Regulation of Mec1 (ATR) signaling in budding yeast

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Nicole Hustedt

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auf Antrag von

Prof. Dr. Susan Gasser

Prof. Dr. Philippe Pasero

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Prof. Dr. Jörg Schibler (Dekan)

THESIS OVERVIEW

This PhD thesis is based on the following publications:

Hustedt, N., Seeber, A., Sack, R., Bhullar, B., Vlaming, H., van Leeuwen, F., Guenole A., van Attikum, H., Srivas, R., Ideker, T., Shimada K., Gasser, S.M. Yeast PP4 interacts with ATR homologue Ddc2-Mec1and regulates checkpoint signaling. *under revision at Molecular Cell*

Hustedt, N., Gasser, S.M., and Shimada, K. (2013). Replication checkpoint: tuning and coordination of replication forks in s phase. Genes 4, 388-434.

Hegnauer, A.M*., Hustedt, N*., Shimada, K., Pike, B.L., Vogel, M., Amsler, P., Rubin, S.M., van Leeuwen, F., Guenole, A., van Attikum, H., et al. (2012). An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. EMBO J 31, 3768-3783. * These authors contributed equally to this work

This thesis consists of five chapters. Each chapter starts with a title sheet stating if and where parts or the whole chapter were published. When projects were collaborative I list my contributions, clarifying as well the contributions of others.

In the first chapter, the current knowledge of the replication checkpoint with a specific focus on *S. cerevisiae* is summarized. A large part of this chapter (Sections 1 – 5 and 6.2) is published as a review in *Genes (Basel), 2013. 4(3): p. 388-434*. Small updates and modifications were added when appropriate. Section 6.1 called "Phosphatases downregulate the checkpoint" was modified and extended because of its special relevance to my thesis.

Chapters 2, 3 and 4 are experimental chapters. In chapter 2 the relationship between the PP4 phosphatase complex Psy2-Pph3 with the checkpoint kinase Ddc2-Mec1 is investigated. Data is presented supporting the idea that PP4 negatively regulates Mec1 checkpoint signaling. The work presented in this chapter is under revision for publication in *Molecular Cell*.

Chapter 3 contains additional data on characterization of the S-phase defective allele *mec1-100*. Several hypotheses about the cause of the specific defect are developed and tested. Furthermore, intragenic mutations that suppress the sensitivity of *mec1-100* to hydroxyurea (HU) are characterized and studied.

Chapter 4 focuses on the role of the RPA-interacting domain in the RecQ helicase Sgs1 in replication checkpoint signaling and replication fork stabilization. We show that this domain is targeted by Mec1 and once phosphorylated, can serve to recruit Rad53. Thus, we propose that Sgs1 acts as a checkpoint mediator, recruiting Rad53 to stalled replication forks for activation. This project was started by a former PhD student, Anna Maria Hegnauer, and finished as part of the PhD work presented here. It was published in *EMBO J, 2012. 31(18): p. 3768-83*.

In the last chapter, the main conclusions from this work are summarized and future directions for this research are discussed.

SUMMARY

Cells are continuously challenged by various sources of DNA damage that can contribute to cancer formation if not appropriately repaired. To cope with this threat, cells have conserved mechanisms called the DNA damage checkpoints that sense damaged DNA, stop the cell cycle, and upregulate DNA repair. Central players in these checkpoints are the PI3K-like kinases ATM and ATR (*S.c*. Tel1 and Mec1). Mec1 senses single stranded DNA (ssDNA) that is exposed at stalled replication forks and activates the S phase checkpoint. However, ssDNA, which is generated at the lagging strand during normal replication, does not cause detectable checkpoint activation. It is unknown how Mec1 is regulated in S phase. To study this, we took advantage of a mutant allele of MEC1, *mec1-100*, which is proficient for the G2 DNA damage checkpoint, but is compromised in G1-S and intra-S-phase checkpoints.

In the first part of this thesis we aimed at identifying regulatory factors. We screened for spontaneous survivors on a lethal dose of the replication fork-stalling agent hydroxyurea (HU) for *mec1-100* cells. We mapped additional mutations in *mec1-100* or mutations in either *PPH3* or *PSY2*, which form a highly conserved phosphatase (PP4) complex. In a second, more unbiased, high-throughput screen we combined *mec1-100* with a collection of 1525 gene deletions involved in chromatin processes and scored double mutants for HU sensitivity. *pph3*Δ and *psy2*Δ were among the top *mec1-100* suppressor hits, confirming a strong genetic interaction. Suppression by *pph3*Δ was correlated with the phosphorylation of the downstream kinase Rad53. However, it did not depend exclusively on Rad53, because residual suppression of *mec1-100* by *pph3*Δ could also be observed in *rad53*Δ cells. We tested whether Psy2-Pph3 might regulate Mec1 directly, and found a physical interaction between Psy2 and Ddc2-Mec1. Moreover, we found that a phosphorylation site within Mec1 (S1991) is downregulated in *mec1-100* cells and restored when Pph3 is also lost. However, we were unable to demonstrate that Pph3 dephosphorylates Mec1 directly *in vitro*. Phosphorylation required both Mec1 kinase activity and Rad53. Thus, we speculate that Mec1 phosphorylation is achieved through Rad53, which is in turn regulated by Pph3, indicating the existence of a feedback loop from Rad53 back to Mec1. Mutation of the phosphorylation site renders cells sensitive to the radiomimetic drug Zeocin, indicating an important role in the survival of DNA damage. Finally, we applied quantitative phosphoproteomics to identify Mec1 and Pph3 targets. We found that the levels of the majority of the phosphopeptides that are affected by a *tel1*Δ *mec1-100* mutation but not by *rad53*Δ can be rescued due to additional deletion of *PPH3*. The data presented here support a model in which Pph3 is a major regulator of Mec1 signaling.

In a second part *mec1-100* was further characterized in order to understand the mechanism by which its two point mutations outside of the catalytic domain (F1179S, N1700S) cause defects in the replication checkpoint. We find that the mutations leave kinase activity *in vitro*, oligomerization and Ddc2-Mec1 interaction intact. Genetic analysis shows that *mec1-100* is additive, rather than epistatic with mutation or deletion of any of the canonical checkpoint activating proteins Ddc1, Dna2, Dpb11, Rad24, Mrc1, Rad9, Tel1 or Chk1. Thus, we conclude that *mec1-100* does not impair function of any of these proteins. We hypothesized that the mutated region might constitute a regulatory domain that is bound by a yet unknown factor. IP experiments followed by mass spectrometry analysis did not show reproducibly decreased interaction of any protein. Additional detailed biochemical analysis is needed to fully understand the mechanism of the two *mec1-100* mutations.

We further characterize intragenic *mec1-100* suppressor mutations by mapping them to a homology model. While some mutations reside within the kinase domain, and could influence catalytic activity, others might as well be involved protein-protein interactions. We asked whether

suppression would involve Rad24 dependent Mec1 activation. Interestingly, we find that suppression by mutations in residues that might make protein-protein contacts completely requires Rad24. Other suppressor mutations relied less on Rad24. Thus, we conclude that intragenic suppression of *mec1-100* HU sensitivity employs at least two different mechanisms: one that is Rad24-dependent and a second that is Rad24–independent. These unpublished results will help in understanding Mec1 function and regulation once structural data is available.

The third experimental part resolves the role of the RecQ helicase Sgs1 in replication checkpoint signaling. It was shown before that Sgs1 and Mec1 synergistically contribute to replication fork stabilization under replication stress. Both interact with the ssDNA binding protein RPA. Here, we created a mutant, *sgs1-r1*, which lacks the RPA interaction domain. While *sgs1-r1* is proficient to stabilize stalled forks under replication stress, it is synthetic lethal with *mus81*Δ, *slx4*Δ, *slx5*Δ and *slx8*Δ. These could provide alternative means to recover stalled forks by resolving crossover structures, DNA repair or break induced replication. . Sgs1 was previously shown to promote Rad53 activation in a manner independent of its helicase activity. We show here that Sgs1 checkpoint function requires the R1 domain. Mec1 phosphorylates Sgs1 in this domain and Sgs1 phosphorylation allows its binding to Rad53 *in vitro* and *in vivo*. We thus propose that Sgs1 serves as a mediator in checkpoint signaling by recruiting Rad53 to stalled replication forks for activation.

This work provides new insights into Mec1 signaling by elucidating the checkpoint function of Sgs1 and defining Psy2-Pph3 as a major regulator of this pathway.

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CHAPTER 1: INTRODUCTION

Hustedt, N., Gasser, S. M., and Shimada K.

Friedrich Miescher Institute for Biomedical Research, Maulbeerstrasse 66, CH-4058 Basel, Switzerland

Based on the published review

Hustedt, N., S.M. Gasser, and K. Shimada, Replication Checkpoint: Tuning and Coordination of Replication Forks in S Phase. *Genes (Basel), 2013. 4(3): p. 388-434.*

(part of a special issue on DNA replication)

CONTENT AND AUTHOR CONTRIBUTIONS

Sections 1 to 5 and 6.2 from this chapter were published in *Genes (Basel), 2013. 4(3): p. 388-434*, but slightly modified and updated where appropriate. Section 6.1 was extended and modified because of special interest to this work. NH independently wrote the introduction (Section 1), sections on Replication checkpoint initiation (Section 2), Effector kinase activation (Section 3) and phosphatases (Section 6.1). KS contributed to sections on checkpoint targets (Section 4), ATM/ATR coordination (Section 5), and phosphatase-independent checkpoint downregulation (Section 6.2) and SMG made editorial corrections.

SUMMARY

Checkpoints monitor critical cell cycle events such as chromosome duplication and segregation. They are highly conserved mechanisms that prevent progression into the next phase of the cell cycle when cells are unable to accomplish the previous event properly. During S phase, cells also provide a surveillance mechanism called the DNA replication checkpoint, which consists of a conserved kinase cascade that is provoked by insults that block or slow down replication forks. The DNA replication checkpoint is crucial for maintaining genome stability, because replication forks become vulnerable to collapse when they encounter obstacles such as nucleotide adducts, nicks, RNA-DNA hybrids, or stable protein-DNA complexes. These can be exogenously induced or can arise from endogenous cellular activity. Here, we summarize the initiation and transduction of the replication checkpoint as well as its targets, which coordinate cell cycle events and DNA replication fork stability.

1. INTRODUCTION

Dividing cells go through cycles of cell growth, DNA replication, chromatin condensation, chromosome segregation, and cell division. All these highly complicated processes need to be accurately performed and tightly controlled in order to produce viable offspring. Checkpoints were initially characterized as mechanisms that ensure that a certain process is started only after the previous one has been successfully completed (Hartwell and Weinert, 1989). Originally, yeast genetic studies identified checkpoint genes that ensured cell survival and delayed the onset of mitosis during DNA replication arrest, yet many of these factors are now known to be involved in the DNA damage response (Allen et al., 1994; Friedel et al., 2009; Weinert et al., 1994). Thus, in addition to preserving the order of events, checkpoints factors contribute to the maintenance of genome stability (Harper and Elledge, 2007). The loss of genome stability has extremely deleterious consequences, including malignant transformation or cell death (Haering and Nasmyth, 2003).

Cells are exposed to many types of exogenous and endogenous stress that can modify or damage the DNA. These include oxidative stress, ionizing or UV-light mediated irradiation, and chemical damage, as well as inherent DNA compaction, tightly bound DNA binding proteins, and transcription. Even excessive or premature initiation of replication can cause replicative stress (Halazonetis et al., 2008), arguing that normal DNA metabolism itself can interfere with DNA replication (Aguilera and Gomez-Gonzalez, 2008). This is particularly true in cells with perturbed G1/S control, such as oncogene-transformed cells. In response to excessive DNA damage, wild-type cells arrest the cell cycle in G1 phase, before starting DNA replication, or in G2 phase before entering mitosis (Elledge, 1996). On the other hand, replication fork-associated damage provokes a response that delays progression through S phase, by controlling forks and initiation events (Santocanale and Diffley, 1998; Shirahige et al., 1998; Tercero and Diffley, 2001).

At the heart of all DNA damage checkpoint responses, are the two kinases Tel1 (telomere maintenance 1; ATM in mammals, see Table 1.1 for an overview of checkpoint protein names in several model organisms) and Mec1 (Mitosis Entry Checkpoint 1; ATR in mammals) (Figure 1.1)) (Friedel et al., 2009). Both are phosphoinositide 3-kinase (PI3K)-related kinases (PIKKs) that share significant sequence homology and phosphorylate an overlapping set of substrates. Both show a preference for serine or threonine residues followed by glutamine ([S/T] Q) or a hydrophobic residue (Chan et al., 1999; Cortez et al., 1999; Kim et al., 1999; Sweeney et al., 2005). Often these target sites are found in SQ/TQ cluster domains (SCDs) (Traven and Heierhorst, 2005). All PIKKs, not only Mec1 and Tel1, share a common domain architecture in which the kinase domain is flanked by both FRAPP, ATM, TRRAP (FAT), and FAT C-terminal (FATC) domains (Figure 1.2A), all being conserved alpha-helical regions (Bosotti et al., 2000; Cimprich and Cortez, 2008). Because FAT and FATC domains are always present in combination, it has been suggested that these two domains interact with each other, potentially providing a scaffold or binding sites for other proteins (Bosotti et al., 2000).

In budding yeast, Mec1 is active even in an unperturbed S phase, as it can regulate dNTP levels and replication initiation without blocking cell cycle progression (Randell et al., 2010; Zhao et al., 2001). ATR^{Mec1} becomes hyperactivated in response to a wide variety of DNA insults and is essential for cell viability, whereas ATM^{Tel1} is activated primarily by double-strand breaks (DSBs) and its loss in budding yeast is not lethal. Nonetheless, in mammalian cells, mutation of either homolog leads to an elevated predisposition towards cancer (Cimprich and Cortez, 2008). Once localized to the site of DNA damage and activated by DNA damage sensing proteins, either kinase can initiate a signaling cascade that transduces the signal through mediator proteins Mrc1 and Rad9 (Claspin, BRCA1, MDC1 and 53BP1 in mammals) to the effector kinases Rad53 and Chk1 (CHK2 and CHK1 in mammals) (Figure 1.1) (Alcasabas et al., 2001; Pellicioli et al., 1999; Sanchez et al., 1999; Sanchez

et al., 1996). Effector kinases are transiently recruited to sites of DNA damage and are released after their activation (Gilbert et al., 2001; Katou et al., 2003), allowing transmission of the checkpoint response to a range of effector proteins (Gardner et al., 1999). In addition to the effector kinases, Mec1 and Tel1 also phosphorylate proteins bound at sites of damage, such as budding yeast histone H2A (the H2AX variant in mammals), generating γH2AX, to provoke local chromatin changes (Downs et al., 2000).

DNA damage occurs in all stages of the cell cycle, yet cells are particularly vulnerable to insults during DNA replication, when the double helix is unwound. Indeed, in S phase, defects in one strand can have serious consequences on the integrity of the daughter chromosome. Moreover, the single-stranded DNA (ssDNA) that is generated during replication, is intrinsically more labile than double-stranded (dsDNA) (Lindahl, 1993). To cope with this danger, cells provide a surveillance mechanism called intra-S-phase or DNA replication checkpoint (Figure 1.1A). This checkpoint slows genome replication by inhibiting the firing of late origins (Santocanale and Diffley, 1998; Shirahige et al., 1998), and protects stalled replication forks by preventing their conversion to DSBs and/or reducing recombination events (Cobb et al., 2005; Sogo et al., 2002; Tercero et al., 2003). Consistently, it has been shown that the loss of replication checkpoint factors provokes high levels of spontaneous gross chromosomal rearrangements in budding yeast (Myung et al., 2001). The factors involved in this checkpoint are highly conserved and many, including ATR itself, have tumor suppressor roles in mammals (Aguilera and Gomez-Gonzalez, 2008).

Table 1.1: Conserved checkpoint proteins and their functions.

S. cerevisiae	***S. pombe***	***H. sapiens***	**Function**
Rad24-RFC	Rad17-RFC	RAD17-RFC	RFC-like complex, 9-1-1 clamp loader
Ddc1-Rad17-Mec3	Rad9-Rad1-Hus1	RAD9-RAD1-HUS1	9-1-1 complex, DNA damage checkpoint clamp, Mec1 activation
Dpb11	Cut5/Rad4	TOPBP1	Mec1 ATR activation
Dna2	Dna2	DNA2	Mec1 activation in S phase
Mre11-Rad50-Xrs2	Mre11/Rad32-Rad50-Nbs1	MRE11-RAD50-NBS1	MRX/MRN complex, DSB resection, Tel1/ATM recruitment
Mec1-Ddc2	Rad3-Rad26	ATR-ATRIP	checkpoint signaling kinase
Tel1	Tel1	ATM	checkpoint signaling kinase
Mrc1	Mrc1	Claspin	fork-associated, checkpoint mediator
Rad9	Crb2	53BP1, BRCA1	checkpoint mediator
Sgs1	Rqh1	BLM, WRN	fork-associated, Rad53 activation
Rad53	Cds1	CHK2	effector kinase
Chk1	Chk1	CHK1	effector kinase

Gene name abbreviations: Rad24 (radiation sensitive 24), RFC (replication factor c), Ddc1 (DNA damage checkpoint 1), Mec3 (Mitosis entry checkpoint 3), Hus1 (hydroxyurea sensitive 1), Dpb11 (DNA polymerase B 11), Cut5 (cell untimely torn 5), TOPBP1 (DNA topoisomerase 2 binding protein 1), Dna2 (DNA synthesis defective 2), Mre11(meiotic recombination 11), Xrs2 (X-ray sensitive 2), Nbs1 (Nijmegen breakage syndrome 1), ATR (ATM and Rad3-related), ATRIP (ATR interacting protein), Tel1 (telomere maintenance 1), ATM (Ataxia telangiectasia mutated), Mrc1 (mediator of the replication checkpoint 1), Crb2 (cut5 repeat binding 2), 53BP1 (tumor suppressor p53 binding protein 1), BRCA1 (breast cancer 1, early-onset), Sgs1 (slow growth suppressor 1), rqh1 (RecQ-type DNA helicase 1), BLM (Bloom syndrome protein), WRN (Werner syndrome ATP-dependent helicase), Cds1 (checking DNA synthesis 1), CHK2 (checkpoint kinase 2), CHK1 (checkpoint kinase 1).

Here we review recent findings on the replication checkpoint. We will first discuss the nature of the DNA lesions that provoke a checkpoint response. We then describe the mechanism of ATR^{Mec1} activation and summarize the functions served by the replication checkpoint, especially with respect to replication fork stability. We will discuss how cells downregulate the checkpoint signal to resume the cell cycle after the insult has been removed, and finally examine the coordination between two checkpoint PIKK kinases, ATR^{Mec1}and ATM^{Tel1}. Although we focus primarily on insights from studies in budding yeast, we relate those findings to results obtained from other organisms.

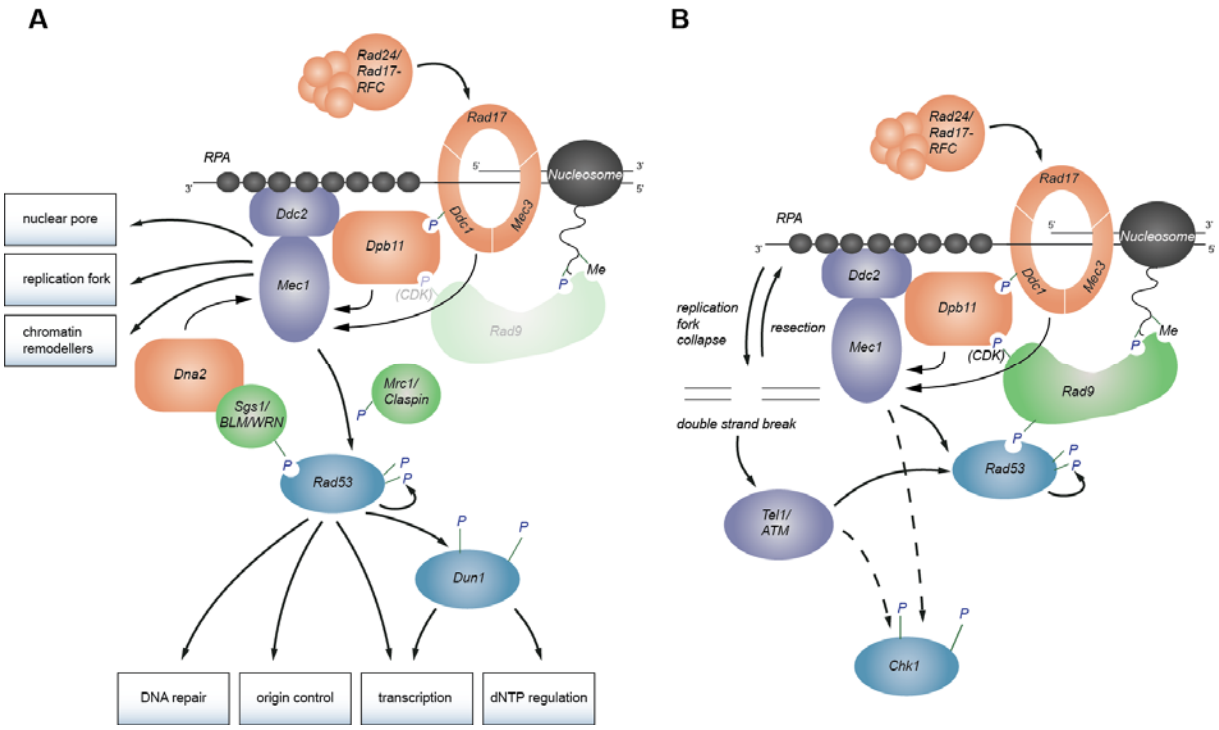

Figure 1.1: Checkpoint signaling network. (**A**) Replication checkpoint signaling. The yeast equivalent to ATRIP, Ddc2, binds ssDNA that is covered with RPA, while the 9-1-1 checkpoint clamp is loaded onto ds/ssDNA junctions. Dpb11, 9-1-1, and Dna2 (checkpoint sensors, orange) can activate Ddc2-Mec1 (checkpoint kinase, purple). Checkpoint mediators like Mrc1 and Sgs1 (green) help activate Rad53 (checkpoint transducing kinase, blue). Rad53 activates Dun1 and other downstream responses. (**B**) DNA damage checkpoint signaling. Crosstalk between Mec1 and Tel1 (DSB response) can occur, if stalled replication forks collapse, since they can generate DSBs. These are resected to generate ssDNA which activates Mec1. Rad9, the DNA damage checkpoint mediator, can be recruited by histone modifications and also binds, once phosphorylated by CDK, to Dpb11. In addition, both Mec1 and Tel1 can activate the Chk1 kinase.

