

**Supplementary materials for**

**Intra- and inter-specific variations of gene expression levels in yeast are largely neutral**

Yang, Maclean, Park, Zhao, and Zhang (jianzhi@umich.edu)

Supplementary materials include:

Legends for supplementary figures

Figures S1-S3

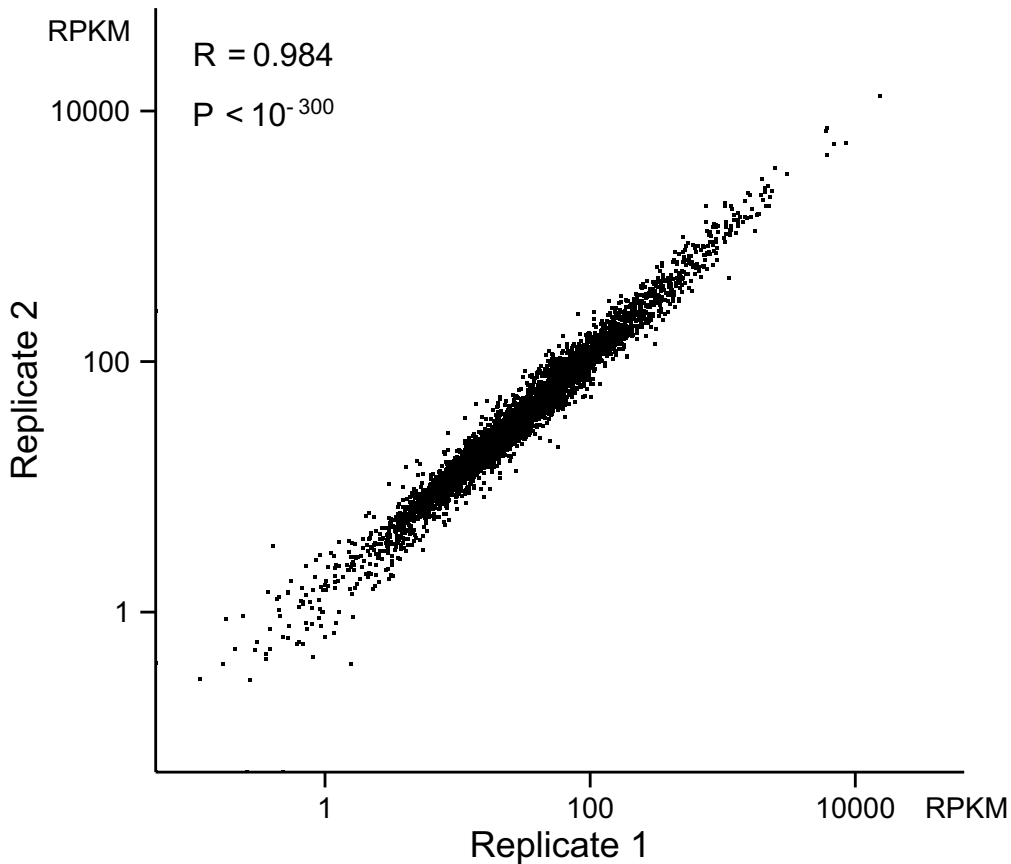
Table S1

## LEGENDS OF SUPPLEMENTARY FIGURES

**Figure S1.** High correlation ( $R$ ) between the gene expression levels of strain YPS606 measured in two biological replicates. Each dot is a gene. RPKM, reads per kilobases per million reads.

**Figure S2.** Transcriptome trees showing no clustering of wild strains. Panels (A)-(B) are equivalent to Fig. 1A, except that TPM instead of RPKM is used to measure gene expression levels (A), or expression level is quantile-normalized across samples (B). Panels (C)-(E) are equivalent to Fig. 1B-D, respectively, except that the data from the two biological replicates of YPS606 are not merged. Panel (F) is similar to the GO-based analysis in Fig. 1G, except that here we respectively perform biochemical pathway-based (“Biochemistry”) and gene deletion phenotype-based (“Phenotype”) analyses.

