# Supplemental materials

# The Interactome of the Atypical Phosphatase Rtr1 in *Saccharomyces cerevisiae*

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## Supplemental methods

### Characterization of the Rtr1 interactome using SAINT

All SAINT and fold change (FC-A and FC-B) scores were calculated through www.crapome.org. Input tables were formatted according to the guidelines outlined on the website and in various SAINT publications. FC-A is the least stringent score and compares the enrichment values in the affinity purification to the average number of PSMs for a given protein in mock controls. FC-B is a more stringent fold-change calculation and takes the PSM values from the three mock purifications in which the protein was most frequently detected. This allows for removal of contaminant proteins that are sometimes detected at high levels depending on the degree of contamination or carryover (Choi et al., 2011; Mellacheruvu et al., 2013). The SAINT probability values are determined through modeling of each prey-bait pair with mixture-model analysis of the PSM distributions (Choi et al., 2011). As mentioned in the main text, the TAP double affinity purifications had significantly higher numbers of PSMs for Rtr1 and high-level interacting partners such as the subunits of RNAPII. As such, we chose to perform SAINT analysis of the single affinity and double affinity purifications separately to identify both stable and transient Rtr1 interactions (Tables S2, S4, S6, S7). We also performed SAINT express analysis of the combined datasets as reported in Table S7 and Figure S1. Since analysis of the Rtr1 *ctk1Δ* interactome using both TAP and FLAG tagged Rtr1, the comparison of SAINT values for the WT and *ctk1Δ* interactome used both the TAP and FLAG affinity purifications as independent replicates (Table S8). The Rtr1-V5 data was not included in the analysis in Table S8 since no data was obtained on Rtr1-V5 *ctk1Δ*.

### In vitro interaction analyses

Ctk1 and Ctk2 were cloned into pYES-DEST52 (Invitrogen) and transformed into

BY4741. Each strain, Ctk1 and Ctk2 pYES-DEST52 was grown overnight in 6 mL cultures of Sc-Ura/2% glucose. The next day, these cultures were centrifuged, washed with water, and then grown overnight in 400 mL cultures of Sc-Ura 2% Raffinose. The next morning, cultures were diluted to $OD_{600}$ ~1.5-2.5 in 400 mL cultures of 3X YEP/6% Galactose (3% yeast extract, 6% peptone, 6% Galactose) and fusion proteins were induced for 6 hours. After induction, cells were centrifuged, washed with water and frozen at $-80^0$C until lysis.

Ctk1 and Ctk2 pellets were resuspended in lysis buffer (40mM Hepes-KOH, pH 7.5; 10% glycerol; 100mM NaCl; 0.1% Tween-20; 2X protease inhibitors and 0.5mM DTT). After clarification, each lysate was then incubated with 200 uL of anti-V5 agarose for at least 3 hours at $4^0$ C on a rotating wheel. Following incubation with anti-V5 agarose, the supernatant was separated from the resin via gravity flow. To each immobilized V5 protein, 2 ug of Rtr1-GST was added, and incubated at $4^0$ C on a rotating wheel, overnight. In addition to the two samples, 2 ug of Rtr1-GST was also added to 200 uL of anti-V5 agarose to serve as a negative control. The next day, the resin was then washed with 20 mL of lysis buffer containing 350 mM NaCl. Following wash, the resin from each sample and control were resuspended in 200 uL of 1X SDS buffer and prepped for SDS PAGE analysis.

## Description of Supplemental Materials

**Figure S1: Identification of the Rtr1 interactome by AP-MS followed by SAINT.** A. Overview of the interactions identified by SAINT in double affinity Rtr1-TAP purifications. Graph compares the FC-B score against the SAINT probability scores. The dashed line represents the 0.75 probability cut-off. Proteins of interest are indicated with a label. All identifiers for these data are included in Table S6. B. High confidence Rtr1 interaction network illustrating the unique and shared interactions identified with a SAINT probability score of ≥ 0.8. A legend describing all nodes and edges is shown below the network.

**Figure S2: The interaction between Rtr1 and RNAPII is significantly decreased in the absence of Ctk1.** A. The number of peptide-spectrum matches (PSMs) for each protein of interest was summed from each purification as indicated at the top of the heat map. An intensity scale of the number of PSMs is shown below the figure. B. FC-B scores for Rtr1 affinity purifications from WT(black bars) and *CTK1* deletion (red bars) yeast strains for proteins of interest.

**Figure S3: Analysis of the interaction between Rtr1 and CTDKI subunits.** A. Double co-immunoprecipitation of Ctk1-TAP followed by TEV cleavage and V5-IP for Rtr1-V5. The input material (whole cell extract – WCE) and IP material was separated by SDS-PAGE and then subjected to western blot with either anti-calmodulin binding peptide or anti-V5 antibodies as indicated. The expected mobility of each tagged protein is indicated to the right with arrows. C. *In vitro* analysis of the Rtr1-Ctk1 and Rtr1-Ctk2 interactions. Ctk1- or Ctk2-V5 were overexpressed in yeast through galactose induction in the pYES system. After affinity capture on anti-V5 agarose, recombinant Rtr1-GST was added to check for direct interactions. The antibody used for western detection is indicated to the right and the sample type is indicated at the bottom of the figure below the lane numbers.

**Table S1: Full Rtr1 interactome dataset with all control and Rtr1 affinity purifications.** The NCBI gene accession number and protein sequence annotations are provided in the table along with the standard yeast protein name according to the Saccharomyces Genome Database (SGD, www.yeastgenome.org). For each purification, the percent protein sequence coverage (%SC), number of unique peptides (UP), and number of peptide spectrum matches (PSMs, also known as spectral counts) are given. Since this table is over 300 printed pages, it is provided as a separate supplemental file.

**Table S2: Single affinity purification (V5/FLAG) SAINT analysis.** Output list from SAINT express analysis of the Rtr1-V5 and Rtr1-FLAG affinity purifications compared to mock controls. Table includes the SGD protein ID acronym, the fold-change A value (FC_A), the fold-change B value (FC_B), and the SAINT probability. In addition, the presence (1) or absence (0) of each interaction with Rtr1 in the iRefIndex (**irefindex**.org) database is indicated (iREF). High confidence interactions have a SAINT value of ≥ 0.75 and are shown in green boxes, moderate confidence interactions have a SAINT value of 0.45-0.75 shown in yellow boxes, and low confidence interactions have a SAINT value of 0.01-0.44 shown in red boxes.

**Table S3: GOStat analysis output of significant interactions in single affinity purifications.** The top 30 GO terms enriched in the Rtr1-FLAG/V5 dataset true interactions (SAINT ≥ 0.75). The GO term, significant gene IDs for proteins identified in the Rtr1 interactome belonging to each term, the number of IDs in the Rtr1 interactome for each term (count), total number of genes associated with each term (Total), and p-value are given in the table.

**Table S4: Output list from SAINT express analysis of the Rtr1-FLAG affinity purifications compared to mock controls.** Table includes the SGD protein ID acronym, the fold-change A value (FC_A), the fold-change B value (FC_B), and the SAINT probability. In addition, the presence (1) or absence (0) of each interaction with Rtr1 in the iRefIndex (**irefindex**.org) database is indicated (iREF). High confidence interactions have a SAINT value of ≥ 0.75 and are shown in green boxes, moderate confidence interactions have a SAINT value of 0.45-0.75 shown in yellow boxes, and low confidence interactions have a SAINT value of 0.01-0.44 shown in red boxes.

**Table S5: GOStat analysis output of significant interactions in Rtr1-FLAG purifications.** The top 30 GO terms enriched in the Rtr1-FLAG dataset true interactions (SAINT ≥ 0.75). The GO term, significant gene IDs for proteins identified in the Rtr1 interactome belonging to each term, the number of IDs in the Rtr1 interactome for each term (count), total number of genes associated with each term (Total), and p-value are given in the table.

**Table S6: Output list from SAINT express analysis of the Rtr1-TAP affinity purifications compared to mock controls.** Table includes the SGD protein ID acronym, the fold-change A value (FC_A), the fold-change B value (FC_B), and the SAINT probability. In addition, the presence (1) or absence (0) of each interaction with Rtr1 in the iRefIndex (**irefindex**.org) database is indicated (iREF). High confidence interactions have a SAINT value of ≥ 0.75 and are shown in green boxes, moderate confidence interactions have a SAINT value of 0.45-0.75 shown in yellow boxes, and low confidence interactions have a SAINT value of 0.01-0.44 shown in red boxes.

**Table S7: Output list from SAINT express analysis of the combined Rtr1 affinity purifications compared to mock controls.** Table includes the SGD protein ID acronym, the fold-change A value (FC_A), the fold-change B value (FC_B), and the SAINT probability. In addition, the presence (1) or absence (0) of each interaction with Rtr1 in the iRefIndex (**irefindex**.org) database is indicated (iREF). High confidence interactions have a SAINT value of ≥ 0.75 and are shown in green boxes, moderate confidence interactions have a SAINT value of 0.45-0.75 shown in yellow boxes, and low confidence interactions have a SAINT value of 0.01-0.44 shown in red boxes.

**Table S8: Output list from SAINT express analysis of the Rtr1-WT and Rtr1-*ctk1Δ* affinity purifications compared to mock controls.** Table includes the SGD protein ID acronym, the fold-change A value (FC_A), the fold-change B value (FC_B), and the SAINT probability. In addition, the presence (1) or absence (0) of each interaction with Rtr1 in the iRefIndex (**irefindex**.org) database is indicated (iREF). High confidence interactions have a SAINT value of ≥ 0.75 and are shown in green boxes, moderate confidence interactions have a SAINT value of 0.45-0.75 shown in yellow boxes, and low confidence interactions have a SAINT value of 0.01-0.44 shown in red boxes.

**Table S9: Yeast strains used in this study.** The strain name, genotype, and source for each strain are provided.

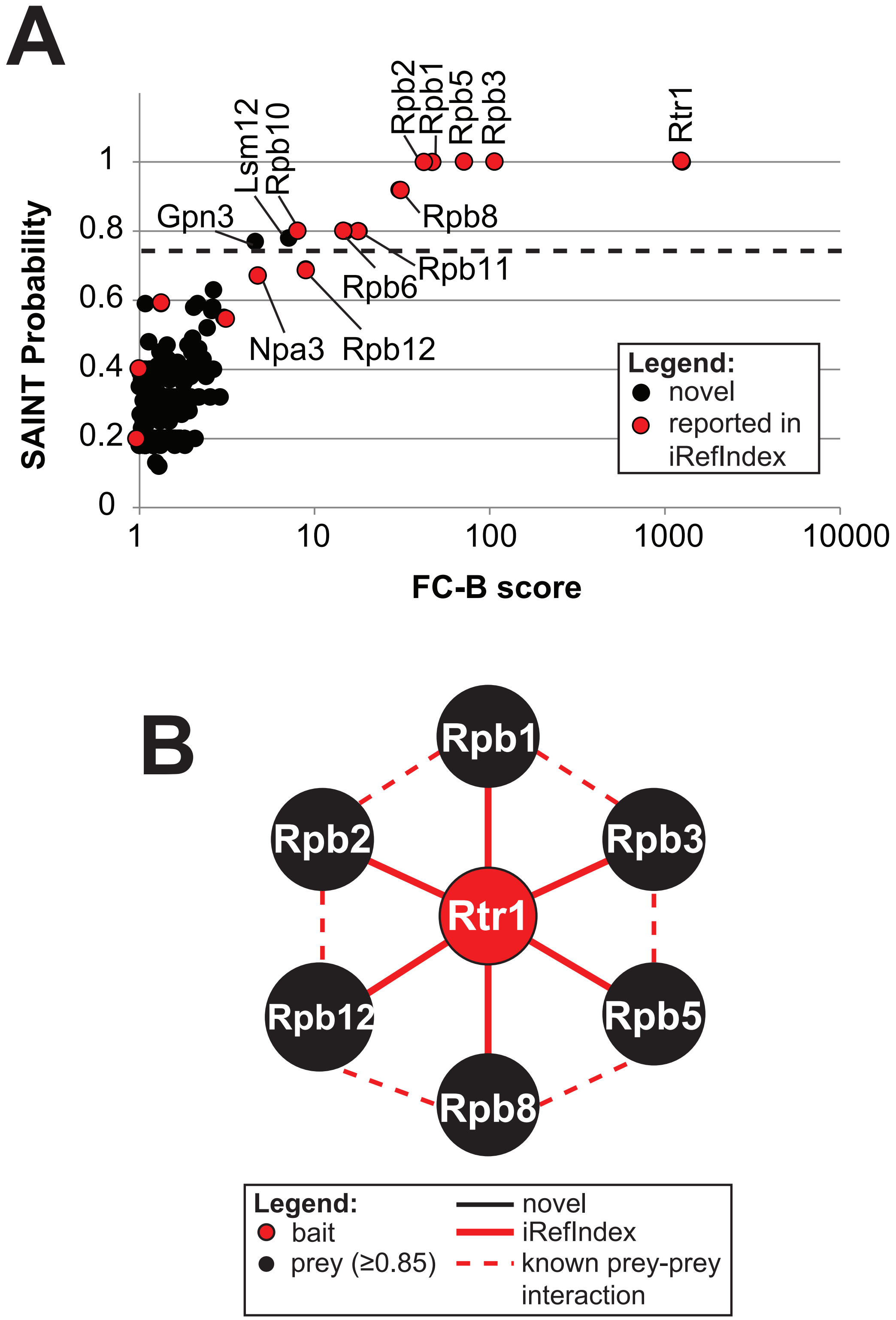
A
Rpb2
Rpb1
Rpb5
Rpb3
Rtr1
Lsm12
Rpb10
Gpn3
Rpb8
Rpb6
Rpb11
Npa3
Rpb12
1
0.8
0.6
0.4
0.2
0
SAINT Probability
1
10
100
1000
10000
FC-B score
Legend:
novel
reported in iRefIndex
B
Rpb1
Rpb2
Rpb3
Rtr1
Rpb12
Rpb5
Rpb8
Legend:
bait
prey (≥0.85)
novel
iRefIndex
known prey-prey interaction

Figure S1

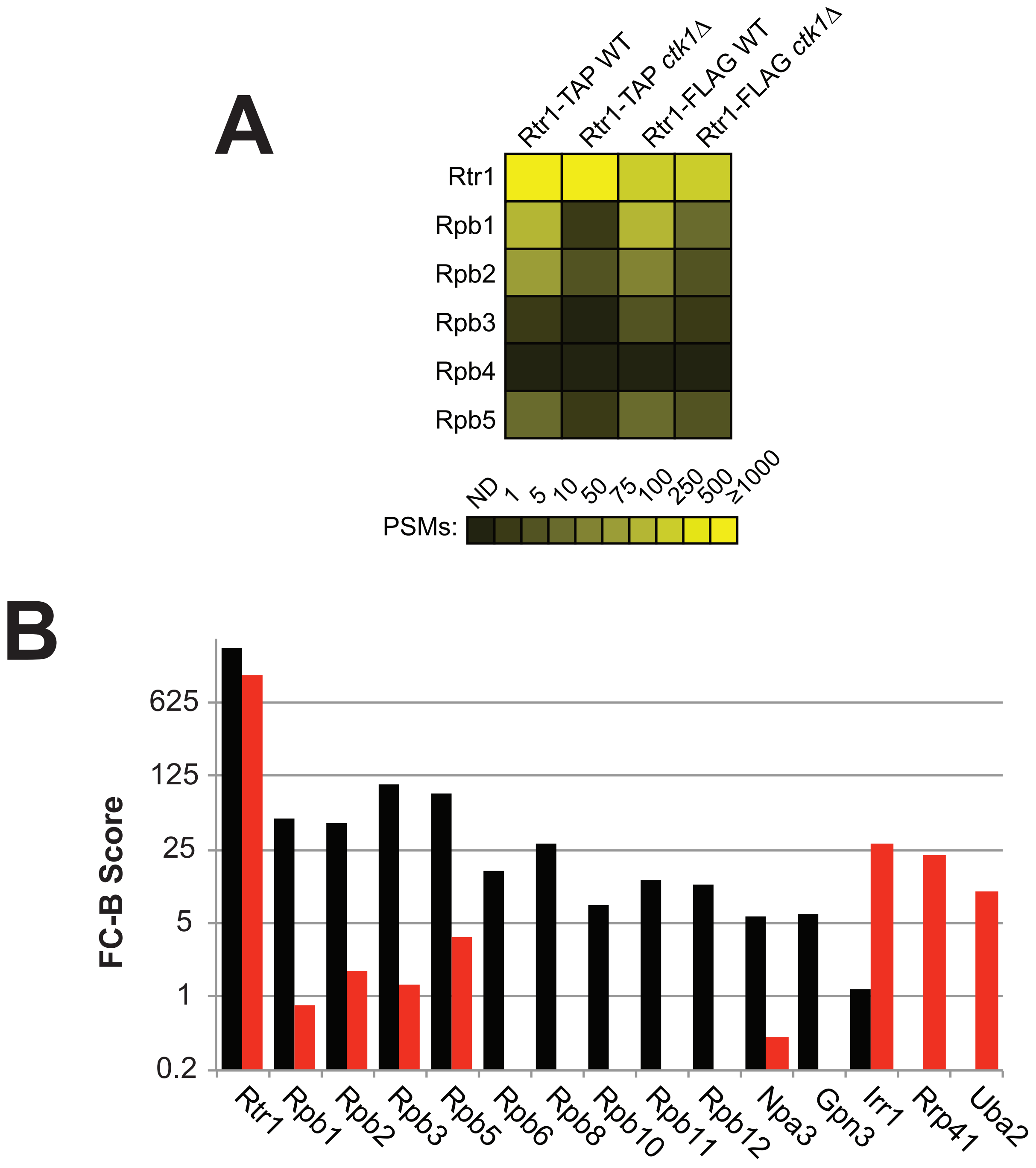
A
Rtr1-TAP WT
Rtr1-TAP *ctk1Δ*
Rtr1-FLAG WT
Rtr1-FLAG *ctk1Δ*
Rtr1
Rpb1
Rpb2
Rpb3
Rpb4
Rpb5
PSMs:
ND
1
5
10
50
75
100
250
500
≥1000
B
FC-B Score
625
125
25
5
1
0.2
Rtr1
Rpb1
Rpb2
Rpb3
Rpb5
Rpb6
Rpb8
Rpb10
Rpb11
Rpb12
Npa3
Gpn3
Irr1
Rrp41
Uba2

Figure S2

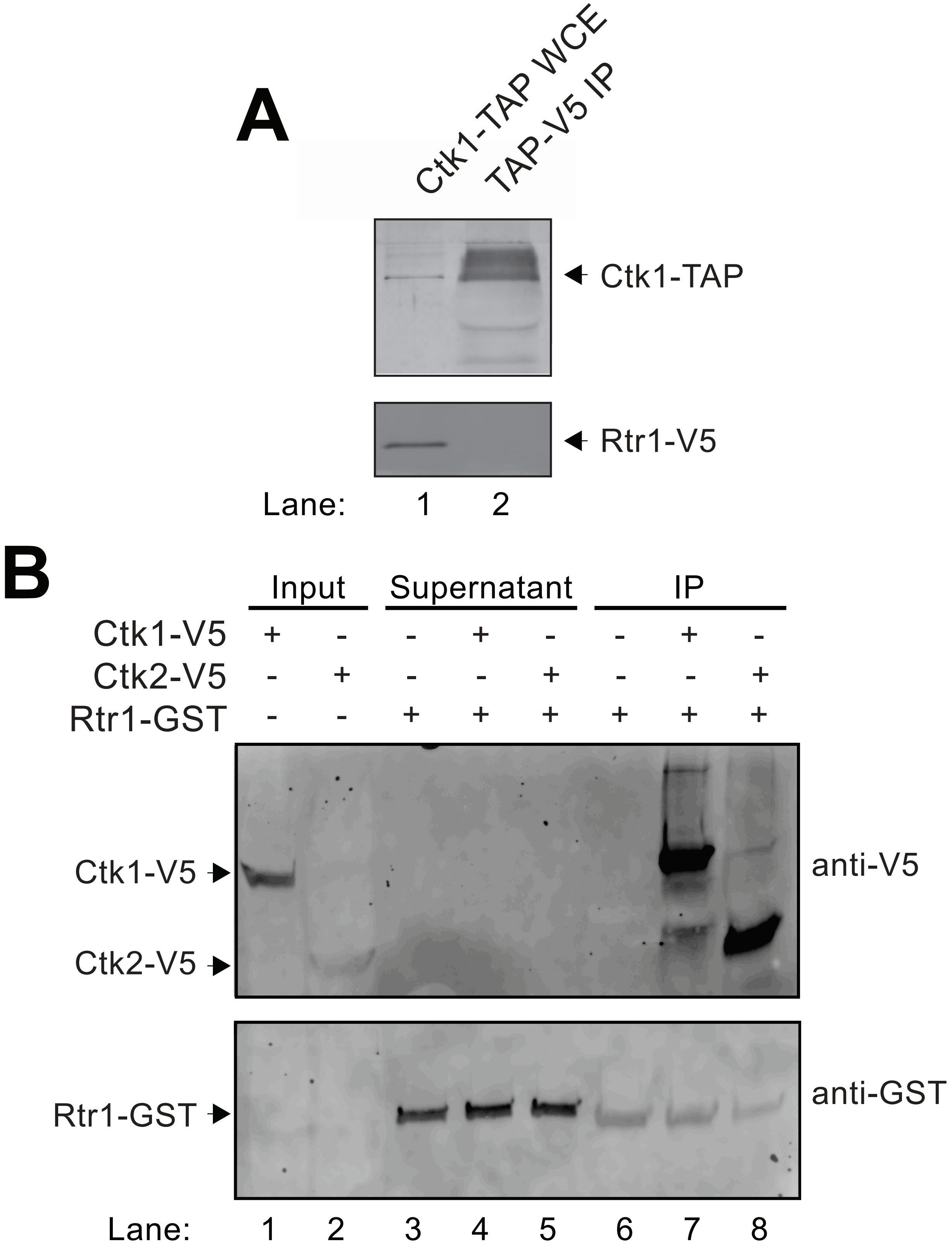
A
Ctk1-TAP WCE
TAP-V5 IP
Ctk1-TAP
Rtr1-V5
Lane: 1 2
B
Input
Supernatant
IP
Ctk1-V5 + - - + - - + -
Ctk2-V5 - + - - + - - +
Rtr1-GST - - + + + + + +
Ctk1-V5
Ctk2-V5
anti-V5
Rtr1-GST
anti-GST
Lane: 1 2 3 4 5 6 7 8