2. REPLICATION CHECKPOINT INITIATION

2.1 LESIONS THAT ACTIVATE THE CHECKPOINT

Replication forks themselves play a critical role in inducing a checkpoint signal. Only when a critical number of replication forks initiate and encounter lesions, will the replication checkpoint signal become robust (Shimada et al., 2002; Tercero et al., 2003). This has seeded the notion of a threshold for activation of the replication checkpoint. After treatment with a replication stress-inducing drug (hydroxyurea, HU), long stretches of ssDNA (about 200 nucleotides) are exposed at stalled forks (Sogo et al., 2002). These extended stretches of ssDNA themselves contribute to the induction of the checkpoint response, but they are not sufficient: a double-stranded primer with a free 5′ end is also required (MacDougall et al., 2007). The ds-ssDNA junction structure can arise from a variety of replication and repair processes, such as lagging strand DNA synthesis, nucleotide excision repair (Huang et al., 1992), or from resection at DSBs. This structure is recognized by the 9-1-1 checkpoint clamp and its loading factor (see below and Figure 1.1AB). At DSBs ATM^{Tel1} is recruited and activated initially by the $Mre11\text{-}Rad50\text{-}Nbs1^{Xrs2}$ complex, which then promotes resection. Resection generates ssDNA and a ds-ssDNA junction, which in turn activate ATR^{Mec1} (Costanzo et al., 2001; Jazayeri et al., 2006; Myers and Cortez, 2006; Shiotani and Zou, 2009) (see also Section 5). Both at resected DSBs and at stalled replication forks, ssDNA is rapidly coated with the trimeric ssDNA binding complex RPA (replication protein A) (Alani et al., 1992). RPA-bound ssDNA interacts with $ATRIP^{Ddc2}$, an essential cofactor of the ATR^{Mec1} kinase (Ball et al., 2005; Zou and Elledge, 2003) (Figure 1.1). Mutations in RPA that disrupt its interaction with $ATRIP^{Ddc2}$ reduce checkpoint activation (Ball et al., 2007; Dubrana et al., 2007; Kim and Brill, 2001; Zou and Elledge, 2003). In budding yeast, the RPA-Ddc2 interaction also requires Mec1, suggesting either that there may be an independent RPA binding surface on Mec1, or that Mec1 changes Ddc2 conformation in a way that favors RPA interaction (Nakada et al., 2005).

The ds-ssDNA junctions are recognized by the Rad24-RFC complex that loads the 9-1-1 checkpoint clamp (Ddc1, Rad17 and Mec3 in *S. cerevisiae*). *In vitro* analysis argues that 9-1-1 can be loaded at both 3′and 5′ junctions, although if RPA is bound to the ssDNA, the 9-1-1 complex prefers to load at 5′ junctions. These structures, together with RPA, are sufficient to activate the ATR^{Mec1} checkpoint in a cell-free system (MacDougall et al., 2007; Majka et al., 2006a). In budding yeast, Mec1 phosphorylates the Ddc1 subunit (human RAD9) of the 9-1-1 complex, which can then recruit Dpb11 (human TopBP1). $TopBP1^{Dpb11}$ further stimulates ATR^{Mec1} kinase activity (Delacroix et al., 2007; Furuya et al., 2004; Lee et al., 2007; Mordes et al., 2008a; Mordes et al., 2008b; Paciotti et al., 1998; Puddu et al., 2008). This indicates that in addition to its loading onto ssDNA, ATR^{Mec1}-$ATRIP^{Ddc2}$ needs to contact an activator in order to induce the checkpoint response (see Section 2.3). In addition to this, several studies have suggested that mismatch repair factors at the site of DNA damage provide an alternative means to recruit and activate ATR^{Mec1} (Liu et al., 2010; Pabla et al., 2011; Wang and Qin, 2003)[1].

2.2 DRUGS USED TO INDUCE AND STUDY CHECKPOINT RESPONSES

As mentioned above, special DNA structures initiate the ATR^{Mec1} checkpoint response. To study the replication checkpoint and downstream responses *in vivo*, a variety of DNA-damaging and fork stalling agents are used, and these provoke the checkpoint response in different ways (summarized in Table 1.2). Natural replication fork stalling can also occur, generally due to secondary

[1] Morevoer, a recent study suggested that ATR^{Mec1} can localize to the nuclear envelope independently of RPA or DNA damage (Kumar, et al., 2014).

DNA structures (e.g. G-quadruplexes), RNA-DNA hybrids found at genes, tightly bound transcription complexes (e.g. at rDNA or tRNA genes) or specific protein-DNA complexes, like that formed by the replication fork barrier protein (Fob1), which prevents forks from colliding with RNA PolI in the rDNA repeats (Azvolinsky et al., 2009; Lambert and Carr, 2005). Natural fork pausing, however, does not provoke a global checkpoint response. We note that the proteins involved in a chemically induced checkpoint response depend on the type of damage induced and can vary with the dose applied, as demonstrated recently for camptothecin (Ray Chaudhuri et al., 2012). Further complexity in the checkpoint network stems from differences in cell type or genetic background. For example, the checkpoint response is more prone to be activated in cells deficient for DNA repair, such as the *rad18* mutant, which is deficient for post-replication repair (Hishida et al., 2009; Huang et al., 2013). Other lesions that expose primed ssDNA and activate the replication checkpoint arise when replicative helicase and polymerase functions are uncoupled (Byun et al., 2005) (Figure 1.3A, B). Here we summarize commonly used treatments that induce the checkpoint response, and highlight differences in the responses they elicit.

Table 1.2: *S. cerevisiae* checkpoint responses differ, depending on the treatment.

Treatment/Impediments	Mode of action	Result	Responders (*S.cerevisiae*)
hydroxurea (HU)	inhibits ribonucleotide reductase—dNTP pools become depleted	uncoupling of helicase and polymerase function; ssDNA is exposed	Mec1, Mrc1, Sgs1
aphidicolin	inhibits DNA polymerases	uncoupling of helicase and polymerase function; ssDNA is exposed	Mec1, Mrc1
methylmethanesulfonate (MMS)	alkylates DNA	uncoupling of helicase and polymerase function; ssDNA is exposed; in addition DNA repair takes place, that also leads to ssDNA; requires replication forks to induce checkpoint response	Mec1, Rad9 (Mrc1, Sgs1)
ultraviolet light/4-NQO	induces Thymidine dimerization	induces DNA repair, that leads to ssDNA	Mec1, Rad9, Mrc1
crosslinking agents (cisplatin/nitrogen mustard)	causes DNA inter-strand crosslinks	both helicase and polymerase are blocked; in addition DNA repair takes place, that also leads to ssDNA	Mec1/Tel1, Rad9
ionizing irradiation (IR)/bleomycin	causes single and double strand breaks	breaks are directly recognized by MRX-Tel1; resection leads	Mec1/Tel1; Rad9

		to ssDNA	
camptothecin (CPT)	inhibits Topoisomerase I, keeps it in a DNA-bound confirmation	both helicase and polymerase are blocked; double strand breaks are actively induced by DNA repair machinery	Mec1/Tel1, Rad9
natural fork barriers (rDNA, t-RNA genes, transcription	slow down replisome progression	both helicase and polymerase are slowed down	-

One commonly used means to trigger the replication checkpoint is to treat cells with either hydroxyurea (HU) or aphidicolin. HU inhibits ribonucleotide reductase (RNR) by reducing the reactive tyrosyl radical in the active center of the enzyme (Eklund et al., 2001). When replication is initiated, dNTP pools are rapidly depleted if RNR is inhibited (Poli et al., 2012), and this leads to a stalling of DNA polymerases. Aphidicolin, on the other hand, directly inhibits DNA polymerases (Ikegami et al., 1978) without affecting the replicative helicase (Pacek and Walter, 2004). Accordingly, polymerases are blocked, but MCM helicases continue to move, generating long stretches of ssDNA that trigger the replication checkpoint (MacDougall et al., 2007). It should be noted that HU also induces an oxidative stress and a transcriptional response to DNA damage, even in G1 phase.

Interstrand crosslinks (ICs), such as those caused by cisplatin, do the opposite: they tend to block the MCM helicase in front of the replication fork. There is no uncoupling of helicase and polymerase, and hence no immediate activation of the replication checkpoint. However, often the replication forks pause 20-40 nucleotides before reaching the IC lesion, and often structure-specific nucleases will process the template or nascent strand, generating ssDNA (Lambert et al., 2003; Raschle et al., 2008), which in turn leads to checkpoint activation.

Methyl methane sulfonate (MMS) creates bulky lesions by alkylating DNA. Alkylation alone does not elicit the checkpoint response, but requires that the replication fork collides with the DNA adduct. Therefore, MMS-induced checkpoint responses are restricted to S-phase cells (Tercero et al., 2003). Although both MMS and HU activate an S-phase checkpoint, it is important to note that they do not provoke equivalent responses (Ball et al., 2007; Emili, 1998; Liu et al., 2003; Pellicioli et al., 1999). In response to MMS, cells activate several repair pathways, including base excision repair (BER), DNA damage tolerance pathways such as trans-lesion synthesis (Vazquez et al., 2008), and homologous recombination (HR). However, since DSBs are not detected on MMS, it is not clear whether it is the repair process itself, or an uncoupling of leading and lagging strand synthesis, that provokes what appears to be a combined replication/DNA damage checkpoint response (Lundin et al., 2005).

Ionizing radiation (IR) or treatment with bleomycin or its derivatives (e.g. Zeocin®) cause DSBs, which activate the DNA damage response initially through the ATM^{Tel1} kinase, and after processing, through ATR^{Mec1} (Povirk, 1996). It should be kept in mind that IR or bleomycin derivatives induce oxidative damage and single-strand nicks much more efficiently than DSBs. At sufficiently high doses, UV light also provokes an ATR^{Mec1}-dependent response (Jazayeri et al., 2006), for the pyrimidine dimers caused by UV treatment are recognized by the nucleotide excision repair (NER) machinery, which itself creates a ssDNA patch during the repair process which is extended by Exo1 (Giannattasio et al., 2010; Huang et al., 1992). While these lead to ATR^{Mec1} activation, the

pathway involves Rad9 (homologue of 53BP1 or BRCA1), a mediator typically implicated at DSBs (Neecke et al., 1999). In mammals, Mre11-Rad50-Nbs1^{Xrs2} (MRN) nuclease has been shown to be involved in UV-dependent ATR^{Mec1} activation, possibly again by creating a single-strand patch (Olson et al., 2007).

Camptothecin inhibits topoisomerase I (Top1) by blocking religation after the enzyme has made a ssDNA nick and becomes covalently linked to the DNA end (Hsiang et al., 1985). These structures arrest replication forks and are cytotoxic (Hsiang et al., 1989), yet they only provoke a mild checkpoint response (Redon et al., 2003), presumably because the lesion is not accompanied by helicase-polymerase uncoupling nor extensive resection. The so-called replication run-off model (Strumberg et al., 2000) has indicated that replication forks running into these ssDNA nicks are converted into DSBs, which generally depend on a recombination-dependent mechanism for replication fork restart (Ray Chaudhuri et al., 2012; Regairaz et al., 2011). Recent data indicate that torsional stress generated by Top1 inhibition may lead to fork slowing, and suggest that the formation of a DSB is an active process involving cleavage by the endonuclease Mus81. An artificial system that generates a similar lesion uses a mutant form of the site-specific Flp recombinase to generate a covalent protein-DNA complex, adjacent to a ssDNA nick (Nielsen et al., 2009). This lesion, like the Top1-camptothecin complex, does not induce a checkpoint response in wild-type yeast, but recruits the recombination machinery for repair following collision with a replication fork (L. Bjergbaek, personal communication). This illustrates the broad range of responses elicited by exogenous agents, and underscores the importance of highlighting the type of damaging agent used.

2.3 MEC1/ATR ACTIVATION

An accumulation of RPA-coated ssDNA recruits ATR^{Mec1}-ATRIP^{Ddc2}, just like a DSB bound by MRN^{MRX} recruits ATM^{Tel1}. However, whereas MRN^{MRX} also activates ATM^{Tel1}, ssDNA-RPA is not sufficient to induce ATR^{Mec1} activation. As discussed above, ds-ssDNA junctions that recruit the 9-1-1 checkpoint clamp are also required for activation (see Section 2.1). In budding yeast, Ddc1, a subunit of the 9-1-1 complex that binds the ds-ssDNA junction, has been shown to be capable of activating Mec1 alone under low salt conditions *in vitro* (Majka et al., 2006b; Navadgi-Patil and Burgers, 2009), just as the artificial juxtaposition of multiple Ddc1 and Ddc2 molecules can activate Mec1 *in vivo* (Bonilla et al., 2008). In higher organisms, on the other hand, RAD9^{Ddc1} instead creates a binding site for the ATR^{Mec1} activator TopBP1^{Dpb11} (Delacroix et al., 2007; Furuya et al., 2004; Lee et al., 2007). TopBP1^{Dpb11} contains eight BRCA1 C-terminal (BRCT) domains (Figure 1.2A) and interacts with phosphorylated RAD9^{Ddc1} through its BRCT domains 1 and 2. In addition, the MRN^{MRX} complex has been shown to recruit TopBP1^{Dpb11} through its BRCT domains 3-6 (Figure 1.2B) (Duursma et al., 2013). Overexpression of a domain of TopBP1^{Dpb11} that sits between its BRCT motifs 6 and 7 (called AAD for ATR activation domain), also leads to ATR^{Mec1} activation. Indeed, one can bypass the need for the intact 9-1-1 clamp by tethering the AAD to PCNA or histone H2B (Delacroix et al., 2007; Kumagai et al., 2006). TopBP1^{Dpb11} itself binds to ATRIP^{Ddc2}, and mutations within its TopBP1^{Dpb11} binding region can block ATR^{Mec1} activation. Finally, a region of ATR^{Mec1}, between the kinase and the FATC domain, is important for TopBP1^{Dpb11}-mediated ATR^{Mec1} activation (Mordes et al., 2008a) (Figure 1.2A, B). Here, however, molecular details are scarce, as there are no structural data available for ATR^{Mec1}. This RAD9^{Ddc1}-TopBP1^{Dpb11} pathway for ATR^{Mec1} activation is also found in budding yeast. Dpb11 is recruited by Ddc1, which is phosphorylated by Mec1 (Puddu et al., 2008), although either Ddc1 or Dpb11 can activate Mec1 on its own (Mordes et al., 2008b; Navadgi-Patil et al., 2011; Wang and Elledge, 2002). The responsible regions of Dpb11 and Ddc1 have been mapped to their unstructured C-terminal tails, within which two conserved hydrophobic residues are important for Mec1 activation (Navadgi-Patil and Burgers, 2009; Navadgi-Patil et al., 2011; Pfander and Diffley, 2011).

How Ddc1 and Dpb11 act together to activate Mec1 is still under debate, and it may vary in a cell-cycle dependent manner (Figure 1.2C). Burgers' laboratory suggests that whereas the 9-1-1 subunit Ddc1 is responsible for the activation of Mec1 in response to DNA damage in G1 phase, 9-1-1 and Dpb11 cooperate to activate Mec1 in G2/M phase (Navadgi-Patil and Burgers; Navadgi-Patil et al., 2011). Dpb11 interacts with phosphorylated Rad9, which is modified by a cell-cycle regulated Cyclin-dependent kinase (CDK). Since CDK is not active in G1, this could explain why Dpb11 function is cell-cycle specific (Pfander and Diffley, 2011). In contrast, Puddu et al. have shown that Dpb11 and 9-1-1 act together in G1, while 9-1-1 is the predominant Mec1 activator in G2 (Puddu et al., 2011). Fission yeast Rad4/Cut5^{Dpb11} similarly assists Rad3^{Mec1} activation in G1, when DSB resection is restricted (Lin et al., 2012). This observation suggests that Rad4/Cut5^{Dpb11} compensates for limited ssDNA to promote full Rad3^{Mec1} activation in G1 phase (Lin et al., 2012).

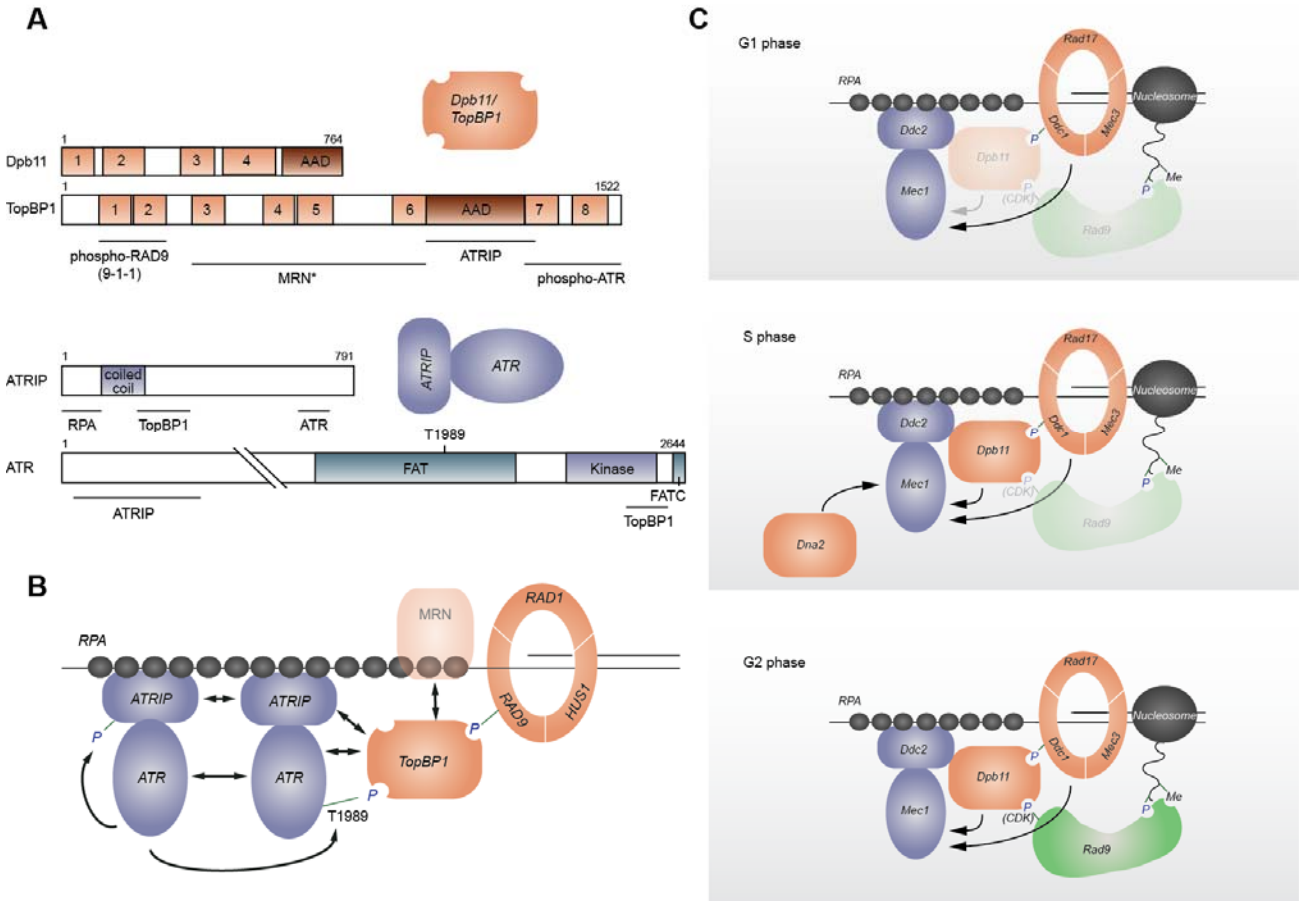

Figure 1.2: ATR/Mec1 activation. (**A**) Domain architecture of *S. cerevisiae* Dpb11, human TopBP1^{Dpb11}, human ATRIP^{Ddc2}, and human ATR^{Mec1}**.** Numbered brown boxes indicate BRCA1 C-terminal (BRCT) domains. Underlined regions interact with indicated proteins. *MRN^{MRX} interaction shown for *Xenopus* TopBP1^{Dpb11}. (**B**) Mammalian ATR^{Mec1} activation. TopBP1^{Dpb11} is recruited by RAD9^{Ddc1} phosphorylation and interacts with ATRIP^{Ddc2} and ATR^{Mec1}. *Xenopus* TopBP1^{Dpb11} may be recruited through MRN^{MRX}. ATR^{Mec1} autophosphorylates, and this may also contribute to interaction with TopBP1^{Dpb11}. ATRIP^{Ddc2} and ATR^{Mec1} form higher-order oligormers. (**C**) Cell cycle specific *S. cerevisiae* Mec1 activation. In G1 phase Ddc1, a subunit of the 9-1-1 checkpoint clamp, is the predominant Mec1 activator. In S phase, Ddc1, Dpb11, and Dna2 are able to activate Mec1. In G2 phase, both Ddc1 and Dpb11 can activate Mec1. Dpb11 is recruited through phosphorylated Ddc1 and CDK-mediated phosphorylation of Rad9, which in turn binds to modified histones. AAD—ATR/Mec1 activation domain; FAT—FRAP, ATM, TRRAP domain; kinase—kinase domain; FATC—FAT C-terminal domain.

