

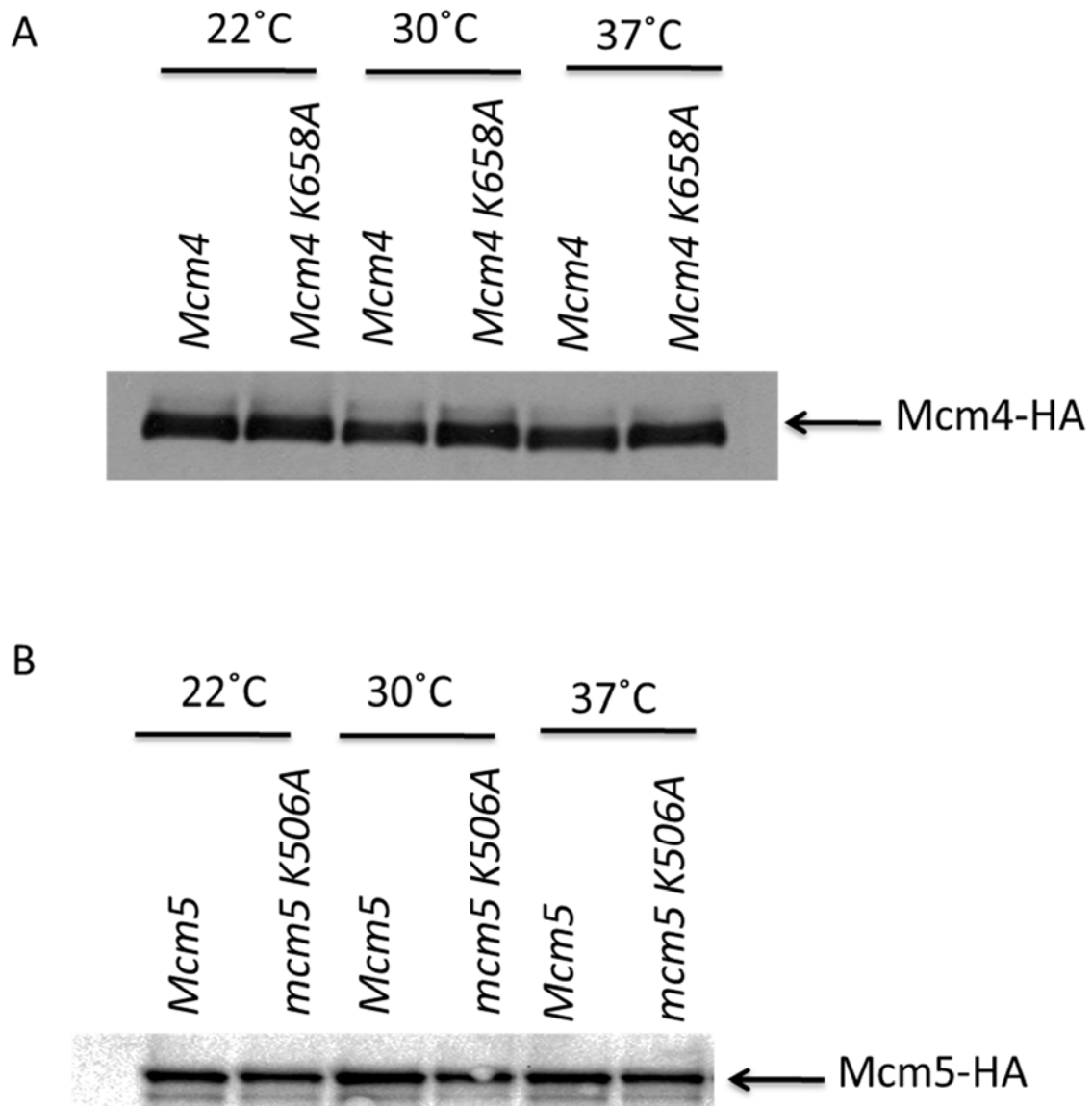
**Functional Conservation of the Pre-Sensor One Beta-finger Hairpin (PS1-hp) Structures in MCM Proteins of *Saccharomyces cerevisiae* and Archaea**

