Proteomic and Genomic Analyses of the Rvb1 and Rvb2 Interaction Network upon Deletion of R2TP Complex Components

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The highly conserved yeast R2TP complex, consisting of Rvb1, Rvb2, Pih1, and Tah1, participates in diverse cellular processes ranging from assembly of protein complexes to apoptosis. Rvb1 and Rvb2 are closely related proteins belonging to the AAA+ superfamily and are essential for cell survival. Although Rvbs have been shown to be associated with various protein complexes including the Ino80 and Swr1 chromatin remodeling complexes, we performed a systematic quantitative proteomic analysis of their associated proteins and identified two additional complexes that associate with Rvb1 and Rvb2: the chaperonin-containing T-complex and the 19S regulatory particle of the proteasome complex. We also analyzed Rvb1 and Rvb2 purified from yeast strains devoid of PIH1 and TAH1. These analyses revealed that both Rvb1 and Rvb2 still associated with Hsp90 and were highly enriched with RNA polymerase II complex components. Our analyses also revealed that both Rvb1 and Rvb2 were recruited to the Ino80 and Swr1 chromatin remodeling complexes even in the absence of Pih1 and Tah1 proteins. Using further biochemical analysis, we showed that Rvb1 and Rvb2 directly interacted with Hsp90 as well as with the RNA polymerase II complex. RNA-Seq analysis of the deletion strains compared with the wild-type strains revealed an up-regulation of ribosome biogenesis and ribonucleoprotein complex biogenesis genes, down-regulation of response to abiotic stimulus genes, and down-regulation of response to temperature stimulus genes. A Gene Ontology analysis of the 80 proteins whose protein associations were altered in the PIH1 or TAH1 deletion strains found ribonucleoprotein complex proteins to be the most enriched category. This suggests an important function of the R2TP complex in ribonucleoprotein complex biogenesis at both the proteomic and genomic levels. Finally, these results demonstrate that deletion network analyses can provide novel insights into cellular systems. Molecular & Cellular Proteomics 15: 10.1074/mcp.M115.053165, 960–974, 2016.

The Saccharomyces cerevisiae R2TP complex consists of Rvb1, Rvb2, Pih1 (protein interacting with Hsp90) and Tah1 (TPR (tetratricopeptide repeat)-containing protein associated with Hsp90) proteins. Although, the R2TP complex was initially discovered in yeast as an Hsp90-associated complex (1), R2TP subunits are conserved in higher eukaryotes and the R2TP complex was recently identified and purified from human cells (2). The R2TP complex has been implicated in various cellular processes such as assembly of small nucleolar ribonucleoprotein (snoRNP) (3) (small nucleolar ribonucleoprotein) complex (3, 4), RNAPII (RNA polymerase II) complex (5), apoptosis (6), and PIKK (phosphatidylinositol 3-kinase-related protein kinases) signaling (7). The involvement of R2TP in assembling various complexes seems to be in part because of Pih1 and Tah1, which serve as adapter/recruiter proteins. For example; the

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cytoplasmic assembly of human RNAPII complex involves a cochaperone, the Prefoldin-like complex. Both the Prefoldin-like complex and RNAPII complex are recruited by the R2TP complex (8). Tah1 has been shown to directly interact with Rpb1 (the largest subunit of RNAPII) and possibly bring the R2TP and Prefoldin-like complexes together to facilitate RNAPII complex assembly (5). Similar examples illustrate an adapter/recruiter function for Pih1 in recruiting the Hsp90 chaperone to other complexes. These include the recruitment of Hsp90 to the yeast box C/D snoRNP assembly via an interaction between Pih1 and Nop58 (4) and the activation of PIKK signaling by recruitment of Hsp90 to PIKK via an interaction between Pih1 and the PIKK subunit Tel2 (9).

Rvb1 and Rvb2 (Tip49 and Tip48 in humans) are members of the AAA+/adenosine triphosphatase associated with diverse cellular activities) superfamily possessing both ATPase as well as helicase activities (10). Rvb1 and Rvb2 are similar in both sequence and structure across various species and are essential for cell survival (11). This comes as no surprise, because they are involved in several biological processes ranging from assembly of macromolecular complexes (with or without the involvement of Pih1 and Tah1), chromatin remodeling and the regulation of gene transcription (12, 13). Rvb1 and/or Rvb2 have also been linked to human diseases and are overexpressed in lung, liver, and colon cancers (12). Both Rvb1 and Rvb2 form higher order oligomers either by themselves or together, which can influence their activity, function and association with other protein complexes (14–17). Electron microscopy studies on Swr1 indicate that Rvb1 and Rvb2 exist as heterohexamer (16, 18), whereas instances of both single heterohexameric and dodecameric ring structures have been observed in the Ino80 complex (15, 18). The oligomerization of Rvb1/Rvb2 in several complexes is an intense field of study, and it is becoming widely accepted that the molecular organization of these proteins are complex and species dependent. Based on structural studies, Rvb1 and Rvb2 have been divided into three domains. The N and C terminus of Rvbs form part of the AAA+ domain (domain I and II respectively, which includes the classical Walker A and B motifs, Sensors and Arginine finger) and the enigmatic insertion region (domain II) which is ~174 amino acids long and protrudes from the ring like oligomeric structures formed by Rvbs (19). The insertion region has been proposed to play roles in the activity of Rvb1/2, nucleic acid binding and in protein-protein interactions.

Pih1 (originally known as Nop17 and referred to as Pih1D1 in humans) is a ~40 KDa protein which is unstable on its own, but is stable when bound to Tah1 (20). Pih1 is predominantly localized in the nucleolus. Pih1 contains a Pih1 domain at its N terminus, two IDRs (intrinsically disordered regions) and a C-terminal region, which is highly susceptible to degradation. Using bioinformatics analysis and mutational studies, Paci et al. (20) have shown that the IDR1 of Pih1 is largely responsible for Rvb1/Rvb2 binding, and the IDR2 and C terminus are needed for binding to Tah1. Tah1 (RPAP3 or hSpagh in humans) is the smallest member of the complex with 111 amino acids and connects Pih1 to Hsp90. Tah1 contains 2 TPR (tetra-tricopeptide repeat) motifs which are responsible for binding to the C terminus (MEEVD motif) of Hsp90 and the unfolded C-terminal segment (93–111) of Tah1 is responsible for binding to and stabilizing Pih1 (21).