In S-phase cells, several proteins have been reported to activate Mec1, apparently in a redundant manner. The 9-1-1 complex is recruited to stalled replication forks, and facilitates Rad53 phosphorylation (Bjergbaek et al., 2005; Katou et al., 2003). However, *dpb11* or *ddc1* mutations that

interfere with Mec1 activation (or a mutation defective in 9-1-1 loading such as *rad24*Δ), alone or in combination, show only mild defects in Rad53 phosphorylation in response to replication stress (Berens and Toczyski, 2012; Navadgi-Patil and Burgers, 2009; Navadgi-Patil et al., 2011). Recently, Burgers' laboratory has reported that Dna2, a conserved nuclease-helicase that is essential for Okazaki fragment maturation, has a role in Mec1 activation in S phase. *TEL1* and *DDC1* deletions (which also compromises Dpb11-mediated Mec1 activation) were combined with a mutation in the Mec1 activation domain of Dna2, and this eliminated Rad53 activation upon HU treatment in S phase (Kumar and Burgers, 2013). These data indicate that Dna2 functions as a third factor contributing to Mec1 activation in S phase. Here it is important to note that Dna2 binds the yeast RecQ helicase Sgs1, and that the two factors co-activate each other (Cejka et al., 2010). Sgs1 also promotes replication stress-dependent checkpoint activation, and the checkpoint defects of a *SGS1* deletion are strongly aggravated by mutations in 9-1-1 or the *RAD24* gene (Bjergbaek et al., 2005; Frei and Gasser, 2000; Fu et al., 2008). Sgs1 directly binds Rad53 in a Mec1-dependent manner, arguing that its loss does not simply generate structures that activate and require Mec1 (Hegnauer et al., 2012).

Whereas Ddc1, Dpb11 and Dna2 were all shown to enhance Mec1 catalytic activity *in vitro,* the molecular details of how they act on Mec1 are unclear. Rather than stimulating Mec1 through its kinase domain, they may serve as scaffolds that bring factors closely together. Indeed, Berens and Toczyski have shown that an artificial co-localization of Ddc2 and the replication checkpoint mediator Mrc1 elicits a downstream Rad53 kinase response in the absence of Dpb11 and Ddc1 (Berens and Toczyski, 2012). It remains possible the Dna2 serves as the crucial activator in this case, and it would be interesting to see how a *dna*2 mutant defective for Mec1 activation, or the *dna2 dpb11* and *dna2 ddc1* double mutants, would behave in the Toczyski assay.

Another level of ATR^{Mec1} regulation may be inherent to the kinase itself. Recently it has been reported that human ATR^{Mec1} can autophosphorylate in *trans*, and that this phosphorylation correlates with ATR^{Mec1} activation (Liu et al., 2011; Nam et al., 2011b). It has been suggested that ATR^{Mec1} autophosphorylation assists its binding to $TopBP1^{Dpb11}$, which further activates the kinase (Liu et al., 2011) (Figure 1.2B). However, another study concluded that mutation of the same autophosphorylation site does not have a strong impact on ATR^{Mec1} function (Nam et al., 2011b), and the relevant target residue, Thr 1989, is not conserved in budding and fission yeast (Nam et al., 2011b). Indeed, a study that mutagenized all [S/T]Q sites in checkpoint proteins in fission yeast did not find a single [S/T]Q residue in $Rad3^{Mec1}$ critical for its function (Yue et al., 2011). However, since the ATR^{Mec1} autophosphorylation site does not match the [S/T]Q consensus (Liu et al., 2011; Nam et al., 2011b), these results are inconclusive. It remains to be seen whether a similar autophosphorylation mechanism exists for $Rad3^{Mec1}$ in fission yeast or for Mec1 in budding yeast.[2]

ATR^{Mec1} may be also controlled by regulated protein complex formation. It has recently been determined that Nek1 (Never in mitosis A-related kinase 1) promotes ATR^{Mec1}-$ATRIP^{Ddc2}$ association in a DNA damage independent manner. The responsible phosphorylation site is unknown, but Nek1 does not seem to target ATR^{Mec1} Thr 1989 directly (Liu et al., 2013). Functional complexes may require disruption of dimers. ATM^{Tel1} forms inactive dimers, which dissociate upon autophosphorylation after DSB induction (Bakkenist and Kastan, 2003). ATR^{Mec1}-$ATRIP^{Ddc2}$ can also form oligomers (Ball and Cortez, 2005; Itakura et al., 2005; Lee et al., 2004; Lindsay et al., 1998;

[2] Mec1 serine 38 phosphorylation was shown to depend on Mec1 (Chen et al., 2010). and fits to the ATR consensus ([S/T]Q), thus it is likely an autophosphorylation site. However, serine 38 mutation does not show a phenotype (Chapter 2). In Chapter 2 we show that Mec1 is also phosphorylated on serine 1991, which is important for resistance to the Zeocin. However, serine 1991 phosphorylation requires not only Mec1 but also Rad53 and thus is unlikely to be a site of autophosphorylation (Chapter 2).

Paciotti et al., 2001) and it has been speculated that the oligomerization of ATR^{Mec1}-ATRIP^{Ddc2} regulates kinase activity, even though oligomerization is independent of DNA damage or replication stress (Itakura et al., 2005; Paciotti et al., 2001). There are conflicting reports on the size of ATR^{Mec1}-ATRIP^{Ddc2} complexes, ranging from 300 to 1000 kD in size (Itakura et al., 2005; Kim et al., 2005; Majka et al., 2006b). In humans, both the coiled-coil domain of ATRIP^{Ddc2} and ATR^{Mec1} contribute to oligomerization (Ball and Cortez, 2005) (Figure 1.2A). Mutation of the human ATRIP^{Ddc2} coiled-coil domain does not impair chromatin binding, but impairs foci formation and signaling. Interestingly, this coiled-coil mutation shows stronger defects in the replication checkpoint than in the G2/M damage checkpoint (Ball and Cortez, 2005; Itakura et al., 2005). In contrast, it has been reported that in *Xenopus* the ATRIP^{Ddc2} coiled-coil domain is dispensable for both oligomerization and CHK1^{Chk1} phosphorylation (Kim et al., 2005), indicating species or cell-type specific differences.

3. ACTIVATION OF EFFECTOR KINASES

Once ATR^{Mec1} and ATM^{Tel1} have been activated, these kinases signal to the downstream effector kinases, Rad53 and Chk1 (Figure 1.1). Although Rad53 is more closely related to CHK2^{Rad53} by sequence, its function is taken over by CHK1^{Chk1} in higher organisms. In response to stalled replication forks, the signaling of the replication checkpoint is mediated primarily through Rad53 in budding yeast, or by its functional homolog CHK1^{Chk1} in mammalian cells. Rad53 contains a kinase domain which is flanked by two Forkhead associated (FHA) domains, that can bind phosphorylated proteins (Durocher and Jackson, 2002). Mutations of critical residues in the FHA domains have revealed that full Rad53 activation requires at least one functional FHA domain, and that mutations of FHA2 show slightly stronger defects (Pike et al., 2003; Schwartz et al., 2003; Sweeney et al., 2005). N-terminal of each FHA domain is an [S/T]Q cluster domain (Lee et al., 2003), which becomes modified at multiple residues by either Mec1 or Tel1 (Pellicioli et al., 1999; Sanchez et al., 1996; Sun et al., 1996). Nonetheless, genetic evidence indicates that either Mec1 or Tel1 is required, but not sufficient, for Rad53 activation (de la Torre-Ruiz et al., 1998; Emili, 1998). Rad53 activation is facilitated by at least two mediator proteins: the budding yeast Rad9 fulfills this role in the DNA damage checkpoint, while Mrc1 serves as mediator during replication checkpoint activation (Alcasabas et al., 2001; de la Torre-Ruiz et al., 1998; Navas et al., 1996; Sweeney et al., 2005). Interestingly, Rad53 also appears to be phosphorylated in a cell-cycle dependent manner, and this phosphorylation may fine-tune the checkpoint response (Schleker et al., 2010). Here we will first summarize the well-characterized molecular mechanism of Rad53 activation by Rad9, and then review current knowledge about Mrc1.

3.1 RAD53 ACTIVATION IS MEDIATED BY RAD9 IN RESPONSE TO DNA DAMAGE

Rad9 was the first cell-cycle checkpoint protein identified in budding yeast, and it has a key role as an adaptor for activating Rad53 in the DNA damage response, yet it has little or no role in the replication checkpoint triggered by HU-arrested forks (Weinert and Hartwell, 1988; Weinert et al., 1994). Rad9 does not possess enzymatic activity, but contains both tandem Tudor and BRCA1 C-terminal (BRCT) domains. Thus, the mammalian proteins BRCA1, MDC1 and 53BP1 are all considered to be functional homologs of Rad9. The Rad9 tandem Tudor domains can bind to histone H3 methylated on lysine 79 (Grenon et al., 2007), which is deposited throughout the genome by the methyltransferase Dot1 (van Leeuwen et al., 2002). In addition, Rad9 binds histone H2A phosphorylated on serine 129, using its tandem BRCT domains (Hammet et al., 2007). The H2A phosphorylation is mediated by both Tel1 and Mec1 at sites of DNA damage (Cobb et al., 2005; Downs et al., 2000; van Attikum et al., 2004), and both H3K79 methylation and phosphorylated H2A are thought to recruit Rad9 to damaged sites. Consistently, strains bearing *dot1*Δ or phospho-acceptor

mutations in H2A show defects in the G1 checkpoint activation (Giannattasio et al., 2005; Grenon et al., 2007; Hammet et al., 2007; Wysocki et al., 2005). The G2 checkpoint, on the other hand, still functions in the *dot1* mutant. Because the G2 checkpoint activity is lost in a *dpb11 dot1* double mutant, it appears that Dpb11 may also recruit Rad9 in G2 (see Section 2.3) (Pfander and Diffley, 2011; Puddu et al., 2008).

Rad9 becomes phosphorylated by Mec1/Tel1 in response to DNA damage, and is required for efficient Rad53 activation (Emili, 1998). It has been shown that phosphorylated Rad9 can bind to the Rad53 FHA domains, with a preference for FHA2 (Emili, 1998; Schwartz et al., 2002; Schwartz et al., 2003; Sun et al., 1998; Sweeney et al., 2005). This, together with the observation that the autophosphorylation of Rad53 is concentration-dependent, has led to the hypothesis that phosphorylated Rad9 locally increases Rad53 concentration, providing a scaffold for efficient Rad53 autophosphorylation and activation (Gilbert et al., 2001; Ma et al., 2006). In this model, Mec1 would be only required for initial Rad9 phosphorylation, and might not necessarily act directly on Rad53. However, more recent studies have shown that direct phosphorylation of Rad53 by Mec1/Tel1, and not only of Rad9, is required for Rad53 activation (Ma et al., 2006; Sweeney et al., 2005). Indeed, the mutation of Mec1/Tel1 target sites in Rad53's N-terminal [S/T]Q cluster domain reduced viability, replication and damage checkpoint functions, as well as its kinase activity (Lee et al., 2003).

Activation of the mammalian Rad53 homolog CHK2^{Rad53} or *S. pombe* Cds1^{Rad53} requires phosphorylation of one specific residue by upstream kinases (threonine 68 or 11, respectively) (Matsuoka et al., 2000; Tanaka et al., 2001). In the case of Rad53, the [S/T]Q sites in the N-terminal SCD seem to be redundant, and phosphorylation at multiple sites is important for activation (Lee et al., 2003; Sweeney et al., 2005). Once Rad53 has been primed by Mec1/Tel1 and fully activated through autophosphorylation, Rad9 seems to release Rad53, enabling the transduction of the checkpoint responses throughout the nucleus (Gilbert et al., 2001). Mec1/Tel1 phosphorylation of Rad9 also leads to oligomerization of Rad9. The oligomerization may be dispensable for Rad53 activation, whereas it is needed for maintenance of the checkpoint (Usui et al., 2009). Intriguingly, phosphorylation of Rad9 by Rad53 disrupts Rad9 oligomerization, providing a negative feedback mechanism for checkpoint regulation (Usui et al., 2009).

3.2 Mrc1 Serves As a Mediator in the Replication Checkpoint

Whereas Rad9 acts in response to DNA damage in G1 and G2, Mrc1 is a key mediator protein for Rad53 activation in the context of DNA replication (Alcasabas et al., 2001; Osborn and Elledge, 2003; Tanaka and Russell, 2001). Mrc1 is a component of the replisome, and it travels along with replication forks (Katou et al., 2003; Osborn and Elledge, 2003). Mrc1 enhances Rad53 activation during replication stress, but does not activate Mec1 kinase activity per se. Rather, it seems to positively influence the enzyme-substrate interaction between Mec1 and Rad53, and could, therefore, recruit Rad53 to stalled forks to facilitate Rad53-Mec1 interaction (Chen and Zhou, 2009). Analogously, Claspin, the Mrc1 homolog in higher eukaryotes, contributes to replication checkpoint activation by interacting with CHK1^{Chk1}, a functional homolog of Rad53, and facilitating its activation (Chini and Chen, 2003; Kumagai and Dunphy, 2000; Kumagai et al., 2004).

In addition to its checkpoint function, Mrc1 appears to have a structural role in replication fork maintenance, as it binds to the replisome via the Csm3-Tof1 fork protection complex (Bando et al., 2009). Mrc1 interacts with Pol ε and Mcm6 (Komata et al., 2009; Lou et al., 2008), and Tof1 and Csm3 interact with Mcm2 (Bando et al., 2009). Thus, it has been suggested that this complex forms a bridge between the leading strand polymerase ε and the replicative helicase (Lou et al., 2008). Consistently, replisome structure is aberrant in the *mrc1*Δ mutant; *mrc1*Δ cells proceed faster through S phase, show an uncoupling of the replisome from the site of DNA synthesis and have impaired

recovery from HU arrest (Alcasabas et al., 2001; Katou et al., 2003; Szyjka et al., 2005; Tourriere et al., 2005). Mrc1 becomes phosphorylated by Mec1 and a mutant in which all Mrc1 [S/T]Q sites are mutated to AQ, shows a defect only in checkpoint signaling, but not in replisome progression (Alcasabas et al., 2001; Osborn and Elledge, 2003). By using this *mrc1*-AQ mutant, an alternative function for Mrc1 in the replication checkpoint has been suggested, namely, phosphorylation of Mrc1 may stabilize the association of Mec1 with sites of stalled replication forks, thereby creating a positive feedback for Mec1 function (Naylor et al., 2009). Although Mrc1 activates the replication checkpoint in response to replication stress, loss of it can be compensated by Rad9 (Alcasabas et al., 2001). Indeed, Rad9 accumulates at stalled replication forks in *mrc1*Δ cells on HU (Katou et al., 2003). It is therefore likely that loss of Mrc1 checkpoint function creates DSBs or damage structures that provoke Rad9-dependent Rad53 activation. This is a much more likely option than that Mrc1 and Rad9 are equivalent in their mode of action, given that Mrc1 is part of the replisome, and Rad9 clearly is not.

3.3 A Role for Sgs1 in Rad53 Activation

Another factor that has been shown to be involved in replication checkpoint signaling and which helps activate Rad53, is the budding yeast RecQ helicase, Sgs1 (Bjergbaek et al., 2005; Hegnauer et al., 2012). Sgs1 interacts with Dna2, RPA and Rad53, and is constitutively associated with replication forks (Cejka et al., 2010; Cobb et al., 2003; Hegnauer et al., 2012). The deletion of *sgs1* alone destabilizes DNA polymerases α and ε when replication forks are stalled by HU (Cobb et al., 2003), and this effect is far more pronounced when combined with either *mrc1*Δ or the S-phase specific mutant allele of *MEC1*, *mec1-100* (Cobb et al., 2003; Cobb et al., 2005; Lopes et al., 2001; Lucca et al., 2004; Paciotti et al., 2001). This leads to a synergistic arrest of growth and failed fork recovery in response to HU , and a loss of dNTPs incorporation, as both polymerases α and ε are lost from the replisome (Cobb et al., 2003). One explanation of the observed synergy, may be that *mec1-100* generates fold back structures that need Sgs1 for resolution. However, Sgs1 also participates in the activation of Rad53, particularly in response to HU arrest (Bjergbaek et al., 2005). Sgs1 itself contains a [S/TQ] cluster that is phosphorylated in a Mec1-dependent manner *in vivo* and *in vitro* (Hegnauer et al., 2012) (Chapter 4). When phosphorylated, this domain of Sgs1 binds Rad53, again both *in vivo* and *in vitro* (Bjergbaek et al., 2005; Hegnauer et al., 2012) (Chapter 4). Therefore, Sgs1 serves as a replication checkpoint mediator that recruits Rad53 to stalled forks, acting in much the same way as Rad9 acts at DSBs (Chapter 4). Mrc1 and Sgs1 have been found to be epistatic for their function in Rad53 phosphorylation, although Sgs1 functions in parallel with Rad24 and 9-1-1, and the double mutants are highly compromised for the activation of Rad53 at stalled forked (Bjergbaek et al., 2005; Fu et al., 2008). A RecQ homologue in mammals, the WRN^{Sgs1} helicase, has also been shown to facilitate the ATR^{Mec1}-$CHK1^{Chk1}$ checkpoint pathway in response to camptothecin (Patro et al., 2011), indicating that RecQ function in checkpoint signaling may be conserved.

4. TARGETS OF THE REPLICATION CHECKPOINT

An activated replication checkpoint cascade transduces a multitude of stimuli that control cell-cycle and replication-fork recovery. Here, we summarize the downstream pathways that are influenced by the checkpoint. We focus on relevant replication fork targets at the end of this section, to the extent that they are known.

4.1 CELL CYCLE REGULATION

In all eukaryotic species, checkpoint effector kinases play a central role in cell-cycle arrest upon checkpoint activation, even though the mechanism of arrest differs. In fission yeasts and higher eukaryotes, $CHK1^{Chk1}$ and $CHK2^{Rad53}$ negatively regulate $CDC25^{Mih1}$ phosphatases that remove inhibitory phosphorylation on cyclin-dependent kinase (CDK) (Karlsson-Rosenthal and Millar, 2006; Rhind and Russell, 1998; Sanchez et al., 1997; Sorensen and Syljuasen, 2012). Checkpoint-dependent phosphorylation of $CDC25^{Mih1}$ down-regulates its activity through inhibition of its nuclear localization by binding 14-3-3, a nuclear-cytoplasmic shuttling protein, and through degradation by the SCF^{BTrcp} ubiquitin ligase (Busino et al., 2003; Jin et al., 2003; Peng et al., 1997). Therefore, DNA replication and the damage checkpoint down-regulates the CDK cell cycle engine, thereby blocking G2/M transition. In *S. cerevisiae*, however, this cell-cycle arrest by CDK inhibition does not occur (Sorger and Murray, 1992). Nonetheless, checkpoint mutants exhibit a cytologically typical mitotic arrest defect, with elongated spindles in response to blocked replication forks (Allen et al., 1994; Paulovich and Hartwell, 1995; Weinert et al., 1994). Budding yeast cells transmit the checkpoint signal to inhibit progression of mitosis by stabilizing $securin^{Pds1}$, which inhibits the metaphase to anaphase transition, and by stimulating the Bub2/Bfa1 GAP complex which inhibits the mitotic exit network (Clarke et al., 2001; Hu et al., 2001; Sanchez et al., 1999). Microtubule elongation is also blocked (Krishnan et al., 2004).

4.2 ESSENTIAL FUNCTION FOR CELL VIABILITY—DNTP POOL REGULATION AND FORK MAINTENANCE?

Intriguingly, Mec1 and Rad53 and their functional homologs ATR^{Mec1} and $CHK1^{Chk1}$ are essential for cell proliferation, but this is not due to their checkpoint function (Brown and Baltimore, 2000; de Klein et al., 2000; Desany et al., 1998; Liu et al., 2000; Takai et al., 2000; Zhao et al., 1998). In *S. cerevisiae*, the lethality of *mec1* or *rad53* deletions can be bypassed by up-regulating the dNTP pool with another mutation (Desany et al., 1998; Zhao et al., 1998). In *S. pombe*, on the other hand, neither $Rad3^{Mec1}$ nor $Cds1^{Rad53}$ are encoded by essential genes, raising the question of whether the critical dNTP regulating function of these checkpoint kinases is conserved. In mammalian cells NTP pool control through c-Myc appears to be a determinant of dNTP levels (Bester et al., 2011).

In *S. cerevisiae* dNTP levels increase 8-fold in response to DNA damage, an increase that facilitates cell survival, even as it increases the mutation rate (Chabes et al., 2003). Given the pleotropic effects of dNTPs, it is reasonable that cells have multiple pathways that regulate dNTP concentrations, one of which is through the Dun1 kinase, a target of Rad53 (Nordlund and Reichard, 2006) Dun1 phosphorylates Sml1 and Dif1, which inhibit ribonucleotide reductase (RNR), priming them for degradation (Lee et al., 2008; Zhao and Rothstein, 2002). Dun1 also induces RNR gene transcription by inhibiting the transcriptional repressor Crt1 (Huang et al., 1998). Given that the failure to regulate dNTPs is lethal, these pathways are obviously very important in budding yeast.

