

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 OD₆₀₀ ~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°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° 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° 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.

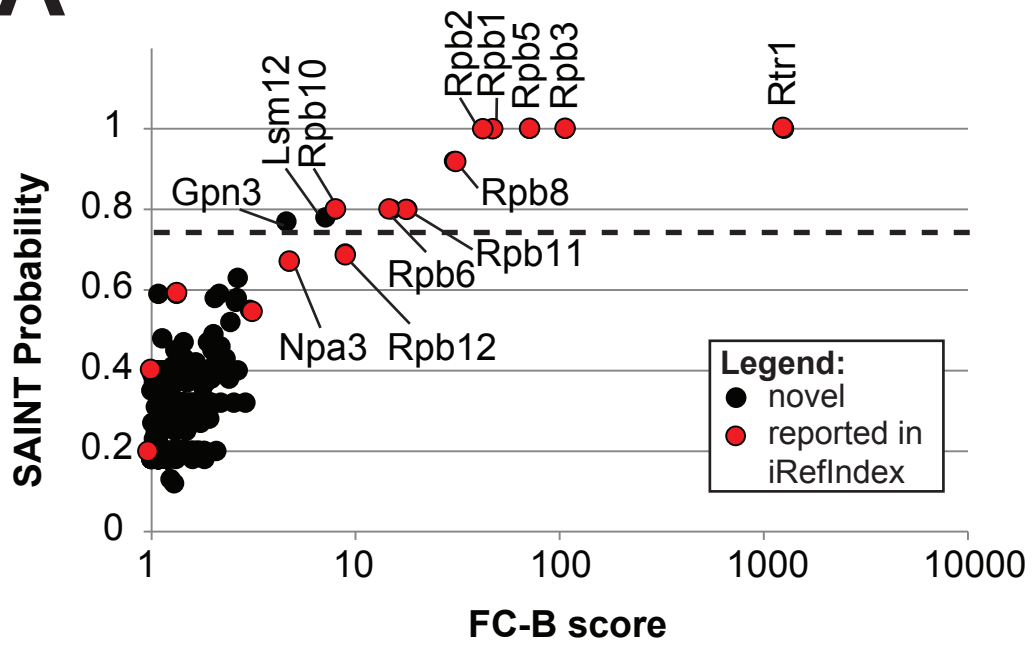
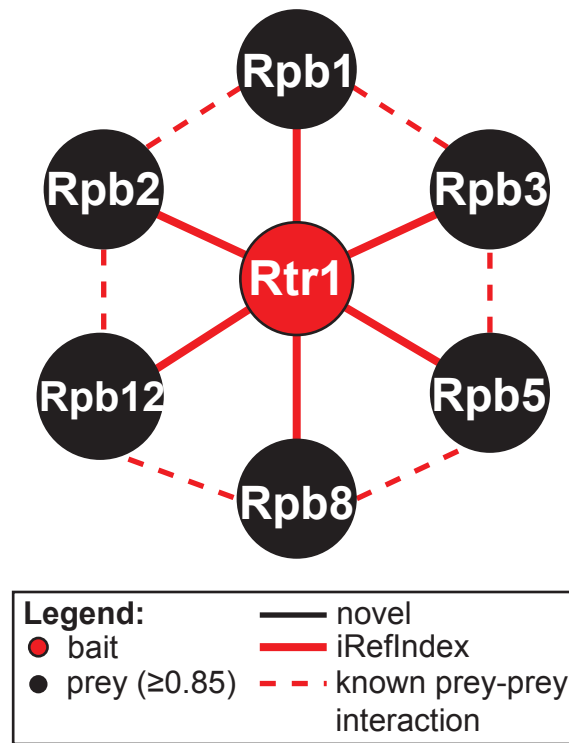
A**B**

