



**Supplementary Figure 5: Change in  $\ln[\text{bias P-value}]$  vs. % identity for globular domain, for Sup35p.** The change in  $\ln[\text{bias P-value}]$  from one Sup35p sequence to another is correlated with percentage sequence identity for pairwise alignment of the globular domain of Sup35p ( $r^2 = 0.07$ ,  $P < 0.001$ ). Redundant sequences were removed as for Figure 3.