

File S7: Gene expression correlation c is high across different cell states or environments.

Figure S1 plots c and the closely related Pearson correlation coefficient r for 21 pairs of tissue-specific expression data sets in humans (Figure S1B) and mouse (Figure S1C). In all tissue pairs, the correlations are substantially above zero, ranging between 0.62 and 0.82 (human), as well as between 0.51 and 0.89 (mouse). In unicellular organisms, c also tends to be high. For example, in the yeast *Scheffersomyces stipitis* RNA sequencing data reveals that 5176 of 5816 genes are expressed uniformly in glucose and xylose-containing environments. Only 67 and 147 genes are preferentially expressed in glucose and xylose, which leads to $c = 0.72$ ($r = 0.78$) (Yuan et al., 2011). Likewise, in the bacterium *Bacillus subtilis* tiling microarrays show that 1974 of 3662 distinct transcriptionally active genomic regions are uniformly active in both minimal and rich media, whereas only 317 and 346 regions are preferentially active in minimal and rich medium, respectively. These numbers yield $c = 0.58$ ($r = 0.52$) (Rasmussen et al., 2009). More generally, multiple older microarray experiments also suggest a positive correlation between expression states. While they usually do not report the total number of expressed genes in any one cell state, they show that only a modest fraction of genes (<1-20 percent) change their expression in a new environment or cell state (Dragosits et al., 2013; Colbourne et al., 2011; Gasch et al., 2000; Henry et al., 2012; Huang et al., 2008; Landis et al., 2004).

References

- Colbourne, J. K., M. E. Pfrender, D. Gilbert, W. K. Thomas, A. Tucker, T. H. Oakley, S. Tokishita, A. Aerts, G. J. Arnold, M. K. Basu, D. J. Bauer, C. E. Caceres, L. Carmel, C. Casola, J. H. Choi, J. C. Detter, Q. F. Dong, S. Dusheyko, B. D. Eads, T. Frohlich, K. A. Geiler-Samerotte, D. Gerlach, P. Hatcher, S. Jogdeo, J. Krijgsveld, E. V. Kriventseva, D. Kultz, C. Laforsch, E. Lindquist, J. Lopez, J. R. Manak, J. Muller, J. Pangilinan, R. P. Patwardhan, S. Pitluck, E. J. Pritham, A. Rechtsteiner, M. Rho, I. B. Rogozin, O. Sakarya, A. Salamov, S. Schaack, H. Shapiro, Y. Shiga, C. Skalitzky, Z. Smith, A. Souvorov, W. Sung, Z. J. Tang, D. Tsuchiya, H. Tu, H. Vos, M. Wang, Y. I. Wolf, H. Yamagata, T. Yamada, Y. Z. Ye, J. R. Shaw, J. Andrews, T. J. Crease, H. X. Tang, S. M. Lucas, H. M. Robertson, P. Bork, E. V. Koonin, E. M. Zdobnov, I. V. Grigoriev, M. Lynch, and J. L. Boore (2011). The ecoresponsive genome of *Daphnia pulex*. *Science* 331(6017), 555–561.
- Dragosits, M., V. Mozhayskiy, S. Quinones-Soto, J. Park, and I. Tagkopoulos (2013). Evolutionary potential, cross-stress behavior and the genetic basis of acquired stress resistance in *Escherichia coli*. *Molecular Systems Biology* 9, 643.

- Gasch, A., P. Spellman, C. Kao, O. Carmel-Harel, M. Eisen, G. Storz, D. Botstein, and P. Brown (2000). Genomic expression programs in the response of yeast cells to environmental change. *Molecular Biology of the Cell* 11, 4241–4257.
- Henry, G. L., F. P. Davis, S. Picard, and S. R. Eddy (2012). Cell type-specific genomics of *Drosophila* neurons. *Nucleic Acids Research* 40(19), 9691–9704.
- Huang, D., W. Wu, S. R. Abrams, and A. J. Cutler (2008). The relationship of drought-related gene expression in *Arabidopsis thaliana* to hormonal and environmental factors. *Journal of Experimental Botany* 59(11), 2991–3007.
- Landis, G. N., D. Abdueva, D. Skvortsov, J. D. Yang, B. E. Rabin, J. Carrick, S. Tavare, and J. Tower (2004). Similar gene expression patterns characterize aging and oxidative stress in *Drosophila melanogaster*. *Proceedings of the National Academy of Sciences of the United States of America* 101(20), 7663–7668.
- Rasmussen, S., H. B. Nielsen, and H. Jarmer (2009). The transcriptionally active regions in the genome of *Bacillus subtilis*. *Molecular Microbiology* 73(6), 1043–1057.
- Yuan, T., Y. Ren, K. Meng, Y. Feng, P. Yang, S. Wang, P. Shi, L. Wang, D. Xie, and B. Yao (2011). RNA-Seq of the xylose-fermenting yeast *Scheffersomyces stipitis* cultivated in glucose or xylose. *Applied Microbiology and Biotechnology* 92(6), 1237–1249.