A recent study from the Longhese laboratory has revealed that the essential functions of Mec1 and Rad53 can also be bypassed by lowering the activity of Cdc28, the budding yeast CDK (Manfrini

et al., 2012). Similarly, a delayed entry into S or M phase provoked by lowered levels of G1- or M-phase cyclins, improves the survival of *mec1Δ* or *rad53Δ* cells on low doses of HU. This suggests that either extending G1, prior to S phase entry, or a reduction in the number of active replication forks, compensates for the lethal effects of checkpoint kinase ablation. Most likely, this suppression is explained by the fact that cells have sufficient time both to generate dNTPs and to complete replication. Surprisingly, lowered rates of microtubule elongation provoked by *cin8* mutation, also suppresses the lethality of *mec1Δ* or *rad53Δ* cells. Both survival on HU and the ensuing completion of replication improve in the *cin8* mutant, suggesting that centromere segregation by a premature mitotic spindle, is another lethal consequence of *mec1* or *rad53* ablation. Similarly, the inhibition of microtubule elongation through nocodazole diminishes Rad52 repair foci, which are induced in cells bearing the temperature-sensitive *mec1-14* mutation at elevated temperatures in S phase (Manfrini et al., 2012). Together, these data suggest that checkpoint kinases also coordinate the completion of replication with microtubule elongation, in line with the original concept of checkpoints: that is, to preserve the order of cell-cycle events. We note, however, that the experiments in the cited study used either no or low dose HU. Indeed, after treatment with a high doses of HU or MMS, the essential function of the replication checkpoint was shown to be its ability to facilitate the restart of replication forks once the lesions have been removed (Desany et al., 1998; Tercero et al., 2003). This may act by preventing the accumulation of aberrant DNA structures and/or fork collapse (Cobb et al., 2003; Cobb et al., 2005; Lopes et al., 2001; Lucca et al., 2004) (see Section 4.6).

Mec1 and ATR^{Mec1} are known to prevent chromosome breakage at fragile sites where replication forks frequently slow down, even in the absence of exogenous damage (Casper et al., 2002; Cha and Kleckner, 2002). Given the fact that ATR^{Mec1} is an essential protein in mammalian cells, and given that there are many more obstacles that impair fork progression in higher eukaryotes, it may well be that overcoming intrinsic replication stress is the essential role for ATR^{Mec1}/$CHK1^{Chk1}$ in higher organisms.

4.3 ORIGIN CONTROL

DNA replication is initiated by a series of steps that proceed in a sequential manner. In the first step, known as licensing, the pre-replicative complex (pre-RC) is loaded onto DNA at the origins of replication in G1 phase, when CDK activity is low. The pre-RC consists of ORC, Cdc6, Cdt1, and Mcm2-7. In the second step, the essential helicase components Cdc45 and GINS, together with DNA polymerases, are brought onto pre-RC by the bridging factors Sld3-Sld7 and Dpb11-Sld2 in a CDK- and DDK- (Dbf4 dependent kinase, $CDC7^{Cdc7}$-$DBF4^{Dbf4}$) dependent manner (Tanaka and Araki, 2010; Zegerman and Diffley, 2009)[3]. Finally, Mcm10 functions in the unwinding step, together with the CMG helicase complex (Cdc45-MCM-GINS), thus initiating DNA replication (Kanke et al., 2012; van Deursen et al., 2012; Watase et al., 2012).

In eukaryotes, there are multiple origins of DNA replication (in *S. cerevisiae* ~500 in a haploid genome), and those initiation events are regulated temporally (Barberis et al., 2010; Gilbert et al., 2010). In budding yeast cells, several factors essential for the initiation of DNA replication are limiting, and those factors appear to be recycled for later initiation events (Mantiero et al., 2011; Tanaka et al., 2011). Recent studies have shown that Rad53 targets and inactivates two of the limiting

[3] DDK promotes DNA replication by phosphorylating Mcm4 (Sheu and Stillman, 2006). in a domain of Mcm4 that integrates multiple kinase signals important for replication initiation and elongation (Sheu et al., 2014). Recently, it was shown that $PP1^{Glc7}$, which is recruited by Rif1, regulates and prevents premature Mcm4 phosphorylation, thus suggesting a role for Rif1 in regulation of replication initiation in budding yeast (Hiraga et al., 2014).

replication factors, Sld2 and Dbf4 (the DDK regulatory subunit). Thus, late-origin firing is suppressed by an activated replication checkpoint (Lopez-Mosqueda et al., 2010; Zegerman and Diffley, 2010). Regulation of replication initiation by the checkpoint also occurs in higher eukaryotic cells, although the targets appear to be different (Karnani and Dutta, 2011). It is interesting to note that in *S. pombe* and mammalian cells, DDK has been shown to have a positive role in replication checkpoint activation (Kim et al., 2008b; Matsumoto et al., 2010; Tenca et al., 2007). DDK also modulates the checkpoint response to facilitate DNA repair and recovery from checkpoint arrest (Furuya et al., 2010; Tsuji et al., 2008) (see Section 4.5).

4.4 Transcription Control

Genome-wide gene expression analyses in budding yeast have revealed that hundreds of genes are up- or down-regulated upon treatment with genotoxic reagents that induce stalled replication forks (Benton et al., 2006; Gasch et al., 2001; Jelinsky and Samson, 1999; van Attikum et al., 2004). This transcriptional regulation is controlled by two branches in the replication checkpoint pathway; one directly by Rad53, the other by Dun1 (Bastos de Oliveira et al., 2012; Huang et al., 1998; Travesa et al., 2012). Dun1 phosphorylates and inhibits Crt1, which recruits repressors Ssn6 and Tup1 to the promoters of DNA damage response genes. Dun1 thereby up-regulates genes involved in DNA repair and ribonucleotide biosynthesis (Gasch et al., 2001; Huang et al., 1998). Two recent studies have revealed that the cell-cycle dependent genes that are transcribed at the G1/S boundary are also induced as a part of the DNA replication and damage response in *S. cerevisiae* (Bastos de Oliveira et al., 2012; Travesa et al., 2012). Over 200 G1/S genes are regulated by the heteromeric transcription factors SBF (Swi4-Swi6 cell-cycle box (SCB) binding factor) and MBF (*MluI* cell-cycle box (MCB) binding factor) (Iyer et al., 2001). While SBF activates transcription in G1, MBF down-regulates transcription outside of G1 through the co-repressor Nrm1, thereby restricting the expression of the target genes in late G1 (Bean et al., 2005; de Bruin et al., 2006). The studies revealed that MBF target genes are up-regulated upon replication stress by inactivation of Nrm1 in a Rad53-dependent Dun1-independent manner (Bastos de Oliveira et al., 2012; Travesa et al., 2012). This transcriptional regulation is also conserved in *S. pombe*, as the Rad53 homolog $Cds1^{Rad53}$ inhibits Nrm1 and promotes G1/S transcription in response to replication stress (de Bruin et al., 2008; de Bruin et al., 2006).

4.5 Coordinating DNA Repair

It seems obvious that the DNA damage checkpoint should be coupled with the up-regulation of DNA repair, and various forms of damage provoke both a checkpoint response and DNA repair. Since ssDNA coated by RPA initiates both checkpoint activation and the loading of Rad51 for repair by HR, the cell has to carefully coordinate these events, particularly at the replication fork where ssDNA exists constitutively. Importantly, studies in budding and fission yeasts have shown that the replication checkpoint actively suppresses the initiation and processing required for HR (Alabert et al., 2009; Barlow and Rothstein, 2009; Meister et al., 2005). Rad52 foci are absent in cells treated with HU, even in the presence of DSBs, as long as the replication checkpoint is intact (Alabert et al., 2009; Barlow and Rothstein, 2009). Consistently, the ATR^{Mec1}-p53 pathway has been shown to suppress the formation of $RAD51^{Rad51}$ foci in response to HU in mammalian cells[4] (Sirbu et al., 2011), although in other cases it has been reported that $CHK1^{Chk1}$ phosphorylates $RAD51^{Rad51}$ and positively regulates HR in response to HU or CPT (Huang et al., 2008; Sorensen et al., 2005). These discrepancies suggest that the checkpoint regulation of HR is fine-tuned with respect to the type and level of damage.

[4] One recent study suggested that hyperphosphorylated RPA2 sequesters Rad51 in the soluble nuclear fraction, thus impairing homologous recombination (Lee et al., 2010).

In addition to the role of 9-1-1 in ATR^{Mec1} activation described above, it has been well documented that 9-1-1 functions in various aspects of DNA repair (see review (Helt et al., 2005)). Indeed, cells may use the multi-tasking capacity of 9-1-1 to coordinate the checkpoint activation with DNA repair. In both *S. cerevisiae* and *S. pombe*, it has been suggested that 9-1-1 functions in DNA damage tolerance pathways (Kai and Wang, 2003; Karras et al., 2013; Paulovich et al., 1998). The budding yeast 9-1-1 complex also contributes to the resection of DSBs, as *rad24* mutants that impair 9-1-1 loading have reduced ssDNA formation and impaired recruitment of Mec1 at HO-induced breaks (Aylon and Kupiec, 2003; Dubrana et al., 2007). Finally, human 9-1-1 physically interacts with factors involved in base excision repair (BER), such as MYH, Polβ, TDG, Fen1, and DNA ligase I, and stimulates their enzymatic activities (Balakrishnan et al., 2009; Chang and Lu, 2005; Gembka et al., 2007; Guan et al., 2007; Toueille et al., 2004; Wang et al., 2004).

How then is 9-1-1 function regulated? Recent studies have indicated that post-transcription modification of 9-1-1 is crucial for its regulation. *S. pombe* Rad9^{Ddc1}, a component of checkpoint clamp, is phosphorylated at multiple sites by Rad3^{Mec1}, and two phosphoacceptor sites in the C-terminal tail that promote Rad9^{Ddc1}-Cut5^{Dpb11} interaction are required for Chk1^{Chk1} activation (Furuya et al., 2004) (see Section 2.1). Interestingly, Rad3^{Mec1}-dependent phosphorylation at T225 on Rad9^{Ddc1} has been shown to facilitate the interaction with Mms2^{Mms2}-Ubc13^{Ubc13}, a ubiquitin-conjugating enzyme, to promote error-free repair (Kai et al., 2007). Finally, a study in human cells has indicated that RAD18^{Rad18} facilitates RAD9^{Ddc1} recruitment at IR-induced damage through an unknown mechanism, although this mode of RAD9^{Ddc1} recruitment has little impact on checkpoint activation: no loss of CHK1^{Chk1} or CHK2^{Rad53} activation was scored in cells depleted for RAD18^{Rad18} (Inagaki et al., 2011).

As mentioned above, Dbf4-Cdc7 also modulates checkpoint activity (Kim et al., 2008b; Matsumoto et al., 2010; Tenca et al., 2007; Tsuji et al., 2008). A recent study by Furuya et al. has shown that the *S. pombe* DDK phosphorylates Rad9^{Ddc1} (Furuya et al., 2010), thereby reducing interaction between Rad9^{Ddc1} and RPA and releasing 9-1-1 from chromatin. This phosphorylation appears to be important for the repair of CPT-induced lesions, as the number of Rad22^{Rad52} repair foci increase in DDK phospho-acceptor site mutants (Furuya et al., 2010). Together, the above studies argue compellingly that 9-1-1 functions at the interface of repair and checkpoint pathways.

4.6 Replication Fork Stability

As briefly discussed in Section 4.2, maintenance of replication fork integrity is the crucial function of the replication checkpoint in response to replication stress (Figure 1.3). Control of the cell cycle, transcription, and origin firing, while important, are non-essential events based on the following considerations: (1) Blocking the transition through M phase by nocodazole is not sufficient to rescue the lethality of high doses of MMS or HU in *rad53* or *mec1* mutant cells (Desany et al., 1998; Tercero and Diffley, 2001); (2) De novo protein synthesis does not contribute to cell viability, nor is it required for the resumption of replication forks after HU treatment (Tercero et al., 2003); and (3) HU treatment of cells that cannot suppress late-origin firing due to phospho-site mutations in both Dbf4 and Sld3, is not lethal (Lopez-Mosqueda et al., 2010; Zegerman and Diffley, 2010). On the other hand, checkpoint mutants fail to resume DNA replication after transient exposure to HU or MMS, and replisome components are not detected by chromatin immunoprecipitation (ChIP) at early origins on HU in *mec1* mutants (Cobb et al., 2003; Cobb et al., 2005; Lucca et al., 2004; Tercero et al., 2003). Finally, upon fork stalling, checkpoint mutants show aberrant DNA structures, such as the formation of reversed forks (so-called chicken-foot structures) and an accumulation of ssDNA (Lopes et al., 2001; Sogo et al., 2002). These observations led to the notion that the replication checkpoint maintains the stable association of replication polymerases at stalled forks.

An important aspect of the replication checkpoint is the fact that the roles of ATR^{Mec1} and the effector kinase, $CHK1^{Rad53}$, are not equivalent, particularly with respect to fork recovery. This is well-documented, yet often overlooked. In *S. cerevisiae* it has been shown that the function of Rad53 that is essential for viability on MMS is largely rescued by deletion of the exonuclease, *EXO1* (Segurado and Diffley, 2008). This suggests that the down-regulation of Exo1 at arrested forks is a major function of Rad53 (Segurado and Diffley, 2008). Interestingly, however, an *EXO1* deletion does not suppress *mec1Δ* lethality, indicating that Mec1 has functions that are crucial for cell survival on MMS, other than the activation of Rad53 (Segurado and Diffley, 2008). Indeed, when forks are arrested by high concentrations of HU, quantitative ChIP assays showed that leading and lagging DNA polymerases are displaced in *mec1* mutant cells, although their association is intact in the absence of Rad53 (Cobb et al., 2003; Cobb et al., 2005; Lucca et al., 2004). Similarly, in *mec1* mutants Cdc45 becomes undetectable at early origins (Cobb et al., 2005; Katou et al., 2003). In *rad53* mutants, on the other hand, ChIP signals for DNA polymerases stay high, yet the distribution of the MCM helicase is altered, underscoring again the distinct roles played by Mec1 and Rad53 at stalled forks (Cobb et al., 2003; Cobb et al., 2005). The exact mechanisms are unclear, yet it appears that Mec1 activity keeps replication polymerases engaged in the presence of HU, while Rad53 acts primarily through the MCM helicase to ensure replication restart (Cobb et al., 2003; Cobb et al., 2005).

Whereas the outcome of checkpoint activation is clear, it is not clear exactly what happens to the stalled replisome complex in the absence of a functional replication checkpoint. ChIP data led to the conclusion that the replication checkpoint stabilizes the replisome and preserves its integrity (Figure 1.3C). Recent biochemical approaches, on the other hand, have shown that intact replisome complexes can be recovered by Sld5-(GINS) pull-down even in *mec1* and *rad53* checkpoint mutants arrested with HU. The replisome complex, even though it is not functionally engaged, may stay chromatin-associated in both checkpoint-proficient and -deficient cells (De Piccoli et al., 2012). ChIP coupled with deep sequencing suggests that the replisome moves away from the last site of DNA synthesis in an uncoordinated manner in checkpoint mutants, possibly still unwinding double-stranded DNA by the helicase, but not incorporating dNTPs (Figure 1.3D). This random sliding of the replisome could explain the apparent "loss" of polymerases from early initiating sites, as well as the accumulation of ssDNA observed by ChIP and electron microscopy analyses (Cobb et al., 2005; De Piccoli et al., 2012; Katou et al., 2003; Lucca et al., 2004; Sogo et al., 2002). This movement, however, was only detected at the very earliest origins (De Piccoli et al., 2012), did not correlate with the incorporation of nucleotides (Crabbe et al., 2010; Katou et al., 2003), and could not account for the majority of forks where both polymerase and helicase seem to persist even in checkpoint mutants (De Piccoli et al., 2012). One model that could reconcile these results suggests that the replication checkpoint keeps the replisome engaged at sites of stalled forks in an as yet undefined way, rather than simply tethering the replisome factors together. Further work is needed to address the molecular mechanisms of how the replication checkpoint facilitates the restart of stalled forks and recovery from replication stress.

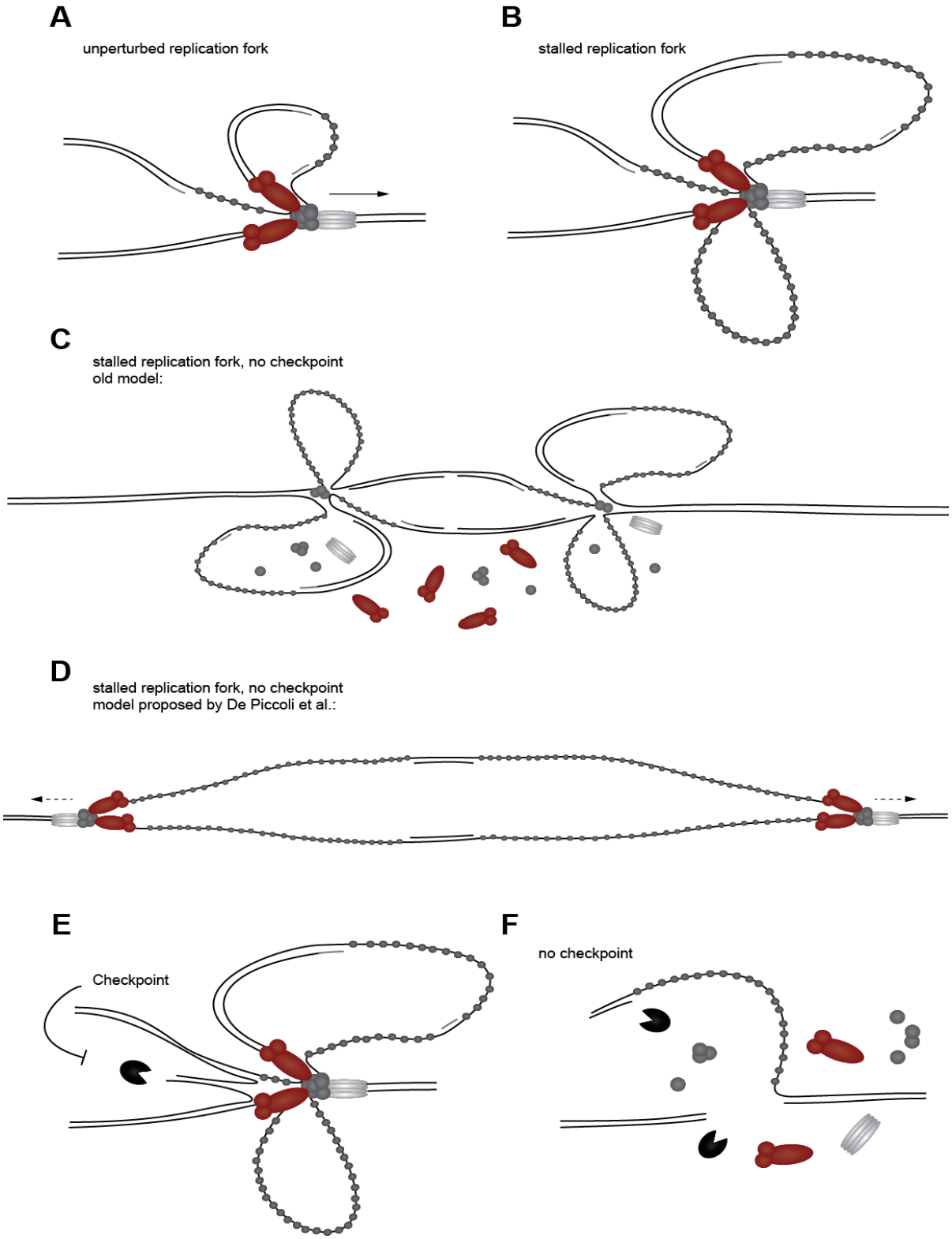

Figure 1.3: Replication fork stabilization. (**A**) A normal replication fork with leading and lagging strand polymerases, replicative helicase, and short ssDNA stretches coated with RPA. (**B**) When replication forks stall and helicase and polymerases become functionally uncoupled, long ssDNA stretches are exposed that lead to checkpoint activation. (**C**) ChIP experiments have indicated that replisome factors are lost from stalled replication forks if the replication checkpoint is not functional. (**D**) New data suggest that replisomes stay intact, but move away from replication origins without incorporating nucleotides. This leads to long ssDNA stretches. (**E**) The checkpoint regulates nucleases that may target structures (e.g. reverse forks) that arise at stalled replication forks. (**F**) If nuclease regulation fails due to checkpoint dysfunction, this may lead to uncontrolled processing and could result in double-strand breaks.

