Materials and Methods

Strains and plasmids

Wild *S. cerevisiae* isolates were obtained from genetic stock centers or were the generous gifts of investigators and consortia indicated in the supplementary information. RM, BY, and their genotyped meiotic segregants have been described previously (*1*) and were kindly provided by L. Kruglyak.

Strains were inoculated in triplicate into 384-well plates containing 40 µL YPD per well and grown to saturation at 23°C (typically 48 h). After re-suspension, QRep polypropylene 384-well pin replicators (Genetix) were used to transfer cells (200-500 nL) to new 384-well plates in duplicate. These new plates were used to assess different growth conditions (Table S2) and also contained 40 µL media per well. The conditions were chosen to cause a measurable growth defect in yeast based either on previous studies or on pilot investigations in BY, RM, segregants from the BYxRM cross, or selected strains from Table S1. All plates were incubated at 23°C, covered and in a humidified chamber unless otherwise noted. Growth was measured approximately every 20 hours by OD_{600} with a Tecan Sapphire2 plate reader (after re-suspension by gentle agitation). Permutation of the positions strains occupied within the plate had no effect on growth. This eliminated the possibility that position effects would be responsible for the traits we observed. In parallel, strains were analogously treated in 384-well plates containing each condition with Hsp90 inhibition (5 µM Rad or GdA). As controls, strains were also grown in control medium (YPD) alone, and in control medium with

Hsp90 inhibitors alone (5 µM Rad or GdA). Rad and GdA stocks (50 mM) were made in molecular biology grade dimethyl sulfoxide (DMSO).

MIC concentrations for Rad and GdA were determined by serial 1.5-fold dilutions of a 200 µM starting concentration of each inhibitor in YPD. These measurements were carried out as above, in 384-well microplates with 40 µL YPD per well. Growth was measured by OD_{600} 66 h post-inoculation in a Tecan Sapphire plate reader. Four replicate measurements were performed for each strain.

NDI1 overexpression was achieved by transforming the *NDI1-*containing clone from the Flexgene overexpression library (*2*) under the control of a galactose-inducible promoter. Plasmid-containing strains were grown in synthetic medium lacking uracil with either 2% glucose as a carbon source (as a control) and or 2% galactose as a carbon source (to induce expression). Strains were treated with 5 mM CDNB for 24 hours and 100 µL of a 10,000-fold dilution was plated on synthetic medium lacking uracil. Images are shown after 3 days of incubation at 30° C.

Data analysis

Growth yield of BYxRM segregants was measured by OD_{600} in a Tecan Sapphire plate reader. Values for growth in each condition with Hsp90 inhibitors were compared to growth in the same condition without Hsp90 inhibitors. At these concentrations, the Hsp90 inhibitors themselves did not affect growth. However, Hsp90 inhibition altered growth of certain segregants in the selective conditions. A variety of patterns emerged. For example, strains with average growth in some conditions (e.g. in Fig. 1C-F, strain 1 in rapamycin and deoxycholate) were sensitive (CDNB) or resistant (HU) in others. Similarly, strains strongly affected by Hsp90 inhibition in some conditions were unaffected in others (e.g. in Fig. 1, strain 1 in hydroxyurea and CDNB vs. rapamycin and deoxycholate). The difference in growth in each condition elicited by Hsp90 inhibition with Rad was used for linkage analysis using R/qtl (*3*). Growth of the segregants in control media (containing DMSO) was used as an additive covariate where appropriate to eliminate the effects of carrier solvent. Linkage analysis was performed using several algorithms within R/qtl (standard maximum likelihood/EM, nonparametric, and binary models). To test significance, growth in each condition was randomly permuted among the segregants and genome-wide mapping was re-performed using the same algorithm. After 200 such permutations and mappings across all conditions, QTL were discarded if their LOD scores did not fall above the top 5% of those obtained by chance for each trait. Based on these empirical permutation tests, 3.2 of the QTL we identified (or less than 1%) would be expected to occur by chance.

The location of the QTL within the genome was defined by calculating approximate Bayesian credible intervals (to 95% confidence) in R/qtl. Virtually all Hsp90-contingent traits could be mapped to one or more QTL. However, we were unable to do so in several cases (Trichostatin A, iodoacetate, and chlorhexidine. It might be that too many genetic determinants contributed under these conditions, obscuring the effects of individual loci. However, trichostatin A and iodoacetate perturb histone modification (*4, 5*). Thus, it seems likely that epigenetic variation operates on these traits.

Published genotypic correlation among sequenced strains was obtained from refs. (*6*) and (*7*). Phenotypic correlations among the strains were determined by linear regression across the conditions in Table S2. Neighbor-joining trees were constructed in PHYLIP (evolution.genetics.washington.edu/phylip.html) from distance matrices derived from these correlations.

