 45 minutes (S). Short and long exposures of the FLAG IBs are shown to detect total Taf12 and P-Taf12, respectively, within the linear range of the chemi-luminescence signal. Anti-tubulin IBs are shown as controls for loading. The star (*) symbol labels an unspecific band detected by the anti-FLAG antibody in *S. pombe*. Shown are IBs that are representative of 2 independent experiments.

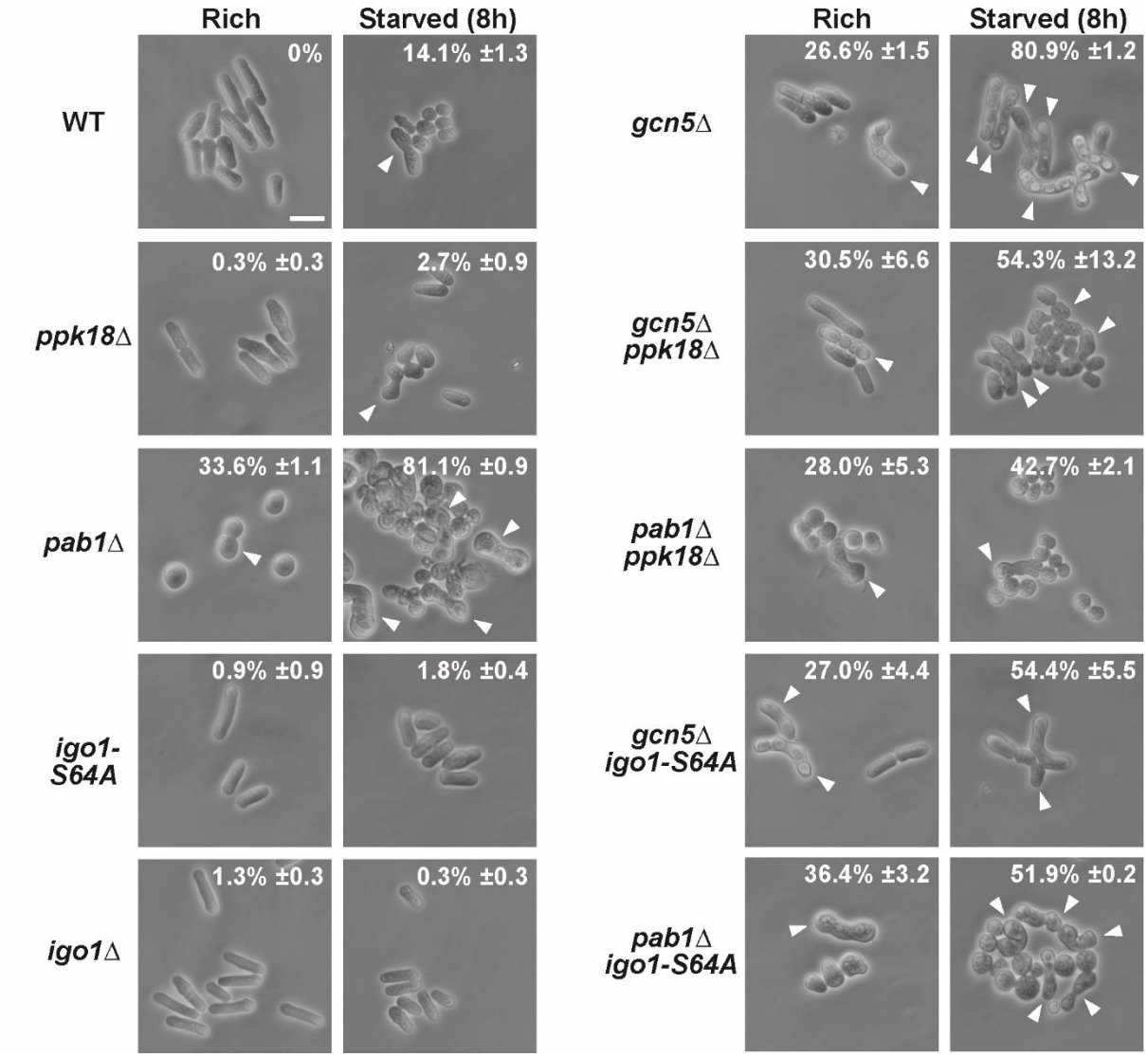
**Appendix Figure S7**




**Appendix Figure S7.** The PP2A regulator Tap42 does not regulate Taf12 phosphorylation.

P-Taf12 was followed by anti-FLAG IB (upper panel) of protein extracts from wild-type (WT) and *nmt41-HA3-tap42* strains. Cells were grown in rich medium (R) or starved for 45 minutes (S). To turn the *nmt41* promoter off, 5 g/L of thiamine was added 4 or 8 hours before shifting cells to starvation conditions, as described on the experimental scheme. The membrane was also immuno-blotted with an anti-HA antibody to follow the loss of Tap42 expression (middle panel). An anti-tubulin IB is shown as a control for loading (lower panel). The star (*) symbol labels an unspecific band detected by the anti-FLAG antibody in *S. pombe*. Shown are IBs that are representative of 2 independent experiments.