Figure S3

## Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 1

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| RTR1 | 261.08 | 144.72 | 1 | 1 |
| RPB3 | 30.32 | 20.62 | 1 | 1 |
| RPB2 | 20.09 | 11.19 | 1 | 1 |
| RPB8 | 13.54 | 10.08 | 1 | 1 |
| RPB1 | 20.38 | 9.66 | 1 | 1 |
| RPB12 | 13 | 6.27 | 1 | 1 |
| RPB5 | 9.37 | 4.34 | 0.99 | 1 |
| RPB11 | 7.19 | 4.16 | 0.99 | 1 |
| FAA4 | 2.75 | 1.51 | 0.98 | 0 |
| RPL33A | 3.89 | 1.34 | 0.98 | 0 |
| IDH2 | 6.51 | 2.55 | 0.95 | 0 |
| VTC4 | 4.83 | 2.24 | 0.94 | 0 |
| VMA8 | 3.98 | 1.65 | 0.93 | 0 |
| CYM1 | 2.82 | 2.05 | 0.91 | 0 |
| SIN4 | 1.75 | 1.58 | 0.9 | 0 |
| RVS167 | 3.06 | 1.36 | 0.88 | 0 |
| DHH1 | 2.01 | 1.02 | 0.87 | 0 |
| ECM29 | 1.87 | 1.13 | 0.86 | 0 |
| ENP1 | 5.1 | 2.24 | 0.85 | 0 |
| ENA1 | 2.35 | 1.15 | 0.85 | 0 |
| YPK1 | 2.14 | 1.05 | 0.81 | 0 |
| HEM14 | 1.76 | 1.33 | 0.8 | 0 |
| NPA3 | 5.57 | 2.05 | 0.79 | 1 |
| YLR413W | 3.58 | 1.44 | 0.7 | 0 |
| HSP26 | 5.24 | 2.12 | 0.69 | 0 |
| VAC8 | 2.11 | 1.32 | 0.69 | 0 |
| PHO84 | 79.33 | 11.08 | 0.67 | 0 |
| TAP42 | 12.11 | 3.13 | 0.67 | 0 |
| ERV25 | 6.45 | 2.7 | 0.67 | 0 |
| DIP5 | 5.42 | 2.33 | 0.67 | 0 |
| PHO81 | 2.56 | 2 | 0.67 | 0 |
| PUF4 | 2.23 | 1.81 | 0.67 | 0 |
| ARO9 | 3.16 | 1.71 | 0.67 | 0 |
| DRS2 | 2.75 | 1.58 | 0.67 | 0 |
| VPS5 | 2.19 | 1.45 | 0.67 | 0 |
| REX4 | 1.84 | 1.43 | 0.67 | 0 |
| CAR2 | 3.15 | 1.41 | 0.67 | 0 |
| VPS13 | 2.65 | 1.32 | 0.67 | 0 |
| TLG2 | 2.56 | 1.29 | 0.67 | 0 |
| RPL33B | 4.13 | 1.01 | 0.67 | 0 |
| TVP18 | 6.9 | 2.8 | 0.66 | 0 |
| HSP42 | 3.47 | 2.11 | 0.66 | 0 |
| AQR1 | 2.72 | 1.91 | 0.66 | 0 |
| AAD14 | 2.33 | 1.84 | 0.66 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| PEP12 | 3.07 | 1.82 | 0.66 | 0 |
| SYN8 | 2.96 | 1.81 | 0.66 | 0 |
| LSB3 | 3.76 | 1.76 | 0.66 | 0 |
| PPN1 | 1.94 | 1.63 | 0.66 | 0 |
| FOL2 | 6.63 | 1.54 | 0.66 | 0 |
| YPR097W | 1.78 | 1.54 | 0.66 | 0 |
| RPC19 | 2.49 | 1.48 | 0.66 | 0 |
| ECM32 | 1.83 | 1.55 | 0.65 | 0 |
| COG4 | 1.67 | 1.46 | 0.65 | 0 |
| TIF4631 | 1.8 | 1.06 | 0.65 | 0 |
| ERG26 | 1.76 | 1 | 0.65 | 0 |
| RLP7 | 4.42 | 1.64 | 0.64 | 0 |
| SSP1 | 3.57 | 1.56 | 0.64 | 0 |
| STH1 | 2.3 | 1.32 | 0.64 | 0 |
| FRD1 | 1.95 | 1.31 | 0.64 | 0 |
| YIP4 | 2.19 | 1.18 | 0.64 | 0 |
| KEX1 | 1.92 | 1.13 | 0.64 | 0 |
| VTC3 | 6.31 | 1.61 | 0.63 | 0 |
| GNP1 | 2.82 | 1.58 | 0.63 | 0 |
| YNR065C | 4.1 | 1.32 | 0.63 | 0 |
| ERG20 | 1.83 | 1.05 | 0.63 | 0 |
| NHX1 | 2.9 | 1.88 | 0.62 | 0 |
| SFL1 | 2.39 | 1.82 | 0.62 | 0 |
| DMA1 | 2.64 | 1.8 | 0.62 | 0 |
| PRP6 | 2.21 | 1.65 | 0.62 | 0 |
| GRX1 | 1.99 | 1.65 | 0.62 | 0 |
| TRA1 | 2.02 | 1.63 | 0.62 | 0 |
| YLR241W | 3.23 | 1.48 | 0.62 | 0 |
| LST8 | 1.77 | 1.48 | 0.62 | 0 |
| PRE2 | 1.68 | 1.47 | 0.62 | 0 |
| KRE9 | 1.64 | 1.45 | 0.62 | 0 |
| YBR238C | 1.56 | 1.4 | 0.62 | 0 |
| JNM1 | 1.9 | 1.23 | 0.62 | 0 |
| BBC1 | 2.79 | 1.2 | 0.62 | 0 |
| LEO1 | 6.5 | 2.52 | 0.61 | 0 |
| ERG5 | 2.19 | 1.57 | 0.61 | 0 |
| ARD1 | 2.4 | 1.55 | 0.61 | 0 |
| EAP1 | 2.18 | 1.54 | 0.61 | 0 |
| YLR422W | 1.73 | 1.51 | 0.61 | 0 |
| RCR1 | 1.71 | 1.45 | 0.61 | 0 |
| CDC24 | 2.03 | 1.42 | 0.61 | 0 |
| SRB8 | 1.53 | 1.38 | 0.61 | 0 |
| GEF1 | 1.53 | 1.38 | 0.61 | 0 |
| YDL073W | 1.55 | 1.37 | 0.61 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| RHB1 | 1.55 | 1.37 | 0.61 | 0 |
| CBK1 | 1.55 | 1.37 | 0.61 | 0 |
| SNX3 | 1.55 | 1.37 | 0.61 | 0 |
| SWI6 | 1.45 | 1.33 | 0.61 | 0 |
| MDM38 | 1.45 | 1.33 | 0.61 | 0 |
| YPR089W | 1.45 | 1.33 | 0.61 | 0 |
| SEC8 | 1.45 | 1.33 | 0.61 | 0 |
| TOR1 | 1.45 | 1.33 | 0.61 | 0 |
| LYS9 | 1.65 | 1.32 | 0.61 | 0 |
| UTR1 | 1.4 | 1.19 | 0.61 | 0 |
| PCM1 | 1.43 | 1.18 | 0.61 | 0 |
| AAP1 | 1.5 | 1.11 | 0.61 | 0 |
| HOC1 | 1.39 | 1.08 | 0.61 | 0 |
| CHS1 | 1.89 | 1.06 | 0.59 | 0 |
| FCY2 | 7.52 | 1.9 | 0.58 | 0 |
| HFA1 | 3.59 | 1.4 | 0.58 | 0 |
| PDS5 | 10.38 | 2.11 | 0.57 | 0 |
| GDE1 | 4.82 | 2.02 | 0.57 | 0 |
| ACS1 | 2.25 | 1.36 | 0.57 | 0 |
| CHS3 | 1.83 | 1.14 | 0.56 | 0 |
| EMC4 | 1.99 | 1.09 | 0.56 | 0 |
| NUS1 | 1.33 | 1.05 | 0.56 | 0 |
| CDC53 | 1.4 | 1 | 0.55 | 0 |
| ATG20 | 4.94 | 1.96 | 0.54 | 0 |
| DUG1 | 2.68 | 1.25 | 0.54 | 0 |
| SEH1 | 1.73 | 1.22 | 0.54 | 0 |
| OSH2 | 1.81 | 1.18 | 0.54 | 0 |
| IFA38 | 1.47 | 1.14 | 0.54 | 0 |
| BIM1 | 1.47 | 1.14 | 0.54 | 0 |
| SCY1 | 1.65 | 1.13 | 0.54 | 0 |
| TIF4632 | 1.57 | 1.13 | 0.54 | 0 |
| MRD1 | 1.47 | 1.09 | 0.54 | 0 |
| KCS1 | 1.45 | 1.06 | 0.54 | 0 |
| HOP | 1.31 | 1.05 | 0.54 | 0 |
| APE3 | 1.31 | 1.05 | 0.54 | 0 |
| CCZ1 | 4.28 | 1.57 | 0.52 | 0 |
| NVJ2 | 1.69 | 1.14 | 0.52 | 0 |
| STE20 | 8.17 | 2.02 | 0.51 | 0 |
| FUM1 | 2.91 | 1.31 | 0.51 | 0 |
| NUP82 | 2.6 | 1.16 | 0.51 | 0 |
| EMP70 | 2.59 | 1.1 | 0.51 | 0 |
| PHO8 | 2.05 | 1.08 | 0.49 | 0 |
| PNC1 | 6.13 | 1.28 | 0.45 | 0 |
| PMT2 | 4.93 | 1.24 | 0.45 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| DNF2 | 4.63 | 1.08 | 0.39 | 0 |
| CCT8 | 2.04 | 1.14 | 0.37 | 0 |
| PFK1 | 3 | 1.37 | 0.34 | 0 |
| SIT1 | 11.74 | 2.97 | 0.33 | 0 |
| FUI1 | 5.77 | 2.3 | 0.33 | 0 |
| PAF1 | 7.81 | 2.29 | 0.33 | 0 |
| FTR1 | 3.98 | 2 | 0.33 | 0 |
| CAB3 | 3.62 | 1.93 | 0.33 | 0 |
| YKL063C | 3.39 | 1.88 | 0.33 | 0 |
| NRT1 | 3.39 | 1.88 | 0.33 | 0 |
| THI7 | 3.39 | 1.88 | 0.33 | 0 |
| AEP2 | 3.3 | 1.86 | 0.33 | 0 |
| OPT1 | 3.09 | 1.81 | 0.33 | 0 |
| SNC1 | 6.45 | 1.76 | 0.33 | 0 |
| CTR9 | 6.23 | 1.67 | 0.33 | 0 |
| LYP1 | 3.59 | 1.67 | 0.33 | 0 |
| GCN3 | 2.53 | 1.66 | 0.33 | 0 |
| PIS1 | 2.92 | 1.58 | 0.33 | 0 |
| ERG28 | 2.92 | 1.58 | 0.33 | 0 |
| EMC1 | 2.92 | 1.58 | 0.33 | 0 |
| SCS7 | 2.84 | 1.56 | 0.33 | 0 |
| FLC1 | 2.19 | 1.56 | 0.33 | 0 |
| BAP2 | 2.19 | 1.56 | 0.33 | 0 |
| AUS1 | 2.19 | 1.56 | 0.33 | 0 |
| VHT1 | 2.19 | 1.56 | 0.33 | 0 |
| MCD4 | 2.19 | 1.56 | 0.33 | 0 |
| MUP1 | 2.19 | 1.56 | 0.33 | 0 |
| ATP25 | 2.09 | 1.53 | 0.33 | 0 |
| TRM8 | 3.98 | 1.48 | 0.33 | 0 |
| NOP16 | 1.92 | 1.47 | 0.33 | 0 |
| CPR4 | 1.89 | 1.46 | 0.33 | 0 |
| SUR1 | 1.89 | 1.46 | 0.33 | 0 |
| RPB6 | 1.89 | 1.46 | 0.33 | 1 |
| ERP2 | 1.89 | 1.46 | 0.33 | 0 |
| HSP30 | 1.89 | 1.46 | 0.33 | 0 |
| PMC1 | 1.89 | 1.46 | 0.33 | 0 |
| NUP192 | 1.89 | 1.46 | 0.33 | 0 |
| EFM1 | 1.89 | 1.46 | 0.33 | 0 |
| MNN10 | 1.89 | 1.46 | 0.33 | 0 |
| YIF1 | 1.87 | 1.45 | 0.33 | 0 |
| OST1 | 2.29 | 1.42 | 0.33 | 0 |
| BUD23 | 1.81 | 1.42 | 0.33 | 0 |
| CLA4 | 1.81 | 1.42 | 0.33 | 0 |
| BRE5 | 1.69 | 1.38 | 0.33 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| HRI1 | 1.69 | 1.38 | 0.33 | 0 |
| SEG1 | 1.69 | 1.38 | 0.33 | 0 |
| PRE10 | 1.69 | 1.38 | 0.33 | 0 |
| RFC4 | 1.69 | 1.38 | 0.33 | 0 |
| SEC16 | 2.08 | 1.36 | 0.33 | 0 |
| VPS53 | 1.65 | 1.36 | 0.33 | 0 |
| SBH1 | 1.65 | 1.36 | 0.33 | 0 |
| TYR1 | 1.65 | 1.36 | 0.33 | 0 |
| RCN1 | 1.65 | 1.36 | 0.33 | 0 |
| CPR8 | 2.02 | 1.34 | 0.33 | 0 |
| DSL1 | 1.6 | 1.34 | 0.33 | 0 |
| GLO1 | 1.6 | 1.34 | 0.33 | 0 |
| SPR28 | 1.6 | 1.34 | 0.33 | 0 |
| MTC4 | 1.6 | 1.34 | 0.33 | 0 |
| DAP2 | 1.6 | 1.34 | 0.33 | 0 |
| PNT1 | 1.6 | 1.34 | 0.33 | 0 |
| KTR6 | 1.6 | 1.34 | 0.33 | 0 |
| PUS1 | 2.71 | 1.33 | 0.33 | 0 |
| BUD27 | 1.58 | 1.33 | 0.33 | 0 |
| AIP1 | 1.58 | 1.33 | 0.33 | 0 |
| SSN3 | 1.58 | 1.33 | 0.33 | 0 |
| TSR1 | 1.58 | 1.33 | 0.33 | 0 |
| RRP46 | 1.58 | 1.33 | 0.33 | 0 |
| RPA43 | 6.17 | 1.28 | 0.33 | 0 |
| SDS22 | 1.46 | 1.28 | 0.33 | 0 |
| THO1 | 1.46 | 1.28 | 0.33 | 0 |
| CFT2 | 1.46 | 1.28 | 0.33 | 0 |
| YNL035C | 1.46 | 1.28 | 0.33 | 0 |
| SGD1 | 1.46 | 1.28 | 0.33 | 0 |
| FIG2 | 1.46 | 1.28 | 0.33 | 0 |
| ASR1 | 1.46 | 1.28 | 0.33 | 1 |
| ECM1 | 2.13 | 1.26 | 0.33 | 0 |
| AIM39 | 1.44 | 1.26 | 0.33 | 0 |
| TOP3 | 1.44 | 1.26 | 0.33 | 0 |
| MSN5 | 1.44 | 1.26 | 0.33 | 0 |
| OCA2 | 1.44 | 1.26 | 0.33 | 0 |
| APM4 | 1.44 | 1.26 | 0.33 | 0 |
| GFD2 | 1.44 | 1.26 | 0.33 | 0 |
| POP2 | 1.44 | 1.26 | 0.33 | 0 |
| FMP21 | 1.44 | 1.26 | 0.33 | 0 |
| YNL115C | 1.44 | 1.26 | 0.33 | 0 |
| RML2 | 1.44 | 1.26 | 0.33 | 0 |
| GYP8 | 1.44 | 1.26 | 0.33 | 0 |
| SPC110 | 1.44 | 1.26 | 0.33 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| CDC73 | 5.32 | 1.23 | 0.33 | 1 |
| HCA4 | 1.66 | 1.23 | 0.33 | 0 |
| CAR1 | 1.66 | 1.23 | 0.33 | 0 |
| YRA2 | 1.66 | 1.23 | 0.33 | 0 |
| MSS4 | 1.35 | 1.22 | 0.33 | 0 |
| PIN3 | 1.35 | 1.22 | 0.33 | 0 |
| VHS2 | 1.35 | 1.22 | 0.33 | 0 |
| POL30 | 1.35 | 1.22 | 0.33 | 0 |
| GRE3 | 1.35 | 1.22 | 0.33 | 0 |
| RTT102 | 1.35 | 1.22 | 0.33 | 0 |
| APM1 | 1.35 | 1.22 | 0.33 | 0 |
| APL3 | 1.35 | 1.22 | 0.33 | 0 |
| YGR169C_A | 1.35 | 1.22 | 0.33 | 0 |
| PBP2 | 1.35 | 1.22 | 0.33 | 0 |
| BOI2 | 1.35 | 1.22 | 0.33 | 0 |
| APN1 | 1.35 | 1.22 | 0.33 | 0 |
| RTC1 | 1.35 | 1.22 | 0.33 | 0 |
| PUS4 | 1.35 | 1.22 | 0.33 | 0 |
| TCO89 | 1.35 | 1.22 | 0.33 | 0 |
| TRM10 | 1.35 | 1.22 | 0.33 | 0 |
| MET22 | 1.35 | 1.22 | 0.33 | 0 |
| LCB5 | 1.35 | 1.22 | 0.33 | 0 |
| IES2 | 1.35 | 1.22 | 0.33 | 0 |
| SOL1 | 1.55 | 1.19 | 0.33 | 0 |
| CAF20 | 5.02 | 1.18 | 0.33 | 0 |
| NPR2 | 2.05 | 1.18 | 0.33 | 0 |
| SUR2 | 1.52 | 1.17 | 0.33 | 0 |
| ERV41 | 1.52 | 1.17 | 0.33 | 0 |
| YCR087C_A | 1.96 | 1.16 | 0.33 | 0 |
| NOP9 | 1.45 | 1.15 | 0.33 | 0 |
| APL5 | 1.45 | 1.15 | 0.33 | 0 |
| UME6 | 1.23 | 1.15 | 0.33 | 0 |
| COX17 | 1.23 | 1.15 | 0.33 | 0 |
| DPH2 | 1.23 | 1.15 | 0.33 | 0 |
| NPC2 | 1.23 | 1.15 | 0.33 | 0 |
| YPL245W | 1.23 | 1.15 | 0.33 | 0 |
| RPB7 | 1.23 | 1.15 | 0.33 | 1 |
| ECM16 | 1.23 | 1.15 | 0.33 | 0 |
| KIN82 | 1.23 | 1.15 | 0.33 | 0 |
| TMA7 | 1.23 | 1.15 | 0.33 | 0 |
| YCL012C | 1.23 | 1.15 | 0.33 | 0 |
| LDB19 | 1.23 | 1.15 | 0.33 | 0 |
| PEP3 | 1.23 | 1.15 | 0.33 | 0 |
| ASE1 | 1.23 | 1.15 | 0.33 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| RCM1 | 1.23 | 1.15 | 0.33 | 0 |
| CBP2 | 1.23 | 1.15 | 0.33 | 0 |
| YFR016C | 1.23 | 1.15 | 0.33 | 0 |
| FCY1 | 1.23 | 1.15 | 0.33 | 0 |
| HAP2 | 1.23 | 1.15 | 0.33 | 0 |
| FPK1 | 1.23 | 1.15 | 0.33 | 0 |
| TGL5 | 1.23 | 1.15 | 0.33 | 0 |
| YGR016W | 1.23 | 1.15 | 0.33 | 0 |
| DPP1 | 1.23 | 1.15 | 0.33 | 0 |
| COQ9 | 1.23 | 1.15 | 0.33 | 0 |
| AGP2 | 1.23 | 1.15 | 0.33 | 0 |
| QRI1 | 1.23 | 1.15 | 0.33 | 0 |
| YBR085C_A | 1.23 | 1.15 | 0.33 | 0 |
| SIP3 | 1.23 | 1.15 | 0.33 | 0 |
| NGL2 | 1.23 | 1.15 | 0.33 | 0 |
| PIH1 | 1.23 | 1.15 | 0.33 | 0 |
| RPN14 | 1.23 | 1.15 | 0.33 | 0 |
| DAT1 | 1.23 | 1.15 | 0.33 | 0 |
| VAM7 | 1.23 | 1.15 | 0.33 | 0 |
| TPT1 | 1.23 | 1.15 | 0.33 | 0 |
| TLG1 | 1.23 | 1.15 | 0.33 | 0 |
| SHG1 | 1.23 | 1.15 | 0.33 | 0 |
| APS3 | 1.23 | 1.15 | 0.33 | 0 |
| PIN2 | 1.23 | 1.15 | 0.33 | 0 |
| SER2 | 1.23 | 1.15 | 0.33 | 0 |
| SIS2 | 1.23 | 1.15 | 0.33 | 0 |
| ATO3 | 1.23 | 1.15 | 0.33 | 0 |
| GYP5 | 1.23 | 1.15 | 0.33 | 0 |
| MON1 | 1.23 | 1.15 | 0.33 | 0 |
| HOS3 | 1.23 | 1.15 | 0.33 | 0 |
| CAF16 | 1.23 | 1.15 | 0.33 | 0 |
| CTK1 | 1.23 | 1.15 | 0.33 | 1 |
| KAP120 | 1.23 | 1.15 | 0.33 | 0 |
| DEP1 | 1.23 | 1.15 | 0.33 | 1 |
| SEC6 | 1.23 | 1.15 | 0.33 | 0 |
| URM1 | 1.23 | 1.15 | 0.33 | 0 |
| IRC8 | 1.23 | 1.15 | 0.33 | 0 |
| SOK1 | 1.23 | 1.15 | 0.33 | 0 |
| KIN4 | 1.23 | 1.15 | 0.33 | 0 |
| SPT2 | 1.23 | 1.15 | 0.33 | 0 |
| CSR2 | 1.23 | 1.15 | 0.33 | 0 |
| YPR117W | 1.23 | 1.15 | 0.33 | 0 |
| OLE1 | 1.97 | 1.12 | 0.33 | 0 |
| CHO2 | 1.75 | 1.12 | 0.33 | 0 |

| V5/FLAG PROTEIN ID | RTR1 V5/FLAG FC_A | RTR1 V5/FLAG FC_B | V5/FLAG SAINT PROB | RTR1 V5/FLAG iREF |
|---|---|---|---|---|
| RUD3 | 1.77 | 1.11 | 0.33 | 0 |
| SOL2 | 1.34 | 1.1 | 0.33 | 0 |
| NMD5 | 1.34 | 1.1 | 0.33 | 0 |
| QNS1 | 1.34 | 1.1 | 0.33 | 0 |
| SLK19 | 1.34 | 1.1 | 0.33 | 0 |
| GUF1 | 1.32 | 1.09 | 0.33 | 0 |
| YDR056C | 1.32 | 1.09 | 0.33 | 0 |
| APE2 | 1.67 | 1.08 | 0.33 | 0 |
| BUL1 | 1.58 | 1.05 | 0.33 | 0 |
| APL2 | 1.58 | 1.05 | 0.33 | 0 |
| SLX9 | 1.24 | 1.05 | 0.33 | 0 |
| DCP2 | 1.24 | 1.05 | 0.33 | 0 |
| COG6 | 1.24 | 1.05 | 0.33 | 0 |
| GAL11 | 1.24 | 1.05 | 0.33 | 0 |
| APL6 | 1.83 | 1.04 | 0.33 | 0 |
| DLD3 | 1.82 | 1.04 | 0.33 | 0 |
| CDC27 | 1.56 | 1.04 | 0.33 | 0 |
| ALG9 | 1.56 | 1.04 | 0.33 | 0 |
| ERV46 | 2.12 | 1.03 | 0.33 | 0 |
| MTC5 | 2.22 | 1.02 | 0.33 | 0 |
| CLU1 | 4.58 | 1.01 | 0.33 | 0 |
| PDR5 | 9.05 | 1 | 0.33 | 0 |
| DMA2 | 1.97 | 1 | 0.33 | 0 |
| PSD1 | 1.68 | 1 | 0.33 | 0 |
| ITC1 | 1.13 | 1 | 0.33 | 0 |
| RLF2 | 1.13 | 1 | 0.33 | 0 |
| YHM2 | 1.41 | 1.03 | 0.32 | 0 |
| SNL1 | 1.36 | 1.02 | 0.3 | 0 |

Table S3: GOStat analysis output of significant interactions in single affinity purifications Page 1

| **Best GOs** (Max: 30) | **Genes** | **Count** 22 | **Total** 6476 | **p-Value** |
|---|---|---|---|---|
| GO:0005665 | rpb12 rpb1 rpb8 rpb5 rpb2 rpb11 rpb3 | 7 | 12 | 5.18E-13 |
| GO:0000428 | rpb12 rpb1 rpb8 rpb5 rpb2 rpb11 rpb3 | 7 | 31 | 4.14E-10 |
| GO:0055029 | rpb12 rpb1 rpb8 rpb5 rpb2 rpb11 rpb3 | 7 | 31 | 4.14E-10 |
| GO:0030880 | rpb12 rpb1 rpb8 rpb5 rpb2 rpb11 rpb3 | 7 | 31 | 4.14E-10 |
| GO:0003899 | rpb12 rpb1 rpb8 rpb5 rpb2 rpb11 rpb3 | 7 | 34 | 6.73E-10 |
| GO:0016591 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 72 | 2.70E-09 |
| GO:0016779 | rpb12 rpb1 rpb8 rpb5 rpb2 rpb11 rpb3 | 7 | 123 | 5.29E-06 |
| GO:0044451 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 313 | 0.00022 |
| GO:0005654 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 334 | 0.000317 |
| GO:0016772 | rpb12 rpb1 rpb5 rpb8 rpb2 rpb11 rpb3 ypk1 | 8 | 342 | 0.000337 |
| GO:0006366 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 346 | 0.000337 |
| GO:0005736 | rpb12 rpb8 rpb5 | 3 | 14 | 0.000369 |
| GO:0005666 | rpb12 rpb8 rpb5 | 3 | 17 | 0.000563 |
| GO:0032991 | rpb12 enp1 rpl33a rpb2 vtc4 vma8 sin4 rpb3 ecm29 idh2 rpb1 dhh1 rpb5 rpb8 rpb11 | 15 | 1705 | 0.000563 |
| GO:0043233 | rpb12 enp1 rpb2 sin4 rpb3 idh2 rpb1 rpb8 rpb5 rpb11 cym1 | 11 | 824 | 0.000563 |
| GO:0031974 | rpb12 enp1 rpb2 sin4 rpb3 idh2 rpb1 rpb8 rpb5 rpb11 cym1 | 11 | 824 | 0.000563 |
| GO:0043234 | rpb12 rpb2 vtc4 vma8 sin4 rpb3 ecm29 idh2 rpb1 dhh1 rpb5 rpb8 rpb11 | 13 | 1225 | 0.000727 |
| GO:0031981 | rpb12 enp1 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 9 | 611 | 0.00183 |
| GO:0006351 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 523 | 0.00362 |
| GO:0032774 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 525 | 0.00362 |
| GO:0006360 | rpb12 rpb8 rpb5 | 3 | 35 | 0.00362 |
| GO:0006383 | rpb12 rpb8 rpb5 | 3 | 38 | 0.00442 |

| **Best GOs** (Max: 30) | **Genes** | **Count** 22 | **Total** 6476 | **p-Value** |
|---|---|---|---|---|
| GO:0006350 | rpb12 rpb2 sin4 rpb3 rpb1 rpb8 rpb5 rpb11 | 8 | 568 | 0.00559 |
| GO:0016070 | rpb12 enp1 rpb2 sin4 rpb3 rpb1 dhh1 rpb8 rpb5 rpb11 | 10 | 1056 | 0.0191 |
| GO:0016740 | rpb12 rpb1 rpb5 rpb8 rpb2 rpb11 rpb3 ypk1 | 8 | 703 | 0.0216 |
| GO:0044452 | rpb12 enp1 rpb8 rpb5 | 4 | 182 | 0.0392 |
| GO:0044446 | rpb12 enp1 rpl33a rpb2 vtc4 vma8 sin4 rpb3 idh2 rpb1 rvs167 rpb5 rpb8 rpb11 cym1 | 15 | 2309 | 0.0392 |
| GO:0044422 | rpb12 enp1 rpl33a rpb2 vtc4 vma8 sin4 rpb3 idh2 rpb1 rvs167 rpb5 rpb8 rpb11 cym1 | 15 | 2309 | 0.0392 |
| GO:0004729 | hem14 | 1 | 1 | 0.0429 |
| GO:0010324 | rvs167 vtc4 ypk1 | 3 | 96 | 0.0483 |

## Table S4: FLAG affinity purification SAINT analysis PAGE 1

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| RTR1 | 260.61 | 155.33 | 1 | 1 |
| PHO84 | 118.6 | 52.33 | 1 | 0 |
| RPB3 | 28.16 | 22.56 | 1 | 1 |
| RPO21 | 25.76 | 13.53 | 1 | 1 |
| RPB8 | 12.94 | 11.63 | 1 | 1 |
| TAP42 | 17.95 | 10.68 | 1 | 0 |
| RPB2 | 17.62 | 10.13 | 1 | 1 |
| RPB5 | 12.86 | 8 | 1 | 1 |
| RPC10 | 13.69 | 6.5 | 1 | 1 |
| ERV25 | 9.25 | 5.83 | 1 | 0 |
| DIP5 | 7.78 | 5.3 | 1 | 0 |
| PFK26 | 6.53 | 2.87 | 1 | 0 |
| DRS2 | 3.75 | 2.72 | 1 | 0 |
| CAR2 | 4.45 | 2.65 | 1 | 0 |
| TLG2 | 3.53 | 2.25 | 1 | 0 |
| FOL2 | 9.8 | 4.12 | 0.99 | 0 |
| SYN8 | 4.01 | 3.13 | 0.99 | 0 |
| ARO9 | 4.33 | 2.92 | 0.99 | 0 |
| TVP18 | 9.85 | 5.52 | 0.98 | 0 |
| TRR1 | 3.71 | 3.1 | 0.98 | 0 |
| AQR1 | 3.58 | 3.04 | 0.98 | 0 |
| RPB11 | 2.76 | 2.76 | 0.98 | 1 |
| PPN1 | 2.41 | 2.38 | 0.98 | 0 |
| TAL1 | 2.75 | 1.37 | 0.98 | 0 |
| PEP12 | 4.19 | 3.25 | 0.97 | 0 |
| ECM32 | 2.24 | 2.17 | 0.97 | 0 |
| SRP1 | 3.04 | 1.94 | 0.92 | 0 |
| YIP4 | 2.95 | 1.83 | 0.9 | 0 |
| STE2 | 2.37 | 1.13 | 0.9 | 0 |
| NHX1 | 3.86 | 2.93 | 0.89 | 0 |
| CYM1 | 3.41 | 2.71 | 0.89 | 0 |
| GNP1 | 3.81 | 2.48 | 0.89 | 0 |
| GRX1 | 2.48 | 2.41 | 0.89 | 0 |
| KRE9 | 1.97 | 1.96 | 0.89 | 0 |
| FRD1 | 2.54 | 1.96 | 0.89 | 0 |
| RCR1 | 2.07 | 1.94 | 0.88 | 0 |
| SRB8 | 1.79 | 1.79 | 0.88 | 0 |
| SIN4 | 1.79 | 1.79 | 0.88 | 0 |
| GEF1 | 1.79 | 1.79 | 0.88 | 0 |
| ERG20 | 2.4 | 1.57 | 0.85 | 0 |
| OYE2 | 2.26 | 1.36 | 0.84 | 0 |
| YNR065C | 5.93 | 2.94 | 0.83 | 0 |
| FAA4 | 2.35 | 1.26 | 0.83 | 0 |

## Table S4: FLAG affinity purification SAINT analysis PAGE 2

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| LEO1 | 9.29 | 4.9 | 0.82 | 0 |
| DUG1 | 3.56 | 2.77 | 0.82 | 0 |
| ARD1 | 3.14 | 2.26 | 0.82 | 0 |
| YLR241W | 4.46 | 2.39 | 0.81 | 0 |
| BMS1 | 2.87 | 2.19 | 0.81 | 0 |
| FET4 | 5.71 | 2.05 | 0.81 | 0 |
| UTR1 | 1.65 | 1.48 | 0.8 | 0 |
| VTC4 | 5.72 | 2.47 | 0.79 | 0 |
| AAP1 | 1.84 | 1.44 | 0.79 | 0 |
| GDE1 | 6.81 | 3.67 | 0.76 | 0 |
| ENP1 | 6.84 | 3.39 | 0.76 | 0 |
| FCY2 | 10.92 | 3.63 | 0.75 | 0 |
| CHS1 | 2.49 | 1.5 | 0.73 | 0 |
| SKN1 | 2.12 | 1.21 | 0.73 | 0 |
| ATG20 | 7 | 3.55 | 0.72 | 0 |
| SEH1 | 2.18 | 1.69 | 0.72 | 0 |
| ECM29 | 1.99 | 1.21 | 0.72 | 0 |
| RFC3 | 1.68 | 1.08 | 0.72 | 0 |
| TSA2 | 3.95 | 2.12 | 0.71 | 0 |
| UTP22 | 2.04 | 1.39 | 0.7 | 0 |
| YLR413W | 4.85 | 2.05 | 0.69 | 0 |
| SCY1 | 2.07 | 1.48 | 0.69 | 0 |
| CHS3 | 2.34 | 1.54 | 0.68 | 0 |
| ENA1 | 2.34 | 1.36 | 0.68 | 0 |
| ALD6 | 2.51 | 1.32 | 0.68 | 0 |
| CCZ1 | 6.04 | 2.57 | 0.66 | 0 |
| HOP | 1.53 | 1.28 | 0.66 | 0 |
| APE3 | 1.53 | 1.28 | 0.66 | 0 |
| RPT6 | 2.06 | 1.13 | 0.66 | 0 |
| IDH1 | 2.03 | 1.06 | 0.66 | 0 |
| RVS167 | 3.74 | 1.54 | 0.65 | 0 |
| PHO90 | 1.87 | 1.24 | 0.65 | 0 |
| YDL124W | 1.87 | 1.42 | 0.64 | 0 |
| VTI1 | 1.96 | 1.09 | 0.64 | 0 |
| VTC3 | 8.99 | 2.59 | 0.62 | 0 |
| ENO2 | 3.14 | 1.83 | 0.62 | 0 |
| GDI1 | 1.94 | 1.16 | 0.62 | 0 |
| FUM1 | 4.07 | 2.29 | 0.6 | 0 |
| CHC1 | 2.88 | 1.66 | 0.59 | 0 |
| KRE6 | 2.68 | 1.26 | 0.59 | 0 |
| EMP70 | 3.6 | 1.73 | 0.58 | 0 |
| KRI1 | 1.86 | 1.2 | 0.57 | 0 |
| RFC2 | 1.59 | 1.17 | 0.57 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 3

