Isw1 complex mutants

RNA was harvested from *isw1*, *ioc2*, *ioc3*, and *ioc2ioc3* and *wild-type* cultures grown to OD_{660}=0.7. DNA microarray analyses were done using 30 µg total RNA from each strain labeled with Cy5 or Cy3 dyes and hybridized to ORF-based arrays containing all putative *S. cerevisiae* open reading frames. Four independent microarray hybridizations were performed for *ioc2* vs. *w.t.*, *ioc3* vs. *w.t.*, and *ioc2ioc3* vs. *w.t.*, samples. Three independent microarray hybridizations were performed for *isw1* vs. *w.t.*, samples.

We utilized a number of different previously described methods to normalize our expression data. Briefly, a Bayesian background correction method was applied to reduce the variance of spots of low intensity (Kooperberg, 2002; Fazzio, 2001). This corrected data from each microarray slide was then normalized to account for bias due to spot intensity (Intensity-dependent normalization using a lowess smoother to account for nonlinearity) and each cDNA's position on the array grid (Within-print-tip-group normalization). In addition, conversely labeled slide pairs were normalized to each other to account for dye-specific differences in labeling efficiency and/or dye stability (Paired-slides normalization); and separate slides were normalized to each other to reduce absolute expression differences that introduce bias when making slide to slide comparisons (Multiple slide normalizations) (Yang, 2001).

The expression changes for each gene were then determined by calculating the median value from these normalized values.

File is a tab-delimited text file.

isw1_ioc2_ioc3.txt

Platform: ORF-based array
Cell source: Cells grown in YEPD to OD_{660}=0.7
RNA prep: Hot phenol extraction
Taxonomy: *Saccharomyces cerevisiae*
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Submission Date: July 2002
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