Several studies have indicated that the checkpoint regulates the action of nucleases and helicases at stalled forks (Figure 1.3E, F). Indeed, in *S. cerevisiae* the exonuclease Exo1 is modified and inhibited by the DNA damage checkpoint (Morin et al., 2008; Segurado and Diffley, 2008), and deletion of *EXO1* has been shown to suppress the accumulation of ssDNA in checkpoint-deficient cells on HU (Cotta-Ramusino et al., 2005). Similarly, human EXO1 undergoes ubiquitin-mediated degradation on HU, in a manner partly dependent on phosphorylation by ATR^{Mec1} (El-Shemerly et al., 2008). Recently it has also been shown that the nuclease/helicase Dna2 is a target of the replication checkpoint, and that phosphorylation facilitates its association to DNA following exposure to HU (Hu et al., 2012). Dna2 nuclease activity is thought to prevent ssDNA formation by cleaving off ssDNA tails that arise from stalled fork regression (Hu et al., 2012). A structure-specific nuclease Mus81-Eme1 is also a target of Cds1^{Rad53} in *S. pombe*, and is released from chromatin upon fork stalling (Kai et al., 2005). Finally, as mentioned above, the Sgs1 helicase is a target of Mec1, and its helicase activity has an important role in replication fork stability (Cobb et al., 2003; Cobb et al., 2005; Frei and Gasser, 2000; Hegnauer et al., 2012). Specifically, when *sgs1*Δ is combined with either *mrc1*Δ or *mec1-100*, an S phase-specific *mec1* mutant (Paciotti et al., 2001), then total fork collapse occurs in the presence of HU, and neither DNA polymerases nor RPA can be detected at the collapsed fork by ChIP analysis (Cobb et al., 2003; Cobb et al., 2005; Frei and Gasser, 2000; Hegnauer et al., 2012). This results in a dramatic increase in gross chromosomal rearrangements and high levels of cell lethality. The mammalian RecQ helicases BLM^{Sgs1} and WRN^{Sgs1} are also phosphorylated by ATR^{Mec1} and ATM^{Tel1} (Davies et al., 2004; Pichierri et al., 2003), and are implicated in replication fork recovery after stress (Ammazzalorso et al.; Davies et al., 2004; Davies et al., 2007). Whereas Sgs1 helicase does help transduce the checkpoint signal by activating Rad53, the prevention of fork collapse requires its helicase activity, and not simply its ability to bind Rad53. (Cobb et al., 2003; Cobb et al., 2005; Frei and Gasser, 2000; Hegnauer et al., 2012). Together, these data suggest that ATR^{Mec1} and CHK1^{Rad53} target distinct sets of nucleases and helicases to suppress the formation of pathological fork structures that impair replication fork resumption after removal of the damage.

A number of studies has been carried out to identify the targets of the replication and DNA damage checkpoints, and to determine their relevance for the checkpoint response. In Table 1.2, we list the replication fork associated factors in addition to those mentioned above, that are phosphorylated upon checkpoint activation (Bennetzen et al., 2010; Blasius et al., 2011; Chen et al.; Matsuoka et al., 2007; Mu et al., 2007; Smolka et al., 2007; Stokes et al., 2007). While phosphoproteomic studies have identified many, only a few checkpoint targets have been elucidated in depth. For example, RPA1^{Rfa1}, the large subunit of RPA, is crucial for ATR^{Mec1} recruitment at the site of damage and is a documented Mec1 target (Brush et al., 1996), yet the function of its phosphorylation remains unclear. In human cells, the second RPA subunit, RPA32^{Rfa2}, is phosphorylated by ATR^{Mec1} and by another PIKK, DNA-PK, upon replication stress, and this phosphorylation is required for a robust checkpoint response and for recovery from fork arrest (Liu et al., 2012b). DNA polymerase α, the lagging strand polymerase, is a checkpoint target (Pellicioli et al., 1999), and has an important role in the initiation of the replication checkpoint (Michael et al., 2000). Interestingly, the gap-filling lagging strand polymerase, DNA polymerase δ, has been shown to be a target of Mec1 in response to MMS (Chen et al., 2010), although the importance of its phosphorylation in replication fork stability is unclear. The active replicative helicase CMG complex (Cdc45-MCM-GINS) is one of the common targets of the replication and damage checkpoint in different organisms; MCM2^{Mcm2} (primarily a target of ATR^{Mec1} (Cortez et al., 2004; Trenz et al., 2008; Yoo et al., 2004)), MCM3^{Mcm3} (primarily a target of ATM^{Tel1}-CHK2^{Rad53} (Cortez et al., 2004; Ilves et al., 2012; Shi et al., 2007)), MCM4^{Mcm4} (a target of both ATR^{Mec1} and ATM^{Tel1} pathways (Bailis et al., 2008; Ilves et al., 2012; Ishimi et al., 2003)), GINS component Psf1 (a Mec1 target (De Piccoli et al., 2012)), and PSF2^{Psf2} (a CHK2^{Rad53} target (Ilves et al., 2012)) are all phosphorylated upon checkpoint

activation. $CHK2^{Rad53}$ phosphorylation of the CMG inhibits its helicase activity (Ilves et al., 2012), whereas phosphorylation of Mcm2 has been shown to recruit $Plk1^{Cdc5}$ (polo-like kinase 1) on chromatin and promote checkpoint recovery (Trenz et al., 2008) (see also Section 6). Finally, analyses in both budding yeast and human cells have identified specific phosphopeptides of the GINS complex and DNA polymerase ε targeted by ATR^{Mec1} and/or ATM^{Tel1}, and not by downstream effector kinases $CHK1^{Rad53}$ (see Table 1.3 (Chen et al., 2010; Matsuoka et al., 2007)), consistent with the distinct roles played by ATR^{Mec1} and the downstream effector kinase $CHK1^{Rad53}$. It is of utmost relevance to find out whether, and how, phosphorylation of these factors impacts replication fork integrity and fork restart.

Table 1.3: Replication factors modified by replication and damage checkpoint kinases.[5]

	Function	References
***S. cerevisiae* (targeted by)**		
Rfa1 (Mec1/Tel1)	a subunit of RPA	(Brush and Kelly, 2000; Chen et al., 2010; Smolka et al., 2007)
Rfa2 (Mec1/Tel1)	a subunit of RPA	(Brush et al., 1996; Chen et al., 2010)
Pol1 (Rad53)	a subunit of DNA polα	(Chen et al., 2010)
Pol31 (Mec1/Tel1)	a subunit of DNA polδ	(Chen et al., 2010)
Dpb4 (Mec1/Tel1)	a subunit of DNA polε and ISW2	(Chen et al., 2010; Smolka et al., 2007)
Mcm4(Mec1)	a subunit of MCM	(Randell et al., 2010)
Mcm6 (Mec1)	a subunit of MCM	(Randell et al., 2010)
Psf1 (Mec1)	a subunit of GINS	(De Piccoli et al., 2012)
Mrc1 (Mec1, Rad53)	checkpoint mediator	(Alcasabas et al., 2001; Chen et al., 2010)
Tof1 (Rad53)	fork protection complex	(Smolka et al., 2007)
Ctf4 (Rad53)	polα interactor	(Smolka et al., 2007)
Dbf4 (Rad53)	a subunit of DDK	(Chen et al., 2010; Lopez-Mosqueda et al., 2010; Weinreich and Stillman, 1999; Zegerman and Diffley, 2010)
Sgs1 (Mec1)	Rec Q helicase	(Hegnauer et al., 2012)
Higher eukaryotes		
RPA1 (ATR/ATM)	a subunit of RPA	(Matsuoka et al., 2007; Stokes et al., 2007)
POLE (ATR/ATM)	a subunit of polε	(Matsuoka et al., 2007)
POLEE4 (ATR/ATM)	a subunit of polε	(Matsuoka et al., 2007)
POLL (ATR/ATM)	a subunit of polλ	(Matsuoka et al., 2007)
MCM2 (ATR/ATM)	a subunit of MCM	(Bennetzen et al., 2010; Matsuoka et al., 2007; Stokes et al., 2007)
MCM3 (ATR/ATM)	a subunit of MCM	(Matsuoka et al., 2007)
MCM4 (ATR/ATM, Chk1)	a subunit of MCM	(Bennetzen et al., 2010; Ishimi et al., 2003; Matsuoka et al., 2007)
MCM5 (Chk1)	a subunit of MCM	(Blasius et al., 2011)
MCM6 (ATR/ATM,	a subunit of MCM	(Bennetzen et al., 2010; Matsuoka et al., 2007)

[5] Many additional checkpoint kinase substrates are known from large scale phosphoproteomics studies from this work (Chapter 2) and other laboratories (Marcus Smolka, unpublished data, Chen et al., 2010) that have not been directly located at replication forks yet may also help to keep polymerases engaged and enable replication fork restart.

MCM7 (ATR/ATM)	a subunit of MCM	(Matsuoka et al., 2007)
POLDIP3 (ATR/ATM)	Polδ interacting factor	(Matsuoka et al., 2007)
MCM10 (ATR/ATM)	replication initiation factor	(Matsuoka et al., 2007)
HELB (ATR/ATM)	DNA helicase B	(Matsuoka et al., 2007)
RFC1 (ATR/ATM)	clamp loader	(Bennetzen et al., 2010; Matsuoka et al., 2007; Stokes et al., 2007)
RFC3 (ATR/ATM)	clamp loader	(Matsuoka et al., 2007)
PSF2 (ATR/ATM)	a subunit of GINS	(Ilves et al., 2012; Matsuoka et al., 2007; Stokes et al., 2007)
ORC3 (ATR/ATM)	a subunit of ORC	(Matsuoka et al., 2007)
ORC6 (ATR/ATM)	a subunit of ORC	(Matsuoka et al., 2007)
DBF4 (ATR/ATM)	a subunit of DDK	(Matsuoka et al., 2007)
Claspin (ATR/ATM)	checkpoint mediator	(Matsuoka et al., 2007; Stokes et al., 2007)
CAF-1B (ATR/ATM)	histone assembly	(Stokes et al., 2007)
CTF18 (ATR/ATM)	POLH interactor	(Matsuoka et al., 2007; Stokes et al., 2007)
TopBP1 (ATR/ATM, Chk1)	initiation and ATR activation	(Blasius et al., 2011; Matsuoka et al., 2007; Stokes et al., 2007)
WDHD1 (ATR/ATM)	Polα interactor	(Stokes et al., 2007)
BLM (ATR/Chk1)	RecQ helicase	(Blasius et al., 2011; Davies et al., 2004)
FEN1 (Chk1)	5' flap endonuclease	(Blasius et al., 2011)
DNA Ligase 1 (Chk1)	DNA ligase	(Bennetzen et al., 2010; Blasius et al., 2011)
TIPIN (ATR/ATM)	fork protection complex	(Matsuoka et al., 2007)
WRN (ATR/ATM)	RecQ helicase	(Matsuoka et al., 2007; Pichierri et al., 2003)

In addition to direct fork-associated proteins, enzymes that modulate long-range chromatin organization are also shown to be targets of the replication checkpoint. For instance, the Ino80 and Isw2 chromatin remodelers are confirmed targets of the DNA damage checkpoint (Chen et al., 2010; Morrison et al., 2007). These ATP-dependent chromatin remodeling complexes are shown to be recruited at the stalled replication forks and to promote the recovery of stalled forks (Falbo et al., 2009; Papamichos-Chronakis and Peterson, 2008; Shimada et al., 2008; Vincent et al., 2008). Loss of Ino80 chromatin remodeling activity results in a poor resumption of stalled forks and an increase in DNA repair response (Falbo et al., 2009; Papamichos-Chronakis and Peterson, 2008; Shimada et al., 2008). This correlates with a proposed action of removing nucleosomes to allow fork progression, although INO80 contains a 5' to 3' DNA helicase activity in its Rvb1 and Rvb2 subunits, which may also be involved in altering fork structure (Shen et al., 2000). Another study has suggested a role in checkpoint down-regulation, although how chromatin remodeling reduces a checkpoint response is unknown ((Au et al., 2011) see also Section 6.2).

A recent study has proposed that the replication checkpoint releases topological tension generated by a transcribed gene that is tethered to components of the nuclear pore (Bermejo et al., 2011). DNA replication forks frequently pause at transcribed genes, and this pausing is independent of the directionality between replication and transcription (Azvolinsky et al., 2009). Bermejo et al. (Bermejo et al., 2011) have determined that mutations in THO, TREX-2, or inner basket nucleoporins enhance the survival of *rad53* mutants on HU, and rescue fork reversal, which occurs in the checkpoint mutants on HU (Bermejo et al., 2011). The replication checkpoint appears to target Mlp1, a nucleoporin, and

counteracts its function for gene tethering to the nuclear pore. A phospho-mimicking *mlp1* mutation suppresses *rad53*Δ lethality on HU, suggesting that releasing topological impediments generated by gene gating is one task of the replication checkpoint. However, the interpretation may be rather complicated since loss of Mlp1 also releases and alters the activity of the SUMO-protease Ulp1 which plays a key role in DNA repair (Palancade et al., 2007).

A bioinformatics approach has also indicated that ATR^{Mec1} and ATM^{Tel1} may be involved in regulating a broad range of cellular structures, such as the spindle pole body/centrosome and actin cytoskeleton (Cheung et al., 2012). It will be interesting to explore whether those less canonical Mec1/Tel1 targets function at replication forks to ensure genome stability.

5. COORDINATION BETWEEN ATR^{MEC1} AND ATM^{TEL1}

While ATR^{Mec1} and $CHK1^{Chk1}$ serve distinct roles in the replication checkpoint, it is also clear that ATR^{Mec1} and ATM^{Tel1} do not have identical roles. ATM^{Tel1} initiates the DSB checkpoint response, while ATR^{Mec1} is the first responder to the replication-associated DNA damage. As mentioned above, MRX/MRN recognizes DSBs and recruits ATM^{Tel1} kinase. However, there are also a range of overlapping functions between ATM^{Tel1} and ATR^{Mec1}. At DSBs, budding yeast Tel1 phosphorylates Mre11, Xrs2, and Sae2. Sae2 activates MRX nuclease activity, which initiates 5'–3'end resection (Mimitou and Symington, 2011). Extended ssDNA formation is followed by Exo1, Sgs1-Top3-Rmi1, and Dna2 helicase/nuclease activity, with the aid of Fun30 (SMARCAD1), a recently identified chromatin remodeler (Chen et al., 2012; Costelloe et al., 2012; Eapen et al., 2012; Mimitou and Symington, 2011). Extended RPA-coated ssDNA leads to the recruitment and subsequent activation of ATR^{Mec1}-$ATRIP^{Ddc2}$ (Jazayeri et al., 2006) (see Figure 1.1). Recently, Peterson et al. have shown that ATR^{Mec1} in mammals also phosphorylates $CtIP^{Sae2}$, and this phosphorylation stimulates $CtIP^{Sae2}$ chromatin interaction and end-resection (Peterson et al., 2011). Thus, checkpoint signaling after DSB induction involves both the ATR^{Mec1} and ATM^{Tel1} pathways. A recent biochemical analysis has suggested a mechanism for a consecutive switch from ATM^{Tel1} to ATR^{Mec1} through swapping the recruiter MRN^{MRX} for RPA at the DSB damage site during end-resection (Shiotani and Zou, 2009). We note that in higher eukaryotes another PIKK, DNA-PK, also participates in the signaling of the DSB damage response (Hill and Lee, 2010).

Although ATR^{Mec1}-$ATRIP^{Ddc2}$ is the major regulator of the replication-associated checkpoint, the vulnerable nature of replication forks can generate DSBs through fork collapse (Figure 1.1), which then might require ATM^{Tel1} activation to protect the break and facilitate fork restart. In a *Xenopus* replication system, both ATM^{Tel1} and ATR^{Mec1} appear to play an important role in preventing DSB formation during replication (Trenz et al., 2006). In the absence of ATM^{Tel1} and ATR^{Mec1}, DSBs accumulate and DNA polymerase ε is displaced from CPT- or mitomycin C-damaged chromatin. It has also been demonstrated that MRN^{MRX} is redistributed to the restarting forks, in a manner dependent on ATM^{Tel1} and ATR^{Mec1}. This appears to be important for preventing persistent DSB formation (Trenz et al., 2006). Consistently, Doksani et al. have shown that in the absence of Tel1 or MRX function, abnormal DNA intermediates accumulate when the replication fork encounters an induced DSB. They suggest that the MRX-Tel1 pathway prevents the formation of cruciform structures at the fork-DSB junction (Doksani et al., 2009), a pathway that may depend on crosstalk between ATR^{Mec1} and ATM^{Tel1}.

The mechanism of ATR-ATM crosstalk is somewhat lesion specific. For instance, ATR^{Mec1} phosphorylates ATM^{Tel1} at serine 1981, which promotes the dissociation of inactive ATM^{Tel1} dimers

into active monomers, in response to HU or UV. This results in CHK2^{Rad53} activation and a robust G2/M arrest (Stiff et al., 2006). In contrast, in the presence of IR-induced damage, ATM^{Tel1} auto-phosphorylates this same residue, resulting in self-activation (Bakkenist and Kastan, 2003; Stiff et al., 2006). A screen for novel *tel1* mutations in budding yeast has shown that there are overlapping functions between Mec1 and Tel1 with respect to stalled forks, and that some *tel1* gain-of-function mutants can even compensate for Mec1 functions. These dominant *TEL1-hy* mutants suppress *mec1Δ* deficiency in respect to Rad53 activation and cell survival to different extents, in response not only to DSBs but also to UV, MMS, and HU in S phase (Baldo et al., 2008). Some Tel1-hy proteins have higher catalytic activity than the wild-type Tel1, yet others show equivalent or even lower activity, suggesting that changes in specificity can also result in suppression. In addition, checkpoint restoration by *TEL1-hy* mutants in response to DSBs requires Xrs2 interaction, suggesting that Tel1-hy recruitment to damage through MRX is still crucial for the suppression phenotype (Baldo et al., 2008).

In agreement with the above observations, MRX has been shown to have a role in replication checkpoint signaling, in parallel to its well-characterized function in the DSB response (D'Amours and Jackson, 2001; Olson et al., 2007). Indeed, budding yeast *mre11* mutants show reduced Rad53 activation in response to HU (D'Amours and Jackson, 2001). In mammals, as well, MRN^{MRX} has been shown to function upstream of ATR^{Mec1} in response to UV and HU, and to interact with ATR^{Mec1}-ATRIP^{Ddc2} through the FHA and BRCT domains of Nbs1^{Xrs2} (Olson et al., 2007). These data would suggest that MRN^{MRX} functions as a regulator for both ATM^{Tel1} and ATR^{Mec1}. Recently, MRN^{MRX} has also been found to assist in TopBP1^{Dpb11} recruitment to ssDNA-dsDNA junctions, explaining how this complex might help activate ATR^{Mec1} in *Xenopus* egg extracts (Duursma et al., 2013; Lee and Dunphy, 2013). It is proposed that MRN^{MRX} recruits TopBP1^{Dpb11}, after which the interaction between 9-1-1 and TopBP1^{Dpb11} subsequently exposes the ATR^{Mec1} activation domain (AAD) of TopBP1^{Dpb11} to fully activate ATR^{Mec1} (Duursma et al., 2013). On the other hand, the Mre11 nuclease activity has also been implicated in checkpoint activation, possibly by generating ssDNA (Lee and Dunphy, 2013). In budding yeast MRX is also recruited to stalled replication forks, where it contributes to the maintenance of stalled polymerases (Tittel-Elmer et al., 2009). Another study by the same group has demonstrated that MRX has an important role in cohesin association behind the fork in response to HU, which is necessary for fork restart (Tittel-Elmer et al., 2009; Tittel-Elmer et al., 2012). Whereas the full molecular details of how MRX contributes to fork stability and cohesin recruitment remain to be clarified, current results suggest that it may be its structural properties, rather than its nuclease activity, that are crucial (Tittel-Elmer et al., 2009; Tittel-Elmer et al., 2012). In mammalian cells cohesin is also important for CHK2^{Rad53} activation in the intra-S and the G2/M damage checkpoints, and this role is independent of cohesin's role in sister chromatid cohesion (Watrin and Peters, 2009). In *S. pombe,* the N-terminus of the MRN component Nbs1^{Xrs2} is required for the Rad3^{Mec1}-Rad26^{Ddc2}-dependent telomere recruitment of Tel1, while the well-studied Tel1-binding C-terminal Nbs1^{Xrs2} domain is not needed (Subramanian and Nakamura, 2010). These observations further emphasize the significant cooperation that exists between ATR^{Mec1} and ATM^{Tel1}, and the important role MRN^{MRX} plays in coordinating their interplay.

6. CHECKPOINT RECOVERY

6.1 PROTEIN PHOSPHATASES DOWN-REGULATE THE CHECKPOINT

The kinase cascade of DNA replication and damage checkpoints must be down-regulated to continue the cell cycle once the impediment is removed (Figure 1.4). This process is known as recovery, and correlates with the disappearance of hyper-phosphorylated Rad53 in *S. cerevisiae* (Pellicioli et al., 2001). Recovery is distinct from "adaptation", which refers to the down-regulation of the checkpoint despite the persistence of unrepaired DNA damage (see review (Clemenson and Marsolier-Kergoat, 2009)). A reasonable way to counteract the kinase cascade would be through protein phosphatases.