**Figure S3.** Principal component analysis of gene expression levels of the nine strains. (A-B) Same as Fig. 2B, except that the (A) 75% or (B) 50% most highly expressed genes instead of all genes are used. (C) Frequency distribution (bars) of the mean distance between two *S. cerevisiae* strains ( $d_{Sc-Sc}$ ) divided by the mean distance between a *S. cerevisiae* strain and a *S. paradoxus* strain ( $d_{Sc-Sp}$ ) in the transcriptome PCA plot made with 1000 random sets of 219 genes. The arrow shows the corresponding ratio in the morphology PCA plot with 219 traits.



**Figure S1**

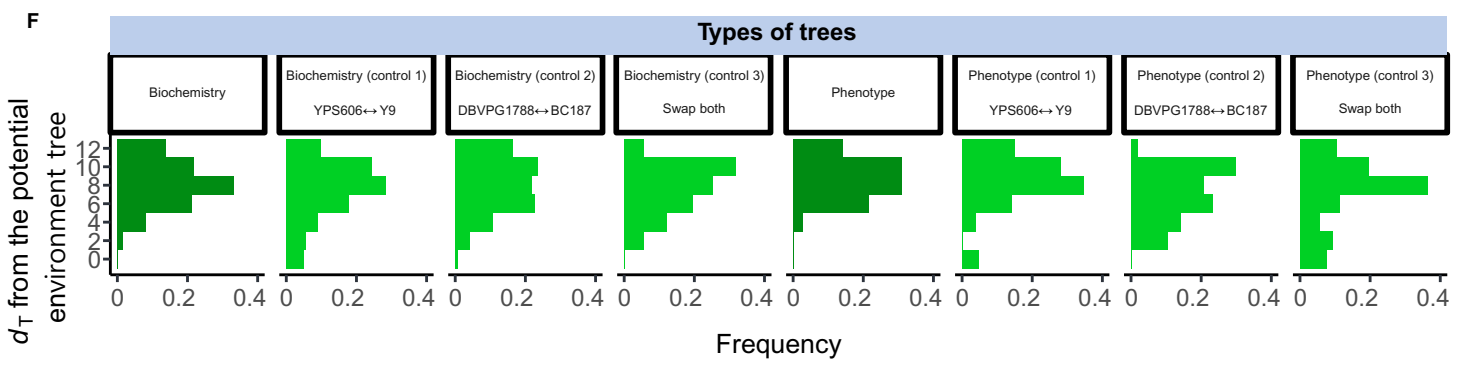
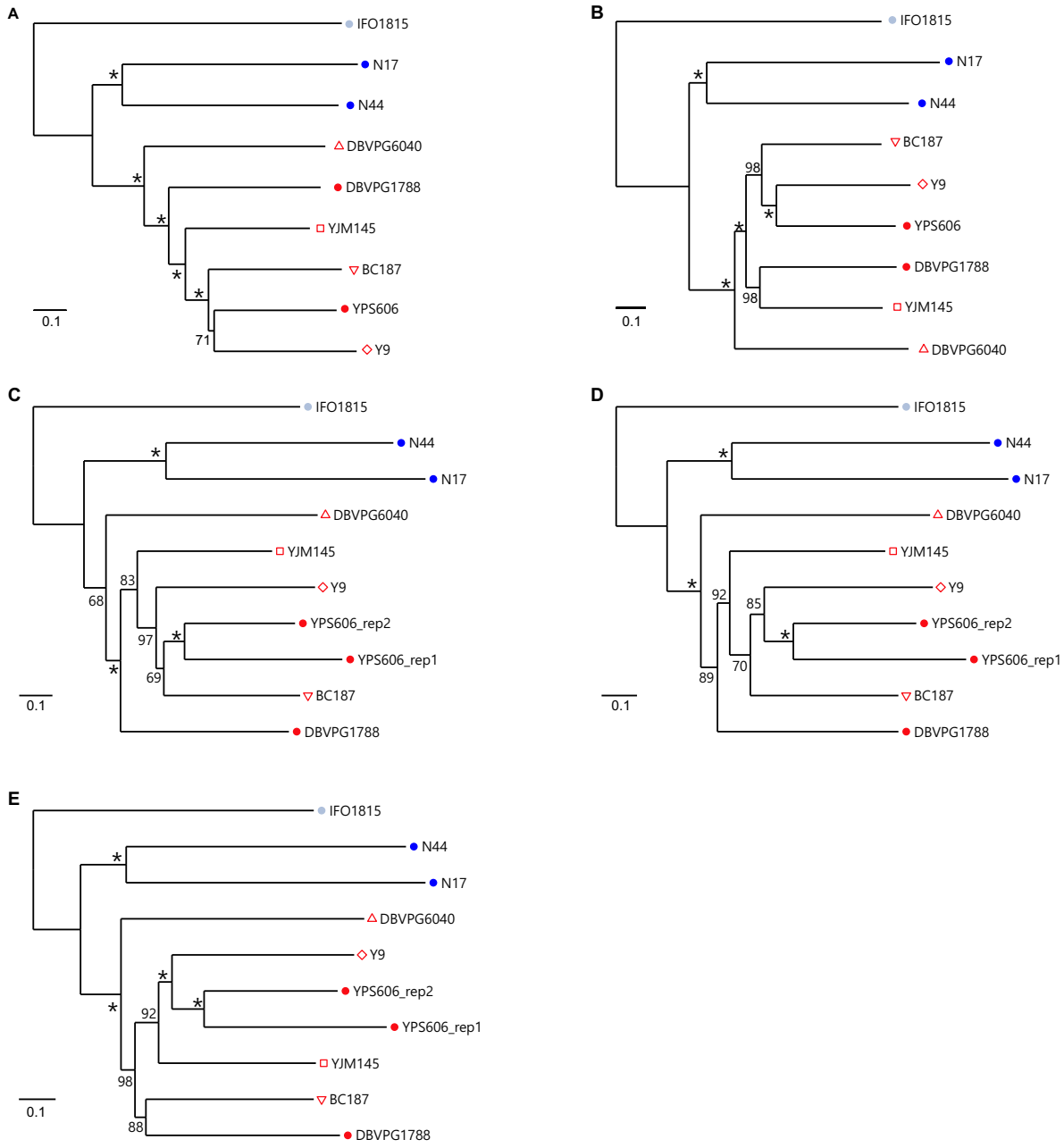
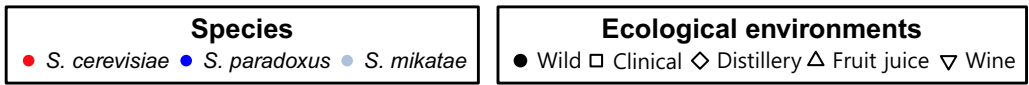
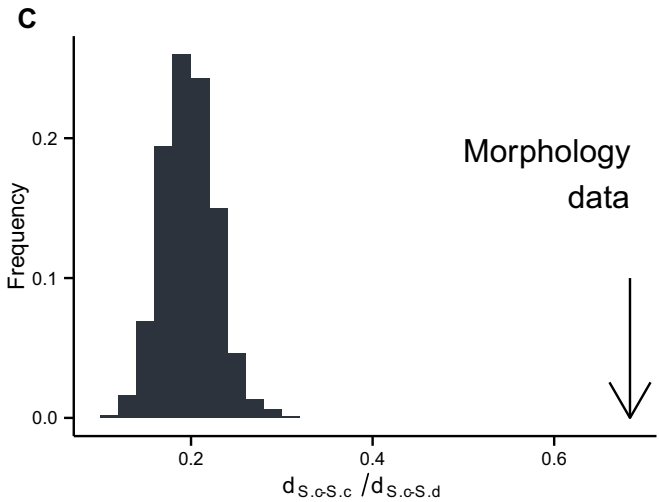
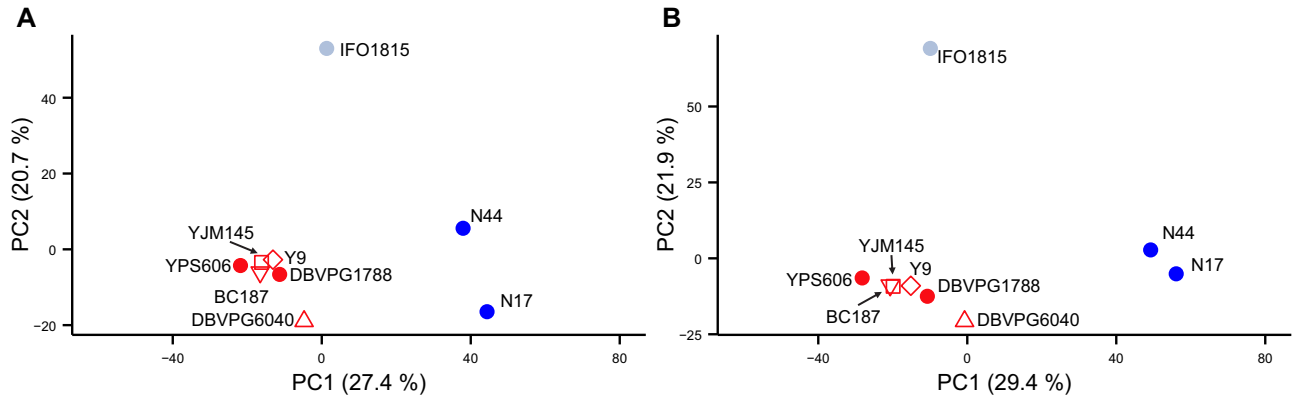
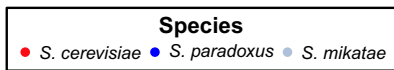