Despite recent advances in characterizing the Rvb1, Rvb2, and the R2TP complex, there is no comprehensive information available on associations between the members of this complex and other cellular proteins. Here, we have used a combination of AP-MS (affinity purification-mass spectrometry) based proteomic analysis and deletion network analysis to create a protein association network centered on Rvb1/Rvb2. We show that yeast Rvb1 and Rvb2 together associate with several protein complexes, which we ranked based on quantitative proteomic data. AP-MS analyses using yeast strains lacking PIH1 and TAH1 indicate that Rvb1/Rvb2 associate independently with both Hsp90 and the RNAPII complex. In support of this independent association, in vitro binding studies suggest direct interactions between Rvb1/Rvb2 and Hsp90 or between Rvb1/2 and the RNAPII complex. Intriguingly, we noticed an enhanced interaction between Rvb1/Rvb2 and Hsp90/RNAPII complex in the absence of Pih1. RNA-Seq analysis of these deletion strains yielded unexpected links to gene expression changes in ribosome biogenesis, ribonucleoprotein complex biogenesis, abiotic stimulus, and response to temperature stimulus. Finally, a GO analysis of the 80 proteins found altered in protein associations in all four deletion strains found ribonucleoprotein complex proteins to be the most enriched category suggesting an important function of the R2TP complex in this process.

**EXPERIMENTAL PROCEDURES**

**Cloning and Expression of Recombinant Proteins from Insect Cells**—Rvb1, Rvb2 and Hsp90 from Saccharomyces cerevisiae were amplified using custom designed primers (supplemental Table S1) and cloned in pBACPAK8™ vector (Clontech Laboratories, Mountain View, CA) for recombinant expression in a Baculovirus system. Rvb1 contained TEV (tobacco etch virus) protease cleavable 6xHis tag, Rvb2 contained FLAG tag and Hsp90 contained TEV protease cleavable Halo tag (Promega, Madison, WI) at their respective N termini. Tags for Rvb1 and Rvb2 were introduced by incorporating the corresponding sequences in primers, whereas TEV cleavable Halo tag was first introduced into pBACPak™ vector before cloning the Hsp90 gene. pBACPak™ vectors containing the genes of interest were used to generate baculoviruses using the BacPAK™ expression system (Clontech Laboratories). 500 ml of ~1 million Sf21 cells/ml cultured at 27 °C in SF-900III SFM media (Life Technologies, Grand Island, NY) were infected with baculoviruses containing individual His-Rvb1, FLAG-Rvb2 and Halo-Hsp90 (separately or together). Infected cells were harvested after 48 h and stored at ~80 °C until required.

**Purification of Recombinant Proteins from Insect Cells**—Sf21 cells expressing His-Rvb1 were resuspended in 25 ml of lysis buffer (50 mM Tris, pH 7.5, 300 mM NaCl, 10 mM imidazole) containing protease inhibitors (0.1 mM benzamidine HCl, 55 μM phenanthroline, 10 μM bestatin, 20 μM leupeptin, 5 μM pepstatin A and 1 mM PMSF (phen-
yethylmethylsulfonyl fluoride) and passed five times through an 18-gauge needle for lysis. Lysed cells were centrifuged at 19,000 RPM (revolutions per minute) for 40 min in Beckman Coulter Avanti J20-XPI centrifuge using a Ti25.50 rotor (Beckman Coulter, Brea, CA). Clarified lysates were mixed with Ni-NTA Agarose resin (Qiagen, Valencia, CA) that was equilibrated with lysis buffer and incubated for 1 h at 4 °C followed by collection of the flow-through. The resin was washed with 10 bed volumes of wash buffer (lysis buffer containing imidazole at a final concentration of 20 mM). The protein was eluted by adding lysis buffer containing imidazole at a final concentration of 200 mM. Flag tagged Rvb2 was purified similarly to Rvb1 using ANTI-FLAG® M2 affinity gel (Sigma-Aldrich, St. Louis, MO) but with different buffers. Lysis buffer for Rvb2 purification contained: 50 mM Tris, pH 7.5, 150 mM NaCl and protease inhibitors. Wash buffer contained 50 mM Tris, pH 7.5, 300 mM NaCl and protease inhibitors. The protein was eluted by incubating the resin with 150 ng/μl 3× FLAG peptide (Sigma-Aldrich) for 1 h at 4 °C. Halo tagged Hsp90 was also purified similarly to Rvb1 but using 1× PBS (phosphate buffered saline) (10 mM phosphate buffer, pH 7.4, 2.7 mM KCl, 137 mM NaCl). Hsp90 was eluted by incubating Hsp90 bound HaloLink™ Sepharose resin (Promega) with His tagged AcTEVTM protease (Life Technologies) for 1 h at 4 °C in TEV cleavage buffer. The eluted proteins were dialyzed overnight in 25 mM HEPEs, pH 7.5, 50 mM KCl, 1 mM DTT (dithiothreitol) buffer. Dialyzed Hsp90 was passed through Ni-NTA resin and the flow-through was collected to remove the AcTEV protease. The proteins were further purified by anion exchange chromatography (1 ml HiTrap DEAE Sepharose FF resin (GE Healthcare Bio-Sciences)) using the AKTA protein purification system (GE Healthcare Bio-Sciences).