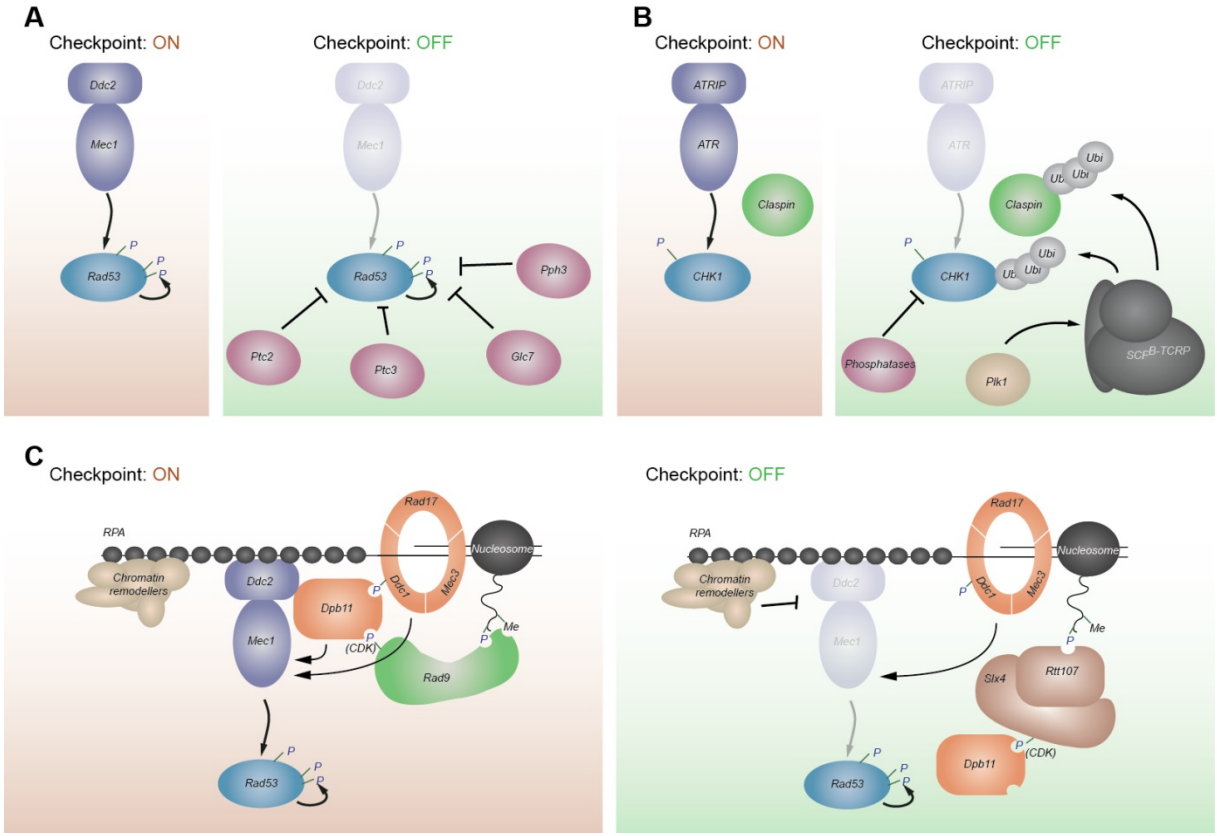

Figure 1.4: Checkpoint down-regulation. (**A**) The phosphatases Ptc2, Ptc3, Glc7, and Pph3 have been implicated in dephosphorylating Rad53 in *S. cerevisiae*. (**B**) In the mammalian replication checkpoint, $CHK1^{Chk1}$ activation by ATR^{Mec1} is facilitated through the checkpoint mediator $Claspin^{Mrc1}$. During checkpoint down-regulation, both $CHK1^{Chk1}$ and $Claspin^{Mrc1}$ are targeted for ubiquitin-mediated degradation, which is promoted by $Plk1^{Cdc5}$. In addition, phosphatases lead to $CHK1^{Chk1}$ dephosphorylation. (**C**) Phosphatase-independent down-regulation in *S. cerevisiae*. Left: The Mec1 activator Dpb11 interacts with phosphorylated Rad9. Rad9 is recruited by chromatin modifications like histone H2A phosphorylation and methylated histone H3, and assists in Rad53 activation. Right: A complex of Slx4 and Rtt107 down-regulates the checkpoint. Slx4 competes with Rad9 for Dpb11 binding, and may sequester Dpb11 away. Rtt107 can interact with phosphorylated H2A, and may compete with Rad9 for that. Chromatin remodelers may also have a role in checkpoint down-regulation. Ubi—Ubiquitin.

42 yeast genes are annotated as having protein phosphatase activity (Figure 1.5). Protein phosphatases can be subdivided into protein tyrosine phosphatases (PTPs), serine/threonine phosphatases and dual specificity phosphatases (see reviews (Moorhead et al., 2007; Stark, 1996)). Since all the checkpoint kinases belong to the family of serine/threonine kinases, we will focus on serine/threonine phosphatases here. Serine/threonine phosphatases were initially classified into either class I (PP1) and class II (PP2A, PP2B and PP2C). While PP1 enzymes are sensitive to the endogenous protein inhibitor-1, all class II enzymes are insensitive (Ingebritsen and Cohen, 1983). Unlike PP2A, PP2B enzymes are calcium and PP2C enzymes magnesium dependent. Thus, PP2C

enzymes are also called "phosphatases, magnesium-dependent" (PPMs), in contrast to phosphoprotein phosphatases (PPPs), which refer to PP1, PP2A and PP2C (see reviews (Moorhead et al., 2007; Shi, 2009)). Both PPPs and PPMs employ ions for their catalytic mechanisms (see review (Shi, 2009)). Three histidine, two aspartate and one asparagine residue, all highly conserved, coordinate two metal ions (e.g. Mn^{2+} and Fe^{2+} for PP1) that are thought to activate a water molecule for the nucleophilic attack on the phosphorous atom (Egloff et al., 1995; Goldberg et al., 1995). Subsequent cloning of phosphatase genes led to the discovery of additional PPPs. PP4 and PP6 are closely related to PP2A, while PP5 and PP7 are slightly distinct. An additional class of serine/threonine phosphatases represents aspartate-based phosphatases. They do not employ metal ions but instead use aspartate residues for catalysis. Two subclasses of aspartate-dependent phosphatases have been described. The first subclass is comprised of FCP/SCP (TFIIF-associating component of CTD phosphatase / small CTD phosphatase), which predominantly target the C-terminal domain (CTD) of RNA polymerase II. A second, less characterized subclass consists of several enzymes of the HAD (halocacid dehalogenase) enzyme superfamily with phosphatase activity (see review by (Moorhead et al., 2007)).

Most PPPs and PPMs are conserved in yeast (see Figure 1.5). While one or two genes encode for the PPP enzymes PP1 (*GLC7*), PP4 (*PPH3*), PP5 (*PPT1*), PP6 (*SIT4*), PP2A (*PPH21* and *PPH22*) and PP2B (*CNA1* and *CMP2*), seven genes encode for PP2C enzymes (*PTC1-7*). Yeast does not have a PP7 homolog, but has several reported PP1-related enzymes (Ppq1, Ppz1 and Ppz2) and Ppg1, which seems to be closely related to $PP4^{Pph3}$ and $PP6^{Sit4}$ (Stark, 1996). While $PP2C^{Ptc1-7}$, $PP5^{Ppt1}$ and PP7 enzymes contain both catalytic and regulatory domains in the same protein, $PP1^{Glc7}$, $PP2A^{Pphh21/22}$, $PP4^{Pph3}$ and $PP6^{Sit4}$ rather employ additional regulatory subunits, which confer substrate specificity. Most $PP1^{Glc7}$ regulatory subunits have an RVXF motif in common, through which they bind the catalytic subunit (Terrak et al., 2004; Zhao and Lee, 1997). However, the probably best studied phosphatase complex is $PP2A^{Pph21/22}$, which besides the catalytic subunit (subunit C) contains two regulatory subunits, a HEAT repeat containing scaffolding subunit A (Tpd3 in yeast) and a third regulatory subunit B. Distinct B subunits (e.g. Cdc55, Rts1 and Rts3 in yeast) (and additional A subunits in mammals) lead to a variety of PP2A complexes, even though only two genes encode for PP2A catalytic subunits. $PP6^{Sit4}$ and $PP4^{Pph3}$ also associate with additional subunits. Sit4 binds to Sit4-associated proteins (SAPs). Human $PP4^{Pph3}$ was found in three distinct complexes with R1, $Tap42^{Tap42}$ and CCT, and $R2^{Psy4}$ and $R3^{Psy2}$ (Gingras et al., 2005). In the same study, yeast Pph3 was found to interact with Psy2, Psy4 and Tap42. Tap42 in combination with Tip41 also interacts with Sit4 and Pph21/22, the latter complex playing a role in TOR signaling.

Additional proteins seem to assist in phosphatase complex assembly. Rrd2 interacts with $PP2A^{Pph21/22}$ during holocomplex biogenesis (Hombauer et al., 2007). Rrd2 is one of two yeast homologs (i.e. Rrd1 and Rrd2) of phosphotyrosyl phosphatase activator (PTPA). While Rrd2 preferentially interacts with Pph21/22, Rrd1 can bind to Pph3, Sit4 and Ppg1 (Van Hoof et al., 2005). Rrd2 is thought to assist in Pph21/22 activation through ATP-dependent cis/trans prolyl isomerization (Jordens et al., 2006). $PTPA^{Rrd2}$ was also shown to stimulate a normally weak PP2A phosphor tyrosine phosphatase activity *in vitro* (Cayla et al., 1990). However, the relevance of $PTPA^{Rrd2}$ in $PP2A^{Pph21/22}$ activation *in vivo* remains unclear. More recently, Rrd1 was shown to act on the same pathway as Pph3 in promoting telomere formation at a DSB site, indicating that it may function in Pph3 activation (Zhang and Durocher, 2010). In contrast, in Chapter 2 we show that *rrd1*Δ is not epistatic with *pph3*Δ in suppressing *mec1-100* HU sensitivity.

Several phosphatases have been implicated in the process of checkpoint recovery in *S. cerevisiae*. Among them are the two PP2C enzymes Ptc2 and Ptc3 (Leroy et al., 2003; Marsolier et al., 2000), the PP1 enzyme Glc7 (Bazzi et al., 2010) and the PP4 enzyme Pph3 (O'Neill et al., 2007; Szyjka et al., 2008). Interestingly, distinct phosphatases are employed depending on the type of

damage that led to Rad53 activation (reviewed by (Heideker et al., 2007)). Ptc2, Ptc3 and Pph3 have been shown to function in the recovery from and repair of a HO endonuclease-induced single DSB response (Guillemain et al., 2007; Keogh et al., 2006; Kim et al., 2011; Leroy et al., 2003). Rad53 down-regulation requires Pph3 and Ptc2 in response to MMS (O'Neill et al., 2007; Szyjka et al., 2008) and another PP1 phosphatase, Glc7, in response to HU (Bazzi et al., 2010) (Figure 1.4A). Dephosphorylation of Rad53 is important for the resumption of stalled replication forks after removal of the drugs (Bazzi et al., 2010; Szyjka et al., 2008). It has been suggested that the phosphatases non-redundantly target Rad53 in response to different types of damage (DSBs vs. MMS) (Heideker et al., 2007). However, the loss of several of those phosphatases at the same time impairs cell growth, suggesting that they have overlapping functions that support cell viability (Bazzi et al., 2010; Szyjka et al., 2008; Travesa et al., 2008). In addition to Rad53, regulation of γH2AX (phosphorylated H2AX, or H2A in budding yeast) phosphorylation has been well studied in both budding yeast and mammalian cells and a conserved function of $PP4^{Pph3}$ was found in γH2AX dephosphorylation (Chowdhury et al., 2008; Keogh et al., 2006; Nakada et al., 2008). Although this role of PP4 is conserved, additional phosphatases have been implicated in $H2AX^{H2A}$ dephosphorylation in mammalian cells (i.e. $PP2A^{Pph21/22}$, the PP2C-type phosphatase Wip1 and $PP6^{Sit4}$) (reviewed in (Shimada and Nakanishi, 2013)).

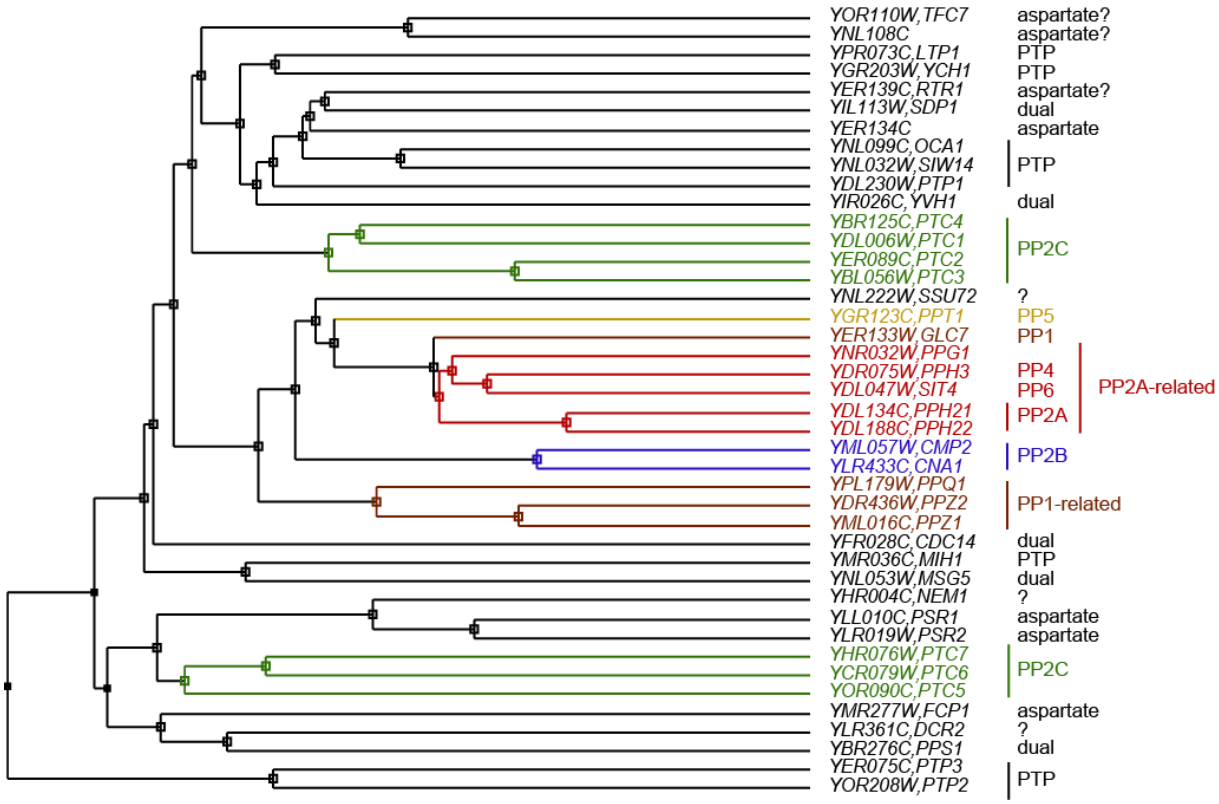

Figure 1.5: Relationship between yeast phosphatase catalytic domain genes. All yeast genes annotated with phosphatase activity (list downloaded from SGD (Saccharomyces Genome Database, http://www.yeastgenome.org/) were manually filtered for phosphoprotein phosphatase catalytic domains, multiple sequence alignment of protein sequences performed with Clustal Omega (Sievers et al., 2011) and a phylogenetic tree generated using jalview (Waterhouse et al., 2009). Phosphatases were classified depending on their annotation in the SGD database and based on a previous review (Stark, 1996). Phosphoprotein phosphatase (PPP) and metal-dependent phosphatase (PPM) classes are color coded. Aspartate: aspartate based phosphatase; PTP phosphotyrosyl phosphatase; dual: dual specificity phosphatase; question marks indicate unclear annotation.

Much more about the role of phosphatases in checkpoint down-regulation can be learned from other organisms than budding yeast: PP1 phosphatase $Dis2^{Glc7}$ negatively regulates $Chk1^{Chk1}$ in *S. pombe* (den Elzen and O'Connell, 2004) and, in metazoans, various phosphatases have been found to function in checkpoint down-regulation (see reviews (Freeman and Monteiro, 2010; Shimada and

Nakanishi, 2013)). ATM^{Tel1} is targeted by PP2A$^{Pph21/22}$, PP1^{Glc7} and the PP2C-type phosphatase Wip1 (Wild-type p53-induced phosphatase 1) (Goodarzi et al., 2004; Peng et al., 2010; Shreeram et al., 2006). While PP2A$^{Pph21/22}$ and PP1^{Glc7} seem to dissociate from ATM^{Tel1} upon DNA damage (Guo et al., 2002; Peng et al., 2010), Wip1 is constitutively ATM^{Tel1}-associated (Shreeram et al., 2006). However, its activity is cell-cycle regulated by both protein level and phosphorylation, and thus it has been suggested that Wip1 protein regulation fine-tunes the global DDR response (Macurek et al., 2013). In contrast to the other phosphatases, PP5^{Ppt1} rather promotes ATM^{Tel1} as well as ATR^{Mec1} activation and signaling through an unknown mechanism (Ali et al., 2004; Zhang et al., 2005). CHK1^{Chk1} and CHK2^{Rad53} are also targeted by PP2A$^{Pph21/22}$ and Wip1 (Fujimoto et al., 2006; Liang et al., 2006; Lu et al., 2005; Oliva-Trastoy et al., 2007), while PP4^{Pph3} has been further implicated in dephosphorylation of the ATM/ATR$^{Mec1/Tel1}$ targets KAP1, 53BP1 and RPA2^{Rfa2} (Lee et al., 2014; Lee et al., 2012; Lee et al., 2010; Liu et al., 2012a). Also, genetic interactions of Pph3 with deletions of checkpoint proteins have been described (Bandyopadhyay et al., 2010; O'Neill et al., 2007). In particular, pph3Δ shows positive (suppressive) interactions with deletions of upstream checkpoint proteins and negative interactions with loss of proteins known to negatively regulate checkpoint signaling, like *sae2*Δ and *ptc2*Δ (Bandyopadhyay et al., 2010; Clerici et al., 2006; Guenole et al., 2013; Keogh et al., 2006; Marsolier et al., 2000; O'Neill et al., 2007). Thus both in budding yeast and other organisms several different phosphatases are employed to prevent untimely checkpoint protein phosphorylation and provide rapid checkpoint recovery after the checkpoint trigger has been removed. ATR^{Mec1} and Mec1 are phosphorylated as well (Chen et al., 2010; Liu et al., 2011; Nam et al., 2011b). However, the role of phosphatases in the control of Mec1/ATR^{Mec1} themselves is largely unexplored. In Chapter 2 we show that Psy2-Pph3 (PP4) regulates not only Mec1 phosphorylation but also phosphorylation of many of its targets.

6.2. Phosphatase-Independent Mechanisms of Checkpoint Down-Regulation

In addition to the phosphatase-dependent down-regulation, the ubiquitin proteasome pathway also plays a role in checkpoint recovery in higher organisms (Figure 1.4B). CHK1 has been shown to be targeted by cullin 1—(CUL1) or cullin 4A—(CUL4A) dependent proteolysis (Leung-Pineda et al., 2009; Zhang et al., 2009). Claspin^{Mrc1} is also targeted by SCF$^{B\text{-}TRCP}$ for degradation[6] (Mailand et al., 2006; Mamely et al., 2006; Peschiaroli et al., 2006), and this effect is counteracted by USP7, a deubiquitylating enzyme, called ubiquitin-specific protease 7 (Faustrup et al., 2009). PLK1^{Cdc5} (polo-like kinase 1) promotes Claspin^{Mrc1} degradation by promoting SCF$^{B\text{-}TRCP}$-dependent ubiquitination (Mailand et al., 2006; Mamely et al., 2006; Peschiaroli et al., 2006), and this PLK1^{Cdc5} activity is prompted by Aurora A and Greatwall kinases (Macurek et al., 2008; Peng et al., 2011). The role of PLK1^{Cdc5} in checkpoint down-regulation may be conserved, since the *S. cerevisiae* PLK1 homolog, Cdc5, is important for adaptation from an irreparable DSB, although the action of Cdc5 appears to be different (Donnianni et al., 2010; Schleker et al., 2010; Toczyski et al., 1997; Vidanes et al., 2010). PLK1^{Cdc5} has also been shown to facilitate DNA replication under replication stress. Namely, the *Xenopus* PLK1^{Cdc5}, Plx1^{Cdc5}, is recruited to chromatin through ATR^{Mec1}-dependent phosphorylation of MCM2^{Mcm2} at serine 92 upon fork stalling, and Plx1^{Cdc5} recruitment is important for origin firing near stalled forks (Trenz et al., 2008). In human cells, it has been shown that PLK1^{Cdc5} phosphorylates ORC2^{Orc2} on serine 188. This phosphorylation promotes DNA replication under replication stress (Song et al., 2011). In summary, checkpoint recovery is promoted by two opposing enzymatic activities; multiple phosphatases directly quench the checkpoint kinases and the effectors, while polo-

[6] Similarly, yeast Mrc1 was recently shown to be degraded in a SCF^{Dia2}-dependent manner during checkpoint recovery (Fong, et al., 2013).

like kinase promotes the degradation of checkpoint factors and facilitates the initiation of replication to complete S phase.

Srs2 helicase and Sae2 in *S. cerevisiae* appear to facilitate checkpoint recovery by eliminating or reducing the source of the sensor kinase activation. Srs2 restrains homologous recombination by dislodging the Rad51 recombination protein from ssDNA (Krejci et al., 2003; Veaute et al., 2003). Consistently, *SRS2* deletion impairs the down-regulation of the checkpoint after repair of HO-induced DSBs (Jain et al., 2009; Vaze et al., 2002). A recent study has demonstrated that *srs2*Δ cells retain Ddc2- and RPA-focus formation and chromatin association, even when the bulk of the DSB repair has been completed (Yeung and Durocher, 2011). Yeung and Durocher suggest that Srs2 dismantles Rad51, which results in elimination of ssDNA and a suppression of Mec1 signaling. Sae2 (CtIP in vertebrates) is involved in meiotic and mitotic DSB processing, together with the Mre11-Rad50-Xrs2 (NBS1 in vertebrates) complex (Clerici et al., 2005; McKee and Kleckner, 1997; Prinz et al., 1997; Rattray et al., 2001). MRN^{MRX} recognizes DSBs very rapidly and recruits ATM^{Tel1} kinase. Several studies have shown that *sae2* mutants show a defect in checkpoint recovery, whereas overexpression of *SAE2* counteracts checkpoint activation (Clerici et al., 2006; Guenole et al., 2013; Kim et al., 2008a). Deletion of *SAE2* results in an increased level of MRX at DSBs, whereas overexpression of *SAE2* has the opposite effect, suggesting that Sae2 evicts MRX at the damage site and thereby limits Tel1 checkpoint signaling (Clerici et al., 2006; Kim et al., 2008a). This Sae2 function may facilitate switching from Tel1/ATM to Mec1/ATR signaling (see Section 5).