Figure S1

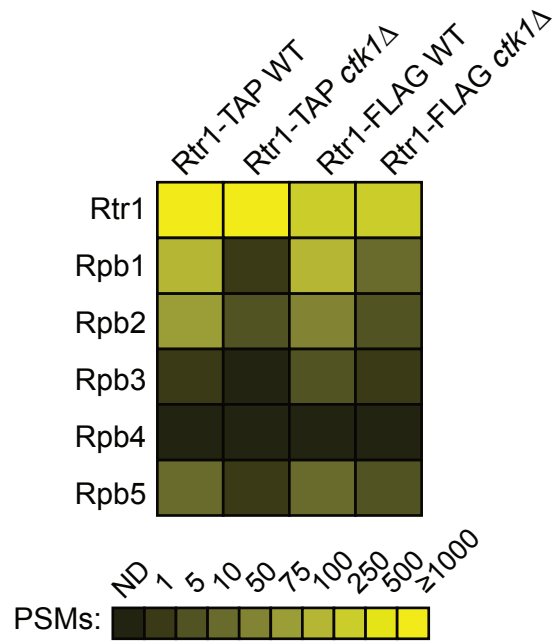
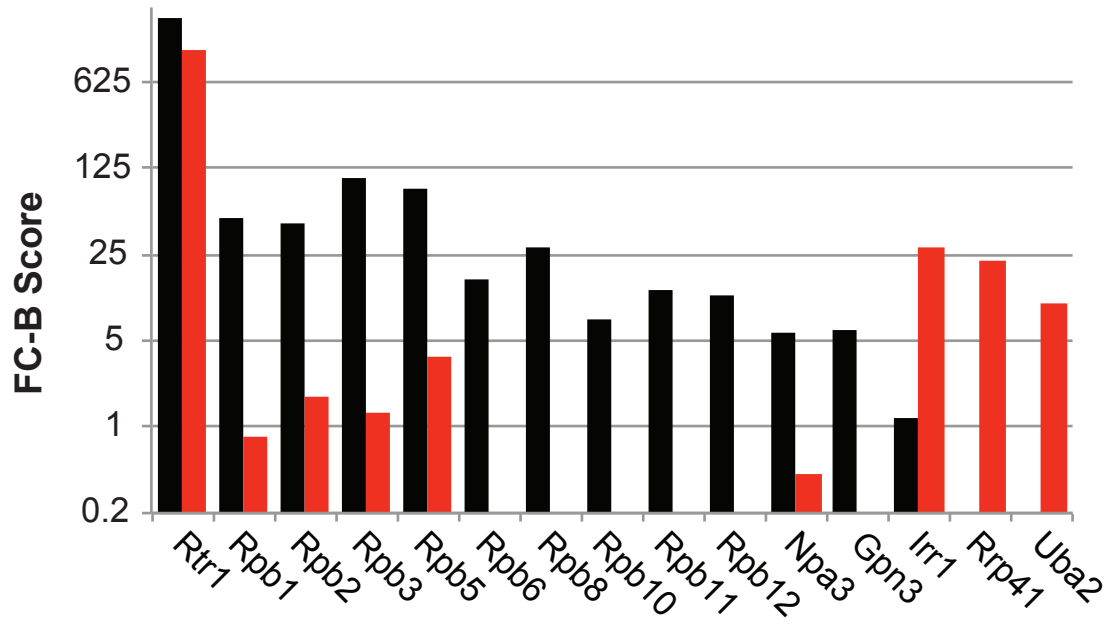
A**B**