**Cloning, Expression and Purification of Proteins from Saccharomyces cerevisiae**—All Saccharomyces cerevisiae (yeast) BY4741 strains used in this study were obtained from GE Healthcare Dharmacon Research’s yeast collection (formerly Open Biosystems). TAP (tandem affinity purification) tags were introduced at the 3′ end of Rvb1 and Rvb2 (in PIH1 and TAHI1 deletion strains) by homologous recombination using an ampiclon that contained a selection marker (S.D.-URA) and gene sequence corresponding to the TAP tag (custom designed primers, supplemental Table S1). TAP tagged wild-type Rvb1, Rvb2 and Rpb1 strains were purchased from GE Healthcare. Cells were grown in YPD (yeast peptone dextrose) media to an OD$_{600}$ of 1.25–1.50 and protein purification was performed as described previously (22). RNAP1 complex was prepared by first performing a TAP tag purification using TAP tagged Rpb1 (similarly to Rvb1 and Rvb2) followed by anion exchange chromatography (1 ml HiTrap DEAE Sepharose FF resin (GE Healthcare Bio-Sciences)) using the AKTA protein purification system (GE Healthcare Bio-Sciences). The buffers used were 25 mM HEPEs, pH 7.5, 50 mM KCl, 0.5 mM DTT, 10% (v/v) glycerol (buffer A) and 25 mM HEPEs, pH 7.5, 500 mM KCl, 0.5 mM DTT, 10% (v/v) glycerol (buffer B).

**Analyses of RNA Levels**—Total RNA was isolated from ~5 ml yeast cells grown to an OD$_{600}$ of 1.2–1.5 using the MasterPure™ yeast RNA purification kit (Epicenter, Madison, WI) followed by enrichment of poly(A) ± RNA by oligo(dT) selection which was then used to construct individually barcoded libraries with the TruSeq RNA Sample preparation kit (Illumina, San Diego, CA). All measurements were performed in triplicate. One replicate of Rvb1-TAP was discarded from further analysis after it was discovered that the sample had been mislabeled (data not shown). Sequenced libraries were aligned to the UCSC sacCer3 reference genome with TopHat (23). Read counts for each of the 7126 gene transcripts (6692 coding genes, 413 non coding genes, and 21 pseudogenes) were generated with the RsuRead package in R (24). FPKM (fragments per kilobase of exon per million fragments mapped) values were calculated in R using the DESeq2 library (25). All data files have been deposited at the GEO (gene expression omnibus) repository and can be accessed using the accession number: GSE69220.

Rvb1-TAP and Rvb2-TAP samples were compared with Rvb1/2-TAP purified PiH1 and Tah1 deletion strains using DESeq2 (25). DESeq2 models read counts as a negative binomial distribution and fits a generalized linear model for each gene. Genes were considered differentially expressed if they had a p value < 0.01 and a log2 fold change > 0.7. An additional filtering step removed lowly expressed genes with an average FPKM < 10. To visualize the differences between the top genes from each comparison we clustered the regularized log2 transformed data from DESeq2 using the default hierarchical clustering method in R with a Euclidean distance measure. The resulting data is displayed as a heatmap created with the R package heatmap (Raivo Kolde (2015)). heatmap: Pretty Heatmaps. R package version 1.0.2. http://CRAN.R-project.org/package=heatmap. The data is shown with standard row scaling to highlight the differences of individual genes across samples. To perform qPCR, total RNA was reverse transcribed using iScript™ Reverse Transcription Supermix (Bio-Rad, Hercules, CA) and analyzed using the MyiQ™ real-time PCR detection system (Bio-Rad). The primers used for qPCR are listed in supplemental Table S1.

**Mass Spectrometry Analyses**—TAP tag purified proteins were precipitated overnight with 25% (v/v) TCA (trichloroacetic acid) and washed twice with ice cold acetone, air dried, resuspended in 100 mM Tris-HCl, pH 8.5, 8 M urea, followed by incubation with 5 mM TCEP (tris(2-carboxyethyl)-phosphine hydrochloride) then with 10 mM CAM (chloroacetamide) to reduce and alkylate disulfide bonds respectively. 0.5 μg of Sequencing grade Endoprotease Lys-C (Roche, Indianapolis, IN) was added to the samples and incubated at 37 °C for 6 h, diluted with 100 mM Tris, pH 8.5 to reduce the concentration of Urea to 2 M, supplemented with 2 mM CaCl$_2$ and further incubated with 0.5 μg sequencing grade Trypsin (Promega) (overnight) and quenched with 5% (v/v) formic acid (J.T.Baker, Center Valley, PA). Tryptic digests were loaded on to tri-phasic 100 μm fused silica micropipette columns that were placed in-line with an HPLC (Agilent, Santa Clara, CA) coupled LTQ mass spectrometer (Thermo Scientific, Waltham, MA) and 12, ~2 h MudPIT steps were performed as described in Florens et al. (26). Database matching and data analyses were performed as described in Banks et al. (27). Briefly, the raw files from the MS runs were processed by in-house generated RAWDistiller v. 1.0 software (28) to generate .ms2 files from which the MS/MS spectra were matched to a database using SEQUEST algorithm (Version 27, rev.9) (29). Mass tolerance for precursor ion was set at 3 Da and fragment ion tolerance was set to the default value of 0.01 in the sequest, params file. To account for carboxamidomethylation, a static modification of +57 Da was added to cysteine residues. To account for oxidation of methionine residues, variable search was carried out with +16 Da. No enzyme specificity was imposed during searches. The database used for the search was from NCBI (national center for biotechnology information, release date April 26, 2011) and contained a total of 11,990 sequences, out of which 5819 belonged to non-redundant Saccharomyces cerevisiae proteins. The rest of the sequences comprised of 176 commonly found contaminants (such as IgGs, human keratin and proteolytic enzymes) and shuffled sequences of Saccharomyces cerevisiae proteins and contaminants to estimate false discovery rates. The spectral FDR (false discovery rate) and protein FDR are 0.32 ± 0.16% and 4.39 ± 1.98% respectively (from 5 controls and 18 experimental samples of yeast TAP purifications) (supplemental Table S2). The database used for searching proteins that were produced in insect cells were from release date April 24, 2011 and contained a total of 150,494 sequences out of which 58,776 belonged to non-redundant proteins. The rest of the sequences comprised of 181 commonly found contaminants (such as IgGs, human keratin and proteolytic enzymes). The spectral FDR was
RESULTS