Recent studies in *S. cerevisiae* have shed light on yet another mechanism of the checkpoint attenuation that involves a scaffold complex called Slx4-Rtt107 (Figure 1.4C). The Mec1 activator Dpb11 binds Rad9 and up-regulates Rad53 activation (see Section 2.4) (Pfander and Diffley, 2011), and the Mec1/Tel1 phosphorylation of H2A at Ser129 (H2A-p; γH2AX in mammals) recruits Rad9 to damage sites, also leading to the activation of Rad53 (Javaheri et al., 2006). Intriguingly, the DNA repair scaffold complex Slx4-Rtt107 can also bind Dpb11 in a Mec1-dependent manner (Ohouo et al., 2010), and the C-terminal tandem BRCT domain of Rtt107 interacts with H2A-P (Li et al., 2012). In a recent study, the Smolka group argues that the Slx4-Rtt107 complex negatively regulates Rad53 by competing with Rad9 for both Dpb11 and H2A-p, two positive checkpoint regulators (Ohouo et al., 2013).

Finally, a recent study suggests that both Isw2 and Ino80, confirmed targets of checkpoint kinases, interact with RPA and function to attenuate the checkpoint activity (Au et al., 2011). Molecular mechanisms of the remodeler function in checkpoint recovery are unclear, but a similar competition may exist where Ino80 and Isw2 exclude excess Mec1 from RPA binding.

7. SCOPE OF MY PROJECTS

7.1 YEAST PP4 INTERACTS WITH DDC2-MEC1 AND REGULATES CHECKPOINT SIGNALING

Checkpoint recovery through Rad53 dephosphorylation is well studied and several phosphatases have been implicated in this process (see Section 6.1), yet it is still unknown if and how the upstream checkpoint kinase Mec1 is regulated by phosphorylation/dephosphorylation cycles. Even though more ssDNA accumulates when replication forks stall, the structures that recruit Mec1 and its activators (ssDNA-dsDNA junctions; see Section 2.1) are also present during normal, discontinuous replication on the lagging strand (Sogo et al., 2002). However, normal replication does not lead to detectable checkpoint activation (Sanchez et al., 1996). Rather it has been described, that in S phase the threshold for checkpoint activation is even lower than in G2 phase and that a certain number of replication forks has to be generated in order to robustly sense and signal replication stress (Shimada et al., 2002; Tercero et al., 2003). One potential mechanism how this threshold could be generated is through cell cycle dependent modification and thus modulation of Rad53 activity (Schleker et al., 2010). Another hypothesis is that Mec1 might be regulated in a way that prevents aberrant checkpoint activation. Supporting this hypothesis, a recent study suggests that Mec1 is active during normal replication and phosphorylates proteins, especially chromatin modulating enzymes. Checkpoint activation may merely induce a switch that results in Mec1 phosphorylating a different set of targets (M. Smolka, unpublished data). However, the nature of this switch and how it is regulated remains unknown. The aim of this project was to identify novel factors involved in Mec1 checkpoint signaling. We were especially interested in potential negative regulators of Mec1. We reasoned that loss of function of a negative inhibitor might rescue HU sensitivity of replication checkpoint deficient *mec1-100* cells. Thus, we screened for suppressors of *mec1-100* HU sensitivity in two independent experiments and characterized the top hit, a conserved phosphatase complex, Psy2-Pph3 and its role in Mec1 signaling in this project.

7.2 CHARACTERIZATION OF *MEC1-100*, AN S PHASE DEFECTIVE ALLELE

The Longhese laboratory discovered a mutant allele of Mec1 that is specifically defective in activating the G1/S and replication checkpoint, but leaves the G2 checkpoint intact (Paciotti et al., 2001). It has two point mutations outside of the catalytic domain. F1179S resides in a helical region N-terminal of the conserved FAT domain, while N1700S is located within the FAT domain. Both residues are predicted to be in turns or loops between helices and therefore might be available for protein-protein contacts (see Chapter 3). A similar allele has been described in human ATR^{Mec1} with three mutations just N-terminal of the FAT domain (Figure 3.1) (Nam et al., 2011a). Therefore, we hypothesized that the mutated residues might reside in a regulatory region with a conserved function for the replication checkpoint. The aim of this project was to understand the mechanism by which these mutations cause a defect in replication checkpoint signaling. Several hypotheses, (e.g. mutations reduce kinase activity, impair oligomerization or disrupt a protein-protein interaction) were developed and tested during the course of this work. By studying intragenic suppressors that were identified in one of the genetic screens described in Chapter 2, we also hoped to better understand the mechanism of the *mec1-100* mutations.

7.3 AN ACIDIC DOMAIN IN SGS1 INTERACTS WITH RPA AND RECRUITS RAD53

Sgs1 is the sole RecQ helicase in yeast and plays an important role in genome stability (Cobb et al., 2003). One of its functions is the resolution of homologous recombination intermediates (Ira et al., 2003). However, it is also involved in the stabilization of stalled replication forks (Cobb et al., 2003; Cobb et al., 2005). Both *sgs1*Δ and *mec1-100* mutations have been shown to be HU sensitive

and to lead to a partial loss of DNA polymerases from sites of stalled forks, as single mutants. The combination of both mutations is synthetic lethal on even low doses of HU and results in a complete loss of polymerase and RPA signals at replication forks stalled on HU (Cobb et al., 2005). Both Mec1 (through Ddc2) and Sgs1 interact with the single stranded binding protein RPA (Cobb et al., 2003; Zou and Elledge, 2003). We hypothesized that the Sgs1-RPA interaction might be key to understanding the role of Sgs1 in the response to replication stress. Although *sgs1*Δ is synergistic with *mec1-100* in regard to stabilization of stalled forks, suggesting that they act on two parallel pathways, it is also involved in Mec1-dependent Rad53 phosphorylation in a manner epistatic with the replication checkpoint mediator Mrc1 (Bjergbaek et al., 2005). In this context Sgs1 was shown to interact with Rad53 by co-immunoprecipitation and yeast two-hybrid assays (Bjergbaek et al., 2005). However, the mechanism through which Sgs1 contributes to replication checkpoint signaling and stabilizing polymerases at stalled forks remained unknown. By separating two of the Sgs1 functions, helicase activity and RPA binding, we aimed at dissecting and better understanding the role of Sgs1 in these processes.

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CHAPTER 2: YEAST PP4 INTERACTS WITH ATR HOMOLOGUE DDC2-MEC1 AND REGULATES CHECKPOINT SIGNALING

Nicole Hustedt[1,2], Andrew Seeber[1,2], Ragna Sack[1], Monika Tsai[1] Bhupinder Bhullar[3], Hanneke Vlaming[4],Fred van Leeuwen[4], Aude Guénolé[5], Haico van Attikum[5], Rohith Srivas[6], Trey Ideker[6], Kenji Shimada[1] and Susan M. Gasser[1,2]

1. Friedrich Miescher Institute for Biomedical Research, Maulbeerstrasse 66, CH-4058 Basel, Switzerland 2. University of Basel, Faculty of Sciences, CH-4056 Basel, Switzerland 3. Novartis Institutes for Biomedical Research, Novartis Pharma AG, Fabrikstrasse 22, CH-4056 Basel, Switzerland 4. Division of Gene Regulation, Netherlands Cancer Institute, Plesmanlaan 121, 1066 CX Amsterdam, The Netherlands 5. Department of Toxicogenetics, Leiden University Medical Center, Einthovenweg 20, 2333 ZC Leiden, The Netherlands 6. Departments of Bioengineering & Medicine, University of California, San Diego, La Jolla, CA 92093, USA

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AUTHOR CONTRIBUTIONS:

NH planned and performed most experiments, evaluated results, made all figures and wrote the paper, AS planned, performed and evaluated the FRET studies, KS supervised NH and assisted in spontaneous suppressor screen experiments, RS performed all mass spectroscopy analyses, MT performed β-galactosidase assays, BB performed genome-wide sequencing of yeast mutants, HV and FvL supervised and hosted NH for the EMAP analysis, AG and HvA provided strains and know-how for the EMAP analysis, TI and RS helped analyse the EMAP results and SMG supervised NH and KS; evaluated and planned experiments, and edited the paper.

SUMMARY

To study regulators of the central intra-S-phase checkpoint kinase, Mec1-Ddc2, we took advantage of a catalytically active yeast *mec1* mutant that compromises the intra-S-phase checkpoint, while retaining association with Ddc2 and stalled replication forks. A screen for spontaneous survivors of hydroxyurea (HU) in *mec1-100* cells yielded mutations that inactivate Pph3 or Psy2, both conserved PP4 phosphatase subunits. In a large-scale screen for synthetic growth effects, *pph3Δ* and *psy2Δ* were the strongest suppressors of *mec1-100* lethality on HU. Restored Rad53 phosphorylation accounts for part, but not all, of the *pph3*Δ-mediated survival. Physical interaction between Pph3 and Mec1, mediated by cofactors Psy2 and Ddc2, is shown biochemically and through FRET in subnuclear foci in HU-treated cells. Phosphoproteomic analysis confirmed that 90% of the *mec1-100*-compromised targets are PP4-regulated, including a phosphoacceptor residue within Mec1 itself, mutation of which confers Zeocin-sensitivity. This establishes a physical and functional Mec1-PP4 unit for regulating the checkpoint response.

INTRODUCTION

Cells are constantly exposed to DNA damage. Lesions can arise either from exogenous agents (e.g. DNA damaging drugs) or endogenous events (e.g. replication forks encountering barriers) (Aguilera and Garcia-Muse, 2013). To preserve the genetic information cells have evolved DNA damage checkpoints to sense damage, stop the cell cycle and induce DNA repair events (Friedel et al., 2009). Key to those signaling cascades are the PI3K-like (PI3KK) kinases ATM and ATR, in budding yeast Tel1 and Mec1 (Cimprich and Cortez, 2008). ATR and Mec1 genes are essential for cell viability, although the absence of Mec1 in yeast can be tolerated by concomitantly up-regulating ribonucleotide reductase (i.e. by deleting the gene encoding the ribonucleotide reductase inhibitor, Sml1) (Zhao et al., 1998). PIKKs are generally large proteins, about 2,500 amino acids in length, with a C-terminal kinase domain which is flanked by a FAT (FRAP ATM TRAPP) and FATC (FAT C-terminal) domains (Cimprich and Cortez, 2008).

Whereas ATM is primarily activated in response to DNA double strand breaks (DSBs), ATR can sense a variety of lesions (Cimprich and Cortez, 2008). Most ATR activation, however, appears to involve single stranded (ss) DNA which is coated by the ssDNA binding protein replication protein A (RPA). ATR requires its cofactor ATRIP (ATR interacting protein, Ddc2 in yeast) to bind these structures (Zou and Elledge, 2003). Experiments in *Xenopus* egg extracts indicate an additional requirement of dsDNA adjacent to the ssDNA stretch for ATR dependent checkpoint activation (MacDougall et al., 2007). The Rad17-RFC2-5 clamp loading complex (Rad24-Rfc2-5 in yeast) recognizes these structures and loads the 9-1-1 clamp, consisting of Rad9, Rad1 and Hus1 in metazoans and Rad17, Mec3 and Ddc1 in *S. cerevisiae*. Phosphorylation of the Rad9 (*S.c*. Ddc1) subunit recruits TopBP1 (*S.c*. Dpb11), which can activate ATR-ATRIP *in vitro* (Mordes et al., 2008), yet the exact mechanism of TopBP1 mediated activation remains unclear. In budding yeast not only Dpb11, but also Ddc1 and Dna2 were shown to enhance Mec1 kinase activity *in vitro* through their N- or C-terminal unstructured tails (reviewed in (Hustedt et al., 2013).

In the checkpoint cascade Mec1 activation leads to phosphorylation of the downstream kinases Rad53 (functionally related to human CHK1) and Chk1 in yeast (Friedel et al., 2009). Activation of those effector kinases requires mediator proteins. In the case of Mec1 activation in response to DSB or DNA adducts (MMS treatment) in S phase, the checkpoint protein Rad9 (53BP1 in mammals) recruits Rad53 and prepares it for Mec1 phosphorylation (Hustedt et al., 2013). In response to hydroxyurea (HU)-induced replication stress the fork components Mrc1 and Sgs1 facilitate Rad53 phosphorylation instead (Alcasabas et al., 2001; Bjergbaek et al., 2005; Frei and Gasser, 2000). In S-phase cells higher levels of damage are required to activate the Mec1-dependent checkpoint, suggesting a threshold for intra-S checkpoint activation (Shimada et al., 2002). This threshold may ensure that the occurrence of ssDNA found at normal replication forks does not trigger the global checkpoint response (Shimada et al., 2002; Tercero et al., 2003).

While checkpoint activation has been extensively studied, how the replication checkpoint is downregulated and how aberrant checkpoint induction is prevented during a normal, unperturbed S phase, are not well understood. A number of phosphatases have been shown to dephosphorylate Rad53 and there seems to be some specificity among the phosphatases depending on the type of damage that led to Rad53 activation (Heideker et al., 2007). The PP1 phosphatase Glc7 was reported to promote Rad53 dephosphorylation after exposure to HU (Bazzi et al., 2010). Furthermore, while the PP2C phosphatases Ptc2 and Ptc3 have been implicated in dephosphorylating Rad53 after a DSB (Leroy et al., 2003), the PP4 phosphatase Pph3 was implicated instead in checkpoint recovery after MMS treatment (O'Neill et al., 2007; Szyjka et al., 2008), although Ptc2/3 may compensate for loss Pph3 and *vice versa* during DSB repair and recovery from MMS treatment (Kim et al., 2011; Travesa et al.,

2008). PP4 was also implicated in dephosphorylation of other Mec1 substrates Zip1 (Falk et al., 2010), Cdc13 (Zhang and Durocher, 2010) and Cbf1 (Bandyopadhyay et al., 2010). Similarly, dephosphorylation of histone H2A has been linked to the PP4 phosphatase Psy2-Pph3. However, this required a third subunit, Psy4 (Keogh et al., 2006).

In human cells the data on phosphatases and checkpoints is no less complicated: both downstream kinases CHK1 and CHK2 are counteracted by both the PP2C (Wip1) and PP2A phosphatase, and, as in yeast, PP4 was shown to dephosphorylate γH2AX (phosphorylated H2AX) in human cells (Chowdhury et al., 2008; Freeman and Monteiro, 2010; Nakada et al., 2008). PP4 was also implicated in dephosphorylation of RPA2 in *C. albicans* and mammals (Lee et al., 2010; Wang et al., 2013), and mammalian 53BP1, KAP-1 and CHD4 (Lee et al., 2014; Lee et al., 2012). Other mechanisms that downregulate the checkpoint act by means of proteasome-mediated degradation of Mrc1 or human CLASPIN (Fong et al., 2013; Mailand et al., 2006; Peschiaroli et al., 2006) or by sequestration of Rad9 by Rtt107-Slx4 (Ohouo et al., 2013). However, there is no study examining whether Mec1-Ddc2 activity itself is under negative control through phosphorylation or other regulation.

Here we describe a novel interaction between the Ddc2-Mec1 checkpoint kinase and the yeast PP4 phosphatase Psy2-Pph3. A strong genetic relationship between mutants in both complexes was identified in two independent screens, involving both forward and reverse genetics. Furthermore, we found that Mec1-Ddc2 and PP4 co-regulate many Mec1-dependent phosphorylation targets in response to HU stress , including Rad53 and H2A, suggesting that this interaction maintains a balance of phosphorylation that is important for surviving fork-associated stress. We also identify a phosphoacceptor site within Mec1 itself that is regulated in a Pph3-dependent manner, and which contributes to survival of Zeocin-induced damage.

RESULTS

SPONTANEOUS *MEC1-100* SUPPRESSOR MUTATIONS MAP TO *PSY2* AND *PPH3* GENES

To study how the replication checkpoint is controlled we used a mutant allele of the checkpoint kinase Mec1, *mec1-100,* which shows a delayed activation of Rad53 in S-phase, but robust Rad53 phosphorylation in G2-phase cells (Paciotti et al., 2001). In this allele two residues outside of the catalytic domain are mutated, one (N1700S) within and one (F1179S) flanking the FAT domain (Paciotti et al., 2001). Despite these mutations, the mutant kinase activity is intact: the mec1-100 kinase recovered from cell lysates by co-precipitation with Ddc2-GFP phosphorylates a well-characterized target peptide (Sgs1 aa404-604) (Hegnauer et al., 2012) as efficiently as wild-type Mec1 (Figure.S2.1A). Its recruitment to stalled forks is also equivalent to that of wild-type Mec1 (Cobb et al., 2005), yet on HU, *mec1-100* allows partial loss of engaged polymerases from stalled forks and fails to prevent late origin firing (Cobb et al., 2005). The mutation also leads to complete fork collapse on HU in the absence of the RecQ helicase Sgs1, which is not observed in *sgs1*Δ *rad53*Δ mutants (Cobb et al., 2005). This suggests that mec1-100 fails to modify a select set of S-phase specific Mec1 targets that ensure survival of replicative stress.

While working with *mec1-100* cells, we realized that spontaneous suppressor mutations arise quite frequently, conferring HU resistance (Figure 2.1A). This is not seen for *mec1*Δ strains. Since suppression could stem from either loss of negative regulators or up-regulation of downstream Mec1 targets, we analysed 31 suppressor colonies by sequencing, after backcrossing 2-3 times with the parental wild-type strain. The suppressors fell into two classes: in the first, the suppressing mutation co-segregated with a marker integrated close to the *MEC1* locus ("intragenic"), and in the second, the suppressors segregated independently ("extragenic"). Consistently, all co-segregating suppressors had acquired one additional mutation in *mec1-100*, rendering them HU-resistant (Figures 2.1B; S2.1B). Remarkably, genome-wide sequencing showed that all twelve extragenic suppressors had mutations in one of two genes, *PSY2* or *PPH3*, which encode subunits of the PP4 phosphatase (Figures 2.1B, S2.1C). In case of *PPH3,* the mutations were found throughout the phosphatase domain, while in *PSY2,* we found premature STOP codons after either 39 or 182 aa (Figure 2.1B). HU sensitivity was restored to the *mec1-100 psy2* or *pph3* double mutants by transformation with wild-type *PSY2* or *PPH3* genes, respectively (data not shown). We conclude that loss of Psy2 or Pph3 function confers HU resistance to *mec1-100* cells.

EMAP PROFILING GROUPS *MEC1-100* WITH REPLICATION CHECKPOINT DEFICIENT MUTATIONS

To better characterize *mec1-100* effects, we performed a high-throughput genetic interaction screen based on the previously described Epistatic Miniarray profiling (EMAP) method (Collins et al., 2007; Collins et al., 2006; Schuldiner et al., 2006). We combined 35 query strains bearing mutations in 35 genes implicated in DNA replication fork or checkpoint function, with an array of 1525 deletions and a few DAmP (Decreased Abundance by mRNA Perturbation) mutants, all representing functions that are required for chromatin-based processes (Guenole et al., 2013). The resulting double mutants were scored for their growth in the presence of 0, 20 and 100 mM HU. Quantitative genetic interaction scores were calculated as previously described (Collins et al., 2006) (Figure 2.1C). A positive score indicates suppression (or potentially, epistasis), while a negative score shows additivity and synthetic sickness. Quality control of the data led to the exclusion of 214 mutants (see Supplementary Procedures), leaving 35x1311 scored double mutants (Tables S2.1).