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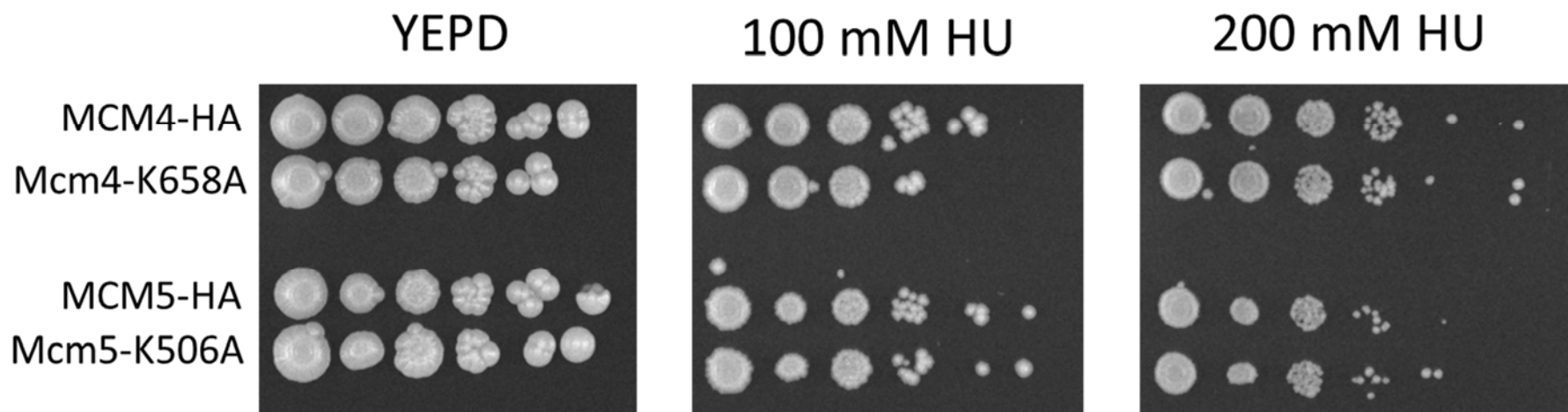
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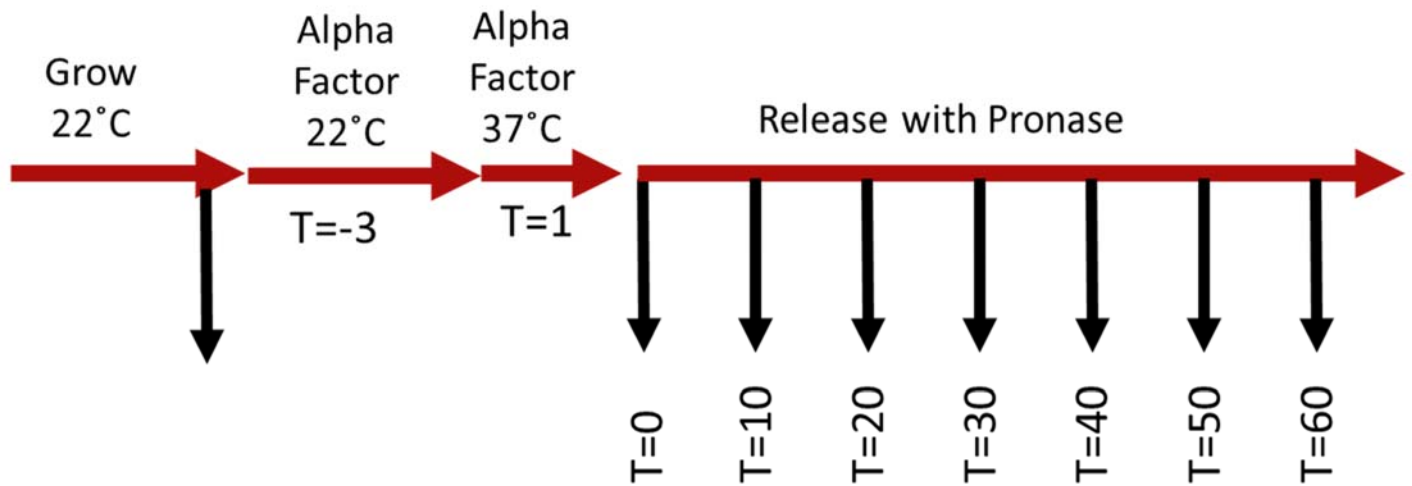
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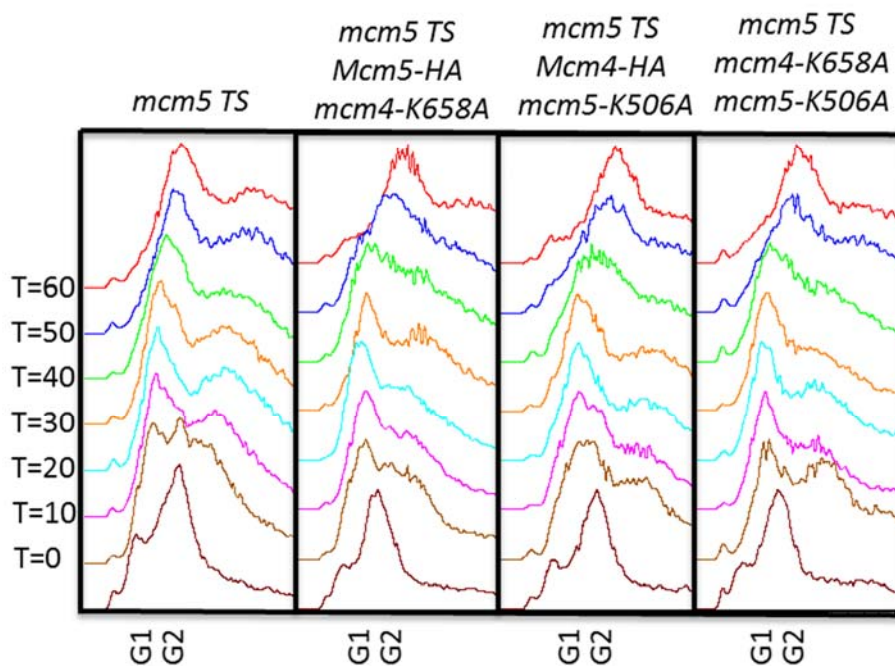
**Figure S1 Protein stability of PS1-hp mutants of Mcm5p and Mcm4p.** A) Western blot analysis of *mcm4p*-K658A-HA stability compared to *Mcm4p*-HA stability at 22°C, 30°C and 37°C. B) Western blot analysis of *mcm5p*-K506A-HA stability compared to *Mcm5p*-HA stability at 22°C, 30°C and 37°C.