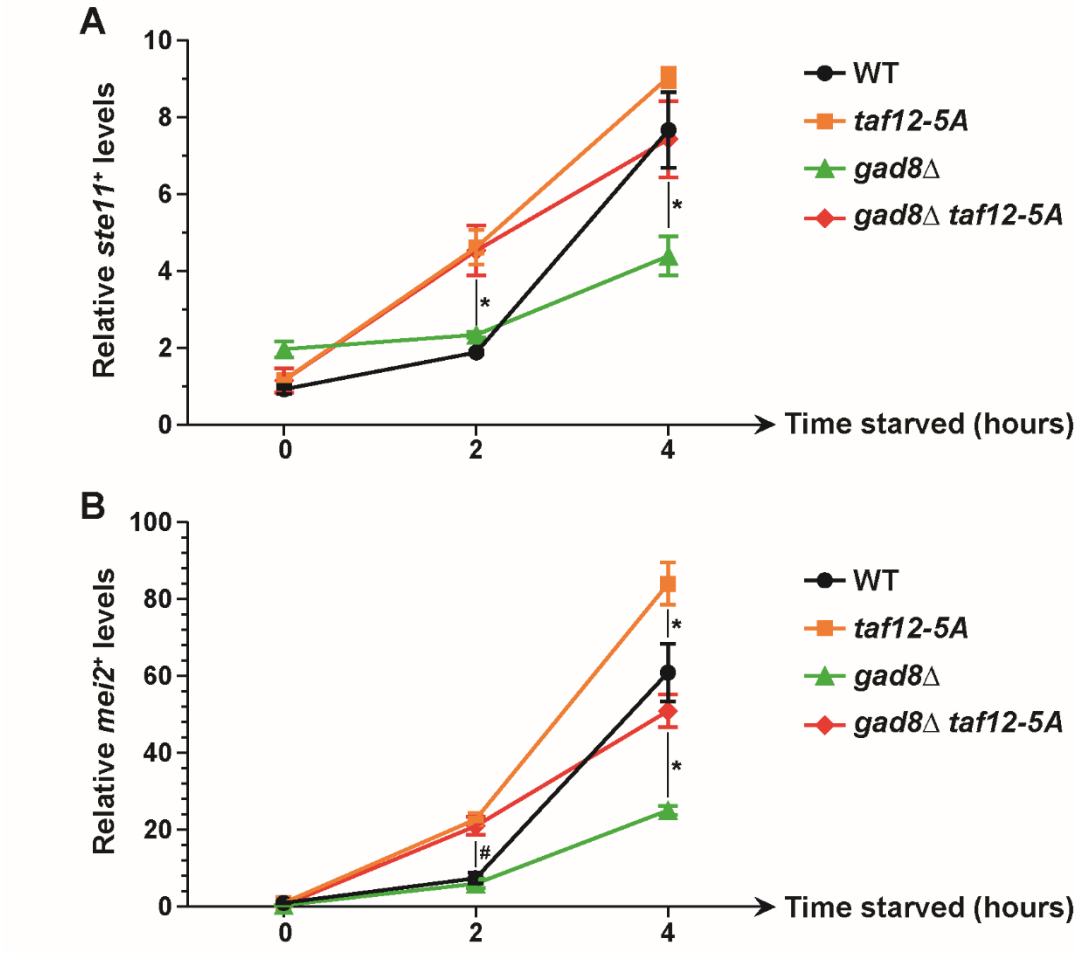
**Appendix Figure S8**




**Appendix Figure S8.** Epistasis analysis of sexual differentiation between Ppk18$^{Gwl}$-Igo1, PP2A-Pab1, and SAGA-Gcn5.

Cells were grown to mid-log phase either in rich medium or starved for 8 hours. Cells of the following genotypes were analyzed: wild-type isogenic controls (WT), *gcn5*Δ, *ppk18*Δ, *gcn5*Δ *ppk18*Δ, *pab1*Δ, *pab1*Δ *ppk18*Δ, *igo1-S64A*, *gcn5*Δ *igo1-S64A*, *pab1*Δ *igo1-S64A*, *igo1*Δ. Zygotes and tetrads, which correspond to differentiated cells, were counted under a light microscope. Each value represents the mean percentage and SE of differentiating cells to the total number of cells, averaged from 3 independent experiments. At least 200 cells from the indicated genotypes were counted in each experiment. White arrowheads indicate zygotes or tetrads. Scale bar, 10 μm.