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| MDN1 | 2.11 | 1.08 | 0.55 | 0 |
| VPS13 | 3.43 | 1.88 | 0.54 | 0 |
| KGD2 | 2.6 | 1.24 | 0.54 | 0 |
| LCD1 | 7.57 | 3.78 | 0.53 | 0 |
| HOR2 | 4.9 | 2.12 | 0.53 | 0 |
| YGL039W | 3.35 | 1.42 | 0.53 | 0 |
| MMF1 | 2.79 | 1.52 | 0.52 | 0 |
| TMA19 | 4.53 | 2.5 | 0.51 | 0 |
| NPA3 | 6.15 | 1.85 | 0.51 | 1 |
| APT1 | 1.81 | 1.17 | 0.51 | 0 |
| SIT1 | 17.11 | 5.76 | 0.5 | 0 |
| PAF1 | 11.26 | 4.04 | 0.5 | 0 |
| FUI1 | 8.16 | 3.91 | 0.5 | 0 |
| FBA1 | 4.85 | 3.24 | 0.5 | 0 |
| FTR1 | 5.47 | 3.15 | 0.5 | 0 |
| STE20 | 11.63 | 3.04 | 0.5 | 0 |
| PDS5 | 14.82 | 2.99 | 0.5 | 0 |
| SNC1 | 9.29 | 2.93 | 0.5 | 0 |
| YKL063C | 4.58 | 2.86 | 0.5 | 0 |
| NRT1 | 4.58 | 2.86 | 0.5 | 0 |
| THI7 | 4.58 | 2.86 | 0.5 | 0 |
| AEP2 | 4.45 | 2.81 | 0.5 | 0 |
| CTR9 | 8.96 | 2.76 | 0.5 | 0 |
| OPT1 | 4.13 | 2.7 | 0.5 | 0 |
| SMT3 | 7.52 | 2.53 | 0.5 | 0 |
| LYP1 | 4.94 | 2.52 | 0.5 | 0 |
| MEC1 | 5.22 | 2.37 | 0.5 | 0 |
| RFA3 | 7.13 | 2.31 | 0.5 | 0 |
| RPA49 | 7.16 | 2.27 | 0.5 | 0 |
| TRM8 | 5.57 | 2.24 | 0.5 | 0 |
| SCS7 | 3.8 | 2.24 | 0.5 | 0 |
| FLC1 | 2.79 | 2.14 | 0.5 | 0 |
| BAP2 | 2.79 | 2.14 | 0.5 | 0 |
| AUS1 | 2.79 | 2.14 | 0.5 | 0 |
| VHT1 | 2.79 | 2.14 | 0.5 | 0 |
| MCD4 | 2.79 | 2.14 | 0.5 | 0 |
| MUP1 | 2.79 | 2.14 | 0.5 | 0 |
| RPA43 | 8.97 | 2.12 | 0.5 | 0 |
| CDC73 | 7.71 | 2.01 | 0.5 | 1 |
| LSB3 | 4.63 | 1.97 | 0.5 | 0 |
| KSP1 | 7.72 | 1.95 | 0.5 | 0 |
| OST1 | 2.98 | 1.94 | 0.5 | 0 |
| NOP16 | 2.38 | 1.94 | 0.5 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 4

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| RPO26 | 2.34 | 1.92 | 0.5 | 1 |
| AAD14 | 2.34 | 1.92 | 0.5 | 0 |
| CPR4 | 2.34 | 1.92 | 0.5 | 0 |
| SUR1 | 2.34 | 1.92 | 0.5 | 0 |
| ERP2 | 2.34 | 1.92 | 0.5 | 0 |
| HSP30 | 2.34 | 1.92 | 0.5 | 0 |
| PDR5 | 13.31 | 1.92 | 0.5 | 0 |
| PMC1 | 2.34 | 1.92 | 0.5 | 0 |
| NUP192 | 2.34 | 1.92 | 0.5 | 0 |
| EFM1 | 2.34 | 1.92 | 0.5 | 0 |
| MNN10 | 2.34 | 1.92 | 0.5 | 0 |
| CAF20 | 7.26 | 1.89 | 0.5 | 0 |
| PUS1 | 3.66 | 1.86 | 0.5 | 0 |
| PFK1 | 3.52 | 1.86 | 0.5 | 0 |
| BUD23 | 2.21 | 1.85 | 0.5 | 0 |
| CLA4 | 2.21 | 1.85 | 0.5 | 0 |
| DBP9 | 2.21 | 1.85 | 0.5 | 0 |
| TRA1 | 2.21 | 1.85 | 0.5 | 0 |
| RKR1 | 7.9 | 1.83 | 0.5 | 0 |
| PNC1 | 8.65 | 1.83 | 0.5 | 0 |
| DNF2 | 6.68 | 1.82 | 0.5 | 0 |
| SEC16 | 2.66 | 1.82 | 0.5 | 0 |
| CPR8 | 2.56 | 1.78 | 0.5 | 0 |
| EAP1 | 2.51 | 1.76 | 0.5 | 0 |
| BRE5 | 2.04 | 1.75 | 0.5 | 0 |
| RCL1 | 2.04 | 1.75 | 0.5 | 0 |
| FPR3 | 5.12 | 1.75 | 0.5 | 0 |
| HRI1 | 2.04 | 1.75 | 0.5 | 0 |
| SEG1 | 2.04 | 1.75 | 0.5 | 0 |
| PRE10 | 2.04 | 1.75 | 0.5 | 0 |
| RFC4 | 2.04 | 1.75 | 0.5 | 0 |
| PHO81 | 2.04 | 1.75 | 0.5 | 0 |
| HXK2 | 2.55 | 1.73 | 0.5 | 0 |
| GND2 | 7.64 | 1.7 | 0.5 | 0 |
| RPL12B | 2.36 | 1.69 | 0.5 | 0 |
| UBA4 | 3.46 | 1.68 | 0.5 | 0 |
| ECM1 | 2.77 | 1.67 | 0.5 | 0 |
| BUD27 | 1.86 | 1.65 | 0.5 | 0 |
| AIP1 | 1.86 | 1.65 | 0.5 | 0 |
| PUF4 | 1.86 | 1.65 | 0.5 | 0 |
| TSR1 | 1.86 | 1.65 | 0.5 | 0 |
| DBP3 | 6.48 | 1.65 | 0.5 | 0 |
| SSN3 | 1.86 | 1.65 | 0.5 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 5

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| RRP46 | 1.86 | 1.65 | 0.5 | 0 |
| PFK2 | 3.9 | 1.64 | 0.5 | 0 |
| HMF1 | 2.19 | 1.62 | 0.5 | 0 |
| FKS1 | 9.45 | 1.57 | 0.5 | 0 |
| NPR2 | 2.66 | 1.55 | 0.5 | 0 |
| ASR1 | 1.69 | 1.54 | 0.5 | 1 |
| SSP1 | 4.16 | 1.54 | 0.5 | 0 |
| YLR179C | 1.69 | 1.54 | 0.5 | 0 |
| SDS22 | 1.69 | 1.54 | 0.5 | 0 |
| HCA4 | 2.03 | 1.54 | 0.5 | 0 |
| THO1 | 1.69 | 1.54 | 0.5 | 0 |
| ESF1 | 1.69 | 1.54 | 0.5 | 0 |
| PRE2 | 1.69 | 1.54 | 0.5 | 0 |
| CFT2 | 1.69 | 1.54 | 0.5 | 0 |
| YNL035C | 1.69 | 1.54 | 0.5 | 0 |
| SGD1 | 1.69 | 1.54 | 0.5 | 0 |
| FIG2 | 1.69 | 1.54 | 0.5 | 0 |
| UBI4 | 4.84 | 1.53 | 0.5 | 1 |
| CAR1 | 2.03 | 1.53 | 0.5 | 0 |
| YRA2 | 2.03 | 1.53 | 0.5 | 0 |
| RHR2 | 2.94 | 1.52 | 0.5 | 0 |
| RPS20 | 3.12 | 1.52 | 0.5 | 0 |
| YCR087C_A | 2.52 | 1.5 | 0.5 | 0 |
| PTR2 | 8.25 | 1.46 | 0.5 | 0 |
| SOL1 | 1.87 | 1.45 | 0.5 | 0 |
| MAK5 | 2.38 | 1.45 | 0.5 | 0 |
| CLU1 | 6.39 | 1.44 | 0.5 | 0 |
| MSS4 | 1.52 | 1.43 | 0.5 | 0 |
| VHS2 | 1.52 | 1.43 | 0.5 | 0 |
| POL30 | 1.52 | 1.43 | 0.5 | 0 |
| RTT102 | 1.52 | 1.43 | 0.5 | 0 |
| APM1 | 1.52 | 1.43 | 0.5 | 0 |
| APL3 | 1.52 | 1.43 | 0.5 | 0 |
| YGR169C_A | 1.52 | 1.43 | 0.5 | 0 |
| LCB5 | 1.52 | 1.43 | 0.5 | 0 |
| PBP2 | 1.52 | 1.43 | 0.5 | 0 |
| BOI2 | 1.52 | 1.43 | 0.5 | 0 |
| APN1 | 1.52 | 1.43 | 0.5 | 0 |
| RTC1 | 1.52 | 1.43 | 0.5 | 0 |
| PUS4 | 1.52 | 1.43 | 0.5 | 0 |
| TCO89 | 1.52 | 1.43 | 0.5 | 0 |
| TRM10 | 1.52 | 1.43 | 0.5 | 0 |
| PIN3 | 1.52 | 1.43 | 0.5 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 6

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| MET22 | 1.52 | 1.43 | 0.5 | 0 |
| GRE3 | 1.52 | 1.43 | 0.5 | 0 |
| YBR238C | 1.52 | 1.43 | 0.5 | 0 |
| IES2 | 1.52 | 1.43 | 0.5 | 0 |
| YPR097W | 1.52 | 1.43 | 0.5 | 0 |
| TSA1 | 2.54 | 1.4 | 0.5 | 0 |
| RUD3 | 2.24 | 1.4 | 0.5 | 0 |
| GND1 | 2.74 | 1.39 | 0.5 | 0 |
| APL5 | 1.72 | 1.38 | 0.5 | 0 |
| LYS9 | 1.72 | 1.38 | 0.5 | 0 |
| NOP9 | 1.71 | 1.37 | 0.5 | 0 |
| MTC5 | 2.98 | 1.36 | 0.5 | 0 |
| STE6 | 4.17 | 1.35 | 0.5 | 0 |
| RFA1 | 5.24 | 1.34 | 0.5 | 0 |
| APE2 | 2.1 | 1.34 | 0.5 | 0 |
| APL6 | 2.36 | 1.33 | 0.5 | 0 |
| DLD3 | 2.35 | 1.32 | 0.5 | 0 |
| BUL1 | 1.96 | 1.29 | 0.5 | 0 |
| APL2 | 1.96 | 1.29 | 0.5 | 0 |
| KRE2 | 3.89 | 1.29 | 0.5 | 0 |
| SOL2 | 1.55 | 1.28 | 0.5 | 0 |
| NMD5 | 1.55 | 1.28 | 0.5 | 0 |
| APL4 | 1.55 | 1.28 | 0.5 | 0 |
| QNS1 | 1.55 | 1.28 | 0.5 | 0 |
| SLK19 | 1.55 | 1.28 | 0.5 | 0 |
| CPS1 | 4.08 | 1.25 | 0.5 | 0 |
| CDC16 | 2.59 | 1.23 | 0.5 | 0 |
| GSC2 | 12.14 | 1.21 | 0.5 | 0 |
| ITR1 | 3.41 | 1.21 | 0.5 | 0 |
| RPC19 | 2.15 | 1.21 | 0.5 | 0 |
| DCP2 | 1.4 | 1.19 | 0.5 | 0 |
| JNM1 | 1.96 | 1.19 | 0.5 | 0 |
| CPR5 | 1.4 | 1.18 | 0.5 | 0 |
| SLX9 | 1.4 | 1.18 | 0.5 | 0 |
| REX4 | 1.4 | 1.18 | 0.5 | 0 |
| COG6 | 1.4 | 1.18 | 0.5 | 0 |
| GAL11 | 1.4 | 1.18 | 0.5 | 0 |
| STH1 | 2.29 | 1.17 | 0.5 | 0 |
| SKI3 | 1.67 | 1.16 | 0.5 | 0 |
| TIF4632 | 1.67 | 1.16 | 0.5 | 0 |
| SLA1 | 2.47 | 1.15 | 0.5 | 0 |
| MNN5 | 4.03 | 1.15 | 0.5 | 0 |
| YRA1 | 5.1 | 1.14 | 0.5 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 7

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| CHD1 | 1.82 | 1.13 | 0.5 | 0 |
| REX2 | 1.82 | 1.13 | 0.5 | 0 |
| BBC1 | 3.17 | 1.13 | 0.5 | 0 |
| SET2 | 2.14 | 1.12 | 0.5 | 1 |
| CHS5 | 2.14 | 1.12 | 0.5 | 0 |
| ADH3 | 6.26 | 1.11 | 0.5 | 0 |
| BUD20 | 1.84 | 1.1 | 0.5 | 0 |
| PRO2 | 1.96 | 1.1 | 0.5 | 0 |
| MET4 | 1.53 | 1.09 | 0.5 | 0 |
| COQ1 | 1.53 | 1.09 | 0.5 | 0 |
| VPS5 | 1.53 | 1.09 | 0.5 | 0 |
| MRD1 | 1.53 | 1.09 | 0.5 | 0 |
| STU1 | 1.53 | 1.09 | 0.5 | 0 |
| PEP1 | 2.52 | 1.08 | 0.5 | 0 |
| CDC19 | 2.05 | 1.06 | 0.5 | 0 |
| THI20 | 6.71 | 1.04 | 0.5 | 0 |
| GCD11 | 1.82 | 1.01 | 0.5 | 0 |
| OLE1 | 2.57 | 1.45 | 0.49 | 0 |
| SSA3 | 2.33 | 1.34 | 0.49 | 0 |
| TEF4 | 2.31 | 1.34 | 0.49 | 0 |
| DNF1 | 3.21 | 1.18 | 0.49 | 0 |
| ADH1 | 1.76 | 1.17 | 0.49 | 0 |
| KEL3 | 1.39 | 1.02 | 0.49 | 0 |
| GCN1 | 1.77 | 1.01 | 0.49 | 0 |
| GLO1 | 1.89 | 1.67 | 0.48 | 0 |
| SPR28 | 1.89 | 1.67 | 0.48 | 0 |
| DSL1 | 1.89 | 1.67 | 0.48 | 0 |
| MTC4 | 1.89 | 1.67 | 0.48 | 0 |
| DAP2 | 1.89 | 1.67 | 0.48 | 0 |
| PNT1 | 1.89 | 1.67 | 0.48 | 0 |
| KTR6 | 1.89 | 1.67 | 0.48 | 0 |
| HSP42 | 1.74 | 1.39 | 0.48 | 0 |
| RPB7 | 1.35 | 1.3 | 0.48 | 1 |
| CTK1 | 1.35 | 1.3 | 0.48 | 1 |
| DEP1 | 1.35 | 1.3 | 0.48 | 1 |
| UME6 | 1.35 | 1.3 | 0.48 | 0 |
| YMR027W | 1.35 | 1.3 | 0.48 | 0 |
| COX17 | 1.35 | 1.3 | 0.48 | 0 |
| DPH2 | 1.35 | 1.3 | 0.48 | 0 |
| NPC2 | 1.35 | 1.3 | 0.48 | 0 |
| YPL245W | 1.35 | 1.3 | 0.48 | 0 |
| KIN82 | 1.35 | 1.3 | 0.48 | 0 |
| TMA7 | 1.35 | 1.3 | 0.48 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 8

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| YCL012C | 1.35 | 1.3 | 0.48 | 0 |
| LDB19 | 1.35 | 1.3 | 0.48 | 0 |
| UBC4 | 1.35 | 1.3 | 0.48 | 0 |
| PEP3 | 1.35 | 1.3 | 0.48 | 0 |
| ASE1 | 1.35 | 1.3 | 0.48 | 0 |
| RCM1 | 1.35 | 1.3 | 0.48 | 0 |
| CBP2 | 1.35 | 1.3 | 0.48 | 0 |
| SWI6 | 1.35 | 1.3 | 0.48 | 0 |
| YFR016C | 1.35 | 1.3 | 0.48 | 0 |
| SPT2 | 1.35 | 1.3 | 0.48 | 0 |
| MDM38 | 1.35 | 1.3 | 0.48 | 0 |
| ECM16 | 1.35 | 1.3 | 0.48 | 0 |
| FCY1 | 1.35 | 1.3 | 0.48 | 0 |
| HAP2 | 1.35 | 1.3 | 0.48 | 0 |
| FPK1 | 1.35 | 1.3 | 0.48 | 0 |
| TGL5 | 1.35 | 1.3 | 0.48 | 0 |
| YGR016W | 1.35 | 1.3 | 0.48 | 0 |
| DPP1 | 1.35 | 1.3 | 0.48 | 0 |
| COQ9 | 1.35 | 1.3 | 0.48 | 0 |
| AGP2 | 1.35 | 1.3 | 0.48 | 0 |
| QRI1 | 1.35 | 1.3 | 0.48 | 0 |
| YBR085C_A | 1.35 | 1.3 | 0.48 | 0 |
| SIP3 | 1.35 | 1.3 | 0.48 | 0 |
| NGL2 | 1.35 | 1.3 | 0.48 | 0 |
| URM1 | 1.35 | 1.3 | 0.48 | 0 |
| PIH1 | 1.35 | 1.3 | 0.48 | 0 |
| RPN14 | 1.35 | 1.3 | 0.48 | 0 |
| DAT1 | 1.35 | 1.3 | 0.48 | 0 |
| VAM7 | 1.35 | 1.3 | 0.48 | 0 |
| TPT1 | 1.35 | 1.3 | 0.48 | 0 |
| YPR089W | 1.35 | 1.3 | 0.48 | 0 |
| TLG1 | 1.35 | 1.3 | 0.48 | 0 |
| URA1 | 1.35 | 1.3 | 0.48 | 0 |
| SHG1 | 1.35 | 1.3 | 0.48 | 0 |
| APS3 | 1.35 | 1.3 | 0.48 | 0 |
| PIN2 | 1.35 | 1.3 | 0.48 | 0 |
| COG4 | 1.35 | 1.3 | 0.48 | 0 |
| SER2 | 1.35 | 1.3 | 0.48 | 0 |
| SIS2 | 1.35 | 1.3 | 0.48 | 0 |
| ATO3 | 1.35 | 1.3 | 0.48 | 0 |
| GYP5 | 1.35 | 1.3 | 0.48 | 0 |
| MON1 | 1.35 | 1.3 | 0.48 | 0 |
| HOS3 | 1.35 | 1.3 | 0.48 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 9

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| CAF16 | 1.35 | 1.3 | 0.48 | 0 |
| ACB1 | 1.35 | 1.3 | 0.48 | 0 |
| KAP120 | 1.35 | 1.3 | 0.48 | 0 |
| SEC6 | 1.35 | 1.3 | 0.48 | 0 |
| SEC8 | 1.35 | 1.3 | 0.48 | 0 |
| IRC8 | 1.35 | 1.3 | 0.48 | 0 |
| SOK1 | 1.35 | 1.3 | 0.48 | 0 |
| KIN4 | 1.35 | 1.3 | 0.48 | 0 |
| CSR2 | 1.35 | 1.3 | 0.48 | 0 |
| YPR117W | 1.35 | 1.3 | 0.48 | 0 |
| TOR1 | 1.35 | 1.3 | 0.48 | 0 |
| PSD1 | 2.14 | 1.25 | 0.48 | 0 |
| VAC8 | 2.01 | 1.14 | 0.48 | 0 |
| TAN1 | 1.44 | 1.1 | 0.48 | 0 |
| GGA2 | 1.83 | 1.09 | 0.48 | 0 |
| CPR3 | 1.24 | 1.08 | 0.48 | 0 |
| ANB1 | 1.24 | 1.08 | 0.48 | 0 |
| AKL1 | 1.24 | 1.08 | 0.48 | 0 |
| CBP3 | 1.24 | 1.08 | 0.48 | 0 |
| ITC1 | 1.24 | 1.08 | 0.48 | 0 |
| RLF2 | 1.24 | 1.08 | 0.48 | 0 |
| KCC4 | 1.24 | 1.08 | 0.48 | 0 |
| IRC20 | 1.24 | 1.08 | 0.48 | 0 |
| PAP1 | 1.24 | 1.08 | 0.48 | 0 |
| GRH1 | 1.24 | 1.08 | 0.48 | 0 |
| APC1 | 1.24 | 1.08 | 0.48 | 0 |
| HIS1 | 1.24 | 1.08 | 0.48 | 0 |
| VRP1 | 1.24 | 1.08 | 0.48 | 0 |
| RIX7 | 1.24 | 1.08 | 0.48 | 0 |
| ARP4 | 1.24 | 1.08 | 0.48 | 0 |
| RGD1 | 1.24 | 1.08 | 0.48 | 0 |
| ALG5 | 1.24 | 1.08 | 0.48 | 0 |
| MNN1 | 2.12 | 1.05 | 0.48 | 0 |
| PMR1 | 1.52 | 1.04 | 0.48 | 0 |
| FUN26 | 1.21 | 1.04 | 0.48 | 0 |
| IMD2 | 1.52 | 1.01 | 0.48 | 0 |
| CDC27 | 1.92 | 1.27 | 0.47 | 0 |
| ALG9 | 1.92 | 1.27 | 0.47 | 0 |
| IMD4 | 1.86 | 1.1 | 0.47 | 0 |
| KAP95 | 1.66 | 1.1 | 0.47 | 0 |
| STV1 | 1.83 | 1.04 | 0.47 | 0 |
| BRE1 | 1.29 | 1.01 | 0.46 | 0 |
| TAT1 | 2.6 | 1.23 | 0.45 | 0 |

Table S4: FLAG affinity purification SAINT analysis PAGE 10

| RTR1 FLAG PROTEIN ID | RTR1 FLAG FC_A | RTR1 FLAG FC_B | RTR1 FLAG SAINT PROB | RTR1 FLAG iREF |
|---|---|---|---|---|
| MNN9 | 2.35 | 1.08 | 0.45 | 0 |
| ARO1 | 2.34 | 1.03 | 0.44 | 0 |
| SLC1 | 1.68 | 1 | 0.41 | 0 |
| SNL1 | 1.62 | 1.19 | 0.4 | 0 |
| ERG8 | 1.56 | 1.11 | 0.39 | 0 |

Table S5: GOStat analysis output of significant interactions in FLAG purifications

| **Best GOs** | **Genes** | **Count** 50 | **Total** 6476 | **P-Value (Max:0.01)** |
|---|---|---|---|---|
| GO:0005665 | rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3 | 7 | 12 | 4.72E-10 |
| GO:0000428 | rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3 | 7 | 31 | 3.14E-07 |
| GO:0055029 | rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3 | 7 | 31 | 3.14E-07 |
| GO:0030880 | rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3 | 7 | 31 | 3.14E-07 |
| GO:0016591 | rpc10 rpb2 leo1 sin4 rpb3 rpo21 rpb5 rpb8 rpb11 | 9 | 72 | 3.14E-07 |
| GO:0003899 | rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3 | 7 | 34 | 4.70E-07 |
| GO:0016740 | car2 utr1 rpc10 aro9 ard1 rpb2 rpb3 tal1 rpo21 erg20 pfk26 rpb8 rpb5 rpb11 grx1 | 15 | 703 | 0.00276 |
| GO:0016779 | rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3 | 7 | 123 | 0.00276 |
| GO:0044451 | rpc10 rpb2 leo1 sin4 rpb3 rpo21 srb8 rpb5 rpb8 rpb11 | 10 | 313 | 0.00709 |
| GO:0005736 | rpc10 rpb5 rpb8 | 3 | 14 | 0.00861 |
| GO:0005654 | rpc10 rpb2 leo1 sin4 rpb3 rpo21 srb8 rpb5 rpb8 rpb11 | 10 | 334 | 0.00993 |

# Table S6: Double affinity purification (TAP) SAINT analysis Page 1

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| RTR1 | 3057.23 | 1259.61 | 1 | 1 |
| RPB3 | 168.89 | 106.54 | 1 | 1 |
| RPB5 | 146.72 | 71.31 | 1 | 1 |
| RPO21 | 109.1 | 47.26 | 1 | 1 |
| RPB2 | 83.72 | 42 | 1 | 1 |
| RPB8 | 55.67 | 30.46 | 0.92 | 1 |
| RPB11 | 34.99 | 17.97 | 0.8 | 1 |
| RPO26 | 43.25 | 15.06 | 0.8 | 1 |
| RPB10 | 27.14 | 7.98 | 0.8 | 1 |
| LSM12 | 19.37 | 7.12 | 0.78 | 0 |
| GPN3 | 13.44 | 4.58 | 0.77 | 0 |
| RPC10 | 20.25 | 8.9 | 0.69 | 1 |
| NPA3 | 12.63 | 4.74 | 0.67 | 1 |
| PBP1 | 7.81 | 2.65 | 0.63 | 0 |
| RPB9 | 3.54 | 1.33 | 0.59 | 1 |
| TIF4632 | 3.84 | 2.15 | 0.59 | 0 |
| RHR2 | 5.65 | 1.08 | 0.59 | 0 |
| RPS29B | 4.45 | 2.62 | 0.58 | 0 |
| PSP2 | 9.14 | 2.04 | 0.58 | 0 |
| ATP22 | 5.61 | 2.59 | 0.57 | 0 |
| RPB4 | 12.84 | 3.04 | 0.55 | 1 |
| TRA1 | 3.79 | 2.44 | 0.52 | 0 |
| DBP3 | 6.51 | 2.01 | 0.49 | 0 |
| IRR1 | 2.43 | 1.13 | 0.48 | 0 |
| GAL11 | 3.61 | 1.89 | 0.47 | 0 |
| MYO1 | 4.15 | 1.44 | 0.47 | 0 |
| FPR4 | 7.41 | 2.18 | 0.46 | 0 |
| MAK5 | 3.43 | 1.99 | 0.45 | 0 |
| RFC3 | 2.77 | 1.31 | 0.45 | 0 |
| CHD1 | 5.48 | 2.31 | 0.43 | 0 |
| TIF4631 | 3.11 | 1.45 | 0.43 | 0 |
| LIP5 | 3.1 | 1.43 | 0.43 | 0 |
| CTR9 | 2.99 | 1.65 | 0.42 | 0 |
| VMA8 | 4.27 | 1.44 | 0.42 | 0 |
| FUN12 | 13.13 | 2.01 | 0.41 | 0 |
| PRP43 | 3.55 | 1.27 | 0.41 | 0 |
| CMK1 | 4.51 | 1.16 | 0.4 | 1 |
| DBP9 | 5.47 | 2.65 | 0.4 | 0 |
| APL5 | 4.7 | 2.18 | 0.4 | 0 |
| GRX1 | 2.8 | 1.98 | 0.4 | 0 |
| JIP5 | 2.76 | 1.92 | 0.4 | 0 |
| URB1 | 2.63 | 1.87 | 0.4 | 0 |
| UFD4 | 3.18 | 1.85 | 0.4 | 0 |

Table S6: Double affinity purification (TAP) SAINT analysis Page 2

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| ECM16 | 2.44 | 1.84 | 0.4 | 0 |
| BUD27 | 2.67 | 1.81 | 0.4 | 0 |
| ROK1 | 2.77 | 1.81 | 0.4 | 0 |
| RFC4 | 3.13 | 1.8 | 0.4 | 0 |
| GCN3 | 2.87 | 1.79 | 0.4 | 0 |
| SEC16 | 4.65 | 1.77 | 0.4 | 0 |
| NOP10 | 2.67 | 1.72 | 0.4 | 0 |
| ESF1 | 2.09 | 1.69 | 0.4 | 0 |
| RFC5 | 2.52 | 1.69 | 0.4 | 0 |
| KAP122 | 2.16 | 1.65 | 0.4 | 0 |
| MYO4 | 3.14 | 1.38 | 0.4 | 0 |
| RPA49 | 4.04 | 1.38 | 0.4 | 0 |
| YSC84 | 4.65 | 1.29 | 0.4 | 0 |
| NOP9 | 1.61 | 1.26 | 0.4 | 0 |
| RSM25 | 2.71 | 1.26 | 0.4 | 0 |
| NOC2 | 2.79 | 1.24 | 0.4 | 0 |
| SXM1 | 2.84 | 1.23 | 0.4 | 0 |
| DBP10 | 3.64 | 1.21 | 0.4 | 0 |
| UTP20 | 2.21 | 1.17 | 0.4 | 0 |
| MRD1 | 2.15 | 1.17 | 0.4 | 0 |
| SDA1 | 2.23 | 1.15 | 0.4 | 0 |
| LSB3 | 5.32 | 1.15 | 0.4 | 0 |
| DLD3 | 2.62 | 1.14 | 0.4 | 0 |
| SLA1 | 3.98 | 1.09 | 0.4 | 0 |
| NOP58 | 3.98 | 1.06 | 0.4 | 0 |
| SEC1 | 4.06 | 1.06 | 0.4 | 0 |
| APL6 | 1.76 | 1.04 | 0.4 | 0 |
| STE20 | 1.94 | 1.02 | 0.4 | 0 |
| ARO9 | 3.41 | 1.48 | 0.39 | 0 |
| NOP56 | 5.39 | 1.48 | 0.39 | 0 |
| SRP72 | 3.65 | 1.37 | 0.39 | 0 |
| CDC39 | 5.16 | 1.1 | 0.39 | 0 |
| ENP1 | 2.24 | 1.01 | 0.39 | 0 |
| BRE5 | 5.37 | 2.4 | 0.38 | 0 |
| IXR1 | 3.37 | 1.96 | 0.38 | 0 |
| TPT1 | 2.62 | 1.67 | 0.38 | 0 |
| CNA1 | 10.43 | 1.6 | 0.38 | 0 |
| SSF1 | 1.94 | 1.6 | 0.38 | 0 |
| YPK2 | 2.16 | 1.57 | 0.38 | 0 |
| APL3 | 2.16 | 1.57 | 0.38 | 0 |
| NUP60 | 5.02 | 1.56 | 0.38 | 0 |
| APS3 | 1.55 | 1.41 | 0.38 | 0 |
| ENP2 | 1.55 | 1.41 | 0.38 | 0 |