MudPIT Analyses of TAP Tagged Rvb1 and Rvb2 Identify New Complex Associations—To determine the proteins associated with Rvb1 and Rvb2, yeast strains containing a TAP tag at the C-terminal end of either Rvb1 or Rvb2 (referred to as wild-type strains or bait proteins) were cultured and the bait proteins were purified using the TAP tag purification protocol (22). Because the TAP tag was integrated into the yeast genome, endogenous protein expression levels were maintained and spurious associations caused by of protein overexpression were avoided. Three independent purifications for experimental samples (tagged) and five purifications for control (untagged) were subjected to MudPIT analyses. Each sample was split into 3 equal parts and subjected to individual MudPIT runs to account for technical variations (technical replicates). After MudPIT analyses, separate SEQUEST (29) searches were performed on each replicate followed by DTASelect (30). Another round of DTASelect was performed to merge all the technical replicates and subjected to Contrast (30) and NSAF7 software (32) analyses to compare and contrast the different runs. For quantitative comparison, we used the label free spectral counting approach as described in Zhang et al. (32), where distributed spectral counts (based on unique and shared spectra) were used for label-free quantification. MudPIT analyses of TAP tag purified Rvb1 and Rvb2 from wild-type and PIH1 and TAH1 deletion strains show that Tah1 is present only in the presence of Ph1, whereas Ph1 is pulled-down even in the absence of Tah1 (Fig. 1A). Because our method captures complexes that are assembled in vivo, it confirms that Ph1 bridges Rvb1/Rvb2 and Tah1, and is indispensable for the formation of the R2TP complex as has been discussed previously (4).

Using the PLGEM (power law global error model) algorithm (33), we identified a set of proteins (prey) specifically enriched in the wild-type Rvb1 and/or Rvb2 bait purifications, but not in the untagged control purifications. To avoid false positives such as contaminants and nonspecific proteins, only proteins appearing in at least two out of three purifications (>50%) were taken into consideration for PLGEM analysis. PLGEM uses dNSAF values to estimate the likelihood of proteins being enriched in experimental samples over controls and calculates ° values for each prey which are further used to determine FDR using the Benjamini and Hochberg method (34). Only proteins with an FDR of 5% or less were used in further analyses, thus ensuring a stringent selection process. Of the 414 Rvb1 associated proteins and 299 Rvb2 associated proteins that were identified, 236 copurified with both Rvb1 and Rvb2 (Fig. 1B and supplemental Tables S3, S4).

Among the 236 proteins that passed our criteria, 28 proteins are already known to be associated with or interact with both Rvb1 and Rvb2. Examples include proteins from the R2TP, Ino80, Swr1 and ASTRA complexes (Fig. 1C and supplemental Table S5).

We found several protein complexes which had not been previously reported as associating with the Rvb proteins. In particular, we identified a relatively large number of spectra corresponding to subunits of both the CCT (chaperonin-containing T-complex) complex and the proteasome. The CCT complex (GO (gene ontology) id: 0005832) mediates protein folding and the proteasome complex (GO id: 0000502) is involved in protein degradation. Specifically, we were able to capture all 11 proteins belonging to the CCT complex (albeit some with lower spectral counts) and several subunits of the 26S proteasome complex (Fig. 1D, Fig. 1E and supplemental Tables S3–S5). To corroborate our approach, we also analyzed the wild-type data against an unrelated TAP tagged control (Rtt101) (supplemental Tables S3, S4) and found that neither the CCT nor proteasome were enriched in the Rtt101 pull-downs whereas contaminating proteins were generally at the same abundances, ruling out nonspecific interactions via the TAP tag. It is interesting to observe that Rvb1s have been found to be associated with both protein folding and protein degradation machinery in the cells and thus expanding the network of proteins associated with Rvb1s.

Label free quantitative proteomics provides a deeper understanding of the Rvb1 and Rvb2 associated proteins than the qualitative data available in databases like the Saccharomyces Genome Database (SGD) (www.yeastgenome.org), for example (35). In SGD, Rvb1 is listed to have 102 physical interactions, and 82 genetic interactions with 9 identified by both physical and genetic methods. While this is important prior knowledge, these lists provide no ranking of interactions, which quantitative proteomic methods can provide. The top associated proteins of Rvb1-TAP are shown in Fig. 2A sorted from highest to lowest abundance. When summing the abundances of proteins that are only found in specific complexes, the largest abundance originates from Ino80 at 21% followed by Swr1 at 10%, the proteins specific to the R2TP complex at 4%, and then the proteasome at 3% (Fig. 2A). In SGD Rvb2 is listed to have 131 physical interactions and 87 genetic interactions with seven identified by both physical and genetic methods. The top associated proteins of Rvb2-TAP are
showed in Fig. 2B sorted from highest to lowest abundance. When summing the abundances of proteins that are only found in specific complexes, the largest abundance originates from Ino80 at 33% followed by Swr1 at 6%, the proteasome at 4%, and then the proteins specific to the R2TP complex at 3% (Fig. 2B).

The mass spectrometry based estimated copies per cell (CpC) of these proteins from Kulak et al. (36) is shown in Fig. 2C. No value of Tah1 is available in this data set and Act1 at 117,202 CpC was excluded from the graph for visualization purposes. The proteasome components identified in this study are overall about six times more abundant than Ino80 components and 15 times more abundant than Swr1 components based on CpC estimates from Kulak et al. (36). When comparing the CpC estimates in Fig. 2C to the ranked abundances in Figs. 2A and 2B, the increased association of Rvb1 and Rvb2 with Ino80 when compared with Swr1 is likely explained by the larger amount of Ino80 in the cell. Given the much higher abundance of the proteasome and the lower levels of the proteasome associated with Rvb1-TAP and Rvb2-TAP when compared with Ino80 and Swr1, it is likely that Rvb1-TAP and Rvb2-TAP are only associating with a small subpopulation of the proteasome.