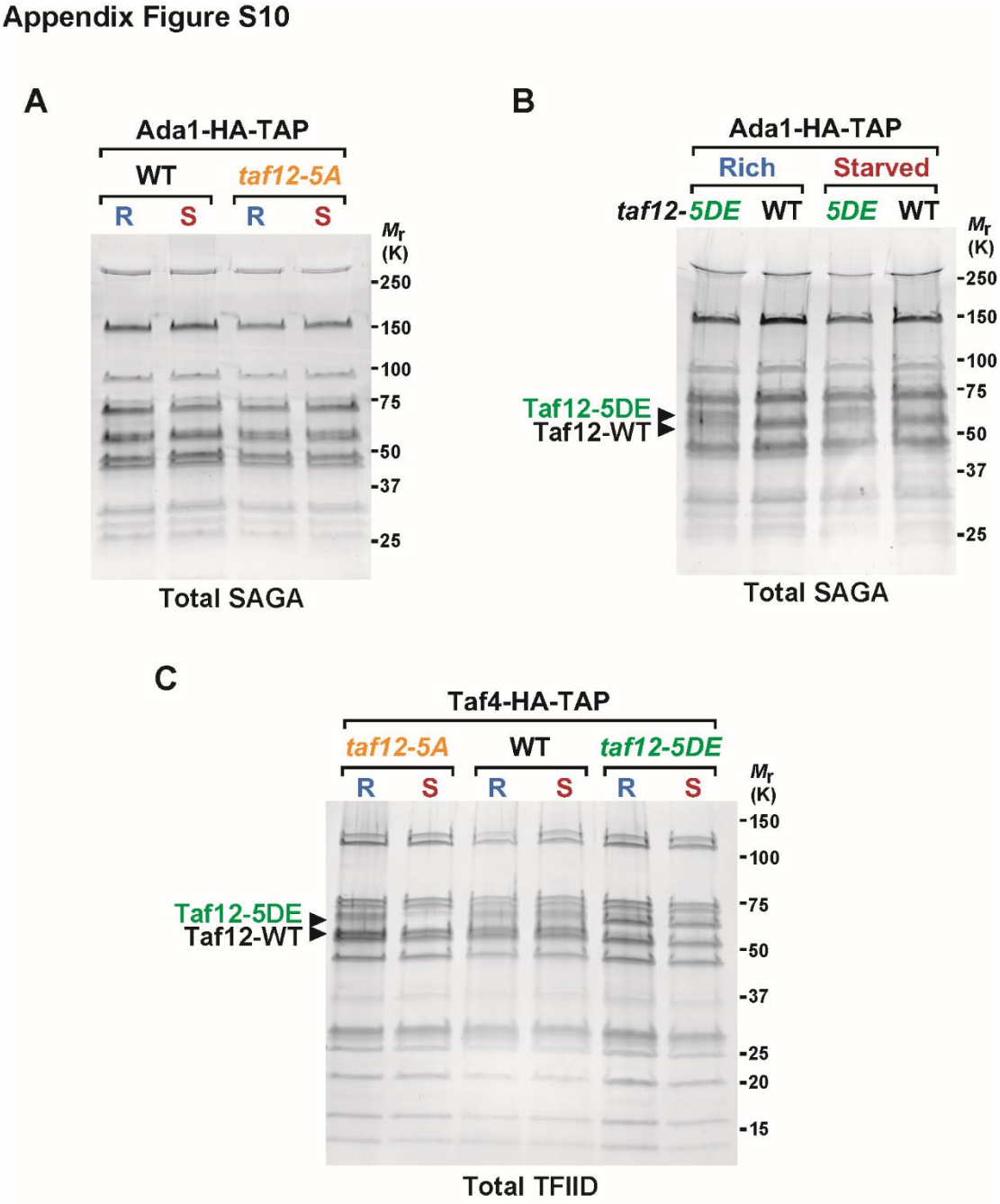
**Appendix Figure S9**




**Appendix Figure S9.** Taf12 phosphorylation is epistatic to Gad8$^{AKT}$ for the inhibition of differentiation gene expression.

(A,B) Expression of *ste11*$^{+}$ (A) and *mei2*$^{+}$ (B) using quantitative RT-PCR of RNA extracted from cells grown either in nutrient rich medium or starved for 2 or 4 hours. Cells of the following genotypes were analyzed: WT, *gad8*Δ, *taf12-5A*, and *gad8*Δ *taf12-5A*. *act1*$^{+}$ served as a control for normalization across samples. Values from a WT strain grown in rich medium were set at 1 to allow comparisons across culture conditions and mutant strains. Each point represents the mean value of at least 3 independent experiments, overlaid with standard error (SE) bars. Statistical significance was determined by 2-way ANOVA followed by Bonferroni's multiple comparison tests (n = 3).

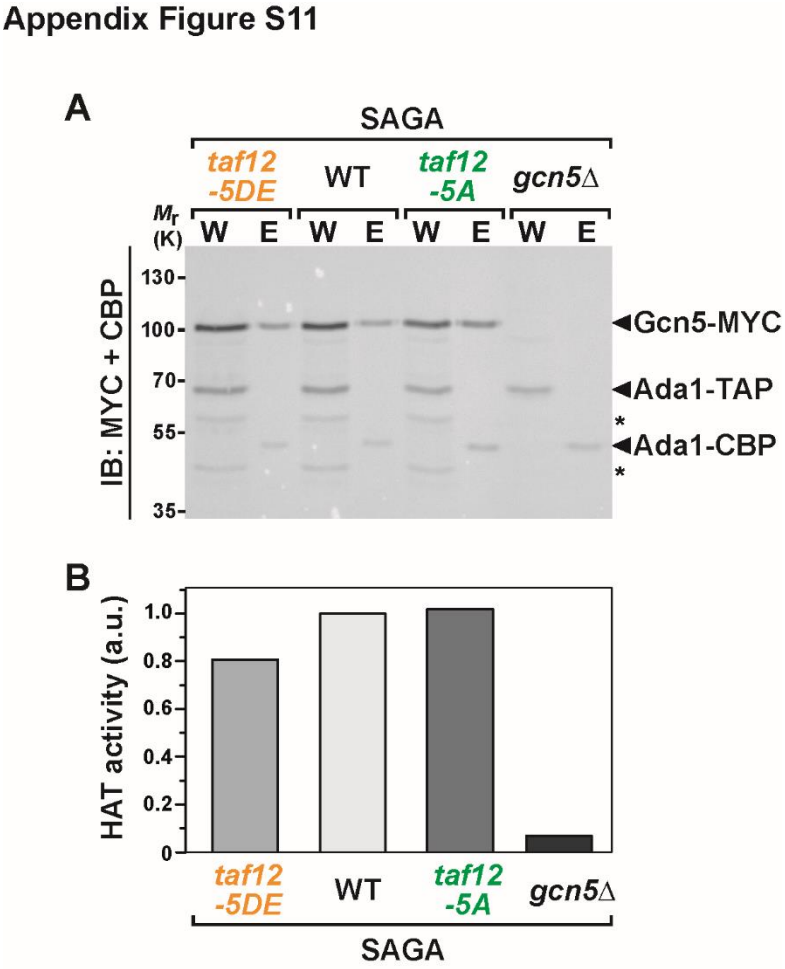
**Appendix Figure S10**




**Appendix Figure S10.** Taf12 phosphorylation does not affect SAGA or TFIID subunit composition.

(A-C) 4-20% gradient SDS-polyacrylamide gel electrophoresis analysis of SAGA (A,B) or TFIID (C) purified from WT, *taf12-5A* or *taf12-5DE* mutant cells, grown either in rich medium (R) or starved for 45 minutes (S). SAGA or TFIID were purified using endogenously TAP-tagged Ada1 or Taf4, respectively. Purification eluates were loaded and stained with silver. In both SAGA and TFIID purifications, Taf12-5DE migrates significantly slower than wild-type Taf12 or Taf12-5A (arrowheads in B,C), presumably because of the negative charge of the five Asp or Glu residues.

**Appendix Figure S11**




**Appendix Figure S11.** Taf12 phosphorylation does not modulate SAGA HAT activity.

SAGA was tandem affinity-purified using endogenously TAP-tagged Ada1, from WT, *taf12-5A* or *taf12-5DE* mutant cells, in which Gcn5 was endogenously MYC-tagged. As a negative control, SAGA was also purified from a *gcn5*Δ strain. TAP-tagged Ada1 was eluted using the TEV protease, releasing a shorter form of the bait (Ada1-CBP). Eluates were then processed either for Western blot analysis (A) or a HAT activity assay (B). (A) 5% of eluates were loaded and immuno-blotted (IB) using anti-CBP and anti-MYC antibodies, together with 1% of either whole cell extracts (WCE), to show equal amounts of Ada1 and Gcn5 in the different purifications. (B) 10% of the same eluates were assayed for HAT activity, using histone substrates. Shown are results that are representative of 2 independent experiments. The star (*) symbol labels unspecific bands detected by the anti-MYC antibody in *S. pombe*.

