



**FIGURE 1** Expression levels of specific gene sets. The responses to the nutrient repletion experiment in Figure 2 were examined for specific gene sets: 137 RP and 230 Ribi genes Jorgensen *et al* (JORGENSEN *et al.* 2004), 79 N catabolite repression (NCR) genes Scherens *et al* (SCHERENS *et al.* 2006), 272 environmental stress response genes (ESR) Gasch *et al* (GASCH *et al.* 2000), 95 Pho4 target genes Harbison *et al* (HARBISON *et al.* 2004), 160 Hsf1 targets Hahn *et al* (HAHN *et al.* 2004), and 241 Rap1 targets Lieb *et al* 2001 (LIEB *et al.* 2001). A) Box plots showing the average log<sub>2</sub> fold-change in expression caused by the indicated nutrient repletion, relative to the initial quiescent state. The black band in the box indicates the median, the upper box limit the 75<sup>th</sup> percentile, the lower box limit the 25<sup>th</sup> percentile and each whisker the minimum and maximum value within 1.5x of the interquartile range respectively. B) Box plots as above, except that the Y-axis shows averaged log<sub>2</sub> signal intensity for the initial nutrient-limited cultures as well as the samples from the nutrient-repleted cultures. This shows how in some cases differences in the starting transcript levels altered the fold-change values as much as the transcript levels after repletion.

**File S1 and Tables S1 and S2**

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