Rvb1 and Rvb2 Interact Directly With Hsp90—Having defined a set of Rvb1 and Rvb2 associated proteins; we noticed that Hsc82 (yeast systematic name: YPL240C and hereafter called Hsp90 for convenience) was present in both wild-type and mutant purifications (Fig 3A). This raises the possibility

![Diagram](https://example.com/diagram.png)

Fig. 1. Rvb1 and Rvb2 both associate with the other R2TP subunits Pih1 and Tah1, and copurify with a functionally diverse group of other protein complexes. A, components of the R2TP complex copurify with Rvb1 and Rvb2. Either Rvb1-TAP or Rvb2-TAP associated proteins were isolated from whole cell extracts of the strains indicated by TAP purification, and identified using MudPIT mass spectrometry. Relative amounts of each protein are estimated using dBNSAF values, where the dNSAF value for each protein was divided by the dNSAF value of the bait protein. The average relative amounts of the four R2TP subunits Rvb1, Rvb2, Pih1, and Tah1 are indicated (average dBNSAF values calculated from 3 biological replicates). Error bars indicate standard deviation. B, Rvb1/Rvb2 associated proteins. Proteins enriched in the Rvb1 and Rvb2 purified wild-type samples described in A, but not in control purifications were identified by PLGEM analysis as previously described (22) (FDR <0.05, except for: the snoRNP subunit Nop56; the CCT complex components Cct2, Cct6, Hsp42, Ssa1 and Ssa2). The area proportional Venn diagram was generated using “Venn Diagram Plotter” (PNNL, http://omics.pnl.gov/). C, protein complexes captured by Rvb1/2. For each complex the number of complex components captured (left) and the total number of known subunits for each complex (right) is indicated. D and E, dBNSAF values of CCT and proteasome complex components that are present in both Rvb1 and Rvb2 purifications.
A

![ quantitative proteomic analysis of top Rvb1/2 interacting proteins A ]

Thirty six of the top proteins interacting with Rvb1 sorted from highest to lowest abundance after contaminant extraction. The focus of the graph is on proteins from the Ino80 complex (I), Swr1 complex (S), the Proteasome (P), the R2TP complex (R), and proteins in both Ino80 and Swr1 (B). The first 33 proteins are the 33 most abundant proteins found in the Rvb1-TAP purification after contaminant extraction. The average and standard deviation is shown for three biological replicates. B.

![ quantitative proteomic analysis of top Rvb1/2 interacting proteins B ]

Thirty six of the top proteins interacting with Rvb2 sorted from highest to lowest abundance after contaminant extraction. The focus of the graph is on proteins from the Ino80 complex (I), Swr1 complex (S), the Proteasome (P), the R2TP complex (R), and proteins in both Ino80 and Swr1 (B). The first 33 proteins are the 33 most abundant proteins found in the Rvb2-TAP purification after contaminant extraction. The average and standard deviation is shown for three biological replicates. C.

![ deletion network analysis of Rvb1/2 without Pih1 or Tah1 C ]

Deletion Network Analysis of Rvb1/2 without Pih1 or Tah1. Thirty six of the top proteins interacting with Rvb1, Flag tagged Rvb2 and Halo tagged Hsp90 and proteins were purified using the Flag resin, we observed 2 predominant bands in Coomassie stained gels, which corresponding to Hsp90 and Rvb1/2 (Fig. 3B, lane F). Western blot analysis of the Flag elution (lane F) confirmed that the upper band corresponds to Halo tagged Hsp90 (~116 kDa) and the other predominant band (~53 kDa) contains both 6xHis-TEV-Rvb1 (~52.9 kDa) and FLAG-Rvb2 (~53 kDa) (Fig. 3B, right panel). In order to test if the co-elution of Hsp90 with Rvb1/2 is because of direct interaction, elution fractions from the FLAG purification were further purified using Ni-NTA chromatography, which enriches for His tagged proteins. Analysis of fractions from the His tag purification by MudPIT mass spectrometry (Fig. 3B lane K) confirmed the presence of Rvb1, Rvb2 and Hsp90 (Fig. 3B), indicating a robust interaction between Hsp90 and Rvb1/2.

To dissect the nature of interactions between the individual subunits, we performed a second series of experiments in which we first purified the Rvb1, Rvb2 and Hsp90 proteins individually, and then mixed the purified proteins together in various combinations to test for protein–protein interactions using affinity chromatography (Fig. 3C). Hsp90 copurified with His-Rvb1 (Fig. 3C second panel), FLAG-Rvb2 (Fig. 3C third panel) as well as in the presence of both Rvb1 and Rvb2 (Fig. 3C end of third panel). It is unlikely that other proteins mediate this interaction as we did not detect significant amounts of other proteins in the eluate when we analyzed it by MudPIT (Fig. 3C fourth panel). To rule out any possibility of nonspecific interactions between Rvb1/2 and Hsp90, we performed the same experiment using yeast alcohol dehydrogenase (Sigma-Aldrich, catalogue no. A7011). No interactions were observed between alcohol dehydrogenase and either of the Rvbs (supplemental Fig. S1), indicating specific and genuine interaction between Rvbs and Hsp90.
Having identified a set of Rvb1/2 associated proteins, we investigated whether Pih1 and Tah1 might have a role in regulating which proteins associate with Rvb1/2. To this end, MudPIT analyses of TAP tag purifications from Pih1 and Tah1 deletion strains were further analyzed using PLGEM statistics (as described above) to identify proteins enriched with Rvb1/2 specifically in these mutant strains. While performing PLGEM statistics, proteins which appeared >50% of the time in the mutant purification and were at least twofold enriched compared with wild-type were considered for further analyses. We used enrichment cut-off instead of FDR, since PLGEM is less reliable when working with smaller datasets. The number of proteins that passed our criteria were 511 (RVB1-TAP PIH1Δ), 585 (RVB1-TAP TAHIΔ), 286 (RVB2-TAP PIH1Δ), and 730 (RVB2-TAP TAHIΔ), of which 80 were present in all mutant purifications. (Fig. 4A and supplemental Table S6). Among these 80 proteins, 16 were exclusively present in the mutant strain purifications (Fig. 4B, Table 1) and GO analysis of these proteins revealed that the majority of them are not part of any complex. However, the GO Slim Mapper function in SGD revealed that the top two most represented GO terms of these 80 proteins was ribonucleoprotein complex and periribosome (supplemental Table S6). Among the proteins that were still present in wild-type purifications albeit in lower proportions, both the RNAPII complex (Rpb1 and Rbp2) and the snoRNP
assembly complex (Nop1 and Nop56) were enriched with Rvb1/2 in much greater amounts in the absence of Pih1 and/or Tah1 (Fig. 4B, Table 2). In particular, the largest subunits of the RNAPII complex, Rpb1 (also known as Rpo21) and Rpb2, copurified with Rvb1 in more than 10 fold greater amounts in the absence of Pih1 (Fig. 4B, Table II).