**Appendix Table S1.** Quantitative mass spectrometry analysis of SAGA subunit composition in rich and starved conditions.

Stable isotope labeling by amino acids in cell culture (SILAC) was performed to compare SAGA purified from cells grown in rich medium or further shifted to starvation conditions for 45 minutes. Shown are the light-to-heavy ratios of the signal intensities observed for all peptides detected for each SAGA subunit. Two experiments were carried out with forward and reverse lysine labeling schemes and are shown in distinct columns.

| SAGA subunit | Uniprot ID | Light (Rich) / Heavy (Starved) intensity ratios | Light (Starved) / Heavy (Rich) intensity ratios |
|---|---|---|---|
| Taf5 | O13282 | 0.97 | 1.05 |
| Taf12 | O13722 | 0.97 | 0.99 |
| Spt20 | O14174 | 0.91 | 1.03 |
| Spt3 | O14311 | 0.95 | 1.03 |
| Spt8 | O60097 | 0.93 | 1.06 |
| Taf10 | O60171 | 0.90 | 1.06 |
| Taf6 | O74462 | 0.93 | 1.01 |
| Hfi1/Ada1 | O94301 | 0.95 | 0.98 |
| Sgf73 | O94397 | 0.85 | 1.16 |
| Spt7 | P87152 | 0.95 | 1.05 |
| Ubp8 | Q09738 | 0.98 | 1.16 |
| Taf9 | Q09869 | 0.94 | 1.08 |
| Sgf11 | Q5FC18 | 0.86 | 1.22 |
| Sus1 | Q7LL15 | 0.84 | 1.22 |
| Tra1 | Q9HFE8 | 0.89 | 1.18 |
| Ada2 | Q9P7J7 | 0.96 | 1.02 |
| Ngg1/Ada3 | Q9USU8 | 0.92 | 0.99 |
| Gcn5 | Q9UUK2 | 0.98 | 1.00 |
| Sgf29 | Q9USW9 | 0.88 | 1.06 |

**Appendix Table S2. List of strains used in this study.**

| Strain | Genotype | Source |
|---|---|---|
| DHP148 | *h*$^{90}$ | Lab Stock |
| DHP290 | *h*$^{90}$ *gcn5*Δ*::kanMX6* | Lab Stock |
| DHP847 | *h*$^{90}$ *cgs2*Δ*::natMX6* | This study |
| DHP850 | *h*$^{90}$ *gcn5*Δ*::kanMX6 cgs2*Δ*::natMX6* | This study |
| DHP867 | *h*$^{90}$ *tor2-L1310P-3p::kanMX6* | F. Tamanoi |
| DHP654 | *h*$^{90}$ *tor2-L1310P-3p::kanMX6 gcn5*Δ*::natMX6* | This study |
| DHP801 | *h*$^{-}$ *leu1-32 rhb1-DA4* | T. Matsumoto |
| DHP946 | *h*$^{90}$ *rhb1-DA4* | This study |
| DHP954 | *h*$^{90}$ *rhb1-DA4 gcn5*Δ*::kanMX6* | This study |
| DHP1200 | *h*$^{-}$ *ssp2*Δ*::natMX6* | This study |
| DHP772 | *h*$^{-}$ *gcn5*Δ*::kanMX6* | This study |
| DHP1201 | *h*$^{-}$ *gcn5*Δ*::kanMX6 ssp2*Δ*::natMX6* | This study |
| DHP1202 | *h*$^{90}$ *sty1*Δ*::natMX6* | This study |
| DHP1203 | *h*$^{90}$ *sty1*Δ*::natMX6 gcn5*Δ*::kanMX6* | This study |
| DHP637 | *h*$^{90}$ *tsc1*Δ*::natMX6* | This study |
| DHP639 | *h*$^{90}$ *gcn5*Δ*::kanMX6 tsc1*Δ*::natMX6* | This study |
| DHP643 | *h*$^{90}$ *tsc2*Δ*::natMX6* | This study |
| DHP645 | *h*$^{90}$ *gcn5*Δ*::kanMX6 tsc2*Δ*::natMX6* | This study |
| DHP43 | *h*$^{-}$ | Lab Stock |
| DHP42 | *h*$^{+}$ | Lab Stock |
| DHP355 | *h*$^{-}$ *ada1-HA3-TAP2::kanMX6* | Lab Stock |
| DHP783 | *h*$^{-}$ *spt7-HA3-TAP2::kanMX6* | Lab Stock |
| DHP815 | *h*$^{-}$ *spt7-HA3-TAP2::kanMX6 gcn5-MYC13::natMX6* | This study |
| DHP828 | *h*$^{-}$ *lys1-131 spt7-HA3-TAP2::kanMX6* | This study |
| DHP898 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP1204 | *h*$^{-}$ *taf12-S217A-T218A-S220A-T221A-T283A-Gly6-FLAG3::kanMX6* | This study |
| DHP1205 | *h*$^{-}$ *taf12-T283A-Gly6-FLAG3::kanMX6* | This study |
| DHP1005 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 pab1*Δ*::natMX6* | This study |
| DHP1206 | *h*$^{-}$ *pab1*Δ*::kanMX6 leu1-32::pJK148-NTAP-pab1+* | S. Lopez-Aviles |
| DHP1207 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 pab1*Δ*::kanMX6 leu1-32::pJK148-NTAP-pab1+* | This study |
| DHP659 | *h*$^{90}$ *ppa2*Δ*::kanMX6* | This study |
| DHP661 | *h*$^{90}$ *pab1*Δ*::kanMX6* | This study |
| DHP945 | *h*$^{90}$ *tsc1*Δ*::natMX6 pab1*Δ*::kanMX6* | This study |
| DHP663 | *h*$^{90}$ *par1*Δ*::kanMX6* | S. Lopez-Aviles |
| DHP1037 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 gcn5*Δ*::kanMX6* | This study |
| DHP1040 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 ppk18*Δ*::natMX6* | This study |
| DHP1208 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 igo1*Δ*::kanMX6* | This study |
| DHP1209 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 igo1-MYC13::kanMX6 ppk18*Δ*::natMX6* | This study |
| DHP1210 | *h*$^{-}$ *igo1-S64A-MYC13::kanMX6* | This study |
| DHP1211 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 igo1-S64A-MYC13::kanMX6* | This study |
| DHP1212 | *h*$^{-}$ *igo1-S64A-MYC13::kanMX6 gcn5*Δ*::natMX6* | This study |
| DHP1213 | *h*$^{-}$ *igo1-S64A-MYC13::kanMX6 pab1*Δ*::hphMX6* | This study |
| DHP1214 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 igo1-S64A-MYC13::kanMX6 pab1*Δ*::hphMX6* | This study |
| DHP1215 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 igo1-S64A-MYC13::kanMX6 gcn5*Δ*::kanMX6* | This study |
| DHP1216 | *h*$^{-}$ *ppk18*Δ*::natMX6 gcn5*Δ*::kanMX6* | This study |
| DHP1217 | *h*$^{-}$ *ppk18*Δ*::natMX6 pab1*Δ*::kanMX6* | This study |
| DHP1218 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 ppk18*Δ*::natMX6 pab1*Δ*::hphMX6* | This study |
| DHP1219 | *h*$^{-}$ *igo1-MYC13::kanMX6* | This study |
| DHP1036 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 ssp2*Δ*::natMX6* | This study |
| DHP1031 | *h*$^{-}$ *taf12-Gly6-FLAG3::kanMX6 sty1*Δ*::natMX6* | This study |
| DHP32 | *h*$^{-}$ *ade6-M210* | Lab Stock |
| DHP45 | *h*$^{-}$ *ade6-M216* | Lab Stock |