**Figure S2 Sensitivity of PS1-hp mutants to replicational stress.** A) Serial dilution analysis (10 fold) of growth indicates no growth defect of Mcm4p PS1-hp or Mcm5p PS1-hp mutants in the presence of the replication inhibitor hydroxyurea.



Take samples for FACs at T=0,10,20,30,40,50,60

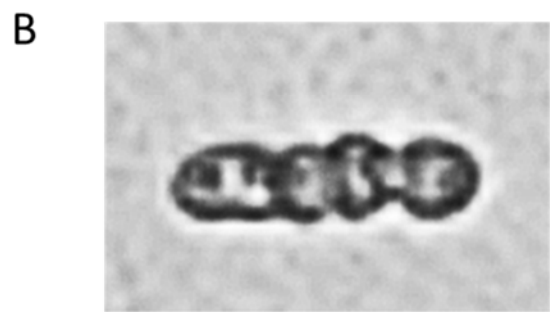


**Figure S3 Time course and flow cytometry analysis of a conditional PS1-hp double mutant.** RSY1148 (*mcm5-TS*), CRY207 (*mcm5-TS, MCM5-HA::URA3, mcm4-HA K658A::TRP1*), CRY208 (*mcm5-TS, mcm5-HA K506A::URA3, MCM4-HA::TRP1*) and CRY209 (*mcm5-TS, mcm5-HA K506A::URA3, mcm4-HA K658A::TRP1*) strains were arrested in alpha factor at 22°C for 3 hours then raised to 37°C for 1 hour. Cells were then released into S Phase at 37°C by the addition of pronase. Cell cycle progress was followed by flow cytometry. Samples were collected every 10 mins for 60 min then processed and analyzed by FACS.

# Synthetic Complete Growth Media (-/+ ) Indicated Nutrient/Drug

A

Number of Tetrads Dissected	YEPD	-URA	-TRP	-LEU	+ G418	-URA + G418	-URA -TRP	-URA -TRP + G418
91	197	131	88	99	44	44	51	0 (22)



**Figure S4 Tetrad analysis of PS1-hp mutants and the terminal MCM phenotype of *mcm4 mcm5* PS1-hp double mutant spores.** A. CRY119 was mated to RSY1345 to form diploids, which were then sporulated. Tetrads were dissected and spores that were  $-Ura^+ G418R$ , which contain both the *mcm5::KanMX4* and *mcm5-HAT K658A::URA3* mutations, were tested for the presence of the *mcm4-HA K658A::TRP1* allele. As *mcm5* and *mcm4* are unlinked, we expected to find 50% (22/44)  $Trp^+$  colonies that carry the *mcm4* PS1-hp mutation. With *mcm5-HA K658A::URA3*, no  $Trp^+$  colonies were found ( $n=44$ ,  $p<0.005$ ). B. The terminal phenotype of the double *mcm4 mcm5* PS1-hp mutant is two large budded cells (magnification=400X).