**LEGEND TO ADJUSTED MICROARRAY DATA**

A total of 13 microarray experiments were performed. The raw data from each experiment is available at: www... The raw data was then processed as described below. For each experiment, a normalization factor was calculated and applied so that the median ratio of the total fluorescence minus the background from one channel versus the other was equal to one. Signal from any particular spot was considered reliable if the total fluorescence minus the background was above a range of 125 to 300 fluorescence units, depending on the particular experiment. Spots whose signal was lower than the cut-off fluorescence are indicated as “DIM”. Genes from which no data was obtainable (as a result of any one of several possible causes, including aberrant spot morphology or uneven hybridization) are indicated with “FLAG”. The “NOTE” columns provide further information on data from any given gene. Spots whose fluorescence data indicate a small bias of incorporation of one cyanine dye over the other are indicated with a “Y”, whereas spots that show a strong bias are indicated with an “X”. For some genes, indicated as “one dir.”, data is only available for experiments performed in one labeling direction – in these cases, therefore, incorporation bias cannot be assessed. Finally, “no data” refers to those genes from which no data is available. The remaining spots, referred to as “GOOD”, show no obvious dye incorporation bias and have at least two data points from experiments performed in both labeling directions. The data for all the experiments after these adjustments is available at: www...All the microarray analyses presented in this article were carried out with data obtained from genes labeled as “GOOD”.

Below is a table with the further details for each experiment:

<table>
<thead>
<tr>
<th>Exp.#</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6\textsuperscript{b}</th>
<th>7\textsuperscript{b}</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12\textsuperscript{b}</th>
<th>13\textsuperscript{b}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Samples\textsuperscript{a}</td>
<td>4/1</td>
<td>4/1</td>
<td>5/2</td>
<td>4/2</td>
<td>6/3</td>
<td>6/3</td>
<td>6/3</td>
<td>9/7</td>
<td>9/7</td>
<td>10/8</td>
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<td>9/7</td>
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</tr>
<tr>
<td>Label</td>
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</tr>
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<tr>
<td>Slide\textsuperscript{c}</td>
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</tr>
</tbody>
</table>

\textsuperscript{a} Different samples were used for the experiments (refer to text for details):
1= HHT2, sample 1 grown at 30˚C
2= HHT2, sample 2 grown at 30˚C
3= HHT2, sample 3 grown at 30˚C
4= hht2-11, sample 1 grown at 30˚C
5= hht2-11, sample 2 grown at 30˚C
6= hht2-11, sample 3 grown at 30˚C
7= HHT2, sample 1 shifted to 14˚C
8= HHT2, sample 2 shifted to 14˚C
9= hht2-11, sample 1 shifted to 14˚C
10= hht2-11, sample 2 shifted to 14˚C

\textsuperscript{b} The reported ratios for these experiments are the inverse of Cy3/Cy5 to facilitate comparisons with Cy5/Cy3 experiments

\textsuperscript{c} The slides were prepared by either the Harvard Medical School Biopolymers Facility (H) or the Whitehead Institute Center for Microarray Technology (W).