| | | | |
|---|---|---|---|
| DHP797 | $h^-$ | *ade6-M21x gcn5 Δ::kanMX6* | This study |
| DHP795 | $h^-$ | *ade6-M21x tor1 Δ::natMX6* | This study |
| DHP890 | $h^+$ | *ade6-M21x tor1 Δ::natMX6 gcn5 Δ::kanMX6* | This study |
| DHP1123 | $h^{90}$ | *gad8 Δ::natMX6* | This study |
| DHP1125 | $h^{90}$ | *gcn5 Δ::kanMX6 gad8 Δ::natMX6* | This study |
| DHP1102 | $h^-$ | *taf12-Gly6-FLAG3::kanMX6 cgs2 Δ::natMX6* | This study |
| DHP1108 | $h^-$ | *taf12-Gly6-FLAG3::kanMX6 gad8 Δ::natMX6* | This study |
| DHP1099 | $h^-$ | *taf12-Gly6-FLAG3::kanMX6 tor1 Δ::natMX6* | This study |
| DHP1220 | $h^-$ | *kanMX6::nmt1-NTAP-gad8 taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP1221 | $h^{90}$ | *taf12-S217A-T218A-S220A-T221A-T283A* | This study |
| DHP1222 | $h^{90}$ | *taf12-S217D-T218E-S220D-T221E-T283E* | This study |
| DHP995 | $h^{90}$ | *natMX6::P41nmt1-HA3-tap42* | This study |
| DHP1223 | $h^-$ | *natMX6::P41nmt1-HA3-tap42 taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP518 | $h^{90}$ | *ade6-M210 leu1 tor2-ts10* | M. Yamamoto |
| DHP1259 | $h^-$ | *tor2-ts10 taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP126 | $h^-$ | *ura4-D18 leu1-32 ade6-M216 ada1-HA3-TAP2::kanMX6+ gcn5D::ura4+* | This study |
| DHP972 | $h^-$ | *spt7-HA3-TAP2::kanMX6 taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP1265 | $h^-$ | *ada1-HA3-TAP2::kanMX6 gcn5-MYC13::natMX6* | This study |
| DHP1266 | $h^-$ | *ada1-HA3-TAP2::kanMX6 gcn5-MYC13::natMX6 taf12-S217A-T218A-S220A-T221A-T283A* | This study |
| DHP1267 | $h^-$ | *ada1-HA3-TAP2::kanMX6 gcn5-MYC13::natMX6 taf12-S217D-T218E-S220D-T221E-T283E* | This study |
| DHP1087 | $h^-$ | *taf4-HA3-TAP2::kanMX6* | This study |
| DHP1090 | $h^-$ | *taf4-HA3-TAP2::kanMX6 taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP1256 | $h^-$ | *taf4-HA3-TAP2::kanMX6 taf12-S217A-T218A-S220A-T221A-T283A* | This study |
| DHP1257 | $h^-$ | *taf4-HA3-TAP2::kanMX6 taf12-S217D-T218E-S220D-T221E-T283E* | This study |
| DHP957 | $h^{90}$ | *ppk18 Δ::natMX6+* | This study |
| DHP1277 | $h^{90}$ | *gcn5 Δ::kanMX6 ppk18 Δ::natMX6+* | This study |
| DHP1290 | $h^{90}$ | *pab1 Δ::kanMX6+ ppk18 Δ::natMX6+* | This study |
| DHP1287 | $h^{90}$ | *igo1-S64A::kanMX6+* | This study |
| DHP1280 | $h^{90}$ | *igo1-S64A-MYC13::kanMX6 gcn5 Δ::natMX6* | This study |
| DHP1283 | $h^{90}$ | *igo1-S64A-MYC13::kanMX6 pab1 Δ::natMX6+* | This study |
| DHP1286 | $h^{90}$ | *igo1 Δ::kanMX6+* | This study |
| DHP1288 | $h^{90}$ | *taf12-S217A-T218A-S220A-T221A-T283A gad8 Δ::natMX6* | This study |
| DHP1304 | $h^-$ | *gad8-HA3::natMX6+* | This study |
| DHP1341 | $h^-$ | *tor1-T1972A taf12-Gly6-FLAG3::kanMX6* | This study |
| DHP1346 | $h^+$ | *taf12-S217A-T218A-S220A-T221A-T283A* | This study |
| DHP1340 | $h^-$ | *tor1-T1972A* | This study |
| DHP1325 | $h^+$ | *tor1-T1972A* | J. Petersen |
| DHP1349 | $h^-$ | *tor1-T1972A taf12-S217A-T218A-S220A-T221A-T283A* | This study |
| DHP1348 | $h^+$ | *tor1-T1972A taf12-S217A-T218A-S220A-T221A-T283A* | This study |