Figure S2

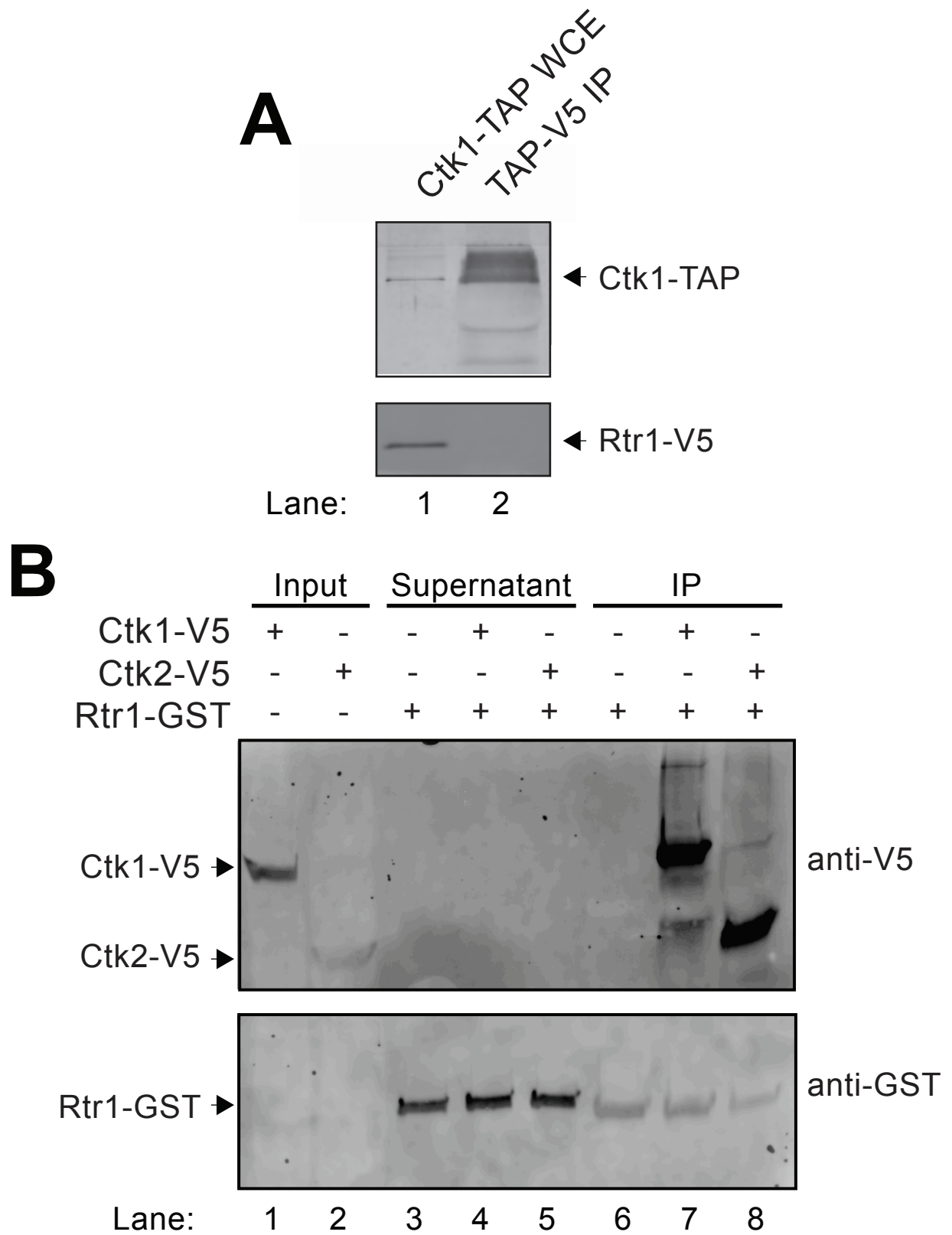


Figure S3

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 2

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 3

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 4

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 5

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 6

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 7

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

Table S2: Single affinity purification (V5/FLAG) SAINT analysis Page 8

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

Table S3: GOSTat analysis output of significant interactions in single affinity purifications Page 2

