

Supplementary Table 6: Overlap of periodic genes between fission and budding yeasts

| <i>S. pombe</i> (ortholog number) ^a | <i>S. cerevisiae</i> (ortholog number) ^b | Ortholog number periodic in both yeasts | Expected overlap in gene number ^c | <i>P</i> -value |
|--|---|---|--|----------------------------|
| All periodic genes (252) | Spellman (322) | 81 | 27.2 | 2.0e-22 |
| All periodic genes (252) | Cho and Spellman (137) | 55 | 11.6 | 7.7e-26 |
| ‘High amplitude’ periodic (87) | Spellman (322) | 54 | 9.4 | 4.3e-32 |
| ‘High amplitude’ periodic (87) | Cho and Spellman (137) | 42 | 4.0 | 2.3e-35 |
| ‘High amplitude’ cluster 1 (28) | Spellman: G1 (127) | 9 | 1.2 | 1.2e-06 |
| ‘High amplitude’ cluster 1 (28) | Spellman: G2/M (74) | 9 | 0.7 | 1.0e-08^d |
| ‘High amplitude’ cluster 2 (36) | Spellman: G1 (127) | 13 | 1.5 | 8.3e-10^d |
| ‘High amplitude’ cluster 2 (36) | Spellman: M/G1 (33) | 3 | 0.4 | 6.9e-03 |
| ‘High amplitude’ cluster 3 (14) | Spellman: S (40) | 10 | 0.2 | 5.4e-17^d |
| ‘High amplitude’ cluster 4 (4) | Spellman: S/G2 (50) | 2 | 0.1 | 1.6e-03^d |

^a Our entire set of periodic genes or the subset of ‘high amplitude’ genes were compared with different lists of genes identified as periodic in *S. cerevisiae*. ‘High amplitude’ genes were also compared for each cluster separately. In parentheses are the numbers of genes with orthologs in *S. cerevisiae* for each list.

^b Lists of periodic genes identified by Spellman et al. (1998), Mol. Biol. Cell 9:3273 or by both Cho et al. (1998), Mol. Cell 2:65 and Spellman et al. (1998) were compared with the *S. pombe* lists. In addition, the five clusters of cell cycle regulated genes defined by Spellman et al. (1998) were also compared separately. In parentheses are the numbers of genes with orthologs in *S. pombe* for each list.

^c Overlap of genes expected by chance, given the sizes of gene sets considered and the total number of 2981 *S. pombe* genes with orthologs.

^d Pairs of gene groups that show the most significant overlap for every *S. pombe* cluster are **in bold**. All other pairwise combinations not shown in this table had *P*-values >0.2.