**Appendix Table S3. List of oligonucleotides used in this study.**

| Gene | Name | Description[a] | Strand[b] | Coordinates[c] | Sequence |
|---|---|---|---|---|---|
| *gcn5+* | DHO 548 | deletion / pFA6a | Fwd | | TTCATCTTGTATCGTTCTTGACAATTTCTGTATCTTCACTTTTTGGATTTATTTGTTTGGATGCGTGGCATAGAATAATCCGGATCCCCGGGTTAATTAA |
| *gcn5+* | DHO 180 | C-terminal tagging / pFA6a | Fwd | | CTTACTATAAAAATGCCGATAGATTGGAAAAGTTTTTCCAGAAAAAACTTCGTGAAACTGAGTATTCACACTTAGCCGATCGGATCCCCGGGTTAATTAA |
| *gcn5+* | DHO 181 | C-terminal tagging or deletion / pFA6a | Rv | | AAAAATTAAAAGGTGAAATGTATATGTTATAATCAATAAAACTTCGGAATAGACGTTTCGATGATAATAAATGTAAATGAGAATTCGAGCTCGTTTAAAC |
| *cgs2+* | DHO 593 | deletion / pFA6a | Fwd | | TAATAAATATGACGTCAACCGACATGTTTTTGTAGACTAGTGCATGCACCGGAGATCTGTAACTCTCCATAAGCCTAGCCCGGATCCCCGGGTTAATTAA |
| *cgs2+* | DHO 594 | deletion / pFA6a | Rv | | AATAAATGGAGAAACCTAAAAGAAATTAAAAAAAAAAAATAAAAATATAATGAATATATGACCATGACCCTGGGATGCTAGAATTCGAGCTCGTTTAAAC |
| *ssp2+* | DHO 476 | deletion / pFA6a | Fwd | | TATCATCTCATGTGACACAACTAAGGATGTATACTATGGCTTTGCCTTCTACCAAATTATATATTTATCTCACACTCTGACGGATCCCCGGGTTAATTAA |
| *ssp2+* | DHO 477 | deletion / pFA6a | Rv | | CACTAAATTCATCAATTCATAAATGTTTCAACAGAAAATGGCGGTAATTAATCCGGACACTAGTATCTTCATGCAACCTTGAATTCGAGCTCGTTTAAAC |
| *sty1+* | DHO 484 | deletion / pFA6a | Fwd | | TACTTTTCGATATAGACGAAGGACGCTTAAATTTTTGAGATTATTGTTGAATAGTCCTTTTTGTAACCAGTTTGAATAAACGGATCCCCGGGTTAATTAA |
| *sty1+* | DHO 485 | deletion / pFA6a | Rv | | TAAATATGATACACGTGAACAAAATAGAGTAATCATAACATACCCCGAGAACAACTTTTAAGGCTTTATCTACAACTTGTGAATTCGAGCTCGTTTAAAC |
| *tsc1+* | DHO 423 | deletion / pFA6a | Fwd | | TTATCAATGCTGCCAAGACTTGCTATCAGTATAATGTCGCATAGTTGTATATCAACGTTGACTTTGCCAACTTTGTACGACGGATCCCCGGGTTAATTAA |
| *tsc1+* | DHO 424 | deletion / pFA6a | Rv | | AATTATTTTATATGGAATGAGCAAGTATGTTTTATCATAATTGACCAGTTCATTTCAAGGACCTTCAAAAATATACCTACGAATTCGAGCTCGTTTAAAC |
| *tsc2+* | DHO 427 | deletion / pFA6a | Fwd | | TTAAGAGTTCAGATTTGCTTTATGTGGTTATTCTGCTGAAGGTCCTAATTTATTGACGTTGAAAAATAAAGGCCACATAGCGGATCCCCGGGTTAATTAA |
| *tsc2+* | DHO 428 | deletion / pFA6a | Rv | | CATATACATGGATACCGTTTCTTTTATTCATCTTCCTTAACATCTTCATTATCTGATCTATAAATAATATTTAAGATTAAGAATTCGAGCTCGTTTAAAC |
| *spt7+* | DHO 490 | C-terminal tagging / pFA6a | Fwd | | TTTTAAATCAATCCTTGAGAAAAAAGCGCTGCCTAAAGGAGAATGAGCAAGGTACTGAGGTAACTACTCTTCCTGAAGAACGGATCCCCGGGTTAATTAA |
| *spt7+* | DHO 491 | C-terminal tagging / pFA6a | Rv | | TTTAAAAGTTATGTCTCCATTGTGGTTGATACACATCTATATACTAGTTGTTTTTGACGTTATAAATAAATACATATGGCGAATTCGAGCTCGTTTAAAC |
| *ada1+* | DHO 488 | C-terminal tagging / pFA6a | Fwd | | CGCCAAGCTACATGCTTGCAAGCAATGATGCGCAAAGTGATAGGAATTCTGTTGCTTCCCTTTTAGATGAAGTGCTTTCACGGATCCCCGGGTTAATTAA |
| *ada1+* | DHO 489 | C-terminal tagging / pFA6a | Rv | | TAATCAAGTCTTGTATATTTGCGAGCTGAAACGCTTGAAGAATAGCCCTTGAAGCTTTTAAGATTGTAAATAAATAAAGCGAATTCGAGCTCGTTTAAAC |
| *ppk18+* | DHO 610 | deletion / pFA6a | Rv | | ATATAAATATTGACACAGTCATCAAGAGCCACCCACGTTCATAAATTGGGTGTTTGATTAGAATATCAATTGGTTACCGTCGGATCCCCGGGTTAATTAA |
| *ppk18+* | DHO 611 | deletion / pFA6a | Fwd | | TCGAGAAACAAAAAGGAAAAAATTAAAGAGAGTATGGTAACAACAAAAAATGAGCAATCACGATTAACAAACGTTTGAACGAATTCGAGCTCGTTTAAAC |
| *igo1+* | DHO 511 | deletion / pFA6a | Fwd | | ATCGACAAAATTACGTATGATACCTAATACGTTAACAGTGCGGTATCTTAGGCTTCGGTAGACAAGTGGCCGTGTGGTATCGGATCCCCGGGTTAATTAA |
| *igo1+* | DHO 512 | deletion / pFA6a | Rv | | ACGACAAGCAATACCAAATTTTAAGAGCCAAGCCAAATTAAACCTCCAACCTTGTCGCAAAAATAGCAACGTGTATGACCGAATTCGAGCTCGTTTAAAC |
| *igo1+* | DHO 1108 | mutagenesis *igo1-S64A* / pKSura4 | Fwd | | TTTTCCGTTTGTATGGACGACTTCCTCAGCGAAAGGATCTATTAGTTCAAAAATTACAGCAAGGTAGAAAATACTTTGATCGCCAGGGTTTTCCCAGTCACGAC |
| *igo1+* | DHO 1109 | mutagenesis *igo1-S64A* / pKSura4 | Rv | | TCAGGAGAGGGAATCTCCTTACCAATACAAGTGATACCTGAATCGGAGGCCTTTCCAGCTTTGTTTAAGGCATAGTCGCCAGCGGATAACAATTTCACACAGGA |
| *igo1+* | DHO 512 | C-terminal tagging / pFA6a | Fwd | | ACGACAAGCAATACCAAATTTTAAGAGCCAAGCCAAATTAAACCTCCAACCTTGTCGCAAAAATAGCAACGTGTATGACCGAATTCGAGCTCGTTTAAAC |