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| PPN1 | 1.5 | 1.38 | 0.38 | 0 |
| SRP21 | 1.5 | 1.38 | 0.38 | 0 |
| SHE2 | 1.5 | 1.38 | 0.38 | 0 |
| PPZ2 | 1.45 | 1.34 | 0.38 | 0 |
| PAF1 | 1.38 | 1.15 | 0.38 | 0 |
| SNU13 | 3.39 | 1.07 | 0.38 | 0 |
| TAE2 | 3.35 | 1.04 | 0.38 | 0 |
| HER1 | 4.74 | 1.84 | 0.37 | 0 |
| FPR3 | 8.33 | 1.49 | 0.37 | 0 |
| AAT1 | 1.4 | 1.3 | 0.37 | 0 |
| SWT1 | 1.4 | 1.3 | 0.37 | 0 |
| SSL1 | 1.4 | 1.3 | 0.37 | 0 |
| ARA1 | 1.4 | 1.3 | 0.37 | 0 |
| CDC53 | 1.94 | 1.21 | 0.37 | 0 |
| CKA2 | 1.8 | 1.03 | 0.37 | 0 |
| TAF12 | 6.19 | 1.79 | 0.36 | 0 |
| SRP14 | 2.06 | 1.22 | 0.36 | 0 |
| TAO3 | 1.29 | 1.08 | 0.36 | 0 |
| NOC3 | 2.02 | 1.09 | 0.35 | 0 |
| DBP6 | 1.62 | 1.08 | 0.35 | 0 |
| CAR2 | 1.93 | 1 | 0.35 | 0 |
| NOP7 | 3.04 | 1.28 | 0.33 | 0 |
| GBP2 | 3.39 | 1.11 | 0.33 | 0 |
| PHO81 | 6.54 | 2.89 | 0.32 | 0 |
| PIB2 | 4.71 | 2.54 | 0.32 | 0 |
| SNF6 | 3.64 | 2.19 | 0.32 | 0 |
| YBR139W | 3.43 | 1.96 | 0.32 | 0 |
| RTS1 | 5.32 | 1.94 | 0.32 | 0 |
| YPR097W | 2.69 | 1.94 | 0.32 | 0 |
| SEN1 | 2.52 | 1.86 | 0.32 | 0 |
| PRE10 | 3.49 | 1.75 | 0.32 | 0 |
| SEC8 | 3.33 | 1.73 | 0.32 | 0 |
| HRQ1 | 2.21 | 1.69 | 0.32 | 0 |
| SWP82 | 3.03 | 1.68 | 0.32 | 0 |
| PUP3 | 3.03 | 1.68 | 0.32 | 0 |
| PRI2 | 2.88 | 1.66 | 0.32 | 0 |
| YAT2 | 2.33 | 1.65 | 0.32 | 0 |
| SIN4 | 2.73 | 1.63 | 0.32 | 0 |
| CYC1 | 1.98 | 1.56 | 0.32 | 0 |
| APM1 | 2.27 | 1.55 | 0.32 | 0 |
| HEM1 | 1.96 | 1.47 | 0.32 | 0 |
| PUF4 | 1.81 | 1.43 | 0.32 | 0 |
| SWI6 | 1.81 | 1.43 | 0.32 | 0 |

Table S6: Double affinity purification (TAP) SAINT analysis Page 4

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| BEM4 | 1.81 | 1.43 | 0.32 | 0 |
| YAP1802 | 1.81 | 1.43 | 0.32 | 0 |
| URB2 | 1.64 | 1.43 | 0.32 | 0 |
| YPR089W | 1.81 | 1.43 | 0.32 | 0 |
| NOC4 | 1.81 | 1.43 | 0.32 | 0 |
| YGR016W | 1.54 | 1.39 | 0.32 | 0 |
| HSP26 | 2.91 | 1.39 | 0.32 | 0 |
| UPF3 | 1.66 | 1.38 | 0.32 | 0 |
| ARP7 | 1.66 | 1.38 | 0.32 | 0 |
| KIP2 | 1.66 | 1.38 | 0.32 | 0 |
| HSH155 | 1.51 | 1.33 | 0.32 | 0 |
| NOP8 | 1.35 | 1.28 | 0.32 | 0 |
| IFM1 | 1.35 | 1.28 | 0.32 | 0 |
| URM1 | 1.35 | 1.28 | 0.32 | 0 |
| IRC21 | 1.3 | 1.25 | 0.32 | 0 |
| SSF2 | 1.48 | 1.08 | 0.32 | 0 |
| RSC6 | 1.58 | 1.05 | 0.31 | 0 |
| MRM1 | 4.81 | 1.9 | 0.3 | 0 |
| RSF2 | 2.24 | 1.7 | 0.3 | 0 |
| DAS2 | 2.24 | 1.7 | 0.3 | 0 |
| AIM46 | 1.6 | 1.44 | 0.3 | 0 |
| ELP4 | 1.6 | 1.44 | 0.3 | 0 |
| ISA1 | 1.64 | 1.38 | 0.3 | 0 |
| SSK1 | 1.35 | 1.26 | 0.3 | 0 |
| SSU72 | 1.35 | 1.26 | 0.3 | 0 |
| YTA7 | 1.35 | 1.26 | 0.3 | 0 |
| CFD1 | 1.35 | 1.26 | 0.3 | 0 |
| SPT20 | 1.35 | 1.26 | 0.3 | 0 |
| RGR1 | 1.35 | 1.26 | 0.3 | 0 |
| RAD53 | 1.35 | 1.26 | 0.3 | 0 |
| GYL1 | 1.35 | 1.26 | 0.3 | 0 |
| YML8 | 1.25 | 1.21 | 0.3 | 0 |
| SLM1 | 1.68 | 1.11 | 0.3 | 0 |
| TIM13 | 8.33 | 1.89 | 0.29 | 0 |
| ISW2 | 3.74 | 1.92 | 0.28 | 0 |
| SDS24 | 3.77 | 1.51 | 0.28 | 0 |
| NOP1 | 7.65 | 1.5 | 0.28 | 0 |
| APP1 | 2.19 | 1.49 | 0.28 | 0 |
| HSP42 | 2.72 | 1.47 | 0.28 | 0 |
| YRA2 | 2 | 1.38 | 0.28 | 0 |
| PAP1 | 2.36 | 1.33 | 0.28 | 0 |
| APL4 | 2.08 | 1.28 | 0.28 | 0 |
| PRP28 | 1.67 | 1.19 | 0.28 | 0 |

Table S6: Double affinity purification (TAP) SAINT analysis Page 5

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| HCA4 | 1.47 | 1.18 | 0.28 | 0 |
| AKL1 | 1.52 | 1.15 | 0.28 | 0 |
| RIX7 | 1.38 | 1.1 | 0.28 | 0 |
| ARD1 | 1.29 | 1.1 | 0.28 | 0 |
| FAD1 | 3.19 | 1.74 | 0.27 | 0 |
| UTP25 | 2.93 | 1.6 | 0.27 | 0 |
| RRP8 | 1.25 | 1.05 | 0.27 | 0 |
| PRP2 | 1.24 | 1.04 | 0.27 | 0 |
| CDC25 | 1.24 | 1.04 | 0.27 | 0 |
| NUP84 | 1.24 | 1.04 | 0.27 | 0 |
| CDC24 | 1.15 | 1.01 | 0.27 | 0 |
| OSH2 | 4.57 | 1.48 | 0.25 | 0 |
| KEL3 | 2.31 | 1.31 | 0.25 | 0 |
| UBP13 | 2.36 | 1.1 | 0.25 | 0 |
| GIP3 | 2.11 | 1.07 | 0.25 | 0 |
| GEA1 | 1.99 | 1.05 | 0.25 | 0 |
| FMC1 | 1.92 | 1.09 | 0.24 | 0 |
| GCR2 | 1.56 | 1.05 | 0.24 | 0 |
| ALB1 | 2.09 | 1.07 | 0.23 | 0 |
| RFC2 | 1.73 | 1.03 | 0.23 | 0 |
| ASR1 | 4.72 | 1.81 | 0.2 | 1 |
| RPB7 | 2.76 | 1.58 | 0.2 | 1 |
| BIK1 | 1.91 | 1.41 | 0.2 | 1 |
| CYM1 | 8.52 | 2.08 | 0.2 | 0 |
| CDC9 | 4.66 | 1.81 | 0.2 | 0 |
| NGL3 | 3.79 | 1.72 | 0.2 | 0 |
| GPI15 | 3.79 | 1.72 | 0.2 | 0 |
| STE5 | 3.74 | 1.71 | 0.2 | 0 |
| STU2 | 3.44 | 1.68 | 0.2 | 0 |
| EXO70 | 3.29 | 1.66 | 0.2 | 0 |
| SRO7 | 3.29 | 1.66 | 0.2 | 0 |
| SUA5 | 3.13 | 1.63 | 0.2 | 0 |
| RTT102 | 2.83 | 1.59 | 0.2 | 0 |
| BUD6 | 2.83 | 1.59 | 0.2 | 0 |
| DMC1 | 2.76 | 1.58 | 0.2 | 0 |
| MPE1 | 2.52 | 1.54 | 0.2 | 0 |
| HTA1 | 3.36 | 1.54 | 0.2 | 0 |
| BOI2 | 2.37 | 1.51 | 0.2 | 0 |
| KAP104 | 2.37 | 1.51 | 0.2 | 0 |
| SKN7 | 2.22 | 1.48 | 0.2 | 0 |
| SHE4 | 2.22 | 1.48 | 0.2 | 0 |
| TAF4 | 2.22 | 1.48 | 0.2 | 0 |
| MZM1 | 2.18 | 1.47 | 0.2 | 0 |

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| TSR1 | 2.17 | 1.47 | 0.2 | 0 |
| SIR3 | 2.07 | 1.45 | 0.2 | 0 |
| COG4 | 2.07 | 1.45 | 0.2 | 0 |
| SDS23 | 1.91 | 1.41 | 0.2 | 0 |
| ATG1 | 1.91 | 1.41 | 0.2 | 0 |
| SWI4 | 1.91 | 1.41 | 0.2 | 0 |
| YDR248C | 1.91 | 1.41 | 0.2 | 0 |
| SFP1 | 1.91 | 1.41 | 0.2 | 0 |
| CYK3 | 1.91 | 1.41 | 0.2 | 0 |
| CLA4 | 1.91 | 1.41 | 0.2 | 0 |
| MUK1 | 1.91 | 1.41 | 0.2 | 0 |
| CAF40 | 1.91 | 1.41 | 0.2 | 0 |
| SOK1 | 1.91 | 1.41 | 0.2 | 0 |
| YMR130W | 1.91 | 1.41 | 0.2 | 0 |
| LRG1 | 1.91 | 1.41 | 0.2 | 0 |
| YLR407W | 1.89 | 1.4 | 0.2 | 0 |
| UME6 | 1.76 | 1.37 | 0.2 | 0 |
| PCF11 | 1.76 | 1.37 | 0.2 | 0 |
| ENT4 | 1.76 | 1.37 | 0.2 | 0 |
| MAG1 | 1.76 | 1.37 | 0.2 | 0 |
| CLF1 | 1.76 | 1.37 | 0.2 | 0 |
| ATG26 | 1.76 | 1.37 | 0.2 | 0 |
| RCN1 | 1.76 | 1.37 | 0.2 | 0 |
| PRP18 | 1.76 | 1.37 | 0.2 | 0 |
| YAP1801 | 1.76 | 1.37 | 0.2 | 0 |
| SOD2 | 1.76 | 1.37 | 0.2 | 0 |
| PBP2 | 1.76 | 1.37 | 0.2 | 0 |
| PTP3 | 1.76 | 1.37 | 0.2 | 0 |
| PET54 | 1.76 | 1.37 | 0.2 | 0 |
| ORC5 | 1.76 | 1.37 | 0.2 | 0 |
| COG6 | 2.88 | 1.36 | 0.2 | 0 |
| BEM3 | 2.74 | 1.34 | 0.2 | 0 |
| MOB2 | 1.61 | 1.32 | 0.2 | 0 |
| MOB1 | 1.61 | 1.32 | 0.2 | 0 |
| YMR124W | 1.61 | 1.32 | 0.2 | 0 |
| ECM14 | 1.61 | 1.32 | 0.2 | 0 |
| MSO1 | 1.61 | 1.32 | 0.2 | 0 |
| BEM1 | 1.61 | 1.32 | 0.2 | 0 |
| PSK2 | 1.61 | 1.32 | 0.2 | 0 |
| WHI5 | 1.61 | 1.32 | 0.2 | 0 |
| SCD5 | 1.61 | 1.32 | 0.2 | 0 |
| RPA14 | 1.61 | 1.32 | 0.2 | 0 |
| CLP1 | 1.61 | 1.32 | 0.2 | 0 |

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| EFM1 | 1.61 | 1.32 | 0.2 | 0 |
| SNX3 | 1.61 | 1.32 | 0.2 | 0 |
| LDB19 | 1.61 | 1.32 | 0.2 | 0 |
| AIM17 | 1.61 | 1.32 | 0.2 | 0 |
| ORC4 | 1.61 | 1.32 | 0.2 | 0 |
| MED8 | 2.47 | 1.3 | 0.2 | 0 |
| NMD5 | 2.32 | 1.28 | 0.2 | 0 |
| SWA2 | 2.32 | 1.28 | 0.2 | 0 |
| PRP6 | 1.46 | 1.27 | 0.2 | 0 |
| SMD1 | 1.46 | 1.27 | 0.2 | 0 |
| MED1 | 1.46 | 1.27 | 0.2 | 0 |
| YNL193W | 1.46 | 1.27 | 0.2 | 0 |
| MTF2 | 1.46 | 1.27 | 0.2 | 0 |
| YLR419W | 1.46 | 1.27 | 0.2 | 0 |
| YPL014W | 1.46 | 1.27 | 0.2 | 0 |
| GCN2 | 1.46 | 1.27 | 0.2 | 0 |
| YNL165W | 1.46 | 1.27 | 0.2 | 0 |
| PRP45 | 1.46 | 1.27 | 0.2 | 0 |
| PRE2 | 1.46 | 1.27 | 0.2 | 0 |
| COG2 | 1.46 | 1.27 | 0.2 | 0 |
| CDD1 | 1.46 | 1.27 | 0.2 | 0 |
| BUD7 | 1.46 | 1.27 | 0.2 | 0 |
| GYP6 | 1.46 | 1.27 | 0.2 | 0 |
| RSE1 | 1.46 | 1.27 | 0.2 | 0 |
| YGL082W | 1.46 | 1.27 | 0.2 | 0 |
| SEC5 | 1.46 | 1.27 | 0.2 | 0 |
| RRP46 | 1.46 | 1.27 | 0.2 | 0 |
| CTT1 | 1.44 | 1.26 | 0.2 | 0 |
| LEO1 | 1.9 | 1.21 | 0.2 | 0 |
| YIL002W-A | 1.29 | 1.2 | 0.2 | 0 |
| TMA10 | 1.29 | 1.2 | 0.2 | 0 |
| BRE1 | 3.05 | 1.2 | 0.2 | 0 |
| NPC2 | 1.29 | 1.2 | 0.2 | 0 |
| RRP17 | 1.29 | 1.2 | 0.2 | 0 |
| NMD2 | 1.29 | 1.2 | 0.2 | 0 |
| SWI1 | 3.7 | 1.19 | 0.2 | 0 |
| ECM32 | 1.24 | 1.17 | 0.2 | 0 |
| SEC10 | 1.76 | 1.17 | 0.2 | 0 |
| YHR127W | 1.24 | 1.17 | 0.2 | 0 |
| KIP3 | 1.24 | 1.17 | 0.2 | 0 |
| GLO1 | 1.2 | 1.15 | 0.2 | 0 |
| SRB8 | 1.2 | 1.15 | 0.2 | 0 |
| YLR422W | 1.2 | 1.15 | 0.2 | 0 |

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| MSN4 | 1.62 | 1.14 | 0.2 | 0 |
| GRX4 | 1.62 | 1.14 | 0.2 | 0 |
| RGD1 | 1.62 | 1.14 | 0.2 | 0 |
| SMY2 | 2.41 | 1.13 | 0.2 | 0 |
| IOC2 | 1.15 | 1.12 | 0.2 | 0 |
| ASE1 | 1.15 | 1.12 | 0.2 | 0 |
| PET100 | 1.15 | 1.12 | 0.2 | 0 |
| MTR10 | 1.15 | 1.12 | 0.2 | 0 |
| LAP2 | 1.15 | 1.12 | 0.2 | 0 |
| YBR053C | 1.15 | 1.12 | 0.2 | 0 |
| SEC61 | 1.15 | 1.12 | 0.2 | 0 |
| MET32 | 1.15 | 1.12 | 0.2 | 0 |
| RAD9 | 1.15 | 1.12 | 0.2 | 0 |
| SGD1 | 1.15 | 1.12 | 0.2 | 0 |
| NHP2 | 1.46 | 1.1 | 0.2 | 0 |
| VPS5 | 2.7 | 1.1 | 0.2 | 0 |
| RSC9 | 2.45 | 1.07 | 0.2 | 0 |
| PRP16 | 1.34 | 1.06 | 0.2 | 0 |
| EKI1 | 1.45 | 1.06 | 0.2 | 0 |
| RSC30 | 1.34 | 1.05 | 0.2 | 0 |
| PTA1 | 1.34 | 1.05 | 0.2 | 0 |
| BIM1 | 1.89 | 1.05 | 0.2 | 0 |
| PSR1 | 1.76 | 1.03 | 0.2 | 0 |
| CPR8 | 1.23 | 1.01 | 0.2 | 0 |
| PRE8 | 2.8 | 1.01 | 0.2 | 0 |
| CTR86 | 1.95 | 1 | 0.2 | 0 |
| UBX4 | 1.95 | 1 | 0.2 | 0 |
| CMP2 | 4.16 | 1.07 | 0.19 | 0 |
| UGA3 | 4.76 | 1.82 | 0.18 | 0 |
| PCL7 | 2.86 | 1.59 | 0.18 | 0 |
| MDM38 | 1.59 | 1.32 | 0.18 | 0 |
| HYM1 | 1.3 | 1.2 | 0.18 | 0 |
| SPB4 | 1.3 | 1.2 | 0.18 | 0 |
| BUD4 | 1.3 | 1.2 | 0.18 | 0 |
| STE12 | 1.3 | 1.2 | 0.18 | 0 |
| MRE11 | 1.3 | 1.2 | 0.18 | 0 |
| DPH1 | 1.3 | 1.2 | 0.18 | 0 |
| MED7 | 1.3 | 1.2 | 0.18 | 0 |
| SAP1 | 1.3 | 1.2 | 0.18 | 0 |
| SSN2 | 1.3 | 1.2 | 0.18 | 0 |
| YIL151C | 1.3 | 1.2 | 0.18 | 0 |
| NUF2 | 1.3 | 1.2 | 0.18 | 0 |
| ATG2 | 1.3 | 1.2 | 0.18 | 0 |

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| MAF1 | 1.3 | 1.2 | 0.18 | 0 |
| YPL245W | 1.3 | 1.2 | 0.18 | 0 |
| ARF3 | 1.3 | 1.2 | 0.18 | 0 |
| BYE1 | 1.3 | 1.2 | 0.18 | 0 |
| RTT107 | 1.3 | 1.2 | 0.18 | 0 |
| MSN2 | 1.3 | 1.2 | 0.18 | 0 |
| MAD3 | 1.3 | 1.2 | 0.18 | 0 |
| HAL5 | 1.3 | 1.2 | 0.18 | 0 |
| YMR111C | 1.3 | 1.2 | 0.18 | 0 |
| RKM3 | 1.3 | 1.2 | 0.18 | 0 |
| VPS9 | 1.3 | 1.2 | 0.18 | 0 |
| RET1 | 1.3 | 1.2 | 0.18 | 0 |
| POP2 | 1.3 | 1.2 | 0.18 | 0 |
| PIH1 | 1.3 | 1.2 | 0.18 | 0 |
| MON2 | 1.3 | 1.2 | 0.18 | 0 |
| ELP6 | 1.3 | 1.2 | 0.18 | 0 |
| SEC15 | 1.3 | 1.2 | 0.18 | 0 |
| YKR078W | 1.3 | 1.2 | 0.18 | 0 |
| SIS2 | 1.3 | 1.2 | 0.18 | 0 |
| AVL9 | 1.3 | 1.2 | 0.18 | 0 |
| INN1 | 1.3 | 1.2 | 0.18 | 0 |
| YMR1 | 1.3 | 1.2 | 0.18 | 0 |
| YBP2 | 1.3 | 1.2 | 0.18 | 0 |
| MTQ2 | 1.3 | 1.2 | 0.18 | 0 |
| PRR1 | 1.3 | 1.2 | 0.18 | 0 |
| IES3 | 1.3 | 1.2 | 0.18 | 0 |
| APT2 | 1.3 | 1.2 | 0.18 | 0 |
| ART10 | 1.3 | 1.2 | 0.18 | 0 |
| SRL2 | 1.3 | 1.2 | 0.18 | 0 |
| YMR144W | 1.3 | 1.2 | 0.18 | 0 |
| CIN8 | 1.3 | 1.2 | 0.18 | 0 |
| YLR118C | 1.3 | 1.2 | 0.18 | 0 |
| BIO2 | 1.3 | 1.2 | 0.18 | 0 |
| ORC2 | 1.3 | 1.2 | 0.18 | 0 |
| ORC3 | 1.3 | 1.2 | 0.18 | 0 |
| FLO11 | 1.3 | 1.2 | 0.18 | 0 |
| ZIP2 | 1.46 | 1.09 | 0.18 | 0 |
| IOC4 | 1.1 | 1.08 | 0.18 | 0 |
| AIM34 | 1.1 | 1.08 | 0.18 | 0 |
| BUD21 | 1.1 | 1.08 | 0.18 | 0 |
| BUD14 | 1.1 | 1.08 | 0.18 | 0 |
| ERG25 | 1.1 | 1.08 | 0.18 | 0 |
| MSN5 | 1.1 | 1.08 | 0.18 | 0 |

Table S6: Double affinity purification (TAP) SAINT analysis Page 10

| RTR1 TAP PROTEIN ID | RTR1 TAP FC_A | RTR1 TAP FC_B | RTR1 TAP SAINT PROB | RTR1 TAP iREF |
|---|---|---|---|---|
| RPL39 | 1.1 | 1.08 | 0.18 | 0 |
| CHK1 | 1.1 | 1.08 | 0.18 | 0 |
| YIR024C | 1.1 | 1.08 | 0.18 | 0 |
| RGC1 | 1.1 | 1.08 | 0.18 | 0 |
| YCR015C | 1.1 | 1.08 | 0.18 | 0 |
| FPK1 | 1.1 | 1.08 | 0.18 | 0 |
| TGL1 | 1.1 | 1.08 | 0.18 | 0 |
| RHB1 | 1.1 | 1.08 | 0.18 | 0 |
| PGM2 | 1.1 | 1.08 | 0.18 | 0 |
| PMD1 | 1.1 | 1.08 | 0.18 | 0 |
| YJL133C-A | 1.1 | 1.08 | 0.18 | 0 |
| HXT9 | 1.1 | 1.08 | 0.18 | 0 |
| APN2 | 1.1 | 1.08 | 0.18 | 0 |
| YKL151C | 1.1 | 1.08 | 0.18 | 0 |
| FRT2 | 1.1 | 1.08 | 0.18 | 0 |
| PCD1 | 1.1 | 1.08 | 0.18 | 0 |
| DNL4 | 1.1 | 1.08 | 0.18 | 0 |
| MPS2 | 1.1 | 1.08 | 0.18 | 0 |
| GLE2 | 2.53 | 1.08 | 0.18 | 0 |
| FOL1 | 1.83 | 1.05 | 0.18 | 0 |
| PSY2 | 1.2 | 1 | 0.18 | 0 |
| GRH1 | 1.2 | 1 | 0.18 | 0 |
| SIR4 | 1.2 | 1 | 0.18 | 0 |
| SPT15 | 1.2 | 1 | 0.18 | 0 |
| DST1 | 2.88 | 1.24 | 0.13 | 0 |
| SGN1 | 4.05 | 1.29 | 0.12 | 0 |

## Table S7: Full Rtr1 interactome SAINT analysis Page 1

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| RTR1 | 2258.92 | 694.61 | 1 | 1 |
| RPB3 | 110.35 | 54.8 | 1 | 1 |
| RPB1 | 76.57 | 24.87 | 1 | 1 |
| RPB2 | 59.94 | 24.73 | 1 | 1 |
| RPB12 | 19.39 | 9.3 | 0.89 | 1 |
| RPB5 | 102 | 24.86 | 0.85 | 1 |
| RPB8 | 39.58 | 19.93 | 0.84 | 1 |
| NPA3 | 10.93 | 3.76 | 0.57 | 1 |
| RPB11 | 17.97 | 8.51 | 0.5 | 1 |
| TIF4631 | 2.47 | 1.16 | 0.48 | 0 |
| HSP26 | 3.83 | 1.55 | 0.46 | 0 |
| VPS5 | 2.75 | 1.35 | 0.41 | 0 |
| CAR2 | 2.21 | 1.01 | 0.41 | 0 |
| TIF4632 | 2.55 | 1.46 | 0.4 | 0 |
| DBP3 | 4.68 | 1.46 | 0.39 | 0 |
| ARO9 | 2.18 | 1.24 | 0.39 | 0 |
| PHO81 | 5.62 | 3.01 | 0.38 | 0 |
| RPB10 | 17.44 | 2.31 | 0.37 | 1 |
| IDH2 | 4.84 | 1.14 | 0.37 | 0 |
| RPC19 | 1.88 | 1.12 | 0.37 | 0 |
| VMA8 | 4.47 | 1.58 | 0.36 | 0 |
| GPN3 | 9.76 | 2.49 | 0.35 | 0 |
| RPB6 | 29.99 | 5.86 | 0.34 | 1 |
| MAK5 | 2.44 | 1.38 | 0.33 | 0 |
| NUP60 | 3.97 | 1.36 | 0.33 | 0 |
| CHD1 | 3.58 | 1.38 | 0.32 | 0 |
| RSM25 | 2.41 | 1.26 | 0.32 | 0 |
| DRS2 | 1.78 | 1.03 | 0.32 | 0 |
| GAL11 | 2.94 | 1.6 | 0.3 | 0 |
| LSB3 | 5.04 | 1.3 | 0.3 | 0 |
| PHO84 | 34.45 | 2.2 | 0.29 | 0 |
| LEO1 | 4.01 | 1.8 | 0.29 | 0 |
| PUF4 | 2.07 | 1.69 | 0.29 | 0 |
| TAF12 | 4.83 | 1.55 | 0.29 | 0 |
| PBP1 | 5.73 | 1.34 | 0.29 | 0 |
| ENP1 | 3.41 | 1.33 | 0.29 | 0 |
| VPS13 | 3.64 | 1.25 | 0.29 | 0 |
| RVS167 | 5.25 | 1.21 | 0.29 | 0 |
| RPA49 | 4.28 | 1.2 | 0.29 | 0 |
| CDC53 | 1.82 | 1.15 | 0.29 | 0 |
| RLP7 | 2.93 | 1.13 | 0.29 | 0 |
| LSM12 | 14.1 | 4.01 | 0.28 | 0 |
| SEC16 | 3.92 | 1.59 | 0.28 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 2