Rvb1 and Rvb2 complexes lacking subunits Pih1 or Tah1 have an increased association with components of the RNA polymerase II and snoRNP complexes. A, a subset of proteins associate with Rvb1 and Rvb2 complexes purified without Pih1 or Tah1. Proteins present in the indicated purifications (described in Fig. 1), but not in control purifications, were identified using PLGEM analysis. The Venn diagram was generated using “Venny” (Oliveros, J.C. (2007–2015) Venny. An interactive tool for comparing lists with Venn’s diagrams. http://bioinfogp.cnb.csic.es/tools/venny/). B, increased association of a set of proteins with Rvb1/2 in the absence of Pih1 or Tah1. Table I, representative proteins from the common 80 proteins shown in A, which are enriched in purifications using PIH1Δ or TAH1Δ deletion strains, compared with purifications using the wild-type strains. Average distributed spectral counts (dS) from three biological replicates are shown. Table II, RNAPII and snoRNP subunits are enriched in purifications using the wild-type strains (Fig. 5A, left panel, Fig. 5B and supplementary Fig. S2). Western blot analysis shows no difference in expression levels of Rpb1 protein when comparing the RVB1-TAP PIH1Δ and RVB2-TAP TAH1Δ strains (Fig. 5A, left panel, Fig. 5B and supplementary Fig. S2). Western blot analysis shows no difference in expression levels of Rpb1 protein when comparing the RVB1-TAP PIH1Δ and RVB2-TAP TAH1Δ strains (Fig. 5A, left panel, Fig. 5B and supplementary Fig. S2).
Deletion Network Analysis of Rvb1/2 without Pih1 or Tah1

Fig. 5. Interaction between Rvb1/2 and RNA polymerase II complex. A, left panel, TAP-purified samples of the indicated strains were analyzed by Western blotting. Rvb1/2 proteins were visualized with rabbit anti-TAP polyclonal antibodies and IRDye®800CW anti-rabbit secondary antibodies (green). Rvb1 associated proteins purified from *S. cerevisiae* lacking Pi1 are enriched for the pol II subunit Rpb1. A, right panel, Whole cell extracts prepared from the indicated yeast strains were analyzed for the presence of RNAPII subunit Rpb1 by fractionating samples using SDS-PAGE and detecting proteins by Western blotting. Rpb1 was detected with mouse anti-Rpb1 monoclonal antibodies and IRDye® 680LT anti-mouse secondary antibodies (red); tubulin was detected with rabbit anti-tubulin monoclonal antibodies and IRDye®800CW anti-rabbit secondary antibodies (green). Li-Cor Odyssey software was used for both imaging and band quantitation. Band quantitation was repeated on Western blots for three biological replicates; average values are plotted. B, Rpb1 association with Rvb1 or Rvb2 depends on Pi1 and Tih1. Average dBNSAF values were calculated from the purifications used in Fig. 1. C, the absence of Pi1 or Tah1 does not significantly affect Rpb1 mRNA levels. RNA samples purified from whole cell extracts of the indicated strains were analyzed by either RNA-seq or qPCR as described in Experimental Procedures. D, interaction between RNA polymerase II purified from yeast and either recombinant Rvb1 or Rvb2 isolated from Sf21 insect cells. Representative Silver stained gel showing purified RNAPII complex that was used as input (for inputs of Rvb1 and Rvb2 refer to Fig. 2C left panel). Approximately 10 μg samples of Rvb1, Rvb2 or RNAPII complex were mixed in the combinations indicated, affinity purified, and analyzed by SDS-PAGE and Western blotting.
addition, we analyzed Rpb1 transcript levels using both RNA-seq, and quantitative PCR (Fig. 5C), and again observed small significant differences between the wild-type and mutant strains that are likely not biologically relevant and do reach the magnitude of protein changes. To further investigate the nature of interaction between the RNAPII complex and Rvb1/2, we performed in vitro pull down experiments using recombinant yeast Rvb1 and Rvb2 and the RNAPII complex. Purified Rvb1, Rvb2 and RNAPII complex were mixed in different combinations as shown in Fig. 5D and subjected to either Ni-NTA (His) or FLAG affinity chromatography. The RNAPII complex (identified by the detection of Rpb1 in the elution fractions) copurifies with Rvb1, with Rvb2, and with both proteins together (Fig. 5D). This is consistent with direct interactions between surfaces on RNAPII and both Rvb1 and Rvb2. We were also able to detect all of the RNAPII subunits in elution fractions (Fig. 5D right panel last lane) using MudPIT analysis (data not shown), indicating that Rvb1 might interact with intact RNAPII complexes.

Recruitment of Rvb Proteins to the Chromatin Remodelers Swr-C and Ino80-C—It is well known that Rvbs are essential for cell survival and are part of several protein complexes, but it is unclear how they are recruited to these complexes. After investigating the Pih1 and Tah1 dependent recruitment of Rvb1/2 to RNAPII, we analyzed our proteomics data set to try to determine whether Pih1 and Tah1 are involved in recruitment of the Rvbs to the Ino80 and Swr1 chromatin remodeling complexes. To address this, we analyzed the MudPIT data from wild-type and mutant Rvb1/2-TAP strains to determine the relative amounts of Swr1 or Ino80 subunits copurifying with Rvb1/2 in the presence or absence of Pih1 or Tah1 (Fig. 6A and 6C). In addition, we monitored the transcript levels of Ino80 and Swr1 complex subunits in each strain to exclude the possibility that any effects that we observed resulted from changes in Swr1 or Ino80 gene expression (Fig. 6B and 6D). We found that deleting the PIH1 or TAHI genes did not result in an overall decrease in the amount of Ino80 and Swr1 complex components copurifying with Rvb1 or Rvb2; indicating that the incorporation of Rvb1 into these complexes does not depend on either Pih1 or Tah1. This is in contrast to the findings of Zhao et al. (1), who report that in the absence of Pih1 and Tah1, Rvb1 and Rvb2 are enriched in les2-TAP purifications, a key component of the Ino80 complex. Nevertheless, analysis of transcript levels indicated that the only change observed was the up-regulation of TAF14 from the RVB2-TAP TAHIΔ strain, which is part of Ino80 as well as several other protein complexes (37).