| *igo1+* | DHO 515 | C-terminal tagging / pFA6a | Rv | | GACCCTCAGAGTCCTCGCCTAGTGGTGCCAGTAGCAGAAGGGAATCTGTCACGCGACACGACTTGGAAAGCAATGAAAATCGGATCCCCGGGTTAATTAA |
| *pab1+* | DHO 793 | deletion / pFA6a | Fwd | | AAGATCAAGATCTTCGTATACAATTGAAATTGGCAAAGTGTACCAACGGGAACGAAATCTTAATATAATACGAGTAGAAGCGGATCCCCGGGTTAATTAA |
| *pab1+* | DHO 794 | deletion / pFA6a | Rv | | TCCCGGAAGTTCAATAAAAAAGGAACTATGTTCAGTCTATCCGTAGATCATAAAAACAAACCAAACTCCACATAAGGACAGAATTCGAGCTCGTTTAAAC |
| *ppa2+* | DHO 604 | deletion / pFA6a | Fwd | | CAAGCTGATGATACGCAAGAGTAGCCTGTCACCTCTGTAACGGTCTCAACTTACCAAAAGCAACACACGGTTAGAAAGACCGGATCCCCGGGTTAATTAA |
| *ppa2+* | DHO 605 | deletion / pFA6a | Rv | | TTAACTCAAAAATCAGAAAGGTGGATAAATTTTTTGAAACAATCACAATCGATTGATCACTCATTAGAGAATTGAAACTTGAATTCGAGCTCGTTTAAAC |
| *gad8+* | DHO 860 | deletion / pFA6a | Fwd | | TTAAAAGAAAAGATAGAGGGAAAGCGAGCTTTTAAAAATCAGTTCATTTTTTTTTTTCTACTCCAAACAGACGTTACCGAACGGATCCCCGGGTTAATTAA |
| *gad8+* | DHO 861 | deletion / pFA6a | Rv | | ATGTAAAAGAGGCAAGAAAAGCGGCATGTATGAGTAAAAATGAGAAAACTTTCAAAATAAACAAAGAAGTGTCAAATTCAGAATTCGAGCTCGTTTAAAC |
| *tor1+* | DHO 411 | deletion / pFA6a | Fwd | | ATTGTGATGAATGCCTAAGTGGAAGAATTGAACACCGCGACTATTAGAAAGTCTATCGTTTCACTCGCTCTCTTTGATTCCGGATCCCCGGGTTAATTAA |
| *tor1+* | DHO 412 | deletion / pFA6a | Rv | | CAGAAACGAGCGAATTTATAGACATAAATTAATAACAACACGAAAAAAATTATCATAATCTCAAAAAACAGAAAACATCAGAATTCGAGCTCGTTTAAAC |
| *gad8+* | DHO 925 | C-terminal tagging / pFA6a | Fwd | | CCAATTGGAGCTATCAACGACCAACAACCATTGATACATCCGACGACATTAATACAATAGCACCTGGAAGTGTCATTAGGCGGATCCCCGGGTTAATTAA |
| *gad8+* | DHO 1053 | *nmt1-TAP* N-terminal tagging / pFA6a | Fwd | | ATTAGTCCATAAATACGTTTTTTGTTAGATTGAAGCTTTTTTGCAGCCTCGTTACCTTATTCTTTATCATTTTCGTTATAGAATTCGAGCTCGTTTAAAC |
| *gad8+* | DHO 1054 | *nmt1-TAP* N-terminal tagging / pFA6a | Rv | | AAAAGCTGTTAGTATGAAAAAGAAAGACAGAGTGTGATAACCCGTATTATGGAATACATACTCTTTGTAAGTTTCCAGGACATCGCGCCATAATCAAGTGC |
| *taf12+* | DHO 771 | C-terminal tagging / pFA6a | Fwd | | GCGCTCGTAAGACTGGGCCCACACCTTCATATCAGCAAAAGCAAAACGCTATTGGAACTGCTAAAAGTTTGAATAAGGACCGGATCCCCGGGTTAATTAA |
| *taf12+* | DHO 772 | C-terminal tagging / pFA6a | Rv | | ATTTTTAAAAATTTTGACCTTTTTTCTTTTACATAAGTCCATGAAATCGCATAACAGTATAAAATTCTCTTTCATTGGCGGAATTCGAGCTCGTTTAAAC |
| *taf12+* | DHO 744 | amplification taf12 / DHB60 | Fwd | | ATTCGTTCCATTCAACAATT |
| *taf12+* | DHO 745 | amplification taf12 / DHB60 | Rv | | AAAATTAGTGACTGATTCGA |
| *taf12+* | DHO 854 | assembly DHB62 | Fwd | | AGCTCCACCGCGGTGGCGGCCGCATGAATGGGCAGCATTCAAGCC |
| *taf12+* | DHO 855 | assembly DHB62 | Rv | | AATTGTTGAATGGAACGAAT |
| *taf12+* | DHO 856 | assembly DHB62 | Fwd | | TCGAATCAGTCACTAATTTT |
| *taf12+* | DHO 857 | assembly DHB62 | Rv | | CATATGTTACGCATAGTCAGGAACATCGTATGGGTAGTCCTTATTCAAACTTTTAGC |
| *taf12+* | DHO 858 | assembly DHB62 | Fwd | | TACCCATACGATGTTCCTGACTATGCGTAACATATGCGCCAATGAAAGAGAATTTT |
| *taf12+* | DHO 859 | assembly DHB62 | Fwd | | CGAATTCCTGCAGCCCGGGGGATCCGAAGCTTACATAACCAATTA |
| *taf12+* | DHO 909 | mutagenesis *taf12-S217A-T218A-S220A-S221A* / DHB62 | Rv | | CCTCAACTGATACTAGAAAAGCCGCTGCTGCAGCTCCTCAATTACAACAGACCCA |
| *taf12+* | DHO 910 | mutagenesis *taf12-S217A-T218A-S220A-S221A* / DHB62 | Fwd | | TGGGTCTGTTGTAATTGAGGAGCTGCAGCAGCGGCTTTTCTAGTATCAGTTGAGG |
| *taf12+* | DHO 1035 | mutagenesis *taf12-A217D-A218E-A220T-A221E* / DHB63 | Rv | | CCTCAACTGATACTAGAAAAGACGAAGCTGACGAGCCTCAATTACAACAGACCCA |
| *taf12+* | DHO 1036 | mutagenesis *taf12-A217D-A218E-A220T-A221E* / DHB63 | Rv | | TGGGTCTGTTGTAATTGAGGCTCGTCAGCTTCGTCTTTTCTAGTATCAGTTGAGG |
| *taf12+* | DHO 1037 | mutagenesis *taf12-A283E* / DHB64 | Fwd | | GTTGAAAAGTCACAAGAGCCTTCTTACATGTCA |
| *taf12+* | DHO 1038 | mutagenesis *taf12-A283E* / DHB64 | Rv | | TGACATGTAAGAAGGCTCTTGTGACTTTTCAAC |
| *igo1+* | DHO 1120 | amplification igo1 / DHB61 | Fwd | | CAACAACCATAATCGCCATG |
| *igo1+* | DHO 1121 | amplification igo1 / DHB61 | Rv | | GGAGATTAGCTTTTGTTCAC |
| *tip41+* | DHO 737 | deletion / pFA6a | Fwd | | TGAAAATGATTATAAATATTACCATGAACTAAACGTAATAAACTTGTAAATTGCTTCAACACTCATTCGTTGACAAAAGTGAATTCGAGCTCGTTTAAAC |