Figure S2



**Figure S3**

Table S1. Yeast strains used in this study and their RNA-seq statistics

Strain name	Species	Location isolated	Source	Ecological environment	RNA-seq replicates	Total no. of reads	Total no. of mapped reads	% reads mapped
IFO1815	<i>S. mikatae</i>	Japan	Soil and decayed leaf <sup>1</sup>	Wild	-	66,240,801	64,638,113	97.6
N17	<i>S. paradoxus</i>	Tartastan, Russia	Oak tree <sup>2</sup>	Wild	-	115,346,915	105,734,882	91.7
N44	<i>S. paradoxus</i>	Ternei, Russia	Oak tree <sup>2</sup>	Wild	-	65,760,339	61,681,466	93.8
YPS606	<i>S. cerevisiae</i>	Woodland, PA, USA	Oak tree <sup>2</sup>	Wild	#1	92,306,996	84,425,699	91.5
					#2	72,024,415	68,728,390	95.4
DBVPG1788	<i>S. cerevisiae</i>	Turku, Finland	Soil <sup>2</sup>	Wild	-	66,775,841	64,425,230	96.5
DBVPG6040	<i>S. cerevisiae</i>	Netherlands	Fermenting fruit juice <sup>2</sup>	Fruit juice	-	61,119,979	58,403,789	95.6
Y9	<i>S. cerevisiae</i>	Indonesia	Ragi (similar to sake) <sup>2</sup>	Distillery	-	60,281,732	57,939,014	96.1
BC187	<i>S. cerevisiae</i>	Napa Valley, CA, USA	Barrel fermentation <sup>2</sup>	Wine	-	74,811,125	72,340,238	96.7
YJM145	<i>S. cerevisiae</i>	USA	Lung of an AIDS patient <sup>3</sup>	Clinical	-	69,619,794	65,883,520	94.6

<sup>1</sup> Liti, G., A. Peruffo, S. A. James, I. N. Roberts, and E. J. Louis. (2005) Inferences of evolutionary relationships from a population survey of LTR-retrotransposons and telomeric-associated sequences in the *Saccharomyces sensu stricto* complex. *Yeast* 22: 177–92. doi:10.1002/yea.1200.

<sup>2</sup> Liti, G., D. M. Carter, A. M. Moses, J. Warringer, L. Parts, S. A. James, R. P. Davey, *et al.* (2009) Population genomics of domestic and wild yeasts. *Nature* 458: 337–341. doi:10.1038/nature07743.

<sup>3</sup> Nakayashiki, T., C. P. Kurtzman, H. K. Edskes, and R. B. Wickner. (2005) Yeast prions [URE3] and [PSI+] are diseases. *Proc. Natl. Acad. Sci. USA* 102: 10575–10580. doi:10.1073/pnas.0504882102.