Allele replacement

Allele replacement was performed as described in (*8*) and depicted in fig. S5 for selected QTL within Bayesian credible intervals. Because many traits we examined involved the contribution of alleles from both the RM and BY parents, allele replacement was carried out in the segregants rather than BY or RM. ORFs within the boundaries of each QTL were PCR amplified from both BY and RM and fused to 5' and 3' fragments of *Kluyveromyces lactis* URA3 in a second PCR reaction. After purification these fusion products were co-transformed into recipient segregants. Loss of the URA3 marker was selected for on 5-FOA and allele replacement was confirmed by sequencing. For each gene within a QTL, this procedure was carried out in three segregants with RM and three segregants with BY genotype, each in triplicate. Candidate genes were confirmed by comparing the phenotypes of segregants with RM vs. BY allele replacements. Similar trends were seen across all equivalently allele-replaced strains. To control for the mutagenic effects of transformation, mock replacements (RM for RM and BY for BY) were performed; none of these produced a relevant phenotype.

References:

- 1. R. B. Brem, G. Yvert, R. Clinton, L. Kruglyak, Genetic dissection of transcriptional regulation in budding yeast. *Science* **296**, 752 (2002).
- 2. Y. Hu *et al.*, Approaching a complete repository of sequence-verified proteinencoding clones for Saccharomyces cerevisiae. *Genome Res* **17**, 536 (2007).
- 3. K. W. Broman, H. Wu, S. Sen, G. A. Churchill, R/qtl: QTL mapping in experimental crosses. *Bioinformatics* **19**, 889 (2003).
- 4. M. Yoshida, M. Kijima, M. Akita, T. Beppu, Potent and specific inhibition of mammalian histone deacetylase both in vivo and in vitro by trichostatin A. *J Biol Chem* **265**, 17174 (1990).
- 5. L. Dong, C. W. Xu, Carbohydrates induce mono-ubiquitination of H2B in yeast. *J Biol Chem* **279**, 1577 (2004).
- 6. G. Liti *et al.*, Population genomics of domestic and wild yeasts. *Nature* **458**, 337 (2009).
- 7. J. Schacherer, J. A. Shapiro, D. M. Ruderfer, L. Kruglyak, Comprehensive polymorphism survey elucidates population structure of Saccharomyces cerevisiae. *Nature* **458**, 342 (2009).
- 8. N. Erdeniz, U. H. Mortensen, R. Rothstein, Cloning-free PCR-based allele replacement methods. *Genome Res* **7**, 1174 (1997).

Supplementary Table and Figure Legends:

Table S1 – *S. cerevisiae* strains used in this study.

Table S2 – Growth conditions used to examine phenotypes of *S. cerevisiae* strains. Conditions were chosen based on values previously used in the literature to perturb growth or specific biological processes in *S. cerevisiae*. In some cases the concentrations may seem idiosyncratic. However, these were used because they were simple dilutions of a saturated stock solution or because they were employed at those concentrations in other studies.

Table S3 – Correlations between phenotypic changes produced across wild *S. cerevisiae* isolates when inhibiting Hsp90 with Rad $(5 \mu M)$ or GdA $(5 \mu M)$. Color indicates concordance in phenotype. For approximately 90% of conditions, changes in growth were in the same direction for both inhibitors in each strain. In \sim 10% of conditions a strains showed no effect for one inhibitor but did show an effect for the other. This was almost certainly because (for experimental expediency) we used 5 µM concentrations of each inhibitor on each strain, rather than titrating to achieve exactly the same fraction of the MIC. Supporting this explanation, in all of the conditions we examined, we only very rarely observed an instance where the two inhibitors produced opposite effects in the same strain. Furthermore, a common mechanism of action of Rad and GdA, proceeding via Hsp90 inhibition, has been extensively documented in the literature, most recently using proteome-wide techniques in HeLa cells (*1*).

Table S4 – Quantitative trait loci identified in this study in the absence of Hsp90 inhibition. Permutation of the position strains occupied in plates did not affect the outcome. Growth in each indicated condition was mapped. Where appropriate, growth in DMSO was used as an additive covariate to eliminate any effects of carrier solvent.

Table S5 –Quantitative trait loci that contribute to Hsp90-contingent transitions in phenotype. The difference in OD_{600} between growth with and without Rad was mapped (difference) as was growth for each condition with Rad (with rad). In some cases, perhaps because Hsp90-contingent traits often had a complex genetic basis, either method revealed Hsp90-dependent variation that the other did not. However, significant contribution of each QTL in this table to variation in phenotype was confirmed by a nonparametric Wilcoxon rank test.