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| ERV25 | 3.25 | 1.29 | 0.28 | 0 |
| STE20 | 4.57 | 1.28 | 0.28 | 0 |
| LIP5 | 2.55 | 1.21 | 0.28 | 0 |
| DLD3 | 2.39 | 1.05 | 0.28 | 0 |
| FPR3 | 3.48 | 1 | 0.28 | 0 |
| GGA2 | 2.18 | 1 | 0.28 | 0 |
| APL2 | 1.59 | 1 | 0.28 | 0 |
| PSP2 | 7.03 | 1.6 | 0.27 | 0 |
| MRD1 | 1.9 | 1.1 | 0.27 | 0 |
| SYN8 | 1.75 | 1.08 | 0.27 | 0 |
| GRX1 | 2.08 | 1.64 | 0.26 | 0 |
| EAP1 | 2.27 | 1.62 | 0.26 | 0 |
| APL5 | 2.75 | 1.39 | 0.26 | 0 |
| NOP9 | 1.45 | 1.13 | 0.26 | 0 |
| TRR1 | 1.67 | 1.09 | 0.26 | 0 |
| PEP12 | 1.78 | 1.04 | 0.26 | 0 |
| BMS1 | 1.56 | 1.02 | 0.26 | 0 |
| HFA1 | 2.47 | 1 | 0.26 | 0 |
| HSP42 | 2.11 | 1.39 | 0.25 | 0 |
| BRE5 | 4.42 | 2.2 | 0.24 | 0 |
| DBP9 | 3.52 | 1.77 | 0.24 | 0 |
| GCN3 | 2.85 | 1.76 | 0.24 | 0 |
| PRE10 | 3.04 | 1.7 | 0.24 | 0 |
| NMD5 | 2.1 | 1.28 | 0.24 | 0 |
| MYO1 | 3.22 | 1.14 | 0.24 | 0 |
| REX4 | 1.31 | 1.07 | 0.24 | 0 |
| KGD2 | 4.94 | 1.02 | 0.24 | 0 |
| YPR097W | 2.54 | 2 | 0.23 | 0 |
| OSH2 | 3.92 | 1.51 | 0.23 | 0 |
| PRE2 | 1.62 | 1.44 | 0.23 | 0 |
| APL4 | 1.9 | 1.24 | 0.23 | 0 |
| BIM1 | 1.86 | 1.16 | 0.23 | 0 |
| ATP22 | 4.24 | 1.81 | 0.22 | 0 |
| RFC4 | 2.71 | 1.65 | 0.22 | 0 |
| CLA4 | 2 | 1.52 | 0.22 | 0 |
| COG4 | 2.05 | 1.58 | 0.21 | 0 |
| ISW2 | 2.98 | 1.57 | 0.21 | 0 |
| EFM1 | 1.82 | 1.47 | 0.21 | 0 |
| PPN1 | 1.62 | 1.46 | 0.21 | 0 |
| CTR9 | 3.95 | 1.42 | 0.21 | 0 |
| SLM1 | 1.48 | 1 | 0.21 | 0 |
| BUD27 | 2.23 | 1.55 | 0.2 | 0 |
| RCN1 | 1.82 | 1.46 | 0.2 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 3

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| GDE1 | 2.83 | 1.34 | 0.2 | 0 |
| COG6 | 2.46 | 1.3 | 0.2 | 0 |
| ALB1 | 1.88 | 1.04 | 0.2 | 0 |
| SIN4 | 2.52 | 1.75 | 0.19 | 0 |
| RTT102 | 2.45 | 1.54 | 0.19 | 0 |
| APM1 | 2.02 | 1.46 | 0.19 | 0 |
| SNX3 | 1.67 | 1.44 | 0.19 | 0 |
| PBP2 | 1.69 | 1.39 | 0.19 | 0 |
| RRP46 | 1.57 | 1.37 | 0.19 | 0 |
| HEM14 | 1.33 | 1.03 | 0.19 | 0 |
| HTL1 | 1.48 | 1.01 | 0.19 | 0 |
| CYM1 | 7.15 | 2.41 | 0.18 | 0 |
| ESF1 | 1.52 | 1.34 | 0.18 | 0 |
| BRE1 | 2.55 | 1.14 | 0.18 | 0 |
| YCR087C_A | 1.85 | 1.07 | 0.18 | 0 |
| RSC9 | 2.1 | 1.03 | 0.18 | 0 |
| GRH1 | 1.21 | 1.02 | 0.18 | 0 |
| ASR1 | 3.86 | 1.73 | 0.17 | 1 |
| TVP18 | 3.53 | 1.63 | 0.17 | 0 |
| IXR1 | 2.69 | 1.61 | 0.17 | 0 |
| PRP6 | 1.84 | 1.52 | 0.17 | 0 |
| BOI2 | 2.13 | 1.49 | 0.17 | 0 |
| TPT1 | 2.19 | 1.47 | 0.17 | 0 |
| YRA2 | 1.85 | 1.27 | 0.17 | 0 |
| PAP1 | 2.01 | 1.22 | 0.17 | 0 |
| ARD1 | 1.66 | 1.2 | 0.17 | 0 |
| ERG5 | 1.47 | 1.12 | 0.17 | 0 |
| GIP3 | 1.87 | 1.02 | 0.17 | 0 |
| PIB2 | 3.65 | 1.95 | 0.16 | 0 |
| RPS29B | 3.16 | 1.74 | 0.16 | 0 |
| YBR139W | 2.73 | 1.62 | 0.16 | 0 |
| DMA1 | 1.81 | 1.45 | 0.16 | 0 |
| APL3 | 1.91 | 1.44 | 0.16 | 0 |
| YDR248C | 1.8 | 1.43 | 0.16 | 0 |
| ATG20 | 2.85 | 1.27 | 0.16 | 0 |
| AKL1 | 1.5 | 1.17 | 0.16 | 0 |
| SMY2 | 2.13 | 1.15 | 0.16 | 0 |
| CDC24 | 1.49 | 1.15 | 0.16 | 0 |
| RGD1 | 1.51 | 1.12 | 0.16 | 0 |
| HCA4 | 1.34 | 1.08 | 0.16 | 0 |
| RIX7 | 1.31 | 1.06 | 0.16 | 0 |
| LYS9 | 1.23 | 1.03 | 0.16 | 0 |
| THI7 | 3.37 | 1.89 | 0.15 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 4

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| SWI6 | 1.74 | 1.45 | 0.15 | 0 |
| NOP16 | 1.61 | 1.38 | 0.15 | 0 |
| RPB4 | 8.12 | 1.37 | 0.15 | 1 |
| HER1 | 3.6 | 1.36 | 0.15 | 0 |
| AAD14 | 1.57 | 1.36 | 0.15 | 0 |
| SHE2 | 1.39 | 1.3 | 0.15 | 0 |
| APP1 | 1.83 | 1.26 | 0.15 | 0 |
| DUG1 | 1.68 | 1.17 | 0.15 | 0 |
| SRP72 | 2.73 | 1.04 | 0.15 | 0 |
| ACS1 | 1.54 | 1.02 | 0.15 | 0 |
| MYO4 | 2.22 | 1.01 | 0.15 | 0 |
| GNP1 | 1.69 | 1.01 | 0.15 | 0 |
| SNF6 | 2.89 | 1.75 | 0.14 | 0 |
| SEC8 | 2.82 | 1.66 | 0.14 | 0 |
| PAF1 | 4.08 | 1.49 | 0.14 | 0 |
| SHE4 | 2 | 1.45 | 0.14 | 0 |
| YPR089W | 1.74 | 1.45 | 0.14 | 0 |
| UME6 | 1.64 | 1.35 | 0.14 | 0 |
| WHI5 | 1.53 | 1.31 | 0.14 | 0 |
| COG2 | 1.45 | 1.3 | 0.14 | 0 |
| RCL1 | 1.4 | 1.27 | 0.14 | 0 |
| SDS24 | 2.92 | 1.24 | 0.14 | 0 |
| PIH1 | 1.32 | 1.23 | 0.14 | 0 |
| APS3 | 1.32 | 1.23 | 0.14 | 0 |
| YLR179C | 1.31 | 1.23 | 0.14 | 0 |
| BEM3 | 2.22 | 1.17 | 0.14 | 0 |
| MED8 | 2.02 | 1.15 | 0.14 | 0 |
| SWA2 | 1.92 | 1.13 | 0.14 | 0 |
| SWI1 | 3 | 1.11 | 0.14 | 0 |
| LYP1 | 2.06 | 1.11 | 0.14 | 0 |
| PIS1 | 1.78 | 1.11 | 0.14 | 0 |
| ERG28 | 1.78 | 1.11 | 0.14 | 0 |
| EMC1 | 1.78 | 1.11 | 0.14 | 0 |
| SEC10 | 1.56 | 1.11 | 0.14 | 0 |
| SCS7 | 1.74 | 1.1 | 0.14 | 0 |
| MSN4 | 1.46 | 1.08 | 0.14 | 0 |
| OST1 | 1.51 | 1.06 | 0.14 | 0 |
| PRP28 | 1.42 | 1.04 | 0.14 | 0 |
| CPR8 | 1.39 | 1.03 | 0.14 | 0 |
| CDC27 | 1.68 | 1.02 | 0.14 | 0 |
| HMF1 | 1.28 | 1.01 | 0.14 | 0 |
| DCP2 | 1.16 | 1 | 0.14 | 0 |
| TRA1 | 3.33 | 2.24 | 0.13 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 5

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| SIT1 | 5.6 | 1.65 | 0.13 | 0 |
| RTS1 | 4.1 | 1.63 | 0.13 | 0 |
| CDC9 | 3.66 | 1.59 | 0.13 | 0 |
| STU2 | 2.79 | 1.51 | 0.13 | 0 |
| EXO70 | 2.68 | 1.5 | 0.13 | 0 |
| YKL063C | 2.13 | 1.46 | 0.13 | 0 |
| SDS22 | 1.86 | 1.45 | 0.13 | 0 |
| MPE1 | 2.14 | 1.42 | 0.13 | 0 |
| MDM38 | 1.61 | 1.41 | 0.13 | 0 |
| RFC5 | 2.03 | 1.4 | 0.13 | 0 |
| YPK2 | 1.86 | 1.4 | 0.13 | 0 |
| JIP5 | 1.92 | 1.38 | 0.13 | 0 |
| TAF4 | 1.92 | 1.38 | 0.13 | 0 |
| SOK1 | 1.75 | 1.38 | 0.13 | 0 |
| AQR1 | 1.74 | 1.37 | 0.13 | 0 |
| LDB19 | 1.53 | 1.32 | 0.13 | 0 |
| TIM13 | 6.15 | 1.29 | 0.13 | 0 |
| POP2 | 1.4 | 1.29 | 0.13 | 0 |
| RPA14 | 1.48 | 1.27 | 0.13 | 0 |
| THO1 | 1.31 | 1.23 | 0.13 | 0 |
| GRX4 | 1.42 | 1.04 | 0.13 | 0 |
| YAT2 | 2 | 1.49 | 0.12 | 0 |
| STE5 | 2.96 | 1.47 | 0.12 | 0 |
| SWP82 | 2.46 | 1.47 | 0.12 | 0 |
| HRQ1 | 1.86 | 1.45 | 0.12 | 0 |
| SRO7 | 2.63 | 1.43 | 0.12 | 0 |
| SUA5 | 2.52 | 1.42 | 0.12 | 0 |
| FAD1 | 2.54 | 1.41 | 0.12 | 0 |
| BUD6 | 2.31 | 1.39 | 0.12 | 0 |
| FTR1 | 2.28 | 1.39 | 0.12 | 0 |
| CAB3 | 2.12 | 1.37 | 0.12 | 0 |
| ROK1 | 2.09 | 1.36 | 0.12 | 0 |
| NHX1 | 1.82 | 1.36 | 0.12 | 0 |
| SFL1 | 1.59 | 1.35 | 0.12 | 0 |
| AEP2 | 1.99 | 1.34 | 0.12 | 0 |
| UTP25 | 2.36 | 1.33 | 0.12 | 0 |
| YAP1802 | 1.59 | 1.31 | 0.12 | 0 |
| SOD2 | 1.59 | 1.31 | 0.12 | 0 |
| UPF3 | 1.48 | 1.27 | 0.12 | 0 |
| YPL245W | 1.32 | 1.23 | 0.12 | 0 |
| KRE9 | 1.28 | 1.21 | 0.12 | 0 |
| URM1 | 1.21 | 1.17 | 0.12 | 0 |
| FUI1 | 3.05 | 1.48 | 0.11 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 6

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| DAS2 | 1.88 | 1.46 | 0.11 | 0 |
| UFD4 | 2.42 | 1.41 | 0.11 | 0 |
| PUP3 | 2.42 | 1.41 | 0.11 | 0 |
| PRI2 | 2.31 | 1.39 | 0.11 | 0 |
| SKN7 | 1.92 | 1.38 | 0.11 | 0 |
| NRT1 | 2.02 | 1.35 | 0.11 | 0 |
| KAP104 | 1.98 | 1.34 | 0.11 | 0 |
| YAP1801 | 1.64 | 1.34 | 0.11 | 0 |
| ATG1 | 1.7 | 1.33 | 0.11 | 0 |
| PCF11 | 1.59 | 1.31 | 0.11 | 0 |
| AIM46 | 1.43 | 1.3 | 0.11 | 0 |
| SDS23 | 1.65 | 1.28 | 0.11 | 0 |
| SFP1 | 1.65 | 1.28 | 0.11 | 0 |
| CYK3 | 1.65 | 1.28 | 0.11 | 0 |
| MUK1 | 1.65 | 1.28 | 0.11 | 0 |
| CAF40 | 1.65 | 1.28 | 0.11 | 0 |
| MOB1 | 1.48 | 1.27 | 0.11 | 0 |
| ARP7 | 1.48 | 1.27 | 0.11 | 0 |
| BEM4 | 1.54 | 1.25 | 0.11 | 0 |
| PRP18 | 1.54 | 1.25 | 0.11 | 0 |
| NOC4 | 1.54 | 1.25 | 0.11 | 0 |
| PET54 | 1.54 | 1.25 | 0.11 | 0 |
| SMD1 | 1.38 | 1.24 | 0.11 | 0 |
| SIS2 | 1.32 | 1.23 | 0.11 | 0 |
| LST8 | 1.33 | 1.22 | 0.11 | 0 |
| BUD23 | 1.35 | 1.19 | 0.11 | 0 |
| HRI1 | 1.3 | 1.17 | 0.11 | 0 |
| TMA7 | 1.21 | 1.17 | 0.11 | 0 |
| YGR016W | 1.21 | 1.17 | 0.11 | 0 |
| CBK1 | 1.9 | 1.51 | 0.1 | 0 |
| AIM39 | 1.85 | 1.44 | 0.1 | 0 |
| MZM1 | 1.89 | 1.37 | 0.1 | 0 |
| OPT1 | 1.89 | 1.33 | 0.1 | 0 |
| SIR3 | 1.76 | 1.3 | 0.1 | 0 |
| ELP4 | 1.43 | 1.3 | 0.1 | 0 |
| HEM1 | 1.65 | 1.28 | 0.1 | 0 |
| KAP122 | 1.65 | 1.28 | 0.1 | 0 |
| SWI4 | 1.65 | 1.28 | 0.1 | 0 |
| BIK1 | 1.65 | 1.28 | 0.1 | 1 |
| YMR130W | 1.65 | 1.28 | 0.1 | 0 |
| ENT4 | 1.54 | 1.25 | 0.1 | 0 |
| MAG1 | 1.54 | 1.25 | 0.1 | 0 |
| CLF1 | 1.54 | 1.25 | 0.1 | 0 |

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| PTP3 | 1.54 | 1.25 | 0.1 | 0 |
| VHT1 | 1.51 | 1.24 | 0.1 | 0 |
| MCD4 | 1.51 | 1.24 | 0.1 | 0 |
| ECM14 | 1.44 | 1.22 | 0.1 | 0 |
| AIM17 | 1.44 | 1.22 | 0.1 | 0 |
| KIP2 | 1.44 | 1.22 | 0.1 | 0 |
| RCR1 | 1.31 | 1.21 | 0.1 | 0 |
| CPR4 | 1.38 | 1.2 | 0.1 | 0 |
| YNL193W | 1.33 | 1.19 | 0.1 | 0 |
| RHB1 | 1.24 | 1.18 | 0.1 | 0 |
| UBC4 | 1.21 | 1.17 | 0.1 | 0 |
| TSR1 | 1.25 | 1.15 | 0.1 | 0 |
| SSN3 | 1.25 | 1.15 | 0.1 | 0 |
| ZIP2 | 1.31 | 1.01 | 0.1 | 0 |
| ECM16 | 1.53 | 1.32 | 0.09 | 0 |
| LRG1 | 1.65 | 1.28 | 0.09 | 0 |
| VPS53 | 1.39 | 1.27 | 0.09 | 0 |
| ATG26 | 1.54 | 1.25 | 0.09 | 0 |
| ORC5 | 1.54 | 1.25 | 0.09 | 0 |
| ART10 | 1.35 | 1.25 | 0.09 | 0 |
| FLC1 | 1.51 | 1.24 | 0.09 | 0 |
| BAP2 | 1.51 | 1.24 | 0.09 | 0 |
| MUP1 | 1.51 | 1.24 | 0.09 | 0 |
| HSH155 | 1.38 | 1.24 | 0.09 | 0 |
| ATP25 | 1.47 | 1.23 | 0.09 | 0 |
| MOB2 | 1.44 | 1.22 | 0.09 | 0 |
| MSO1 | 1.44 | 1.22 | 0.09 | 0 |
| BEM1 | 1.44 | 1.22 | 0.09 | 0 |
| CLP1 | 1.44 | 1.22 | 0.09 | 0 |
| YMR124W | 1.44 | 1.22 | 0.09 | 0 |
| ORC4 | 1.44 | 1.22 | 0.09 | 0 |
| SUR1 | 1.38 | 1.2 | 0.09 | 0 |
| ERP2 | 1.38 | 1.2 | 0.09 | 0 |
| HSP30 | 1.38 | 1.2 | 0.09 | 0 |
| YIF1 | 1.37 | 1.2 | 0.09 | 0 |
| MED1 | 1.33 | 1.19 | 0.09 | 0 |
| MTF2 | 1.33 | 1.19 | 0.09 | 0 |
| YPL014W | 1.33 | 1.19 | 0.09 | 0 |
| PRP45 | 1.33 | 1.19 | 0.09 | 0 |
| GYP6 | 1.33 | 1.19 | 0.09 | 0 |
| YGL082W | 1.33 | 1.19 | 0.09 | 0 |
| IES3 | 1.27 | 1.19 | 0.09 | 0 |
| SEG1 | 1.3 | 1.17 | 0.09 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 8

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| TYR1 | 1.28 | 1.17 | 0.09 | 0 |
| AIP1 | 1.25 | 1.15 | 0.09 | 0 |
| YNL035C | 1.2 | 1.13 | 0.09 | 0 |
| POL30 | 1.15 | 1.11 | 0.09 | 0 |
| GPI15 | 3.04 | 1.54 | 0.08 | 0 |
| MON1 | 2.44 | 1.51 | 0.08 | 0 |
| NGL3 | 2.99 | 1.47 | 0.08 | 0 |
| RSF2 | 1.88 | 1.46 | 0.08 | 0 |
| NOP10 | 2.09 | 1.36 | 0.08 | 0 |
| YLR407W | 1.63 | 1.27 | 0.08 | 0 |
| AUS1 | 1.51 | 1.24 | 0.08 | 0 |
| BUD7 | 1.38 | 1.24 | 0.08 | 0 |
| CFT2 | 1.31 | 1.23 | 0.08 | 0 |
| PSK2 | 1.44 | 1.22 | 0.08 | 0 |
| SCD5 | 1.44 | 1.22 | 0.08 | 0 |
| MNN10 | 1.38 | 1.2 | 0.08 | 0 |
| YNL165W | 1.33 | 1.19 | 0.08 | 0 |
| CDD1 | 1.33 | 1.19 | 0.08 | 0 |
| AAT1 | 1.27 | 1.19 | 0.08 | 0 |
| SSL1 | 1.27 | 1.19 | 0.08 | 0 |
| SGD1 | 1.2 | 1.13 | 0.08 | 0 |
| TRM10 | 1.15 | 1.11 | 0.08 | 0 |
| PIN3 | 1.15 | 1.11 | 0.08 | 0 |
| GRE3 | 1.15 | 1.11 | 0.08 | 0 |
| APN1 | 1.15 | 1.11 | 0.08 | 0 |
| PUS4 | 1.15 | 1.11 | 0.08 | 0 |
| IES2 | 1.15 | 1.11 | 0.08 | 0 |
| ECM32 | 1.35 | 1.25 | 0.07 | 0 |
| GYL1 | 1.31 | 1.23 | 0.07 | 0 |
| ISA1 | 1.42 | 1.22 | 0.07 | 0 |
| PMC1 | 1.38 | 1.2 | 0.07 | 0 |
| SPB4 | 1.27 | 1.19 | 0.07 | 0 |
| PPZ2 | 1.27 | 1.19 | 0.07 | 0 |
| SWT1 | 1.27 | 1.19 | 0.07 | 0 |
| YMR1 | 1.27 | 1.19 | 0.07 | 0 |
| YBP2 | 1.27 | 1.19 | 0.07 | 0 |
| YBR238C | 1.24 | 1.19 | 0.07 | 0 |
| SBH1 | 1.28 | 1.17 | 0.07 | 0 |
| GLO1 | 1.26 | 1.16 | 0.07 | 0 |
| PNT1 | 1.26 | 1.16 | 0.07 | 0 |
| KTR6 | 1.26 | 1.16 | 0.07 | 0 |
| HYM1 | 1.22 | 1.14 | 0.07 | 0 |
| MAD3 | 1.22 | 1.14 | 0.07 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 9

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| NUF2 | 1.22 | 1.14 | 0.07 | 0 |
| DPH1 | 1.22 | 1.14 | 0.07 | 0 |
| MED7 | 1.22 | 1.14 | 0.07 | 0 |
| ARF3 | 1.22 | 1.14 | 0.07 | 0 |
| SSU72 | 1.22 | 1.14 | 0.07 | 0 |
| CFD1 | 1.22 | 1.14 | 0.07 | 0 |
| SPT20 | 1.22 | 1.14 | 0.07 | 0 |
| VPS9 | 1.22 | 1.14 | 0.07 | 0 |
| ELP6 | 1.22 | 1.14 | 0.07 | 0 |
| YKR078W | 1.22 | 1.14 | 0.07 | 0 |
| SSF1 | 1.22 | 1.14 | 0.07 | 0 |
| INN1 | 1.22 | 1.14 | 0.07 | 0 |
| ARA1 | 1.22 | 1.14 | 0.07 | 0 |
| SRP21 | 1.22 | 1.14 | 0.07 | 0 |
| MTQ2 | 1.22 | 1.14 | 0.07 | 0 |
| APT2 | 1.22 | 1.14 | 0.07 | 0 |
| SRL2 | 1.22 | 1.14 | 0.07 | 0 |
| YMR144W | 1.22 | 1.14 | 0.07 | 0 |
| YLR118C | 1.22 | 1.14 | 0.07 | 0 |
| BIO2 | 1.22 | 1.14 | 0.07 | 0 |
| ORC2 | 1.22 | 1.14 | 0.07 | 0 |
| FMP21 | 1.19 | 1.13 | 0.07 | 0 |
| VHS2 | 1.15 | 1.11 | 0.07 | 0 |
| NPC2 | 1.1 | 1.08 | 0.07 | 0 |
| RPB7 | 1.1 | 1.08 | 0.07 | 1 |
| YCL012C | 1.1 | 1.08 | 0.07 | 0 |
| FCY1 | 1.1 | 1.08 | 0.07 | 0 |
| SHG1 | 1.1 | 1.08 | 0.07 | 0 |
| ATO3 | 1.1 | 1.08 | 0.07 | 0 |
| ACB1 | 1.1 | 1.08 | 0.07 | 0 |
| MRM1 | 3.68 | 1.53 | 0.06 | 0 |
| RSE1 | 1.33 | 1.19 | 0.06 | 0 |
| SEC5 | 1.33 | 1.19 | 0.06 | 0 |
| SPR28 | 1.26 | 1.16 | 0.06 | 0 |
| MTC4 | 1.26 | 1.16 | 0.06 | 0 |
| YMR111C | 1.22 | 1.14 | 0.06 | 0 |
| SSK1 | 1.22 | 1.14 | 0.06 | 0 |
| MAF1 | 1.22 | 1.14 | 0.06 | 0 |
| STE12 | 1.22 | 1.14 | 0.06 | 0 |
| MSN2 | 1.22 | 1.14 | 0.06 | 0 |
| RKM3 | 1.22 | 1.14 | 0.06 | 0 |
| PRR1 | 1.22 | 1.14 | 0.06 | 0 |
| OCA2 | 1.19 | 1.13 | 0.06 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 10

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| APM4 | 1.19 | 1.13 | 0.06 | 0 |
| GFD2 | 1.19 | 1.13 | 0.06 | 0 |
| RML2 | 1.19 | 1.13 | 0.06 | 0 |
| GYP8 | 1.19 | 1.13 | 0.06 | 0 |
| TOP3 | 1.19 | 1.13 | 0.06 | 0 |
| MET22 | 1.15 | 1.11 | 0.06 | 0 |
| MSS4 | 1.15 | 1.11 | 0.06 | 0 |
| LCB5 | 1.15 | 1.11 | 0.06 | 0 |
| COX17 | 1.1 | 1.08 | 0.06 | 0 |
| HAP2 | 1.1 | 1.08 | 0.06 | 0 |
| DPP1 | 1.1 | 1.08 | 0.06 | 0 |
| COQ9 | 1.1 | 1.08 | 0.06 | 0 |
| DAT1 | 1.1 | 1.08 | 0.06 | 0 |
| VAM7 | 1.1 | 1.08 | 0.06 | 0 |
| TLG1 | 1.1 | 1.08 | 0.06 | 0 |
| SER2 | 1.1 | 1.08 | 0.06 | 0 |
| CAF16 | 1.1 | 1.08 | 0.06 | 0 |
| TAO3 | 1.2 | 1.02 | 0.06 | 0 |
| UGA3 | 3.68 | 1.53 | 0.05 | 0 |
| PCL7 | 2.33 | 1.4 | 0.05 | 0 |
| NUP192 | 1.49 | 1.31 | 0.05 | 0 |
| YLR419W | 1.38 | 1.24 | 0.05 | 0 |
| GCN2 | 1.33 | 1.19 | 0.05 | 0 |
| HAL5 | 1.27 | 1.19 | 0.05 | 0 |
| RTT107 | 1.27 | 1.19 | 0.05 | 0 |
| CIN8 | 1.27 | 1.19 | 0.05 | 0 |
| GEF1 | 1.23 | 1.18 | 0.05 | 0 |
| SEC6 | 1.21 | 1.17 | 0.05 | 0 |
| DSL1 | 1.26 | 1.16 | 0.05 | 0 |
| DAP2 | 1.26 | 1.16 | 0.05 | 0 |
| ENP2 | 1.22 | 1.14 | 0.05 | 0 |
| BYE1 | 1.22 | 1.14 | 0.05 | 0 |
| MRE11 | 1.22 | 1.14 | 0.05 | 0 |
| SEC15 | 1.22 | 1.14 | 0.05 | 0 |
| AVL9 | 1.22 | 1.14 | 0.05 | 0 |
| RAD53 | 1.22 | 1.14 | 0.05 | 0 |
| SAP1 | 1.22 | 1.14 | 0.05 | 0 |
| ORC3 | 1.22 | 1.14 | 0.05 | 0 |
| FLO11 | 1.22 | 1.14 | 0.05 | 0 |
| FIG2 | 1.2 | 1.13 | 0.05 | 0 |
| YGR169C_A | 1.15 | 1.11 | 0.05 | 0 |
| TCO89 | 1.15 | 1.11 | 0.05 | 0 |
| SPT2 | 1.1 | 1.08 | 0.05 | 0 |

Table S7: Full Rtr1 interactome SAINT analysis Page 11

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| QRI1 | 1.1 | 1.08 | 0.05 | 0 |
| RPN14 | 1.1 | 1.08 | 0.05 | 0 |
| URA1 | 1.1 | 1.08 | 0.05 | 0 |
| PIN2 | 1.1 | 1.08 | 0.05 | 0 |
| DEP1 | 1.1 | 1.08 | 0.05 | 1 |
| RET1 | 1.31 | 1.23 | 0.04 | 0 |
| URB1 | 1.33 | 1.19 | 0.04 | 0 |
| YTA7 | 1.27 | 1.19 | 0.04 | 0 |
| RGR1 | 1.27 | 1.19 | 0.04 | 0 |
| YDL073W | 1.24 | 1.18 | 0.04 | 0 |
| GYP5 | 1.21 | 1.17 | 0.04 | 0 |
| YIL151C | 1.22 | 1.14 | 0.04 | 0 |
| YNL115C | 1.19 | 1.13 | 0.04 | 0 |
| SPC110 | 1.19 | 1.13 | 0.04 | 0 |
| YMR027W | 1.1 | 1.08 | 0.04 | 0 |
| DPH2 | 1.1 | 1.08 | 0.04 | 0 |
| YBR085C_A | 1.1 | 1.08 | 0.04 | 0 |
| NGL2 | 1.1 | 1.08 | 0.04 | 0 |
| CTK1 | 1.1 | 1.08 | 0.04 | 1 |
| MON2 | 1.27 | 1.19 | 0.03 | 0 |
| SSN2 | 1.22 | 1.14 | 0.03 | 0 |
| ATG2 | 1.22 | 1.14 | 0.03 | 0 |
| MSN5 | 1.19 | 1.13 | 0.03 | 0 |
| RTC1 | 1.15 | 1.11 | 0.03 | 0 |
| KIN82 | 1.1 | 1.08 | 0.03 | 0 |
| CBP2 | 1.1 | 1.08 | 0.03 | 0 |
| FPK1 | 1.1 | 1.08 | 0.03 | 0 |
| AGP2 | 1.1 | 1.08 | 0.03 | 0 |
| HOS3 | 1.1 | 1.08 | 0.03 | 0 |
| IRC8 | 1.1 | 1.08 | 0.03 | 0 |
| YLR422W | 1.31 | 1.23 | 0.02 | 0 |
| SRB8 | 1.23 | 1.18 | 0.02 | 0 |
| BUD4 | 1.22 | 1.14 | 0.02 | 0 |
| SGN1 | 3.17 | 1.13 | 0.02 | 0 |
| PEP3 | 1.1 | 1.08 | 0.02 | 0 |
| ASE1 | 1.1 | 1.08 | 0.02 | 0 |
| RCM1 | 1.1 | 1.08 | 0.02 | 0 |
| TGL5 | 1.1 | 1.08 | 0.02 | 0 |
| KIN4 | 1.1 | 1.08 | 0.02 | 0 |
| KAP120 | 1.1 | 1.08 | 0.02 | 0 |
| YFR016C | 1.1 | 1.08 | 0.02 | 0 |
| CSR2 | 1.1 | 1.08 | 0.02 | 0 |
| TOR1 | 1.3 | 1.26 | 0.01 | 0 |

| RTR1 ALL PROTEIN ID | RTR1 ALL FC_A | RTR1 ALL FC_B | RTR1 ALL SAINT PROB | RTR1 ALL iREF |
|---|---|---|---|---|
| SIP3 | 1.1 | 1.08 | 0.01 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 1