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)
<u>GO:0005665</u>	rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3	7	12	4.72E-10
<u>GO:0000428</u>	rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3	7	31	3.14E-07
<u>GO:0055029</u>	rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3	7	31	3.14E-07
<u>GO:0030880</u>	rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3	7	31	3.14E-07
<u>GO:0016591</u>	rpc10 rpb2 leo1 sin4 rpb3 rpo21 rpb5 rpb8 rpb11	9	72	3.14E-07
<u>GO:0003899</u>	rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3	7	34	4.70E-07
<u>GO:0016740</u>	car2 utr1 rpc10 aro9 ard1 rpb2 rpb3 tal1 rpo21 erg20 pfk26 rpb8 rpb5 rpb11 grx1	15	703	0.00276
<u>GO:0016779</u>	rpc10 rpo21 rpb5 rpb8 rpb2 rpb11 rpb3	7	123	0.00276
<u>GO:0044451</u>	rpc10 rpb2 leo1 sin4 rpb3 rpo21 srb8 rpb5 rpb8 rpb11	10	313	0.00709
<u>GO:0005736</u>	rpc10 rpb5 rpb8	3	14	0.00861
<u>GO:0005654</u>	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

Table S6: Double affinity purification (TAP) SAINT analysis Page 3

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

Table S6: Double affinity purification (TAP) SAINT analysis Page 6

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

Table S6: Double affinity purification (TAP) SAINT analysis Page 7

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

Table S6: Double affinity purification (TAP) SAINT analysis Page 8

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

Table S6: Double affinity purification (TAP) SAINT analysis Page 9

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

Table S7: Full Rtr1 interactome SAINT analysis Page 7

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

Table S7: Full Rtr1 interactome SAINT analysis Page 12

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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 13

PROTEIN ID	RTR1 WT FC_A	RTR1 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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
OXPI	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

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 18

PROTEIN ID	RTR1 WT FC_A	RTR1 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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
IP13	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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 21

PROTEIN ID	RTR1 WT FC_A	RTR1 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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

Table S8: Rtr1 WT and Rtr1 *ctk1Δ* SAINT analysis Page 22

PROTEIN ID	RTR1 WT FC_A	RTR1 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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 <i>ctk1Δ</i> FC_A	RTR1 WT FC_B	RTR1 <i>ctk1Δ</i> FC_B	RTR1 WT SAINT PROB	RTR1 <i>ctk1Δ</i> 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	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i>	Ghaemmaghami, S, <i>et al.</i> (2003)
<i>rtr1Δ</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> <i>rtr1::KANMX6</i>	Winzeler, E, <i>et al</i> (1999)
Rtr1-TAP WT	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rtr1-TAP:: <i>HIS3MX6</i>	Ghaemmaghami, S, <i>et al.</i> (2003)
Rtr1-TAP WT	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rtr1-TAP:: <i>URA3</i>	This study
Rtr1-TAP <i>ctk1Δ</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rtr1-TAP:: <i>URA3 ctk1::KANMX6</i>	This study
Rtr1-FLAG WT	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rtr1-FLAG:: <i>HIS3MX6</i>	This study
Rtr1-FLAG <i>ctk1Δ</i>	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rtr1-FLAG:: <i>HIS3MX6 ctk1::KANMX6</i>	This study
Rtr1-V5 WT	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rtr1-V5:: <i>HIS3MX6</i>	This study
Rpb3-TAP	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Rpb3-TAP:: <i>HIS3MX6</i>	Ghaemmaghami, S, <i>et al.</i> (2003)
GPD-Rtr1-TAP WT	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> [pAG413GPD-Rtr1-TAP]	This study
GPD-Rtr1-TAP S217A	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> [pAG413GPD-Rtr1-S217A-TAP]	This study
GPD-Rtr1-TAP S217D	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> [pAG413GPD-Rtr1-S217D-TAP]	This study
Ctk1-TAP Rtr1-V5	<i>MATa his3Δ leu2Δ met15Δ ura3Δ</i> Ctk1-TAP:: <i>HIS3MX6</i> Rtr1-V5:: <i>HIS3MX6</i>	This study