Analysis of RNA-Seq Data—Finally, we analyzed the RNA-Seq data to determine the global effects of deleting PIH1 or...
TAH1 from the RVB1-TAP or RVB2-TAP strains. All Pearson correlations were 0.994 or more (supplemental Fig. S3). These high correlation values reflect similar levels of gene expression for the majority of genes in all strains analyzed. In addition, the lower correlation values obtained when we compared some deletion strains with wild-type strains is also consistent with a limited number of gene expression changes. To assess these, we next performed a hierarchical clustering analysis of the complete dataset (Fig. 7A). After clustering, the replicates grouped together. Interestingly, the deletion of PIH1 or TAH1 had different effects depending on whether they were in the RVB1-TAP or RVB2-TAP background. To assess whether these different effects were consistent with previously reported phenotypic data, we compared annotations for mutant phenotypes of all the components of this system listed in the Saccharomyces Genome Database (35). RVB1 has 5 phenotypes, RVB2 has 19 phenotypes, TAH1 has 13 phenotypes, and PIH1 has 29 phenotypes. The shared phenotype function in SGD reports none of these phenotypes are shared between any of the components RVB1, RVB2, PIH1, and TAH1. The different effects that we observed when deleting either PIH1 or TAH1 in the different backgrounds (RVB1-TAP or RVB2-TAP) are consistent with previously reported data that disruptions introduced to any of these four components can have a different set of phenotypic effects.

Next, we compared the deletion strains to their respective wild-type strains to determine changes in gene expression.
We used an adjusted $p$ value of less than 0.01 as the cutoff for all comparisons. A total of 55 genes had significant expression changes in the RVB1-TAP PIH1Δ strain with 43 downregulated and 12 up-regulated when compared with the control RVB1-TAP (supplemental Table S7). Next, 46 genes had significant expression changes in the Rvb1-TAP TAH1Δ strain with 21 downregulated and 25 up-regulated when compared with the control RVB1-TAP (supplemental Table S7). In the case of the RVB2-TAP strains, deletion of PIH1 resulted in 667 statistically significant gene expression changes with 356 downregulated and 311 up-regulated and deletion of TAH1 resulted in 183 statistically significant gene expression changes with 46 downregulated and 137 up-regulated. A Venn diagram analysis of the gene expression changes found in all studies is shown in Fig. 7B. Only seven gene expression changes were found in common in all analyses. The PIH1 and TAH1 deletion strains in Rvb1-TAP background shared 13 genes whose expression was significantly different (Fig. 7B). The two TAH1Δ strains shared 13 genes whose expression was significantly different (Fig. 7B). The two PIH1Δ strains shared 41 genes whose expression was significantly different (Fig. 7B).

We next conducted GO term analysis of these results (supplemental Fig. S4 and supplemental Table S8). In the RVB1-TAP PIH1Δ strain, ribosome biogenesis ($p = 0.022$) was up-regulated, whereas transition metal ion transport ($p = 6.55E-05$) and nucleotide biosynthetic process ($p = 2.57E-04$) were among the larger downregulated GO categories. In the RVB1-TAP TAH1Δ strain, carboxylic acid biosynthetic process ($p = 3.71E-08$), arginine biosynthetic process ($p = 7.80E-08$), and translation elongation (1.05E-04) were up-regulated, whereas response to temperature stimulus (4.07E-07) and transition metal ion transport (0.018874) were among the downregulated GO categories. In the RVB2-TAP PIH1Δ strain, ribosome biogenesis ($p = 2.34E-98$), maturation of SSU-rRNA ($p = 2.13E-36$), RNA modification ($p = 1.66E-34$) including snoRNA 3’ end processing ($p = 0.020299$), and RNA 5’ end processing ($p = 5.24E-20$) were among the many GO categories up-regulated, while response to temperature stimulus (p = 4.09E-37), vacuolar protein catabolic process (p = 1.09E-31), and protein refolding (p = 6.68E-09) were among the many GO categories downregulated. In the RVB2-TAP TAH1Δ strain, ncRNA processing ($p = 1.98E-06$), ribosome biogenesis ($p = 5.14E-05$), and RNA modification ($p = 2.29E-04$) were among the up-regulated GO categories, while polyphosphate metabolic process ($p = 4.49E-05$) and response to temperature stimulus ($p = 0.0088$) were the most enriched downregulated categories. There were common themes among these GO analyses (supplemental Fig. S4 and supplemental Table S8). Ribosome biogenesis and ribonucleoprotein complex biogenesis were up-regulated in the RVB1-TAP PIH1Δ strain, the RVB2-TAP PIH1Δ strain, and the RVB2-TAP TAH1Δ (supplemental Fig. S4A). The RVB1-TAP TAH1Δ strain, RVB2-TAP PIH1Δ strain, and the RVB2-TAP TAH1Δ had downregulated response to abiotic stimulus (supplemental Fig. S4B), and all four strains had downregulated response to temperature stimulus (supplemental Fig. S4B).

**DISCUSSION**

The highly sensitive and reproducible nature of affinity purification mass spectrometry combined with label free quantitative proteomics has played a major role in identification and characterization of new protein associations and interactions (27, 38–40). Although the yeast R2TP complex and its components have been studied before (41, 42), a comprehensive deletion network analysis is still needed. In the present study, we have purified Rvb1 and Rvb2 from wild-type yeast strains and were able to confirm the known protein associations of the Rvbs. Employing stringent selection criteria, we identified new complexes that associate with Rvb1 and Rvb2 and thus expand their association network. In particular, we observe a strong association between Rvb1 and Rvb2 to the 19S regulatory proteasome complex. All the base subunits of the 19S regulatory subcomplex were captured, including the regulatory particle of non-ATPase subunits (Rpn1, Rpn2, Rpn10, and Rpn13) and the regulatory particle of triple AAA-ATPase (Rpt1–6) subunits (43). The strong association between Rvbs and the base subunits of the 19S subcomplex is very intriguing, because the six AAA-ATPase subunits also form heterohexamers as has been observed in Rvbs and it remains to be seen if the Rvbs have any role in the assembly and oligomerization of Rpt1–6. In fact, the biogenesis of the 19S subcomplex and its association with the 20S core particle is largely uncharacterized. Hsp90 has been shown to play a role in this assembly (44), but the exact mechanism is still poorly understood. It would be interesting to determine if Rvbs play a role in recruiting Hsp90 to the 19S proteasome complex or even help in its assembly without the involvement of Hsp90. Further investigation of the association between the Rvbs and the 19S proteasome may shed more light on the assembly of the proteasome complex.