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RTR1 | 3757.31 | 3382.94 | 2083.54 | 1148.79 | 1 | 1 | 1 |
| RPB5 | 171.47 | 7.04 | 86.64 | 3.74 | 1 | 0.57 | 1 |
| RPB1 | 118.71 | 4.36 | 50.15 | 0.85 | 1 | 0.49 | 1 |
| RPB2 | 89.83 | 3.03 | 44.22 | 1.74 | 1 | 0.03 | 1 |
| RPB3 | 170.37 | 1.95 | 101.06 | 1.28 | 1 | 0 | 1 |
| RPB8 | 59.12 | 0 | 28.13 | 0 | 0.95 | 0 | 1 |
| RPB6 | 51.06 | 0 | 15.93 | 0 | 0.75 | 0 | 1 |
| RPB10 | 30 | 0 | 7.34 | 0 | 0.75 | 0 | 1 |
| RPB11 | 26.06 | 0 | 12.75 | 0 | 0.75 | 0 | 1 |
| PBP1 | 9.6 | 0 | 4.35 | 0 | 0.75 | 0 | 0 |
| LSM12 | 23.84 | 0 | 10.53 | 0 | 0.75 | 0 | 0 |
| IRR1 | 2.66 | 132.23 | 1.15 | 28.25 | 0.42 | 1 | 0 |
| RRP41 | 0 | 41.94 | 0 | 22.44 | 0 | 0.98 | 0 |
| UBA2 | 0 | 15.94 | 0 | 10.02 | 0 | 0.93 | 0 |
| GPN3 | 16.31 | 0 | 6.03 | 0 | 0.74 | 0 | 0 |
| RPB12 | 24.18 | 0 | 11.8 | 0 | 0.72 | 0 | 1 |
| ATP22 | 6.73 | 0 | 3.26 | 0 | 0.67 | 0 | 0 |
| NPA3 | 14.94 | 0.87 | 5.89 | 0.41 | 0.64 | 0 | 1 |
| RSM25 | 3.19 | 0 | 1.53 | 0 | 0.5 | 0 | 0 |
| RHR2 | 5.07 | 1.1 | 0.72 | 0.33 | 0.5 | 0 | 0 |
| CMK1 | 5.5 | 0 | 1.55 | 0 | 0.5 | 0 | 1 |
| CNA1 | 12.96 | 0 | 2.57 | 0 | 0.5 | 0 | 0 |
| RPB9 | 3 | 0 | 1.04 | 0 | 0.5 | 0 | 1 |
| LIP5 | 3.63 | 0 | 1.69 | 0 | 0.5 | 0 | 0 |
| TIF4632 | 3.28 | 0 | 1.75 | 0 | 0.5 | 0 | 0 |
| MYO1 | 4.9 | 0 | 1.66 | 0 | 0.5 | 0 | 0 |
| PSP2 | 11.06 | 0 | 2.43 | 0 | 0.5 | 0 | 0 |
| SNF5 | 2.56 | 0 | 0.38 | 0 | 0.5 | 0 | 0 |
| NUP60 | 6.08 | 0 | 1.96 | 0 | 0.49 | 0 | 0 |
| RPS29B | 4.7 | 0 | 2.45 | 0 | 0.49 | 0 | 0 |
| BRE5 | 6.46 | 0 | 2.99 | 0 | 0.49 | 0 | 0 |
| IXR1 | 3.96 | 0 | 2.31 | 0 | 0.49 | 0 | 0 |
| PBP4 | 2.41 | 0 | 0.88 | 0 | 0.49 | 0 | 0 |
| GAL11 | 4.22 | 0 | 2.2 | 0 | 0.49 | 0 | 0 |
| RPB4 | 13.43 | 0 | 2.45 | 0 | 0.48 | 0 | 1 |
| TAF12 | 7.53 | 0 | 2.33 | 0 | 0.48 | 0 | 0 |
| HEM13 | 2.73 | 0 | 1.07 | 0 | 0.47 | 0 | 0 |
| USO1 | 6.33 | 0 | 1.36 | 0 | 0.45 | 0 | 0 |
| YAT2 | 2.67 | 2.38 | 1.87 | 1.94 | 0.45 | 0 | 0 |
| HRQ1 | 2.51 | 0 | 1.93 | 0 | 0.45 | 0 | 0 |
| PIB2 | 5.64 | 0 | 3.2 | 0 | 0.45 | 0 | 0 |
| HER1 | 5.65 | 0 | 2.21 | 0 | 0.45 | 0 | 0 |

## Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 2

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| PHO81 | 7.92 | 2.47 | 3.76 | 1.98 | 0.45 | 0 | 0 |
| YBR139W | 4.04 | 0 | 2.32 | 0 | 0.45 | 0 | 0 |
| TRA1 | 4.3 | 0 | 2.66 | 0 | 0.45 | 0 | 0 |
| YPR097W | 3.12 | 0 | 2.28 | 0 | 0.45 | 0 | 0 |
| SNF6 | 4.3 | 0 | 2.66 | 0 | 0.45 | 0 | 0 |
| SYP1 | 3.19 | 0 | 1.24 | 0 | 0.44 | 0 | 0 |
| RSF2 | 2.54 | 0 | 1.94 | 0 | 0.44 | 0 | 0 |
| AIM46 | 1.75 | 0 | 1.58 | 0 | 0.44 | 0 | 0 |
| SLM1 | 1.9 | 0 | 1.26 | 0 | 0.44 | 0 | 0 |
| DAS2 | 2.54 | 0 | 1.94 | 0 | 0.44 | 0 | 0 |
| ELP4 | 1.75 | 0 | 1.58 | 0 | 0.44 | 0 | 0 |
| IRR1 | 2.66 | 132.23 | 1.15 | 28.25 | 0.42 | 1 | 0 |
| ISW2 | 4.44 | 0 | 2.36 | 0 | 0.42 | 0 | 0 |
| RBA50 | 3.46 | 0 | 1 | 0 | 0.42 | 0 | 0 |
| APP1 | 2.51 | 0 | 1.72 | 0 | 0.42 | 0 | 0 |
| CDC53 | 2.13 | 0 | 1.29 | 0 | 0.42 | 0 | 0 |
| NUP1 | 3.31 | 0 | 0.99 | 0 | 0.42 | 0 | 0 |
| TIM13 | 10.23 | 0 | 2.64 | 0 | 0.42 | 0 | 0 |
| DBP3 | 4.36 | 0 | 1.34 | 0 | 0.42 | 0 | 0 |
| UTP25 | 3.44 | 0 | 1.89 | 0 | 0.41 | 0 | 0 |
| YGL041W_A | 1.81 | 0 | 0.5 | 0 | 0.41 | 0 | 0 |
| RBG2 | 2.68 | 0 | 0.71 | 0 | 0.41 | 0 | 0 |
| FAD1 | 3.76 | 0 | 2.1 | 0 | 0.41 | 0 | 0 |
| CST6 | 3.4 | 0 | 1.09 | 0 | 0.41 | 0 | 0 |
| UBI4 | 5.28 | 0 | 1.06 | 0 | 0.41 | 0 | 1 |
| RTT103 | 1.72 | 0 | 0.63 | 0 | 0.39 | 0 | 0 |
| FPR4 | 4.01 | 0 | 1.38 | 0 | 0.39 | 0 | 0 |
| GND2 | 2.56 | 0 | 0.89 | 0 | 0.39 | 0 | 0 |
| BUD3 | 0.98 | 0 | 0.48 | 0 | 0.38 | 0 | 0 |
| ALB1 | 2.42 | 0 | 1.23 | 0 | 0.36 | 0 | 0 |
| FMC1 | 2.19 | 0 | 1.24 | 0 | 0.36 | 0 | 0 |
| OSH2 | 5.5 | 0 | 1.81 | 0 | 0.36 | 0 | 0 |
| MAK5 | 2.87 | 0 | 1.62 | 0 | 0.36 | 0 | 0 |
| RFC3 | 2.21 | 0 | 1.04 | 0 | 0.36 | 0 | 0 |
| GCR2 | 1.75 | 0 | 1.18 | 0 | 0.36 | 0 | 0 |
| ATP7 | 3.16 | 0 | 0.63 | 0 | 0.34 | 0 | 0 |
| TIF4631 | 2.97 | 0 | 1.24 | 0 | 0.34 | 0 | 0 |
| CHD1 | 5.16 | 16.51 | 1.89 | 3.79 | 0.33 | 0.5 | 0 |
| CTR9 | 2.24 | 0 | 1.28 | 0 | 0.33 | 0 | 0 |
| SRP14 | 2.24 | 0 | 1.28 | 0 | 0.33 | 0 | 0 |
| FMP52 | 4.5 | 0 | 0.8 | 0 | 0.32 | 0 | 0 |
| LYS12 | 3.28 | 0 | 0.58 | 0 | 0.31 | 0 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 3

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| FOL1 | 2.09 | 8.64 | 1.21 | 2.71 | 0.3 | 0.5 | 0 |
| DST1 | 3.42 | 0 | 1.55 | 0 | 0.3 | 0 | 0 |
| VMA8 | 4.83 | 0 | 1.5 | 0 | 0.3 | 0 | 0 |
| GLE2 | 2.99 | 0 | 1.31 | 0 | 0.3 | 0 | 0 |
| FUN12 | 7.25 | 0 | 1.09 | 0 | 0.29 | 0 | 0 |
| KGD2 | 7.19 | 2.27 | 1.17 | 1.01 | 0.28 | 0.2 | 0 |
| PRP43 | 3.73 | 0 | 1.15 | 0 | 0.27 | 0 | 0 |
| HOR2 | 2.8 | 2.08 | 0.51 | 0.52 | 0.26 | 0 | 0 |
| HSP26 | 2.78 | 34.56 | 1.22 | 22.45 | 0.25 | 1 | 0 |
| DLD3 | 2.81 | 6.39 | 1.08 | 2.31 | 0.25 | 0.5 | 0 |
| ATG26 | 1.95 | 5.41 | 1.48 | 3.13 | 0.25 | 0.5 | 0 |
| CAR2 | 1.51 | 8.3 | 0.8 | 2.04 | 0.25 | 0.5 | 0 |
| GEA1 | 2.23 | 8.06 | 1.11 | 2.86 | 0.25 | 0.5 | 0 |
| APL5 | 3.73 | 57.73 | 1.59 | 9.29 | 0.25 | 0.5 | 0 |
| GRX3 | 1.41 | 89.52 | 0.78 | 8.25 | 0.25 | 0.5 | 0 |
| LSB3 | 6 | 6.97 | 1.02 | 1.51 | 0.25 | 0.49 | 0 |
| SWI4 | 2.14 | 3.94 | 1.54 | 2.62 | 0.25 | 0.48 | 0 |
| MAK21 | 1.18 | 1.52 | 0.41 | 0.61 | 0.25 | 0.11 | 0 |
| IDH2 | 3.59 | 1.71 | 0.59 | 0.54 | 0.25 | 0.01 | 0 |
| ARO1 | 2.97 | 2.11 | 0.61 | 0.63 | 0.25 | 0.01 | 0 |
| MYO2 | 1.72 | 2.42 | 0.27 | 0.58 | 0.25 | 0.01 | 0 |
| PRP6 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| HEM1 | 2.14 | 2.47 | 1.54 | 1.98 | 0.25 | 0 | 0 |
| SUA7 | 2.09 | 0 | 0.52 | 0 | 0.25 | 0 | 0 |
| SUA5 | 3.67 | 0 | 1.85 | 0 | 0.25 | 0 | 0 |
| NOP9 | 1.44 | 0 | 1.12 | 0 | 0.25 | 0 | 0 |
| EDC3 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| UTP22 | 2.29 | 0 | 0.82 | 0 | 0.25 | 0 | 0 |
| CIA2 | 1.49 | 0 | 0.76 | 0 | 0.25 | 0 | 0 |
| UTP20 | 1.5 | 0 | 0.86 | 0 | 0.25 | 0 | 0 |
| LAA1 | 1.34 | 0 | 0.58 | 0 | 0.25 | 0 | 0 |
| BUD27 | 2.71 | 0 | 1.67 | 0 | 0.25 | 0 | 0 |
| MOB2 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| MOB1 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| LEO1 | 2.15 | 0 | 1.32 | 0 | 0.25 | 0 | 0 |
| SMD1 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| UME6 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| URK1 | 1.41 | 0 | 0.69 | 0 | 0.25 | 0 | 0 |
| SWP82 | 3.48 | 0 | 1.82 | 0 | 0.25 | 0 | 0 |
| PSE1 | 5.85 | 0 | 0.74 | 0 | 0.25 | 0 | 0 |
| MOT2 | 1.83 | 0 | 0.48 | 0 | 0.25 | 0 | 0 |
| RPN5 | 1.36 | 0 | 0.51 | 0 | 0.25 | 0 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 4

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RPN8 | 1.64 | 0 | 0.26 | 0 | 0.25 | 0 | 0 |
| PCF11 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| UFD4 | 3.48 | 0 | 1.82 | 0 | 0.25 | 0 | 0 |
| ENP1 | 2.15 | 0 | 0.87 | 0 | 0.25 | 0 | 0 |
| NUP82 | 1.76 | 1.66 | 0.81 | 0.96 | 0.25 | 0 | 0 |
| PRO1 | 1.87 | 0 | 0.49 | 0 | 0.25 | 0 | 0 |
| MED1 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| MED8 | 2.85 | 0 | 1.46 | 0 | 0.25 | 0 | 0 |
| YML6 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| RNA1 | 3.32 | 0 | 0.63 | 0 | 0.25 | 0 | 0 |
| MDN1 | 4.95 | 0 | 0.41 | 0 | 0.25 | 0 | 0 |
| YKT6 | 0.97 | 0 | 0.12 | 0 | 0.25 | 0 | 0 |
| WHI4 | 1.64 | 0 | 0.9 | 0 | 0.25 | 0 | 0 |
| DBP10 | 1.57 | 0 | 0.75 | 0 | 0.25 | 0 | 0 |
| SDS24 | 4.42 | 0 | 1.67 | 0 | 0.25 | 0 | 0 |
| SDS23 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| WHI3 | 1.57 | 0 | 0.73 | 0 | 0.25 | 0 | 0 |
| TCP1 | 1.19 | 0.22 | 0.14 | 0.08 | 0.25 | 0 | 0 |
| PSR1 | 1.98 | 0 | 1.12 | 0 | 0.25 | 0 | 0 |
| ROK1 | 2.9 | 0 | 1.71 | 0 | 0.25 | 0 | 0 |
| YLR407W | 2.11 | 0 | 1.53 | 0 | 0.25 | 0 | 0 |
| PRP28 | 1.8 | 0 | 1.23 | 0 | 0.25 | 0 | 0 |
| THR1 | 3.16 | 0 | 0.9 | 0 | 0.25 | 0 | 0 |
| ENT4 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| CHA1 | 1.6 | 0 | 0.69 | 0 | 0.25 | 0 | 0 |
| ECM29 | 2.54 | 0 | 0.68 | 0 | 0.25 | 0 | 0 |
| ECM25 | 2.29 | 0 | 0.88 | 0 | 0.25 | 0 | 0 |
| RIA1 | 2.08 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| MAG1 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| DJP1 | 2.3 | 0 | 0.63 | 0 | 0.25 | 0 | 0 |
| CIC1 | 2.03 | 0 | 0.79 | 0 | 0.25 | 0 | 0 |
| NUP116 | 2.15 | 0.63 | 0.3 | 0.25 | 0.25 | 0 | 0 |
| ATG1 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| SNF12 | 3.21 | 0 | 0.74 | 0 | 0.25 | 0 | 0 |
| TAH11 | 1.48 | 0 | 0.62 | 0 | 0.25 | 0 | 0 |
| GCD1 | 1.69 | 0 | 0.6 | 0 | 0.25 | 0 | 0 |
| RPS29A | 1.21 | 0 | 0.24 | 0 | 0.25 | 0 | 0 |
| CLF1 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| RSC30 | 1.44 | 0 | 1.12 | 0 | 0.25 | 0 | 0 |
| DRS1 | 1.57 | 0 | 0.54 | 0 | 0.25 | 0 | 0 |
| BRE1 | 3.6 | 0 | 1.37 | 0 | 0.25 | 0 | 0 |
| RCN2 | 1.49 | 0 | 0.75 | 0 | 0.25 | 0 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 5

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RCN1 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| MET7 | 1.37 | 0 | 0.65 | 0 | 0.25 | 0 | 0 |
| MET4 | 1.76 | 0 | 1.02 | 0 | 0.25 | 0 | 0 |
| MSN4 | 1.79 | 0 | 1.23 | 0 | 0.25 | 0 | 0 |
| ECM16 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| SLA1 | 4.41 | 0 | 1 | 0 | 0.25 | 0 | 0 |
| SWH1 | 1.1 | 0 | 0.46 | 0 | 0.25 | 0 | 0 |
| GGA2 | 2.7 | 0 | 1.08 | 0 | 0.25 | 0 | 0 |
| JSN1 | 2.22 | 0 | 0.84 | 0 | 0.25 | 0 | 0 |
| RTT102 | 3.29 | 0 | 1.78 | 0 | 0.25 | 0 | 0 |
| AKL1 | 1.62 | 0 | 1.18 | 0 | 0.25 | 0 | 0 |
| LDB19 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| RPS19B | 3.14 | 0.28 | 0.96 | 0.06 | 0.25 | 0 | 0 |
| YPK2 | 2.33 | 0 | 1.59 | 0 | 0.25 | 0 | 0 |
| BIK1 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 1 |
| PUF4 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| PUF2 | 2.78 | 0 | 0.87 | 0 | 0.25 | 0 | 0 |
| OCA1 | 1.5 | 0 | 0.86 | 0 | 0.25 | 0 | 0 |
| NGL3 | 4.49 | 0 | 1.97 | 0 | 0.25 | 0 | 0 |
| IMH1 | 1.94 | 0 | 0.51 | 0 | 0.25 | 0 | 0 |
| RPS17B | 2.5 | 1.71 | 0.52 | 0.15 | 0.25 | 0 | 0 |
| RSC3 | 2.09 | 0 | 0.82 | 0 | 0.25 | 0 | 0 |
| RSC6 | 1.66 | 0 | 1.05 | 0 | 0.25 | 0 | 0 |
| RRP12 | 1.79 | 0 | 0.39 | 0 | 0.25 | 0 | 0 |
| RSC9 | 2.85 | 0 | 1.2 | 0 | 0.25 | 0 | 0 |
| AHA1 | 1.85 | 0 | 0.6 | 0 | 0.25 | 0 | 0 |
| MEU1 | 2.63 | 0 | 0.87 | 0 | 0.25 | 0 | 0 |
| MCA1 | 2.12 | 0 | 0.49 | 0 | 0.25 | 0 | 0 |
| MSO1 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| HSH155 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| YSC84 | 5.07 | 0 | 1.18 | 0 | 0.25 | 0 | 0 |
| SWI6 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| SWI1 | 4.42 | 0 | 1.38 | 0 | 0.25 | 0 | 0 |
| SWI3 | 3.16 | 0 | 0.9 | 0 | 0.25 | 0 | 0 |
| GIP3 | 2.39 | 0 | 1.14 | 0 | 0.25 | 0 | 0 |
| LRG1 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| BEM1 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| BEM3 | 3.2 | 0 | 1.51 | 0 | 0.25 | 0 | 0 |
| BEM4 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| PRP18 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| PRP16 | 1.45 | 0 | 1.12 | 0 | 0.25 | 0 | 0 |
| VPS52 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 6

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| PSK2 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| PSK1 | 1.44 | 0 | 0.81 | 0 | 0.25 | 0 | 0 |
| ECM14 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| YDR248C | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| WHI5 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| YNL193W | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| CMD1 | 0.79 | 0 | 0.13 | 0 | 0.25 | 0 | 0 |
| ATG19 | 1.39 | 0 | 0.88 | 0 | 0.25 | 0 | 0 |
| HOG1 | 1.47 | 0 | 0.41 | 0 | 0.25 | 0 | 0 |
| SOG2 | 1.76 | 0 | 1.02 | 0 | 0.25 | 0 | 0 |
| FPR3 | 3.22 | 0 | 0.81 | 0 | 0.25 | 0 | 0 |
| APM1 | 2.52 | 2.47 | 1.63 | 1.98 | 0.25 | 0 | 0 |
| APM3 | 1.57 | 0 | 0.75 | 0 | 0.25 | 0 | 0 |
| HGH1 | 1.21 | 0 | 0.35 | 0 | 0.25 | 0 | 0 |
| MPE1 | 2.9 | 2.47 | 1.71 | 1.98 | 0.25 | 0 | 0 |
| CDC14 | 2.04 | 0 | 0.74 | 0 | 0.25 | 0 | 0 |
| SFP1 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| CLU1 | 2.79 | 0.17 | 0.31 | 0.07 | 0.25 | 0 | 0 |
| CLC1 | 2.28 | 0.46 | 0.41 | 0.15 | 0.25 | 0 | 0 |
| ATG18 | 1.82 | 0 | 0.86 | 0 | 0.25 | 0 | 0 |
| YAP1802 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| UPF3 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| YAP1801 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| RPS15 | 3.01 | 0.57 | 0.43 | 0.08 | 0.25 | 0 | 0 |
| ASG1 | 2.36 | 0 | 0.87 | 0 | 0.25 | 0 | 0 |
| NUT1 | 2.04 | 0 | 0.62 | 0 | 0.25 | 0 | 0 |
| CBF5 | 1.2 | 0.82 | 0.35 | 0.37 | 0.25 | 0 | 0 |
| RVS167 | 6.89 | 0 | 1.1 | 0 | 0.25 | 0 | 0 |
| RVS161 | 4.76 | 0.44 | 1.04 | 0.21 | 0.25 | 0 | 0 |
| MCM3 | 2.2 | 0 | 0.5 | 0 | 0.25 | 0 | 0 |
| MDS3 | 1.45 | 0 | 0.94 | 0 | 0.25 | 0 | 0 |
| SOD2 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| NMD5 | 2.67 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| APL3 | 2.33 | 0 | 1.59 | 0 | 0.25 | 0 | 0 |
| APL2 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| APL6 | 1.5 | 0 | 0.87 | 0 | 0.25 | 0 | 0 |
| APL4 | 2.32 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| GET4 | 1.72 | 0 | 0.39 | 0 | 0.25 | 0 | 0 |
| NUP159 | 1.23 | 0 | 0.67 | 0 | 0.25 | 0 | 0 |
| YNR029C | 1.76 | 0 | 1.02 | 0 | 0.25 | 0 | 0 |
| STH1 | 1.73 | 0 | 0.79 | 0 | 0.25 | 0 | 0 |
| MTF2 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 7

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| CLP1 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| MED6 | 1.79 | 0 | 0.93 | 0 | 0.25 | 0 | 0 |
| YLR419W | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| GRX1 | 2.14 | 2.38 | 1.54 | 1.94 | 0.25 | 0 | 0 |
| GRX4 | 1.8 | 0 | 1.23 | 0 | 0.25 | 0 | 0 |
| YPL014W | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| ESF1 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| CYK3 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| MZM1 | 2.48 | 0 | 1.62 | 0 | 0.25 | 0 | 0 |
| JIP5 | 2.52 | 0 | 1.63 | 0 | 0.25 | 0 | 0 |
| VPS1 | 0.82 | 0.38 | 0.1 | 0.1 | 0.25 | 0 | 0 |
| VPS5 | 3.17 | 0 | 1.24 | 0 | 0.25 | 0 | 0 |
| YMR124W | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| PRI2 | 3.29 | 0 | 1.78 | 0 | 0.25 | 0 | 0 |
| ARO9 | 1.45 | 0 | 0.94 | 0 | 0.25 | 0 | 0 |
| CDC39 | 6.07 | 0 | 1.1 | 0 | 0.25 | 0 | 0 |
| CDC31 | 0.97 | 0 | 0.27 | 0 | 0.25 | 0 | 0 |
| CDC34 | 3.23 | 1.01 | 0.56 | 0.48 | 0.25 | 0 | 0 |
| GCN2 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| CLA4 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| YPK1 | 2.34 | 0.66 | 0.34 | 0.29 | 0.25 | 0 | 0 |
| TRM732 | 1.64 | 0 | 0.9 | 0 | 0.25 | 0 | 0 |
| VPS29 | 1.53 | 0 | 0.71 | 0 | 0.25 | 0 | 0 |
| YNL165W | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| YHB1 | 3.39 | 0 | 0.38 | 0 | 0.25 | 0 | 0 |
| NRP1 | 1.54 | 0 | 0.8 | 0 | 0.25 | 0 | 0 |
| PBP2 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| PRP45 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| STE5 | 4.43 | 0 | 1.96 | 0 | 0.25 | 0 | 0 |
| DMA2 | 1.67 | 0 | 0.83 | 0 | 0.25 | 0 | 0 |
| URB1 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| SXM1 | 3.06 | 1.96 | 1.17 | 1.23 | 0.25 | 0 | 0 |
| SCD5 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| FUN30 | 2.92 | 0 | 0.56 | 0 | 0.25 | 0 | 0 |
| BOI2 | 2.71 | 0 | 1.67 | 0 | 0.25 | 0 | 0 |
| MUK1 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| TPT1 | 2.9 | 0 | 1.71 | 0 | 0.25 | 0 | 0 |
| CAF40 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| PAP1 | 2.67 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| YPR089W | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| GCN1 | 1.3 | 1.45 | 0.1 | 0.23 | 0.25 | 0 | 0 |
| RPA135 | 1.47 | 0 | 0.41 | 0 | 0.25 | 0 | 0 |

## Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 8

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| GCN3 | 3.1 | 0 | 1.75 | 0 | 0.25 | 0 | 0 |
| SDA1 | 2.08 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| RPA14 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| NOP58 | 2.06 | 0.21 | 0.65 | 0.11 | 0.25 | 0 | 0 |
| KRI1 | 2.41 | 0 | 0.83 | 0 | 0.25 | 0 | 0 |
| MRD1 | 2.23 | 0 | 1.11 | 0 | 0.25 | 0 | 0 |
| SIN4 | 3.1 | 0 | 1.75 | 0 | 0.25 | 0 | 0 |
| VPS13 | 4.38 | 0 | 1.19 | 0 | 0.25 | 0 | 0 |
| SKN7 | 2.52 | 0 | 1.63 | 0 | 0.25 | 0 | 0 |
| CYM1 | 10.4 | 0 | 2.49 | 0 | 0.25 | 0 | 0 |
| SIR2 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| SIR3 | 2.33 | 0 | 1.59 | 0 | 0.25 | 0 | 0 |
| SEC10 | 1.97 | 0 | 1.27 | 0 | 0.25 | 0 | 0 |
| SEC16 | 5.3 | 0 | 1.76 | 0 | 0.25 | 0 | 0 |
| CRM1 | 1.29 | 0 | 0.41 | 0 | 0.25 | 0 | 0 |
| MNP1 | 1.03 | 0 | 0.36 | 0 | 0.25 | 0 | 0 |
| SOK1 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| PRE8 | 3.32 | 1.77 | 1.16 | 1.16 | 0.25 | 0 | 0 |
| PRE5 | 1.46 | 0 | 0.3 | 0 | 0.25 | 0 | 0 |
| PRE7 | 1.25 | 0 | 0.45 | 0 | 0.25 | 0 | 0 |
| PRE6 | 0.92 | 0 | 0.33 | 0 | 0.25 | 0 | 0 |
| PRE2 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| EXO84 | 2.29 | 0 | 0.96 | 0 | 0.25 | 0 | 0 |
| APA1 | 1.79 | 0 | 0.32 | 0 | 0.25 | 0 | 0 |
| PRE10 | 4.05 | 0 | 1.91 | 0 | 0.25 | 0 | 0 |
| STU2 | 4.05 | 0 | 1.91 | 0 | 0.25 | 0 | 0 |
| DCP1 | 1.33 | 0 | 0.69 | 0 | 0.25 | 0 | 0 |
| STU1 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| GPI15 | 4.49 | 0 | 1.97 | 0 | 0.25 | 0 | 0 |
| NOC2 | 1.83 | 0 | 0.87 | 0 | 0.25 | 0 | 0 |
| NOC4 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| COG8 | 1.13 | 0 | 0.62 | 0 | 0.25 | 0 | 0 |
| COG2 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| COG6 | 3.37 | 0 | 1.53 | 0 | 0.25 | 0 | 0 |
| COG5 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| COG4 | 2.33 | 0 | 1.59 | 0 | 0.25 | 0 | 0 |
| CDC9 | 5.57 | 0 | 2.1 | 0 | 0.25 | 0 | 0 |
| SMY2 | 2.8 | 2.1 | 1.27 | 1.41 | 0.25 | 0 | 0 |
| SMY1 | 1.66 | 0 | 0.73 | 0 | 0.25 | 0 | 0 |
| HTL1 | 1.67 | 0 | 1.06 | 0 | 0.25 | 0 | 0 |
| SER1 | 3.29 | 0 | 0.94 | 0 | 0.25 | 0 | 0 |
| CDD1 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 9

