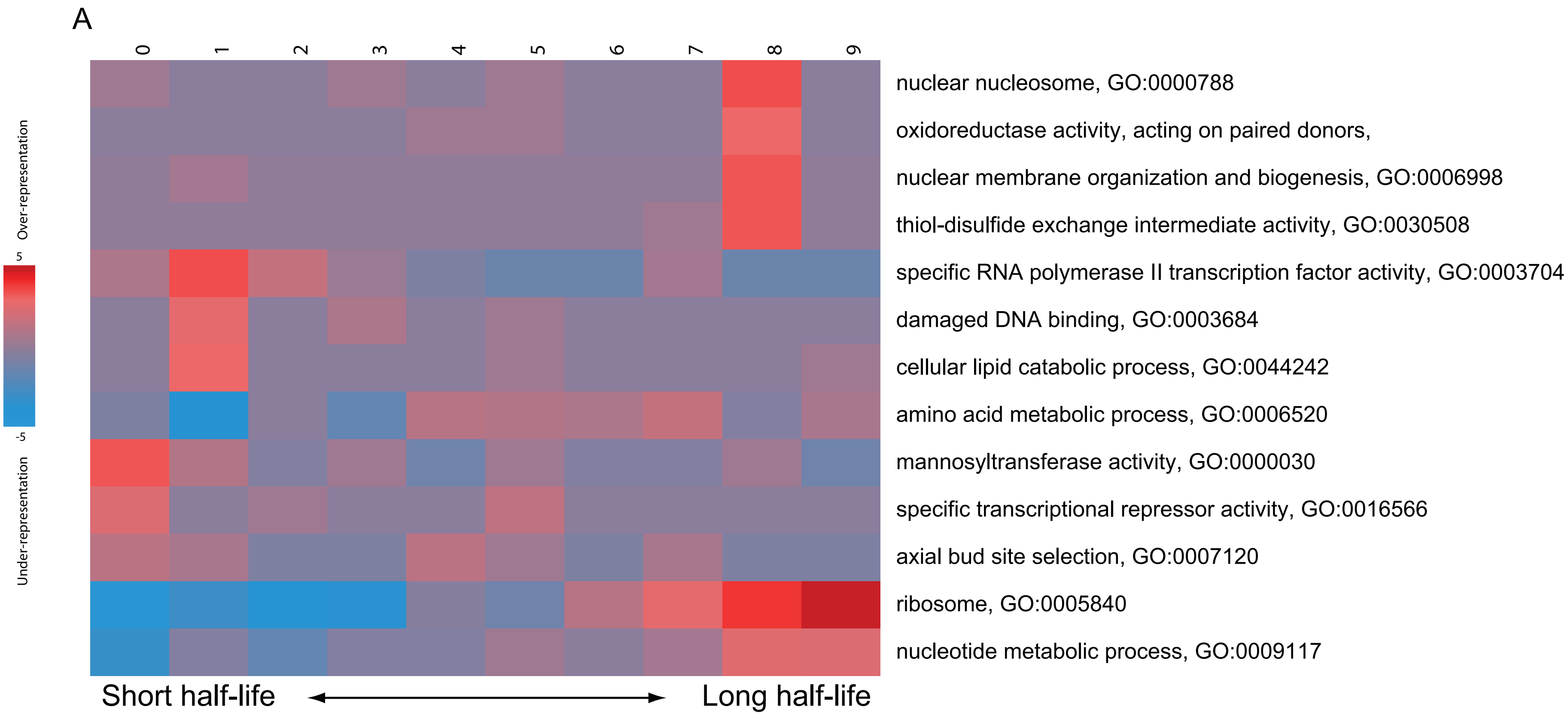

B

Note: GO and domain enrichment are for all proteins with a motif

Motif	**Pos. Bias**	**GO term (p)**	**Domain enrichment**	**Overlap Z-score**
R.[RSY]S		bud neck (p<1e-07)	Pkinase (p<1e-04)	-5.2
K.L[RFS]		protein kinase activity (p<0.001)	Pkinase (p<1e-04)	1.95
L....I		protein kinase activity (p<0.001)	Pkinase (p<0.01)	3.23
I...I[KDY]	Y	protein kinase activity (p<0.001)	Pkinase (p<1e-05)	4.99

Figure S4: GO analysis of protein half-life and enrichment analysis of half-life motifs

(A) iPAGE analysis (http://tavazoielab.princeton.edu/iPAGE/) of quantitative half-life data in *S. cerevisiae*. The half-life values for ~3,750 yeast proteins were sorted and binned into ten equally populated classes, with the shortest half-life proteins comprising the left-most columns and longest half-life proteins comprising the right most columns. The columns represent protein behavior classes and correspond to those in Figure 4. Proteins with short half-lives tend to be enriched for transcription factors whereas proteins with long half-lives are enriched for ribosomal and nucleotide metabolism proteins. (B) Enrichment analysis table for motifs associated with protein half-life. GO and domain enrichment analyses were applied to all proteins containing a motif. Protein kinase domains appear to be enriched for motifs associated with short half-life. While the last three motifs are likely to be domain signatures, the top motif "R.[RSY]S" has a strongly negative overlap Z-score and thus may act as a regulatory motif of protein kinase domains.