Fig. S1 – Experimental schema

Fig. S2 – Immunoblot of Hsp104 to assess the effect of radicicol (Rad) treatment on induction of the heat shock response. A) BY and RM cells were grown with increasing concentrations of Rad to an OD_{600} of 0.8, harvested, and lysed using Y-PER-S yeast protein extraction reagent (Thermo). Protein concentration was determined by BCA protein assay (Thermo). Samples (40 µg total protein) were separated on 12% SDS-PAGE prior to wet-transfer to nitrocellulose membrane and subsequent immunoblot with anti-Hsp104 and anti-PGK1, used as a loading control. B) Hsp104 immunoblot in

BYxRM progeny (numbered as in Fig. 1, bottom) in selective conditions containing 5 µM Rad indicates that this treatment does not produce a heat shock response even in those selective conditions.

Fig. S3 – Growth changes elicited by reducing the Hsp90 buffer in progeny from the BYxRM cross across all segregants and conditions used in this study. Calculations and scale bar as in Fig. 1A.

Fig. S4 – Distribution of QTL identified in this study separated by chromosome. A) Histogram of all QTL from linkage analysis in conditions alone. B) Histogram of QTL from linkage analysis in conditions with reduced Hsp90 buffer. C) Histogram of QTL from linkage analysis of difference in phenotype elicited by reducing the Hsp90 buffer.

Fig. S5 – Schematic of allele replacement strategy employed, described in detail by Erdeniz *et al.* (*2*). Briefly, the allele to be swapped was amplified from BY or RM genomic DNA and, in two subsequent PCR reactions, fused to overlapping 5' and 3' portions of *K. lactis* URA3. These two constructs were simultaneously used to transform recipient segregants, and integration was selected for by growth on SD-URA media. Release of the URA3 marker was then selected for by growth on 5-FOA and allele replacement was confirmed by sequencing.

Fig. S6 – Representative effects of reducing the Hsp90 reservoir on additional Pdr8 dependenent phenotypes in two of six allele replacement strains. Conditions are as

described in Table S2. Growth is normalized to BY allele replacement strain in each condition (set as 100%). Error bars represent standard deviations from three independent biological replicates.

- 1. M. Muroi *et al.*, Application of proteomic profiling based on 2D-DIGE for classification of compounds according to the mechanism of action. *Chem Biol* **17**, 460.
- 2. N. Erdeniz, U. H. Mortensen, R. Rothstein, Cloning-free PCR-based allele replacement methods. *Genome Res* **7**, 1174 (1997).

Table S1. *S. cerevisiae* strains used in this study. Sample origin abbreviations are: (ARSC) Agricultural Research Service Culture Collection; (NCYC) National Collection of Yeast Cultures

Table S2. Conditions used in this study. Treatment was in rich medium (YPD) unless otherwise noted.

Strain	Rad (5 uM)	GdA (5 uM)
Irish Ale	$\overline{\text{R}}$	\overline{R}
Northwest Ale	\overline{R}	\overline{R}
$Y-502$	$\overline{\text{R}}$	$\overline{\text{R}}$
$Y-35$	R	R
Y-5511	R	$\overline{\text{R}}$
Y-7568	R	$\overline{\text{R}}$
WE372	\overline{R}	$\overline{\text{R}}$
Y12	$\overline{\text{R}}$	$\overline{\text{R}}$
Y2034	R	R
$Y-266$	R	R
$Y-645$	$\overline{\text{R}}$	$\overline{\text{R}}$
Trappist Ale	R	NC
$Y-2411$	R	NC
$Y-584$	R	NC
Abbey Ale	S	S
English Ale	S	S
Forbidden Fruit Ale	S	S
Urquell Pilsner	S	S
$Y-865$	S	S
$Y-12659$	S	S
Y-27788	S	S
YJM421	S	S
YJM428	S	S
$Y-139$	S	S
$Y-1527$	S	S
OP7	S	S
T73	S	S
Y-12659	S	S
$Y-269$	S	S
$Y-865$	S	S
ATCC 26249	S	R
Belgian Ale	NC	NC
Y-7327	NC	NC
Y-27806	N _C	N _C
$Y-492$	NC	NC
YJM653	NC	NC
$Y-12657$	N _C	NC
YB-3121	NC	NC
YB-399	NC	N _C
YB-4081	NC	N _C
YB-432	NC	NC
YB-2209	N _C	NC
OP ₁	NC	N _C
OP ₂	NC	N _C

Table S3: Correlation in phenotypes elicited by pharmacological Hsp90 inhibition with Rad and GdA

Growth in maltose. Increased growth (R) highlighted yellow; decreased growth (S) highlighted blue; no change (NC) highlighted green.

Only examples of changed phenotypes shown below:

Growth in novobiocin. Increased growth (R) ; decreased growth (S) ; no change (NC) .

Growth in rapamycin. Increased growth (R); decreased growth (S); no change (NC).

Growth in nickel chloride. Increased growth (R); decreased growth (S); no change (NC).

BY x RM meiotic segregants

Adapted from Erdeniz et al. (1997)