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| EBS1 | 1.23 | 0 | 0.63 | 0 | 0.25 | 0 | 0 |
| NRD1 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| CEX1 | 3.2 | 0 | 0.77 | 0 | 0.25 | 0 | 0 |
| CTR86 | 2.23 | 0 | 1.11 | 0 | 0.25 | 0 | 0 |
| BUD7 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| BUD6 | 3.29 | 0 | 1.78 | 0 | 0.25 | 0 | 0 |
| LSC1 | 0.87 | 0 | 0.14 | 0 | 0.25 | 0 | 0 |
| RTS1 | 6.33 | 0 | 2.17 | 0 | 0.25 | 0 | 0 |
| RIX1 | 1.12 | 0 | 0.54 | 0 | 0.25 | 0 | 0 |
| RIX7 | 1.44 | 2.27 | 1.12 | 1.65 | 0.25 | 0 | 0 |
| PIM1 | 1.32 | 0.51 | 0.32 | 0.29 | 0.25 | 0 | 0 |
| MLC1 | 3.24 | 0.52 | 0.84 | 0.25 | 0.25 | 0 | 0 |
| GYP6 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| EFM1 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| RSE1 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| ARP9 | 3.48 | 0 | 1.01 | 0 | 0.25 | 0 | 0 |
| ARP7 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| PBA1 | 2.27 | 0 | 0.71 | 0 | 0.25 | 0 | 0 |
| PSA1 | 4.79 | 0.43 | 0.23 | 0.07 | 0.25 | 0 | 0 |
| UBP13 | 2.7 | 0 | 1.18 | 0 | 0.25 | 0 | 0 |
| CMP2 | 5.1 | 0 | 1.55 | 0 | 0.25 | 0 | 0 |
| MCX1 | 1.33 | 0 | 0.71 | 0 | 0.25 | 0 | 0 |
| BRO1 | 1.66 | 0 | 0.67 | 0 | 0.25 | 0 | 0 |
| RSC58 | 1.5 | 1.52 | 0.69 | 0.84 | 0.25 | 0 | 0 |
| RPS30B | 3.08 | 0 | 0.79 | 0 | 0.25 | 0 | 0 |
| PTA1 | 1.44 | 2.18 | 1.12 | 1.61 | 0.25 | 0 | 0 |
| RGD1 | 1.79 | 0 | 1.23 | 0 | 0.25 | 0 | 0 |
| RGD2 | 1.62 | 0 | 0.52 | 0 | 0.25 | 0 | 0 |
| DBP9 | 4.81 | 0 | 2.01 | 0 | 0.25 | 0 | 0 |
| DBP6 | 1.66 | 0 | 1.05 | 0 | 0.25 | 0 | 0 |
| DBP5 | 1.82 | 0.71 | 0.25 | 0.48 | 0.25 | 0 | 0 |
| MYO4 | 3.05 | 0 | 1.16 | 0 | 0.25 | 0 | 0 |
| PUP3 | 3.48 | 0 | 1.82 | 0 | 0.25 | 0 | 0 |
| MDJ1 | 1.45 | 0 | 0.81 | 0 | 0.25 | 0 | 0 |
| SHE4 | 2.52 | 0 | 1.63 | 0 | 0.25 | 0 | 0 |
| DOM34 | 1.84 | 0 | 0.8 | 0 | 0.25 | 0 | 0 |
| ETT1 | 3.55 | 0 | 0.56 | 0 | 0.25 | 0 | 0 |
| SNX3 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| SNX4 | 1.79 | 0 | 0.93 | 0 | 0.25 | 0 | 0 |
| BIM1 | 2.15 | 0 | 1.16 | 0 | 0.25 | 0 | 0 |
| STE20 | 1.87 | 0 | 0.9 | 0 | 0.25 | 0 | 0 |
| PTP3 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 10

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| KAP123 | 1.63 | 0.93 | 0.1 | 0.16 | 0.25 | 0 | 0 |
| KAP122 | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| RFC5 | 2.71 | 0 | 1.67 | 0 | 0.25 | 0 | 0 |
| RFC4 | 3.48 | 2.47 | 1.82 | 1.98 | 0.25 | 0 | 0 |
| RFC1 | 1.5 | 0 | 0.54 | 0 | 0.25 | 0 | 0 |
| RRP3 | 2.2 | 0 | 0.39 | 0 | 0.25 | 0 | 0 |
| SRP72 | 3.98 | 0 | 1.27 | 0 | 0.25 | 0 | 0 |
| MCK1 | 1.41 | 0 | 0.52 | 0 | 0.25 | 0 | 0 |
| YDR161W | 2.9 | 0 | 0.99 | 0 | 0.25 | 0 | 0 |
| SWA2 | 2.68 | 0 | 1.43 | 0 | 0.25 | 0 | 0 |
| YKR018C | 2.21 | 0 | 0.48 | 0 | 0.25 | 0 | 0 |
| PPZ1 | 0.99 | 0 | 0.57 | 0 | 0.25 | 0 | 0 |
| YGL082W | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| CKA2 | 1.85 | 0 | 0.99 | 0 | 0.25 | 0 | 0 |
| AIM17 | 1.76 | 2.38 | 1.42 | 1.94 | 0.25 | 0 | 0 |
| SEC28 | 3.72 | 1.44 | 0.95 | 0.85 | 0.25 | 0 | 0 |
| EXO70 | 3.86 | 0 | 1.88 | 0 | 0.25 | 0 | 0 |
| RIM15 | 1.6 | 0 | 0.98 | 0 | 0.25 | 0 | 0 |
| MET10 | 2.02 | 0 | 0.85 | 0 | 0.25 | 0 | 0 |
| MET18 | 3.14 | 0 | 1.06 | 0 | 0.25 | 0 | 0 |
| PET54 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| DHH1 | 2.88 | 0 | 0.79 | 0 | 0.25 | 0 | 0 |
| NOP10 | 2.9 | 0 | 1.71 | 0 | 0.25 | 0 | 0 |
| RMT2 | 1.45 | 0 | 0.71 | 0 | 0.25 | 0 | 0 |
| CCR4 | 1.58 | 0 | 0.41 | 0 | 0.25 | 0 | 0 |
| RPS25A | 3.06 | 0.16 | 0.27 | 0.06 | 0.25 | 0 | 0 |
| IMG2 | 2.04 | 0 | 0.99 | 0 | 0.25 | 0 | 0 |
| UBX4 | 2.23 | 0 | 1.11 | 0 | 0.25 | 0 | 0 |
| SEC1 | 4.69 | 0 | 1.06 | 0 | 0.25 | 0 | 0 |
| SEC5 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| SEC7 | 4.38 | 1.01 | 0.63 | 0.49 | 0.25 | 0 | 0 |
| SEC8 | 3.86 | 0 | 1.88 | 0 | 0.25 | 0 | 0 |
| VMA5 | 1.47 | 0.61 | 0.22 | 0.16 | 0.25 | 0 | 0 |
| NUM1 | 2.53 | 0 | 0.67 | 0 | 0.25 | 0 | 0 |
| RRP46 | 1.57 | 0 | 1.35 | 0 | 0.25 | 0 | 0 |
| NET1 | 1.66 | 0 | 0.53 | 0 | 0.25 | 0 | 0 |
| ASR1 | 5.65 | 0 | 2.1 | 0 | 0.25 | 0 | 1 |
| CYC8 | 1.66 | 0 | 0.73 | 0 | 0.25 | 0 | 0 |
| PRS3 | 1.06 | 0 | 0.2 | 0 | 0.25 | 0 | 0 |
| KAP95 | 3.5 | 0 | 0.66 | 0 | 0.25 | 0 | 0 |
| MOT1 | 1.07 | 0 | 0.64 | 0 | 0.25 | 0 | 0 |
| PBS2 | 4.24 | 0 | 0.94 | 0 | 0.25 | 0 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 11

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| EKI1 | 1.59 | 0 | 1.13 | 0 | 0.25 | 0 | 0 |
| DNM1 | 2.03 | 0 | 0.44 | 0 | 0.25 | 0 | 0 |
| SFH1 | 2.67 | 0 | 1.06 | 0 | 0.25 | 0 | 0 |
| BCH1 | 1.64 | 0 | 0.9 | 0 | 0.25 | 0 | 0 |
| TAF5 | 2 | 0 | 0.74 | 0 | 0.25 | 0 | 0 |
| TAF4 | 2.52 | 0 | 1.63 | 0 | 0.25 | 0 | 0 |
| TAF9 | 1.83 | 0 | 0.79 | 0 | 0.25 | 0 | 0 |
| KIP2 | 1.76 | 2.38 | 1.42 | 1.94 | 0.25 | 0 | 0 |
| RPA49 | 3.72 | 0 | 1.07 | 0 | 0.25 | 0 | 0 |
| SRO9 | 3.43 | 0.31 | 0.69 | 0.11 | 0.25 | 0 | 0 |
| SRO7 | 3.86 | 0 | 1.88 | 0 | 0.25 | 0 | 0 |
| KAP104 | 2.71 | 0 | 1.67 | 0 | 0.25 | 0 | 0 |
| YMR130W | 2.14 | 0 | 1.54 | 0 | 0.25 | 0 | 0 |
| CSR1 | 1.45 | 0 | 0.37 | 0 | 0.25 | 0 | 0 |
| RLP7 | 1.82 | 0 | 0.86 | 0 | 0.25 | 0 | 0 |
| ORC4 | 1.76 | 0 | 1.42 | 0 | 0.25 | 0 | 0 |
| ORC5 | 1.95 | 0 | 1.48 | 0 | 0.25 | 0 | 0 |
| ORC1 | 1.07 | 0 | 0.64 | 0 | 0.25 | 0 | 0 |
| SNF2 | 2.04 | 1.05 | 0.54 | 0.53 | 0.25 | 0 | 0 |
| RTT107 | 1.38 | 84.7 | 1.26 | 12.98 | 0.24 | 0.5 | 0 |
| PRP2 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| HYM1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ATP12 | 1.28 | 0 | 0.67 | 0 | 0.24 | 0 | 0 |
| CPR6 | 1.49 | 0 | 0.3 | 0 | 0.24 | 0 | 0 |
| GAR1 | 1.36 | 0 | 0.31 | 0 | 0.24 | 0 | 0 |
| SPB4 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| PDR16 | 1.28 | 0 | 0.26 | 0 | 0.24 | 0 | 0 |
| SSK1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| BUD4 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| TAE2 | 1.53 | 0 | 0.65 | 0 | 0.24 | 0 | 0 |
| STE12 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| AAT1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MTR2 | 1.29 | 0 | 0.89 | 0 | 0.24 | 0 | 0 |
| HFA1 | 1.63 | 0 | 0.79 | 0 | 0.24 | 0 | 0 |
| ZIP2 | 1.6 | 0 | 1.17 | 0 | 0.24 | 0 | 0 |
| UFD2 | 1.23 | 0 | 0.57 | 0 | 0.24 | 0 | 0 |
| MRE11 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ISW1 | 1.82 | 0 | 0.57 | 0 | 0.24 | 0 | 0 |
| SAP190 | 0.94 | 0 | 0.6 | 0 | 0.24 | 0 | 0 |
| RPC40 | 1.31 | 1.11 | 0.37 | 0.48 | 0.24 | 0 | 0 |
| SKG3 | 0.94 | 0 | 0.6 | 0 | 0.24 | 0 | 0 |
| DPH1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 12

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| PPN1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MED7 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SAP1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SSN2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| KRE33 | 2.3 | 0 | 0.75 | 0 | 0.24 | 0 | 0 |
| YIL151C | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| PPZ2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| NUF2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ATG2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| GCD7 | 1.45 | 1.32 | 0.55 | 0.65 | 0.24 | 0 | 0 |
| ATG20 | 1.29 | 0 | 0.89 | 0 | 0.24 | 0 | 0 |
| SWT1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MAF1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SRB2 | 1.28 | 0 | 0.54 | 0 | 0.24 | 0 | 0 |
| YPL245W | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ARF3 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SLA2 | 1.97 | 0 | 0.38 | 0 | 0.24 | 0 | 0 |
| BYE1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| EMI2 | 1.35 | 0 | 0.83 | 0 | 0.24 | 0 | 0 |
| SSU72 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YTA6 | 1.09 | 0 | 0.78 | 0 | 0.24 | 0 | 0 |
| YTA7 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SUP35 | 1.19 | 0 | 0.23 | 0 | 0.24 | 0 | 0 |
| PCL7 | 3.33 | 0 | 1.79 | 0 | 0.24 | 0 | 0 |
| SSL1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YML13 | 1.3 | 0 | 0.51 | 0 | 0.24 | 0 | 0 |
| CFD1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MSN2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MAD3 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MDM38 | 1.74 | 0 | 1.41 | 0 | 0.24 | 0 | 0 |
| PSY2 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| HAL5 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| BDF1 | 1.29 | 0 | 0.89 | 0 | 0.24 | 0 | 0 |
| MAE1 | 0.86 | 0 | 0.13 | 0 | 0.24 | 0 | 0 |
| GLC7 | 1.37 | 0 | 0.5 | 0 | 0.24 | 0 | 0 |
| EGD1 | 2.61 | 0 | 0.86 | 0 | 0.24 | 0 | 0 |
| VIP1 | 0.83 | 0 | 0.21 | 0 | 0.24 | 0 | 0 |
| HEM15 | 1.14 | 0 | 0.49 | 0 | 0.24 | 0 | 0 |
| COQ1 | 1.29 | 0 | 0.89 | 0 | 0.24 | 0 | 0 |
| YMR111C | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| RKM3 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SPT20 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| TAO3 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| CDC25 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| TPD3 | 1.32 | 0 | 0.52 | 0 | 0.24 | 0 | 0 |
| RPL35A | 1.74 | 0.18 | 0.08 | 0.05 | 0.24 | 0 | 0 |
| NUP84 | 1.27 | 2.18 | 1.05 | 1.61 | 0.24 | 0 | 0 |
| MHP1 | 1.29 | 0 | 0.89 | 0 | 0.24 | 0 | 0 |
| RTT106 | 1.53 | 0 | 0.65 | 0 | 0.24 | 0 | 0 |
| VPS9 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| RPT3 | 0.96 | 0 | 0.17 | 0 | 0.24 | 0 | 0 |
| RET1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| GCD11 | 2.05 | 0.25 | 0.4 | 0.13 | 0.24 | 0 | 0 |
| POP2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| PIH1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| IML2 | 1.29 | 2.03 | 0.89 | 1.32 | 0.24 | 0 | 0 |
| RPN13 | 1.29 | 0.93 | 0.43 | 0.47 | 0.24 | 0 | 0 |
| MON2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SNU13 | 3.24 | 0 | 0.88 | 0 | 0.24 | 0 | 0 |
| SCY1 | 1.29 | 0 | 0.89 | 0 | 0.24 | 0 | 0 |
| ELP6 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| CAF20 | 1.49 | 0 | 0.63 | 0 | 0.24 | 0 | 0 |
| NOP56 | 3.1 | 0 | 0.96 | 0 | 0.24 | 0 | 0 |
| GRH1 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| NUG1 | 1.28 | 0.45 | 0.24 | 0.21 | 0.24 | 0 | 0 |
| URA8 | 1.37 | 0 | 0.29 | 0 | 0.24 | 0 | 0 |
| SRP21 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| RRP8 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| SIR4 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| SEC18 | 1.18 | 0 | 0.25 | 0 | 0.24 | 0 | 0 |
| SEC15 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| HIS5 | 1.48 | 0 | 0.68 | 0 | 0.24 | 0 | 0 |
| PRE9 | 1.06 | 0 | 0.37 | 0 | 0.24 | 0 | 0 |
| APS3 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YML19 | 1.55 | 0 | 0.93 | 0 | 0.24 | 0 | 0 |
| YKR078W | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SPT15 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| RFA3 | 1.65 | 0 | 0.58 | 0 | 0.24 | 0 | 0 |
| PCT1 | 1.09 | 0 | 0.78 | 0 | 0.24 | 0 | 0 |
| SSF1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SIS2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| NOT5 | 1.58 | 0 | 0.54 | 0 | 0.24 | 0 | 0 |
| AVL9 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| CCT6 | 1.55 | 0.44 | 0.2 | 0.16 | 0.24 | 0 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 14

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RVB1 | 0.81 | 0 | 0.08 | 0 | 0.24 | 0 | 0 |
| INN1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YMR1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| RGR1 | 1.38 | 2.47 | 1.26 | 1.98 | 0.24 | 0 | 0 |
| SHE2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YBP2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ARA1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ISA1 | 1.74 | 0 | 1.41 | 0 | 0.24 | 0 | 0 |
| ENP2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| PAF1 | 1.27 | 0 | 1.05 | 0 | 0.24 | 0 | 0 |
| MTQ2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| RAD53 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| PRR1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| UGA3 | 5.7 | 0 | 2.11 | 0 | 0.24 | 0 | 0 |
| IES3 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| APT2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| GYL1 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ART10 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SRL2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YMR144W | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| SEC3 | 0.93 | 0 | 0.29 | 0 | 0.24 | 0 | 0 |
| CIN8 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| YLR118C | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| MRM1 | 5.7 | 0 | 2.11 | 0 | 0.24 | 0 | 0 |
| BIO2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ORC2 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| ORC3 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| FLO11 | 1.38 | 0 | 1.26 | 0 | 0.24 | 0 | 0 |
| END3 | 1.31 | 0.53 | 0.34 | 0.23 | 0.23 | 0 | 0 |
| CFT1 | 1.34 | 0 | 0.95 | 0 | 0.23 | 0 | 0 |
| DEF1 | 0.97 | 0 | 0.41 | 0 | 0.23 | 0 | 0 |
| GCD6 | 1.22 | 0 | 0.38 | 0 | 0.23 | 0 | 0 |
| RNR3 | 1.35 | 0 | 0.24 | 0 | 0.23 | 0 | 0 |
| BEM2 | 1.31 | 1.28 | 0.56 | 0.68 | 0.23 | 0 | 0 |
| MCM2 | 1.04 | 0 | 0.41 | 0 | 0.23 | 0 | 0 |
| COQ8 | 1.29 | 0 | 0.5 | 0 | 0.23 | 0 | 0 |
| ACF4 | 1.79 | 0 | 1.08 | 0 | 0.23 | 0 | 0 |
| GDE1 | 1.34 | 0 | 0.95 | 0 | 0.23 | 0 | 0 |
| RET3 | 1.12 | 0 | 0.5 | 0 | 0.23 | 0 | 0 |
| LOC1 | 1.34 | 0 | 0.96 | 0 | 0.23 | 0 | 0 |
| ARC1 | 1.9 | 0 | 0.36 | 0 | 0.23 | 0 | 0 |
| YRA1 | 3.64 | 0.35 | 0.81 | 0.16 | 0.23 | 0 | 0 |

## Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 15

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| SPN1 | 1.26 | 0 | 0.27 | 0 | 0.23 | 0 | 0 |
| PDC2 | 1.34 | 0 | 0.95 | 0 | 0.23 | 0 | 0 |
| YMR315W | 1.29 | 0 | 0.7 | 0 | 0.23 | 0 | 0 |
| SUP45 | 0.89 | 0 | 0.14 | 0 | 0.23 | 0 | 0 |
| RPC19 | 1.43 | 0 | 0.89 | 0 | 0.23 | 0 | 0 |
| NOP14 | 1.3 | 0 | 0.61 | 0 | 0.23 | 0 | 0 |
| RPA190 | 1 | 0 | 0.19 | 0 | 0.23 | 0 | 0 |
| UTP7 | 1.39 | 0 | 0.88 | 0 | 0.23 | 0 | 0 |
| VMA6 | 1.37 | 0 | 0.22 | 0 | 0.23 | 0 | 0 |
| TAF6 | 2.33 | 0 | 0.8 | 0 | 0.23 | 0 | 0 |
| CMS1 | 1.3 | 0 | 0.61 | 0 | 0.23 | 0 | 0 |
| IVY1 | 2.45 | 0 | 0.94 | 0 | 0.22 | 0 | 0 |
| YNL208W | 0.75 | 0 | 0.16 | 0 | 0.22 | 0 | 0 |
| MDR1 | 0.93 | 0 | 0.52 | 0 | 0.22 | 0 | 0 |
| RPN6 | 1.08 | 0 | 0.24 | 0 | 0.22 | 0 | 0 |
| YLL032C | 1.02 | 0 | 0.52 | 0 | 0.22 | 0 | 0 |
| DPH6 | 1.2 | 0 | 0.79 | 0 | 0.22 | 0 | 0 |
| GCD2 | 1.25 | 0 | 0.52 | 0 | 0.22 | 0 | 0 |
| SRP1 | 0.98 | 0 | 0.31 | 0 | 0.22 | 0 | 0 |
| SHS1 | 1.18 | 0 | 0.4 | 0 | 0.22 | 0 | 0 |
| RSC2 | 1.25 | 0 | 0.52 | 0 | 0.22 | 0 | 0 |
| SUM1 | 1.21 | 0 | 0.79 | 0 | 0.22 | 0 | 0 |
| RPL37A | 1.43 | 0 | 0.39 | 0 | 0.22 | 0 | 0 |
| UBP3 | 3.06 | 0 | 1.08 | 0 | 0.22 | 0 | 0 |
| HAS1 | 1.64 | 0 | 0.61 | 0 | 0.22 | 0 | 0 |
| IDH1 | 0.85 | 1.04 | 0.37 | 0.48 | 0.22 | 0 | 0 |
| SLY1 | 0.92 | 0 | 0.24 | 0 | 0.22 | 0 | 0 |
| SPE3 | 0.98 | 0 | 0.56 | 0 | 0.22 | 0 | 0 |
| SEC65 | 1.12 | 0 | 0.53 | 0 | 0.22 | 0 | 0 |
| RRP6 | 1.16 | 1.56 | 0.64 | 0.87 | 0.22 | 0 | 0 |
| RSC8 | 0.88 | 0 | 0.41 | 0 | 0.22 | 0 | 0 |
| NOC3 | 1.2 | 0 | 0.79 | 0 | 0.22 | 0 | 0 |
| RPO41 | 1.21 | 0 | 0.46 | 0 | 0.22 | 0 | 0 |
| TRP4 | 1.16 | 0 | 0.64 | 0 | 0.22 | 0 | 0 |
| TAF11 | 1.16 | 0 | 0.64 | 0 | 0.22 | 0 | 0 |
| PAT1 | 1.18 | 0 | 0.68 | 0 | 0.22 | 0 | 0 |
| TAP42 | 1.07 | 12.15 | 0.41 | 1.9 | 0.21 | 0.5 | 0 |
| ATP11 | 1.15 | 0 | 0.51 | 0 | 0.21 | 0 | 0 |
| NOP7 | 1.81 | 0 | 0.89 | 0 | 0.21 | 0 | 0 |
| SPA2 | 1.09 | 0 | 0.26 | 0 | 0.21 | 0 | 0 |
| BUL2 | 0.95 | 0 | 0.54 | 0 | 0.21 | 0 | 0 |
| EMW1 | 1.25 | 0 | 0.84 | 0 | 0.21 | 0 | 0 |

## Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 16

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RSC4 | 0.55 | 0 | 0.21 | 0 | 0.21 | 0 | 0 |
| MAK31 | 1.09 | 0 | 0.64 | 0 | 0.21 | 0 | 0 |
| NOP15 | 1.23 | 0 | 0.71 | 0 | 0.21 | 0 | 0 |
| COP1 | 1.21 | 0 | 0.23 | 0 | 0.21 | 0 | 0 |
| GEA2 | 0.74 | 0.9 | 0.34 | 0.45 | 0.21 | 0 | 0 |
| MKT1 | 0.64 | 0.65 | 0.27 | 0.33 | 0.21 | 0 | 0 |
| BNA3 | 1.05 | 0 | 0.46 | 0 | 0.21 | 0 | 0 |
| DUO1 | 1.25 | 0 | 0.84 | 0 | 0.21 | 0 | 0 |
| PAN1 | 2.12 | 0 | 0.49 | 0 | 0.21 | 0 | 0 |
| MCM4 | 0.93 | 0 | 0.33 | 0 | 0.21 | 0 | 0 |
| RCY1 | 1.12 | 1.42 | 0.54 | 0.73 | 0.21 | 0 | 0 |
| SFM1 | 1.26 | 0 | 0.59 | 0 | 0.21 | 0 | 0 |
| SIN3 | 1.23 | 0 | 0.61 | 0 | 0.21 | 0 | 0 |
| COG3 | 0.87 | 2.14 | 0.47 | 1.35 | 0.21 | 0 | 0 |
| CDC55 | 1.24 | 0 | 0.83 | 0 | 0.21 | 0 | 0 |
| SWC4 | 0.92 | 0 | 0.51 | 0 | 0.21 | 0 | 0 |
| CCT8 | 0.94 | 0.13 | 0.15 | 0.07 | 0.21 | 0 | 0 |
| CCT7 | 0.88 | 0.55 | 0.12 | 0.15 | 0.21 | 0 | 0 |
| ADE6 | 1.13 | 1.05 | 0.27 | 0.36 | 0.21 | 0 | 0 |
| RAD51 | 1.25 | 0 | 0.84 | 0 | 0.21 | 0 | 0 |
| YGL039W | 1.07 | 0 | 0.49 | 0 | 0.21 | 0 | 0 |
| GBP2 | 3.51 | 0 | 0.95 | 0 | 0.21 | 0 | 0 |
| MRT4 | 1.04 | 0 | 0.32 | 0 | 0.21 | 0 | 0 |
| MCM7 | 1.12 | 2.4 | 0.67 | 1.2 | 0.2 | 0.16 | 0 |
| IMP2_P | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| SMD2 | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| SGN1 | 4.84 | 0 | 1.49 | 0 | 0.2 | 0 | 0 |
| FKH2 | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| YMR226C | 1.05 | 0 | 0.52 | 0 | 0.2 | 0 | 0 |
| LSM2 | 1.02 | 0 | 0.4 | 0 | 0.2 | 0 | 0 |
| DIS3 | 1.13 | 0 | 0.79 | 0 | 0.2 | 0 | 0 |
| SAR1 | 0.79 | 0.43 | 0.08 | 0.07 | 0.2 | 0 | 0 |
| VHR2 | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| RNT1 | 0.9 | 0 | 0.56 | 0 | 0.2 | 0 | 0 |
| YHR097C | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| TFC4 | 1.48 | 0 | 1 | 0 | 0.2 | 0 | 0 |
| RRP5 | 1.12 | 0 | 0.37 | 0 | 0.2 | 0 | 0 |
| YML16 | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| SSF2 | 1.17 | 0 | 0.89 | 0 | 0.2 | 0 | 0 |
| YNL155W | 1.13 | 0 | 0.84 | 0 | 0.2 | 0 | 0 |
| PUP1 | 1.16 | 0 | 0.74 | 0 | 0.2 | 0 | 0 |
| DBF2 | 1.17 | 0 | 0.89 | 0 | 0.2 | 0 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 17

