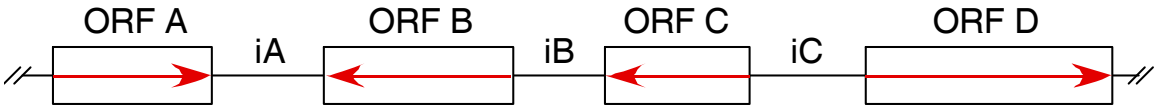
ALIGNMENT

In order to compare intergenic location analysis microarray datasets with expression microarray datasets, intergenic data was separated into loci that were upstream (promoters) or downstream (3') of Pol II-transcribed ORFs. This creates a 1:1 correspondence between ORF and intergenic regions since each ORF can have only one intergenic spot immediately upstream or downstream.

Example:

Schematic of locus



BEFORE:

	LEFT		RIGHT	
Int.	ORF	promoter/3'	ORF	promoter/3'
iA	A	3'	B	3'
iB	B	promoter	C	3'
iC	C	promoter	D	promoter

AFTER:

Promoter

ORF	Int.
B	iB
C	iC
D	iD

3'

ORF	Int.
A	iA
B	iA
C	iB

For convergently transcribed ORFs, the intergenic datapoint for the intervening region is duplicated for the 3' dataset. Similarly, for divergently transcribed ORFs, the intergenic datapoint for the intervening region is duplicated for the promoter dataset. However, in the promoter and 3' lists, each ORF is present no more than once. This allows simple alignment with transcription datasets.

Three alignments were done to align transcription data for each ORF with location analysis for the promoter, the ORF itself, and the 3' region. Following the alignment, we required datapoints to be present in all three datasets (*isw2Δ rpd3Δ* vs. *rpd3Δ* transcription dataset and location analysis datasets for wild-type Isw2p and Isw2-K215Rp). The overlap between Isw2-regulated genes (up or down $\geq$1.7x in the expression arrays) and wild-type Isw2p or Isw2-K215Rp-enriched genes (enriched $\geq$1.5x in the location analyses) was subsequently determined. The significance of the overlap was assessed by random sampling (n=10,000).