| | | | | | | |
|---|---|---|---|---|---|---|
| *tip41+* | DHO | 736 | deletion / pFA6a | Rv | | TATATTTTGCCGTACGCACTCTAAATTGTTACAATAATATAGGGGTCAAGCAACTACTCAAATCACATTATTTAAAGGAGCGGATCCCCGGGTTAATTAA |
| *tap42+* | DHO | 733 | *nmt41-HA3* N-terminal tagging / pFA6a | Fwd | | GAGGAATTCTTCGGATTTGAGAATATAGCTTTACATACGAATATTTTTATTTACTTCAAACGTTTTGAGGATTAAAGGACGAATTCGAGCTCGTTTAAAC |
| *tap42+* | DHO | 735 | *nmt41-HA3* N-terminal tagging / pFA6a | Rv | | GATCTTGTTTTTTCATCTGTGCTTGATGAATCCTTCAGTTTCTCAGTTTCTTCCCATAACTCTCTCAACGACTTCGATTCCATGATTTAACAAAGCGACTATA |
| *act1+* | DHO | 90 | RT-PCR | Fwd | +10 to +29 | GAAATCGCAGCGTTGGTTAT |
| *act1+* | DHO | 91 | RT-PCR | Rv | +186 to +167 | ACGCTTGCTTTGAGCTTCAT |
| *ste11+* | DHO | 175 | RT-PCR | Fwd | +376 to +396 | CCCGAAAAGCCTGTTAATGA |
| *ste11+* | DHO | 176 | RT-PCR | Rv | +635 to +615 | GGACTACCGCTACTGGGTGA |
| *mei2+* | DHO | 206 | RT-PCR | Fwd | -203 to -182 | CAACCATCTAACCCCTTCCTT |
| *mei2+* | DHO | 207 | RT-PCR | Rv | -23 to -43 | AAAGCTGGCCGATAATCCTT |
| *taf4+* | DHO | 799 | C-terminal tagging / pFA6a | Fwd | | AAATGGATAGAGAAGGTGCTGGGCGTATTTTTGGTAGGGGTGCTAAGGCAATGATGCGTGCTTACATTAGGCTAAAAGATCGGATCCCCGGGTTAATTAA |
| *taf4+* | DHO | 800 | C-terminal tagging / pFA6a | Rv | | GAAGGGGTTTTATAAATGAATCCCCGAGATAAATAAATGAGTTAGTCATAACTTTTTAAGGCCATATTAAATTCATAAGTGAATTCGAGCTCGTTTAAAC |
| *taf12+* | DHO | 1393 | cloning pGEX-4T2 / DHB82-83 | Fwd | +439 to +462 | ATCGGATCTGGTTCCGCGTGGATCCCTTTCTACAAATGAAAGATTGGAC |
| *taf12+* | DHO | 1394 | cloning pGEX-4T2 / DHB82-83 | Rv | +1011 to +993 | TCGTCAGTCAGTCACGATGCGGCCGCGTCAAGCTCGTAGTGTGG |

[a] pFA6a, pKSura4 and DHB plasmids are defined in Materials and Methods

[b] Fwd: forward strand; Rv: reverse strand

[c] Coordinates are relative to the ATG of each ORF (A defined as +1)