Although several proteins associated with both Rvb1 and Rvb2 baits from wild-type strains (236), considerably more proteins copurified with Rvb1 (414) than with Rvb2 (299) (Fig. 1B). This difference can be attributed to the instances where both proteins can act independently and even exhibit antagonistic effects (45–48). For example, in prostate cancer cells the metastasis suppressor gene KAI1 which inhibits metastasis by promoting cell adhesion, is activated by the Rvb1/Tip60 complex whereas the Rvb2/β-catenin complex along with HDAC1 (histone deacetylase 1) acts as co-repressor of the transcription of KAI1. Thus, the expression of KAI1 and its metastatic potential is regulated by the antagonistic actions for Rvb1 and Rvb2 (48). It is also worth mentioning that Rvb1 and Rvb2 cannot complement each other and have opposite polarities (Rvb1 displaces DNA from 3’ to 5’ direction (49), whereas Rvb2 displaces from 5’ to 3’ (50)), which may lead to differences in their association with other proteins.
Deletion Network Analysis of Rvb1/2 without Pih1 or Tah1

The proteomic analyses of Rvb1 and Rvb2 purifications from PIH1 and TAH1 deletion strains provide interesting new information. First, purification of Rvb1 and Rvb2 in the PIH1 and TAH1 deletion backgrounds still retains Hsp90. It is highly unlikely that this interaction is mediated by Hsp90 cofactors, because we do not see Hsp90 cofactors associate with Rvb1/2 in stoichiometrically relevant numbers (supplemental Table S9). Further analysis of the interaction between Rvbs and Hsp90 using a biochemical approach revealed that Hsp90 directly interacts with Rvbs. To our knowledge, this is the first time a direct interaction between Rvbs and Hsp90 is being reported. Based on our findings it is clear that in yeast, Rvb1 and Rvb2 can either interact with Hsp90 as part of the R2TP complex or by themselves. Because Hsp90 can interact with Rvbs and can also aid in folding and assembly of several protein complexes, it offers a possible explanation as to why Rvb1 and Rvb2 may possess chaperone-like activity. Further characterization of the interaction between Rvb1/2 and Hsp90, such as the regions required for their interaction and the stoichiometry of the complex would offer clues about their function. Second, our analyses also revealed several interesting proteins that copurified with Rvbs only in the absence of Pih1 or Tah1 (Fig. 4B, Table I). One such interesting protein is Mgm101 (systematic name: YJR144W), which appears in high numbers only in the deletion strain purifications. Mgm101 is a Rad52-type mitochondrial protein that binds to single stranded DNA and has been suggested to play a role in interstrand cross-link repair of mitochondrial DNA (51). Mgm101 also oligomerizes to form rings similar to Rvbs. The bacterial RuvB helicase, which is related to Rvb1 and Rvb2 forms a double hexamer and mediates migration of Holliday junctions in double-strand break repair (52). It has been suggested that Rvbs may also play a role in double strand DNA break repair by assisting Ino80 and Swr1 complexes (53). Taken together, it is possible that Rvbs may also play a similar role in mitochondrial genome maintenance by associating with Mgm101. Finally, we observed an increase of RNAPII complex components in deletion purifications. On further investigation we were able to biochemically confirm that Rvb1/2 interacts with the RNAPII complex. Previous studies have shown that the R2TP complex is involved in the assembly of the RNAPII complex in the cytoplasm, mediated by the interaction between human hSpag1 protein (yeast Tah1 equivalent) and the Rpb1 subunit of RNAPII complex (5). Our findings indicate that yeast Rvb1/2 can interact with RNAPII even in the absence of Pih1 and Tah1, offering clues for the observation of human Ruvb1 in RNAPII complex purifications (11, 54). Rvb1 has also been shown to have a direct role in transcription initiation of ISGs (IFN (interferon)-α-stimulated genes) by recruiting RNAPII complex to its promoter region (55), but it is not known whether Rvb1 is part of yet another unidentified complex that recruits Rvb1 and RNAPII to the transcription start site. From our data it is tempting to speculate that Rvb1 may directly recruit RNAPII complex to the promoter region of ISGs.

In this study we also carried out a systematic RNA-Seq analysis of the TAP tagged strains compared with PIH1Δ and TAH1Δ deletion strains. There were common themes among the gene expression changes like changes in ribosome related GO categories (supplemental Table S8). A comparison of the changed proteins from the quantitative proteomic analysis of the PIH1 and TAH1 deletion strains to the RNA-Seq analysis of the same strains yields an interesting link. GO Slim Mapper analysis of 80 proteins found changed in all deletion strains (Fig. 4A) found ribonucleoprotein complex and periribosome to be the most enriched categories. In the RNA-Seq studies, the ribonucleoprotein complex biogenesis GO category was found enriched in the up-regulated genes in the RVB2-TAP TAH1Δ strain, the RVB2-TAP PIH1Δ strain, and the RVB1-TAP PIH1Δ strain (supplemental Fig. S4). The mechanistic implications of this link are unknown at this time, but warrants further study. Our prior work on deletion network analysis of chromatin remodeling complexes led to architectural insights into the complexes (56, 57) which in the case of the SAGA complex was validated by structural biology studies (56). Here our deletion network analysis of the R2TP complex components from the RVB1-TAP and RVB2-TAP strains have led us in a different direction where changes in protein association found in all deletion strains were also found in gene expression changes in the RNA-Seq analyses. These results demonstrate that deletion network analyses can provide novel and varied insights into cellular systems.

Acknowledgments — The underlying original data not in repositories will be made available in the Stowers Institute Original Data Repository (http://www.stowers.org/research/publications/odr).

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** This article contains supplemental Figs. S1 to S4 and Tables S1 to S8.
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