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| MAS2 | 1.17 | 0 | 0.89 | 0 | 0.2 | 0 | 0 |
| BBC1 | 1.09 | 0 | 0.52 | 0 | 0.2 | 0 | 0 |
| OM45 | 1.43 | 0 | 0.93 | 0 | 0.2 | 0 | 0 |
| PPM1 | 1.17 | 0 | 0.89 | 0 | 0.2 | 0 | 0 |
| PGA3 | 1.77 | 0 | 0.96 | 0 | 0.19 | 0 | 0 |
| CAP1 | 1.22 | 0 | 0.59 | 0 | 0.19 | 0 | 0 |
| PUF3 | 1.12 | 0 | 0.61 | 0 | 0.19 | 0 | 0 |
| KRR1 | 1.07 | 0 | 0.56 | 0 | 0.19 | 0 | 0 |
| SET2 | 1.09 | 0 | 0.67 | 0 | 0.19 | 0 | 1 |
| MRS6 | 1.12 | 0 | 0.61 | 0 | 0.19 | 0 | 0 |
| HSE1 | 1.07 | 1.44 | 0.56 | 0.77 | 0.19 | 0 | 0 |
| TAF10 | 1.29 | 0 | 0.78 | 0 | 0.19 | 0 | 0 |
| SRP68 | 0.74 | 0 | 0.29 | 0 | 0.19 | 0 | 0 |
| BNI1 | 1.04 | 0 | 0.54 | 0 | 0.18 | 0 | 0 |
| SPT5 | 2.8 | 0 | 0.9 | 0 | 0.18 | 0 | 1 |
| UBP2 | 1.04 | 0 | 0.54 | 0 | 0.18 | 0 | 0 |
| OXP1 | 1.01 | 0 | 0.52 | 0 | 0.18 | 0 | 0 |
| NUP188 | 1.03 | 0 | 0.61 | 0 | 0.18 | 0 | 0 |
| SLH1 | 1.03 | 0 | 0.61 | 0 | 0.18 | 0 | 0 |
| KIN1 | 0.62 | 0 | 0.27 | 0 | 0.18 | 0 | 0 |
| RBG1 | 0.77 | 0 | 0.42 | 0 | 0.17 | 0 | 0 |
| RBL2 | 1.09 | 0 | 0.67 | 0 | 0.17 | 0 | 0 |
| SSK2 | 0.48 | 0 | 0.23 | 0 | 0.17 | 0 | 0 |
| ATP2 | 1.11 | 0.47 | 0.13 | 0.09 | 0.17 | 0 | 0 |
| LPD1 | 0.95 | 0 | 0.26 | 0 | 0.17 | 0 | 0 |
| GND1 | 2.46 | 1.1 | 0.8 | 0.32 | 0.17 | 0 | 0 |
| CHS5 | 1.09 | 0 | 0.67 | 0 | 0.17 | 0 | 0 |
| SEC21 | 0.83 | 0.38 | 0.21 | 0.2 | 0.17 | 0 | 0 |
| PRS4 | 1 | 0 | 0.49 | 0 | 0.17 | 0 | 0 |
| EAF3 | 0.77 | 2.08 | 0.44 | 0.89 | 0.16 | 0.32 | 0 |
| NOP1 | 4.47 | 0 | 0.93 | 0 | 0.16 | 0 | 0 |
| ENT5 | 1.06 | 0 | 0.74 | 0 | 0.16 | 0 | 0 |
| MET5 | 0.51 | 0 | 0.23 | 0 | 0.16 | 0 | 0 |
| BMS1 | 1.09 | 0 | 0.78 | 0 | 0.16 | 0 | 0 |
| AFG2 | 0.95 | 0 | 0.53 | 0 | 0.16 | 0 | 0 |
| YGR266W | 1.06 | 1.89 | 0.74 | 1.16 | 0.16 | 0 | 0 |
| SMC2 | 0.68 | 0 | 0.37 | 0 | 0.16 | 0 | 0 |
| TMA64 | 1.06 | 0 | 0.74 | 0 | 0.16 | 0 | 0 |
| ARL1 | 0.95 | 0 | 0.53 | 0 | 0.16 | 0 | 0 |
| DIG1 | 0.99 | 0 | 0.5 | 0 | 0.16 | 0 | 0 |
| YGP1 | 0.77 | 0 | 0.44 | 0 | 0.16 | 0 | 0 |
| IMG1 | 1.06 | 0 | 0.74 | 0 | 0.16 | 0 | 0 |

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| YIR035C | 1.06 | 0 | 0.74 | 0 | 0.16 | 0 | 0 |
| SNF4 | 0.95 | 0 | 0.53 | 0 | 0.16 | 0 | 0 |
| PRO3 | 0.54 | 0 | 0.27 | 0 | 0.15 | 0 | 0 |
| ASC1 | 0.58 | 0 | 0.16 | 0 | 0.15 | 0 | 0 |
| MIS1 | 0.98 | 0 | 0.56 | 0 | 0.15 | 0 | 0 |
| PAA1 | 0.92 | 0.66 | 0.27 | 0.29 | 0.15 | 0 | 0 |
| SFB2 | 0.78 | 0 | 0.46 | 0 | 0.15 | 0 | 0 |
| ALD6 | 0.45 | 0 | 0.14 | 0 | 0.15 | 0 | 0 |
| INP53 | 1 | 0 | 0.63 | 0 | 0.15 | 0 | 0 |
| TPS2 | 1.35 | 1.47 | 0.29 | 0.45 | 0.14 | 0 | 0 |
| ADI1 | 0.96 | 0 | 0.62 | 0 | 0.14 | 0 | 0 |
| ATG17 | 0.96 | 0 | 0.62 | 0 | 0.14 | 0 | 0 |
| MCM6 | 0.79 | 0 | 0.35 | 0 | 0.14 | 0 | 0 |
| YJU2 | 0.96 | 0 | 0.62 | 0 | 0.14 | 0 | 0 |
| LAT1 | 1.05 | 1.63 | 0.24 | 0.32 | 0.14 | 0 | 0 |
| HAP5 | 0.96 | 0 | 0.62 | 0 | 0.14 | 0 | 0 |
| SCL1 | 0.89 | 0 | 0.32 | 0 | 0.13 | 0 | 0 |
| PRO2 | 0.99 | 0 | 0.66 | 0 | 0.13 | 0 | 0 |
| ABF2 | 1.38 | 0 | 0.36 | 0 | 0.13 | 0 | 0 |
| NUP2 | 0.91 | 0 | 0.41 | 0 | 0.13 | 0 | 0 |
| PIK1 | 0.92 | 0 | 0.51 | 0 | 0.13 | 0 | 0 |
| CDC10 | 0.76 | 0 | 0.33 | 0 | 0.13 | 0 | 0 |
| NIF3 | 0.36 | 0 | 0.17 | 0 | 0.13 | 0 | 0 |
| YNK1 | 0.91 | 0 | 0.5 | 0 | 0.13 | 0 | 0 |
| RPT2 | 0.77 | 0 | 0.16 | 0 | 0.13 | 0 | 0 |
| RET2 | 0.9 | 0 | 0.57 | 0 | 0.13 | 0 | 0 |
| CDC33 | 0.65 | 0 | 0.16 | 0 | 0.13 | 0 | 0 |
| SCD6 | 1.3 | 0 | 0.32 | 0 | 0.13 | 0 | 0 |
| GLR1 | 0.93 | 0 | 0.55 | 0 | 0.13 | 0 | 0 |
| SGT1 | 0.99 | 1.71 | 0.74 | 1.13 | 0.13 | 0 | 0 |
| GIN4 | 0.99 | 0 | 0.66 | 0 | 0.13 | 0 | 0 |
| FAP7 | 0.88 | 0 | 0.41 | 0 | 0.13 | 0 | 0 |
| MRI1 | 0.97 | 0 | 0.37 | 0 | 0.12 | 0 | 0 |
| RAD23 | 0.88 | 0 | 0.48 | 0 | 0.12 | 0 | 0 |
| RPT4 | 0.76 | 0.75 | 0.26 | 0.29 | 0.12 | 0 | 0 |
| PAL1 | 0.96 | 0 | 0.63 | 0 | 0.12 | 0 | 0 |
| DOP1 | 0.84 | 0 | 0.44 | 0 | 0.12 | 0 | 0 |
| PRS2 | 0.76 | 2.16 | 0.43 | 0.9 | 0.11 | 0.21 | 0 |
| YKL033W_A | 0.91 | 0 | 0.57 | 0 | 0.11 | 0 | 0 |
| NOP4 | 0.91 | 0 | 0.57 | 0 | 0.11 | 0 | 0 |
| PBI2 | 0.91 | 0 | 0.57 | 0 | 0.11 | 0 | 0 |
| NUP157 | 0.91 | 0 | 0.57 | 0 | 0.11 | 0 | 0 |

## Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 19

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RDH54 | 0.91 | 0 | 0.57 | 0 | 0.11 | 0 | 0 |
| RPA12 | 0.94 | 0 | 0.6 | 0 | 0.11 | 0 | 0 |
| CAB5 | 0.91 | 0 | 0.57 | 0 | 0.11 | 0 | 0 |
| ATP10 | 0.88 | 2.2 | 0.51 | 1 | 0.1 | 0.07 | 0 |
| LSM1 | 0.89 | 0 | 0.55 | 0 | 0.1 | 0 | 0 |
| CMK2 | 1.54 | 0.37 | 0.39 | 0.19 | 0.1 | 0 | 0 |
| YTM1 | 0.72 | 0 | 0.42 | 0 | 0.1 | 0 | 0 |
| SED5 | 0.85 | 1.19 | 0.4 | 0.56 | 0.1 | 0 | 0 |
| ARO4 | 0.69 | 0.63 | 0.19 | 0.37 | 0.1 | 0 | 0 |
| MPP10 | 0.93 | 1.61 | 0.66 | 1.01 | 0.1 | 0 | 0 |
| CAJ1 | 1.42 | 0.2 | 0.27 | 0.09 | 0.1 | 0 | 0 |
| SAP155 | 0.84 | 0 | 0.5 | 0 | 0.1 | 0 | 0 |
| KIN2 | 0.84 | 0 | 0.5 | 0 | 0.1 | 0 | 0 |
| COG7 | 0.71 | 1.59 | 0.39 | 0.72 | 0.09 | 0.02 | 0 |
| IPI3 | 0.84 | 0 | 0.38 | 0 | 0.09 | 0 | 0 |
| SPT6 | 0.72 | 0 | 0.23 | 0 | 0.09 | 0 | 0 |
| SHE3 | 0.81 | 0 | 0.44 | 0 | 0.09 | 0 | 0 |
| GLK1 | 0.82 | 0 | 0.32 | 0 | 0.09 | 0 | 0 |
| MRPS17 | 0.83 | 0 | 0.34 | 0 | 0.09 | 0 | 0 |
| BZZ1 | 0.86 | 6.09 | 0.52 | 1.78 | 0.08 | 0.49 | 0 |
| SPB1 | 0.58 | 0 | 0.25 | 0 | 0.08 | 0 | 0 |
| RXT2 | 0.86 | 0 | 0.52 | 0 | 0.08 | 0 | 0 |
| LSM6 | 0.88 | 0 | 0.59 | 0 | 0.08 | 0 | 0 |
| RPN12 | 0.87 | 0 | 0.19 | 0 | 0.08 | 0 | 0 |
| TWF1 | 0.83 | 0 | 0.18 | 0 | 0.08 | 0 | 0 |
| TSR4 | 0.88 | 0 | 0.6 | 0 | 0.08 | 0 | 0 |
| CCT4 | 0.56 | 1.18 | 0.12 | 0.35 | 0.08 | 0 | 0 |
| YGR126W | 0.35 | 0 | 0.14 | 0 | 0.07 | 0 | 0 |
| CCT5 | 0.62 | 0 | 0.12 | 0 | 0.07 | 0 | 0 |
| PGD1 | 1.43 | 0 | 0.71 | 0 | 0.07 | 0 | 0 |
| NOP2 | 0.79 | 0 | 0.31 | 0 | 0.06 | 0 | 0 |
| RPN2 | 0.8 | 0 | 0.27 | 0 | 0.06 | 0 | 0 |
| EBP2 | 0.84 | 0 | 0.55 | 0 | 0.06 | 0 | 1 |
| URA2 | 1.13 | 0.05 | 0.22 | 0.03 | 0.06 | 0 | 1 |
| TAF14 | 0.82 | 0 | 0.47 | 0 | 0.06 | 0 | 1 |
| CSE1 | 0.59 | 0.71 | 0.26 | 0.34 | 0.06 | 0 | 0 |
| NAT1 | 1.7 | 0 | 0.3 | 0 | 0.06 | 0 | 0 |
| CYS3 | 0.45 | 0 | 0.17 | 0 | 0.06 | 0 | 0 |
| SCP1 | 0.77 | 0 | 0.29 | 0 | 0.06 | 0 | 0 |
| BFR2 | 0.78 | 0 | 0.36 | 0 | 0.05 | 0 | 0 |
| PEP4 | 2.97 | 0.2 | 0.67 | 0.09 | 0.05 | 0 | 0 |
| PUB1 | 0.81 | 0 | 0.28 | 0 | 0.05 | 0 | 0 |

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 20

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RRP15 | 1 | 0 | 0.56 | 0 | 0.05 | 0 | 0 |
| ARP3 | 0.69 | 0 | 0.29 | 0 | 0.05 | 0 | 0 |
| NOP12 | 0.8 | 0 | 0.49 | 0 | 0.05 | 0 | 0 |
| DOT5 | 0.81 | 0 | 0.52 | 0 | 0.05 | 0 | 0 |
| TIM9 | 0.41 | 0 | 0.16 | 0 | 0.04 | 0 | 0 |
| PYK2 | 0.79 | 0 | 0.31 | 0 | 0.04 | 0 | 0 |
| SST2 | 0.75 | 0 | 0.43 | 0 | 0.04 | 0 | 0 |
| DAP1 | 0.79 | 0 | 0.51 | 0 | 0.04 | 0 | 0 |
| LSM5 | 0.78 | 0 | 0.48 | 0 | 0.04 | 0 | 0 |
| AIF1 | 0.68 | 0 | 0.37 | 0 | 0.04 | 0 | 0 |
| RPA43 | 0.77 | 0 | 0.48 | 0 | 0.04 | 0 | 0 |
| UTP15 | 0.74 | 0 | 0.45 | 0 | 0.03 | 0 | 0 |
| DIM1 | 0.92 | 0 | 0.42 | 0 | 0.03 | 0 | 0 |
| MCM5 | 0.68 | 0 | 0.24 | 0 | 0.03 | 0 | 0 |
| SAH1 | 0.6 | 0 | 0.2 | 0 | 0.03 | 0 | 0 |
| RSR1 | 0.71 | 0 | 0.39 | 0 | 0.03 | 0 | 0 |
| SMC1 | 0.52 | 0 | 0.23 | 0 | 0.03 | 0 | 0 |
| HMO1 | 0.76 | 0 | 0.3 | 0 | 0.03 | 0 | 0 |
| CYR1 | 0.71 | 1.26 | 0.39 | 0.61 | 0.03 | 0 | 0 |
| LYS4 | 0.89 | 0 | 0.44 | 0 | 0.03 | 0 | 0 |
| PHO85 | 0.69 | 0 | 0.34 | 0 | 0.03 | 0 | 0 |
| FAA4 | 0.58 | 0 | 0.14 | 0 | 0.03 | 0 | 0 |
| CPR1 | 0.38 | 0.46 | 0.14 | 0.18 | 0.02 | 0 | 0 |
| MTR4 | 0.65 | 0 | 0.25 | 0 | 0.02 | 0 | 0 |
| RPO31 | 0.69 | 0 | 0.4 | 0 | 0.02 | 0 | 0 |
| AIM41 | 0.74 | 0.64 | 0.23 | 0.27 | 0.02 | 0 | 0 |
| UBC1 | 0.67 | 0 | 0.37 | 0 | 0.02 | 0 | 0 |
| GET3 | 0.46 | 0.36 | 0.16 | 0.19 | 0.02 | 0 | 0 |
| YML44 | 0.66 | 0 | 0.29 | 0 | 0.02 | 0 | 0 |
| IRC2 | 0.65 | 0 | 0.29 | 0 | 0.02 | 0 | 0 |
| SRV2 | 0.95 | 1.05 | 0.21 | 0.24 | 0.02 | 0 | 0 |
| IKI3 | 0.68 | 0 | 0.28 | 0 | 0.02 | 0 | 0 |
| ARC19 | 0.68 | 0 | 0.39 | 0 | 0.02 | 0 | 0 |
| AHP1 | 0.33 | 1.89 | 0.11 | 0.35 | 0.01 | 0.08 | 0 |
| VAC8 | 0.65 | 1.76 | 0.46 | 0.93 | 0.01 | 0.03 | 0 |
| RPN7 | 0.96 | 0 | 0.46 | 0 | 0.01 | 0 | 0 |
| RPS16A | 1.3 | 0.47 | 0.26 | 0.09 | 0.01 | 0 | 0 |
| GGA1 | 0.62 | 1.07 | 0.33 | 0.5 | 0.01 | 0 | 0 |
| EMG1 | 0.63 | 0 | 0.35 | 0 | 0.01 | 0 | 0 |
| PHB1 | 1.22 | 0 | 0.48 | 0 | 0.01 | 0 | 0 |
| TIM44 | 1.38 | 0 | 0.36 | 0 | 0.01 | 0 | 0 |
| RSM7 | 0.73 | 0 | 0.47 | 0 | 0.01 | 0 | 0 |

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| TRM44 | 0.61 | 0 | 0.34 | 0 | 0.01 | 0 | 0 |
| NAB6 | 0.42 | 0 | 0.24 | 0 | 0.01 | 0 | 0 |
| SAS10 | 0.64 | 0 | 0.4 | 0 | 0.01 | 0 | 0 |
| SUI2 | 1.06 | 0 | 0.39 | 0 | 0.01 | 0 | 0 |
| TIF6 | 0.64 | 0 | 0.37 | 0 | 0.01 | 0 | 0 |
| SWC7 | 0.68 | 0 | 0.42 | 0 | 0.01 | 0 | 0 |
| RFS1 | 0.52 | 0 | 0.24 | 0 | 0.01 | 0 | 0 |
| MRP1 | 0.54 | 0 | 0.29 | 0 | 0.01 | 0 | 0 |
| HEK2 | 0.31 | 0 | 0.07 | 0 | 0.01 | 0 | 0 |
| TOM1 | 0 | 5.7 | 0 | 2.54 | 0 | 0.52 | 0 |
| MSS2 | 0 | 92.05 | 0 | 13.53 | 0 | 0.5 | 0 |
| YOR093C | 0 | 7.89 | 0 | 3.84 | 0 | 0.5 | 0 |
| PDR10 | 0 | 11.28 | 0 | 4.64 | 0 | 0.5 | 0 |
| BUD21 | 0 | 6.87 | 0 | 3.57 | 0 | 0.5 | 0 |
| SPC97 | 0 | 27.43 | 0 | 7.34 | 0 | 0.5 | 0 |
| MVP1 | 0 | 4.97 | 0 | 2.6 | 0 | 0.5 | 0 |
| TOS8 | 0 | 566.37 | 0 | 33.64 | 0 | 0.5 | 0 |
| DYN1 | 1.09 | 4.97 | 0.96 | 2.6 | 0 | 0.5 | 0 |
| PXL1 | 0 | 9.81 | 0 | 4.32 | 0 | 0.5 | 0 |
| PHO3 | 0 | 12.75 | 0 | 4.95 | 0 | 0.5 | 0 |
| ATG5 | 0 | 165.47 | 0 | 18.16 | 0 | 0.5 | 0 |
| SRB8 | 0 | 40.65 | 0 | 8.96 | 0 | 0.5 | 0 |
| ATF1 | 0 | 62.41 | 0 | 5.79 | 0 | 0.5 | 0 |
| UGA1 | 0 | 12.75 | 0 | 4.95 | 0 | 0.5 | 0 |
| VPH2 | 0 | 46.91 | 0 | 8.37 | 0 | 0.5 | 0 |
| YJR039W | 0 | 15.68 | 0 | 5.51 | 0 | 0.5 | 0 |
| EXO5 | 0 | 24.5 | 0 | 6.93 | 0 | 0.5 | 0 |
| MSH5 | 0 | 18.62 | 0 | 6.02 | 0 | 0.5 | 0 |
| CDC15 | 0 | 6.87 | 0 | 3.57 | 0 | 0.5 | 0 |
| YLR063W | 0 | 8.06 | 0 | 2.86 | 0 | 0.5 | 0 |
| SHQ1 | 0 | 31.84 | 0 | 7.92 | 0 | 0.5 | 0 |
| YGR283C | 0 | 8.34 | 0 | 3.96 | 0 | 0.5 | 0 |
| EMP70 | 0.68 | 10.07 | 0.46 | 2.35 | 0 | 0.5 | 0 |
| VPS35 | 0 | 13.07 | 0 | 4.34 | 0 | 0.5 | 0 |
| YOR111W | 0 | 11.74 | 0 | 4.13 | 0 | 0.5 | 0 |
| RIB2 | 2.16 | 5.41 | 1.54 | 3.13 | 0 | 0.5 | 0 |
| CSF1 | 0 | 6.87 | 0 | 3.57 | 0 | 0.5 | 0 |
| AFI1 | 0 | 18.62 | 0 | 6.02 | 0 | 0.5 | 0 |
| YMR295C | 0 | 25.79 | 0 | 7.11 | 0 | 0.5 | 0 |
| REX3 | 0 | 122.89 | 0 | 15.65 | 0 | 0.5 | 0 |
| YIP5 | 0 | 40.24 | 0 | 5.49 | 0 | 0.5 | 0 |
| CFT2 | 1.19 | 6.87 | 1.15 | 3.57 | 0 | 0.5 | 0 |

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| BRN1 | 0 | 5.41 | 0 | 3.13 | 0 | 0.5 | 0 |
| TID3 | 1.19 | 6.87 | 1.15 | 3.57 | 0 | 0.5 | 0 |
| BCK1 | 0 | 56.8 | 0 | 10.61 | 0 | 0.5 | 0 |
| HXT8 | 0 | 5.41 | 0 | 3.13 | 0 | 0.5 | 0 |
| POL32 | 0 | 8.34 | 0 | 3.96 | 0 | 0.5 | 0 |
| BPH1 | 0 | 20.09 | 0 | 6.26 | 0 | 0.5 | 0 |
| RTN2 | 0 | 5.13 | 0 | 3.04 | 0 | 0.5 | 0 |
| PCD1 | 0 | 5.41 | 0 | 3.13 | 0 | 0.5 | 0 |
| PHO84 | 0 | 10.59 | 0 | 3.14 | 0 | 0.5 | 0 |
| SFI1 | 0 | 9.26 | 0 | 4.19 | 0 | 0.5 | 0 |
| PGK1 | 0.87 | 29 | 0.47 | 7.67 | 0 | 0.5 | 0 |
| FRE7 | 0 | 23.03 | 0 | 6.71 | 0 | 0.5 | 0 |
| ARG7 | 0 | 10.47 | 0 | 3.28 | 0 | 0.5 | 0 |
| BIO3 | 1.19 | 8.34 | 1.15 | 3.96 | 0 | 0.5 | 0 |
| BIO4 | 0 | 8.34 | 0 | 3.96 | 0 | 0.5 | 0 |
| TOR1 | 1.19 | 56.8 | 1.15 | 10.61 | 0 | 0.5 | 0 |
| UPC2 | 0.88 | 4.81 | 0.63 | 1.9 | 0 | 0.49 | 0 |
| LEU2 | 0.47 | 4.7 | 0.22 | 0.85 | 0 | 0.49 | 0 |
| RPS26B | 0 | 7.24 | 0 | 1.47 | 0 | 0.49 | 0 |
| WAR1 | 0 | 5.64 | 0 | 2.37 | 0 | 0.49 | 0 |
| UGP1 | 0.25 | 7.91 | 0.14 | 0.95 | 0 | 0.49 | 0 |
| SPC72 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| HSH49 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| PRM2 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| PEP5 | 0 | 3.62 | 0 | 2.17 | 0 | 0.48 | 0 |
| SPP41 | 0 | 4.44 | 0 | 2.08 | 0 | 0.48 | 0 |
| PPE1 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| SYG1 | 0 | 3.62 | 0 | 2.17 | 0 | 0.48 | 0 |
| FUI1 | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| BIG1 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| PUS1 | 0.98 | 4.44 | 0.76 | 2.08 | 0 | 0.48 | 0 |
| PSO2 | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| IRA1 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| SAK1 | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| COG1 | 1.19 | 3.94 | 1.15 | 2.62 | 0 | 0.48 | 0 |
| CST26 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| RAD2 | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| TAF13 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| BLM10 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |
| DEP1 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 1 |
| ARV1 | 2.16 | 3.75 | 1.54 | 2.55 | 0 | 0.48 | 0 |
| BOR1 | 0 | 3.94 | 0 | 2.62 | 0 | 0.48 | 0 |

# Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 23

| PROTEIN ID | RTR1 WT FC_A | RTR1 *ctk1Δ* FC_A | RTR1 WT FC_B | RTR1 *ctk1Δ* FC_B | RTR1 WT SAINT PROB | RTR1 *ctk1Δ* SAINT PROB | iREF (1= present, 0=absent) |
|---|---|---|---|---|---|---|---|
| RAD26 | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| CCE1 | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| YBL112C | 0 | 3.75 | 0 | 2.55 | 0 | 0.48 | 0 |
| DAL2 | 0 | 4.44 | 0 | 2.08 | 0 | 0.48 | 0 |
| SHM2 | 1.18 | 8.09 | 0.33 | 2.44 | 0 | 0.47 | 0 |
| RPL27B | 0 | 7.11 | 0 | 2.49 | 0 | 0.47 | 0 |
| CHS3 | 0 | 5.44 | 0 | 2.21 | 0 | 0.46 | 0 |
| FOL2 | 0.36 | 6.06 | 0.22 | 1.19 | 0 | 0.45 | 0 |
| PAM1 | 0 | 3.35 | 0 | 1.87 | 0 | 0.4 | 0 |
| ARO3 | 0 | 3.35 | 0 | 1.87 | 0 | 0.4 | 0 |
| NUP120 | 0 | 3.35 | 0 | 1.86 | 0 | 0.4 | 0 |
| PHO90 | 0 | 3.57 | 0 | 1.51 | 0 | 0.39 | 0 |
| RRS1 | 1.19 | 3.01 | 0.84 | 1.53 | 0 | 0.32 | 0 |
| MPD2 | 2.71 | 5.33 | 0.8 | 0.89 | 0 | 0.3 | 0 |
| CIT1 | 0.63 | 1.99 | 0.4 | 0.89 | 0 | 0.27 | 0 |
| ARG5_6 | 0.61 | 3.46 | 0.36 | 1.87 | 0 | 0.18 | 0 |
| RSN1 | 0 | 2.45 | 0 | 1.08 | 0 | 0.16 | 0 |
| NGG1 | 0 | 2.4 | 0 | 1.23 | 0 | 0.15 | 0 |
| PET123 | 0 | 3.43 | 0 | 1.46 | 0 | 0.08 | 0 |
| RPS2 | 0.41 | 4.78 | 0.11 | 0.41 | 0 | 0.08 | 0 |
| ERB1 | 0.39 | 3.71 | 0.23 | 0.93 | 0 | 0.07 | 0 |
| RPL33A | 0.18 | 5.27 | 0.09 | 0.62 | 0 | 0.06 | 0 |
| RPL33B | 0.21 | 4.27 | 0.12 | 0.68 | 0 | 0.04 | 0 |
| ERG11 | 0 | 3.28 | 0 | 0.68 | 0 | 0.03 | 0 |
| THI20 | 0.04 | 6.54 | 0.02 | 0.3 | 0 | 0.03 | 0 |
| EMP24 | 0 | 1.64 | 0 | 0.55 | 0 | 0.02 | 0 |
| RPT6 | 0.4 | 2.6 | 0.18 | 0.54 | 0 | 0.01 | 0 |

Table S9: Yeast strains used in this study

| Strain name | Genotype | Reference(s) |
|---|---|---|
| BY4741 | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* | Ghaemmaghami, S, *et al.* (2003) |
| *rtr1*Δ | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ rtr1::KANMX6* | Winzeler, E, *et al* (1999) |
| Rtr1-TAP WT | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rtr1-TAP*::HIS3MX6* | Ghaemmaghami, S, *et al.* (2003) |
| Rtr1-TAP WT | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rtr1-TAP*::URA3* | This study |
| Rtr1-TAP *ctk1*Δ | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rtr1-TAP*::URA3 ctk1::KANMX6* | This study |
| Rtr1-FLAG WT | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rtr1-FLAG*::HIS3MX6* | This study |
| Rtr1-FLAG *ctk1*Δ | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rtr1-FLAG*::HIS3MX6 ctk1::KANMX6* | This study |
| Rtr1-V5 WT | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rtr1-V5*::HIS3MX6* | This study |
| Rpb3-TAP | *MAT*a *his3Δ leu2Δ met15Δ ura3Δ* Rpb3-TAP*::HIS3MX6* | Ghaemmaghami, S, *et al.* (2003) |
| GPD-Rtr1-TAP WT | MATa *his3Δ leu2Δ met15Δ ura3Δ* [pAG413GPD-Rtr1-TAP] | This study |
| GPD-Rtr1-TAP S217A | MATa *his3Δ leu2Δ met15Δ ura3Δ* [pAG413GPD-Rtr1-S217A-TAP] | This study |
| GPD-Rtr1-TAP S217D | MATa *his3Δ leu2Δ met15Δ ura3Δ* [pAG413GPD-Rtr1-S217D-TAP] | This study |
| Ctk1-TAP Rtr1-V5 | MATa his3Δ leu2Δ met15Δ ura3Δ Ctk1-TAP::HIS3MX6 Rtr1-V5::HIS3MX6 | This study |