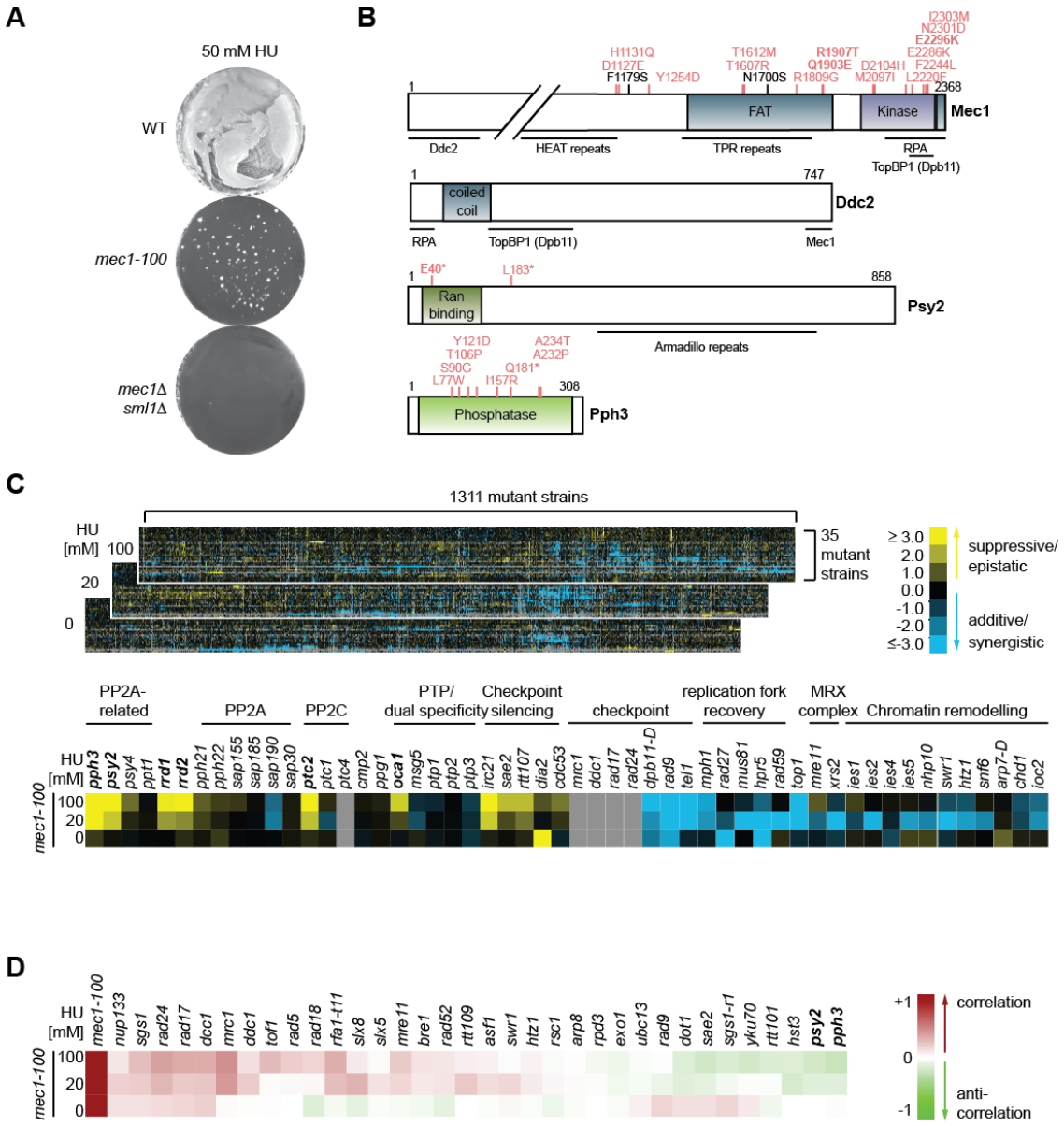


Figure 2.1: Mutations in *PSY2* and *PPH3* genes suppress *mec1-100* HU sensitivity. (A) WT (GA-1981), *mec1-100* (GA-4978) and *mec1*Δ *sml1*Δ (GA-2529) cells were plated on YPAD plates + 50 mM HU for 3 days at 30°C. Colonies appear white on dark background. **(B)** Mec1,Ddc2, Psy2 and Pph3 domain architecture with *mec1-100* mutations indicated in black and *mec1-100* suppressor mutations in red. Bold: mutations found more than once independently. Asterisks: STOP codon at indicated residue. Note that *PSY2-L183** (GA-6610) showed a deletion of a "G" generating a frameshift and stop codon at aa 183. **(C)** Upper panel: Overview of genetic interaction screen (EMAP): 35 mutant "query" strains were combined with 1525 (1311 after quality control) mutant strains. Growth of double mutants was scored in the presence of 0, 20 and 100 mM HU. Genetic interaction scores coding is at right. Lower panel: Selected *mec1-100* genetic interactions are shown, including mutants of other phosphatase classes and additional subunits of multisubunit complexes. Phosphatase mutants showing significant positive interaction with *mec1-100* are in bold. Complete *mec1-100* genetic interactions is in Figure S2.1. (**D)** Heat map showing Pearson correlation coefficients of *mec1-100* genetic interaction profile with the profiles of the other query strains on 0, 20 and 100 mM HU. Code for correlation coefficients at right.

We first compared the overall genetic interaction profile of *mec1-100* with the profiles of the other query mutants. Similar genetic interaction profiles of two mutants indicate related functions of the respective proteins (Collins et al., 2007). As expected, the *mec1-100* profile correlates best with other mutations that compromise the S-phase checkpoint (i.e. *sgs1*Δ, *rad24*Δ, *rad17*Δ, *ddc1*Δ, *mrc1*Δ

and *dcc1*Δ) (Figure 2.1D). In fact, *mrc1*Δ, which is the replication checkpoint mediator, shows the strongest correlation with *mec1-100* in the presence of HU, yet does not correlate in the absence of HU, arguing for cooperation on HU and distinct functions during an unperturbed S phase.

Interestingly, there are two groups of mutants whose genetic correlation patterns change dramatically upon HU treatment. The genetic interaction profiles of several genes implicated in either break-induced replication or translesion synthesis (notably, *rad18*Δ, *slx5*Δ, *slx8*Δ, *mre11*Δ, *rad52*Δ and *bre1*Δ) did not correlate with *mec1-100* in the absence of HU, but the profiles became quite similar on HU, indicating that they have common functions in replication fork stabilization and/or recovery. The opposite was observed for *rad9*Δ, *dot1*Δ, *sae2*Δ, *yku70*Δ, and *sgs1-r1*Δ, an internal deletion upstream of the Sgs1 helicase domain that confers sensitivity to Zeocin, but not HU (Hegnauer et al., 2012). This latter group of genes, which have genetic interaction profiles complementary to *mec1-100* on HU, identify activities involved at DSBs and not in stalled fork recovery. This reinforces the conclusion that *mec1-100* specifically compromises the replication checkpoint response.

If we look specifically at the mutants that interact with *mec1-100* (based on threshold scores of ≥ 2 for suppressive or epistatic and ≤ -2 for additive or synergistically negative interactions) the genetic interactions of *mec1-100* fall into several functional groups, which we discuss below (Figure 2.1C or S2.1D, for full list). However, of the 1311 array mutants scored, *psy2*Δ and *pph3*Δ showed the highest suppressive genetic interaction with *mec1-100*, and clearly promote survival on HU (Figure 2.1C, S2.1D, Table S2.1). This confirms with a comprehensive screen that the alleviating genetic interaction observed by the HU-suppressor screen is robust (Figure 2.1A).

PP4 SUBUNITS PSY2 AND PPH3 COUNTERACT *MEC1-100* SENSITIVITIES

Psy2 and Pph3 form a conserved PP4 phosphatase complex with Pph3 being the catalytic subunit (Heideker et al., 2007). Psy4 has been reported to be a third subunit, but it is not required for dephosphorylation of all targets (Keogh et al., 2006; O'Neill et al., 2007). In our screen, *psy4*Δ showed no genetic interaction with *mec1-100* (Figure 2.1C). When profiles of mutant synergies were compared, we found that *psy2*Δ and *pph3*Δ were strongly anti-correlated with *mec1-100* on HU (Figure 2.1D), arguing that *PSY2* and *PPH3*, but not *PP4*, share a function that opposes that of *mec1-100.*

To see if this was simply a general feature of phosphatase mutants, we examined the impact of loss of *PSY2* and/or *PPH3* in comparison to other phosphatases. Loss of the PP5 phosphatase *ppt1*Δ, showed no genetic interaction with *mec1-100*, nor did deletions of the two PP2A catalytic subunits, *pph21*Δ and *pph22*Δ, or their regulatory subunits, *sap155*Δ, *sap185*Δ, *sap190*Δ, *sap33*Δ (Figure 2.1C). On the other hand, loss of Rrd2, which interacts with and regulates PP2A (Van Hoof et al., 2005), did provide some *mec1-100* suppression, like Rrd1, which interacts physically with the phosphatases Pph3 (PP4), Ppg1 (related to PP4 and PP6) and Sit4 (PP6) (Van Hoof et al., 2005) (Figure 2.1C; 2A). For PP2C we have contradictory results, given that *ptc2*Δ (one of seven genes encoding PP2C subunits) showed suppressive genetic interactions with *mec1-100* in the strain used for the EMAP assay, yet showed weak and variable suppression in a second background (W303; Figure 2.2B). Moreover, two other PP2C phosphatase subunits (*ptc1*Δ and *ptc4*Δ) either showed no genetic interaction or could not be scored in the EMAP assay. This latter can occur either because the double mutants form inefficiently, or because the resulting colonies are too small for accurate growth rate scoring. The only phosphotyrosyl phosphatase mutant interacting genetically with *mec1-100* was *oca1*Δ, yet its effect required 100 mM HU, was significantly less pronounced than *psy2*Δ or *pph3*Δ, and like *ptc2*Δ, was not reproducible in another background (Figure 2.2B). Besides the phosphatase mutants, *mec1-100* was

suppressed by mutations that dampen the checkpoint response such as deletions of *RTT107, SAE2, DIA2, CDC53* or *IRC21* (Clerici et al., 2006; Fong et al., 2013; Guenole et al., 2013; Ohouo et al., 2013) (Figure 2.1C). These factors may act in parallel with phosphatases in checkpoint downregulation.

Indeed, we find *pph3*Δ to be synthetic sick with *ptc2*Δ and *sae2*Δ (Figure S2.1D), which has been previously described (Guenole et al., 2013; Keogh et al., 2006; Kim et al., 2011; O'Neill et al., 2007; Szyjka et al., 2008). Moreover, we find a negative genetic interaction of *pph3*Δ with *dia2*Δ, indicating that *PTC2, SAE2* and *DIA2* act in parallel to *PPH3* to allow cell survival on HU, possibly through redundant targeting of Rad53 (Guillemain et al., 2007; Leroy et al., 2003; O'Neill et al., 2007; Travesa et al., 2008), limiting of Tel1 signaling (Clerici et al., 2006) or Mrc1 degradation (Fong et al., 2013).

MEC1-100 SHOWS SYNTHETIC LETHALITY WITH MUTANTS THAT PERTURB CHECKPOINT ACTIVATION OR REPLICATION FORK RECOVERY

Negative genetic interactions are scored when the loss of a gene renders cells more dependent on another gene for survival. That is, they identify factors acting on parallel pathways to achieve the same function, or in a redundant fashion on the same pathway. As expected, the replication checkpoint deficiency of *mec1-100* rendered cells highly dependent on other checkpoint proteins (i.e. Mrc1, Ddc1, Rad24, Rad17, Dpb11, Rad9 and Tel1) on HU (Figures 2.1C; S2.1D; S2.1E). These mutations also showed a strong correlation with *mec1-100* with respect to overall genetic interaction profiles (Figure 2.1D). Other synergistic genetic interactions included mutants involved in replication fork recovery and damage bypass, the MRX complex and chromatin remodelers, as well as a set of nuclear pore mutations (Figures 2.1D, S2.1D). In addition to the INO80 and SWR1 complexes, we recovered histone acetyltransferases (SAS and AHC) and histone methyltransferases that are closely associated with the transcription machinery (COMPASS) (Figure S2.1D). Interestingly, RNA Pol II subunits and certain translational regulators are far more sensitive to *mec1-100* mutation than to *mrc1* deletion. These may help prevent damage that pushes *mec1-100* cells towards lethality and thus work redundantly with *mec1-100* (Aguilera and Garcia-Muse, 2013).

DELETIONS OF THE PP4 SUBUNITS *PPH3* OR *PSY2* STRONGLY SUPPRESS *MEC1*-100 SENSITIVITY

With two independent suppressor screens yielding mutations in *PPH3* and *PSY2*, we investigated this phosphatase complex further. Previous work suggested that Psy2-Pph3 (PP4) dephosphorylates the checkpoint effector kinase, Rad53, in a manner that is redundant with other phosphatases (Bazzi et al., 2010; Heideker et al., 2007). Specifically, Ptc2, Ptc3 (both PP2C-type phosphatases) and the PP1-type phosphatase Glc7 all appeared to dephosphorylate Rad53, depending on the type of damage used to activate the checkpoint (Bazzi et al., 2010; Leroy et al., 2003; O'Neill et al., 2007; Travesa et al., 2008)(Figure 2.2A). Indeed, it was reported that Pph3 was dispensable for Rad53 dephosphorylation after HU arrest, and that Glc7 might be responsible on HU instead (Bazzi et al., 2010; Travesa et al., 2008).

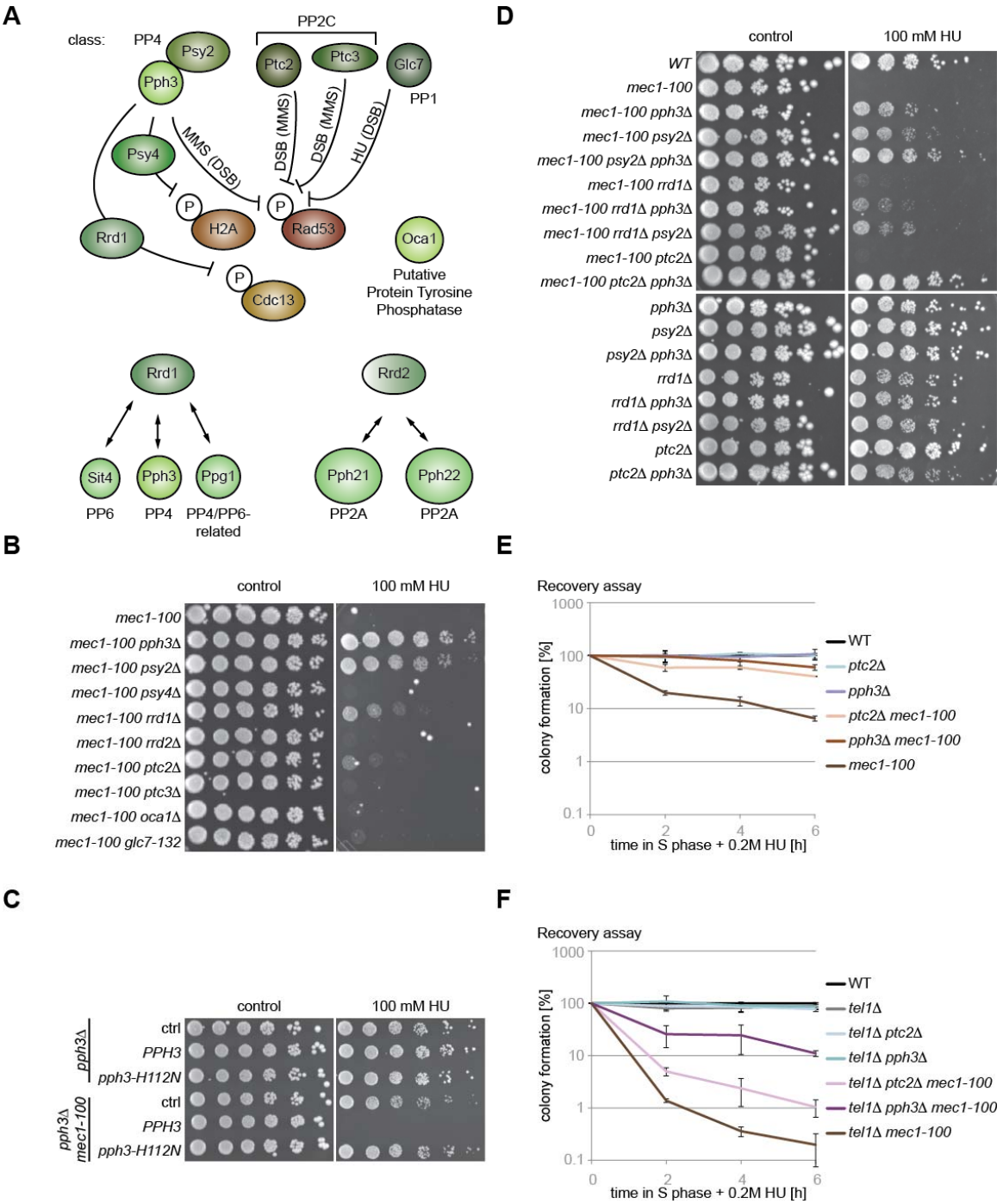


Figure 2.2: Validation of *psy2*Δ and *pph3*Δ as suppressors of *mec1-100* HU sensitivity. (A) Yeast phosphatases and their relationship showing those with substantial genetic interactions with *mec1-100* or those implicated in checkpoint down-regulation, see text. **(B)** Serial 5-fold dilutions of cultures were plated on YPAD ± 100 mM HU. Relevant genotypes of isogenic strains are indicated in the figure. Strains used (Table S2.5) were: GA-6582, GA-7086, GA-7393, GA-7385, GA-7929, GA-7932, GA-7329, GA-7276, GA-7935, and GA-8079. **(C)** *pph3*Δ (GA-7049) or *pph3*Δ *mec1-100* (GA-7086) cells were transformed with *TRP1*-based control plasmid (#286) or plasmids expressing *PPH3* (#3367) or *pph3-H112N* (#3368) from *PPH3* promoter. Cells were grown in SC-TRP medium and serial 5-fold dilutions were plated on SC-TRP ± 100 mM HU. **(D)** Cultures were treated as in (B). Relevant genotypes of isogenic strains are indicated in the figure. Isogenic strains (Table S5) used were: GA-1981, GA-6582, GA-7086, GA-7393, GA-7395, GA-7929, GA-7982, GA-8054, GA-7329, GA-7979, GA-7049, GA-7391, GA-7398, GA-7908, GA-7981, GA-8052, GA-7273 and GA-7977. **(E)** Recovery from replication fork stalling was monitored as colony outgrowth of cells after synchronization in G1 by α-factor arrest and release into S phase with 0.2M HU for the indicated times. Isogenic strains used were: GA-1981, GA-6582, GA-7086, GA-7329, GA-7049 and GA-7273. Error bars indicate standard deviation. **(F)** Cells were treated as in (E). Isogenic strains used were GA-1981, GA-6912, GA-6913, GA-7734, GA-7955, GA-7732 and GA-7953 (Table S2.5). See also Fig. S2.2.

To sort out these contradictions, we created single and double mutants with *mec1-100* in another budding yeast background (W303), and monitored growth on HU. Again, *psy2*Δ and *pph3*Δ were the strongest suppressors among the mutants tested (Figure 2.2B). Consistent with the EMAP result, loss of *RRD1* led to weak suppression, while *ptc2*Δ had almost no effect on the HU sensitivity of *mec1-100*. This latter was true for all other phosphatase mutants, including loss of the PP2A-associated factor Rrd2 (Van Hoof et al., 2005) (Figure 2.2B).

We confirmed that suppression of *mec1-100* by *pph3*Δ was due to loss of Pph3 phosphatase activity, because the catalytically inactive mutant (*pph3-H112N*) (O'Neill et al., 2007) supported *mec1-100* growth on HU to the same extent as *pph3*Δ (Figure 2.2C). Given previous work suggesting that Rrd1 and Pph3 act on the same pathway to dephosphorylate the Mec1 target Cdc13 at breaks (Zhang and Durocher, 2010), we tested whether *rrd1*Δ would be epistatic with *pph3*Δ by combining *rrd1*Δ and *mec1-100* with *psy2*Δ, *pph3*Δ, or both. Surprisingly, coupling *rrd1*Δ with *psy2*Δ or *pph3*Δ reduced the suppression of *mec1-100* sensitivity to HU (Figure 2.2D), arguing that *rrd1*Δ interferes with suppression by *psy2*Δ or *pph3*Δ. In contrast, both the *pph3*Δ *ptc2*Δ and *pph3*Δ *psy2*Δ double mutants were slightly additive for suppression. Furthermore, unlike loss of Psy2 or Pph3, loss of Rrd1 alone enhanced sensitivity to HU (Figure 2.2D), suggesting that Rrd1's suppression of *mec1-100* lethality on HU is distinct from that of PP4.

To examine if PP4-mediated suppression affects viability only (e.g. survival due to checkpoint function) or also helps maintain engaged and stalled replication forks, we tested single and double mutants for their ability to promote colony growth after having synchronously entered S phase and being held in high HU concentrations for 1 to 6 hours (Figure S2.2A). This assay is thought to measure restart of stalled forks, which enables colony outgrowth. In *mec1-100* cells ChIP signals of replicative polymerases are partially lost from sites of early replication by 1h of HU treatment and cells show recovery defects (Cobb et al., 2005). Importantly, the combination of *mec1-100* with *pph3*Δ rescued this defect, while *ptc2*Δ had a weaker effect (Figures 2.2E; S2.2B).

The loss of Tel1 kinase, the yeast ATM homologue, has no effect on fork stability or restart on its own, but it is possible that Tel1 might compensate checkpoint defects and promote cell survival on HU. Therefore we tested the ability of *ptc2*Δ and *pph3*Δ to rescue *mec1-100* in a *tel1*Δ background. Again, we found that *ptc2*Δ and *pph3*Δ rescued *mec1-100* recovery defects, independently of Tel1. Moreover, *pph3*Δ had a 10-fold stronger effect than *ptc2*Δ (Figures 2.2F; S2.2C). We conclude that loss of Pph3 efficiently suppresses both the HU sensitivity and fork recovery defects of *mec1-100*, with no recourse to Tel1/DSB checkpoint response.

RAD53 ACTIVATION CORRELATES WITH LEVEL OF SUPPRESSION

In the S-phase checkpoint cascade, Rad53 is activated by Mec1-mediated phosphorylation, which is compromised by the *mec1-100* mutation in S phase only (Paciotti et al., 2001). Previous work implicated our two suppressor phosphatases, Ptc2 and Pph3, in the dephosphorylation of Rad53 (Leroy et al., 2003; O'Neill et al., 2007; Travesa et al., 2008), although Pph3 was reportedly dispensable after exposure to HU (Travesa et al., 2008). We nonetheless tested the hypothesis that reduced Rad53 phosphorylation in *mec1-100* cells is balanced by loss of Pph3 or Ptc2, using Western blots to detect the hyper-phosphorylated form of Rad53. Cells bearing *mec1-100* in combination with *pph3*Δ or *ptc2*Δ were synchronized in G1 by α-factor, and released into S phase in the presence of HU. The Rad53 Western blot showed that the delayed upshift of Rad53 in the *mec1-100* background was compensated by *pph3*Δ or, albeit weaker, *ptc2*Δ: leading to more rapid Rad53 activation (Figure 2.3A). In *MEC1+* cells, *ptc2*Δ or *pph3*Δ had no effect on the kinetics of Rad53 activation (Figure

2.3A, S2.3A), possibly because the steady-state equilibrium between Rad53 phosphorylation and dephosphorylation is shifted towards dephosphorylation only in *mec1-100* cells. Thus, a compensatory effect by *pph3*Δ can be observed in *mec1-100*, but not in *Mec1+* cells.

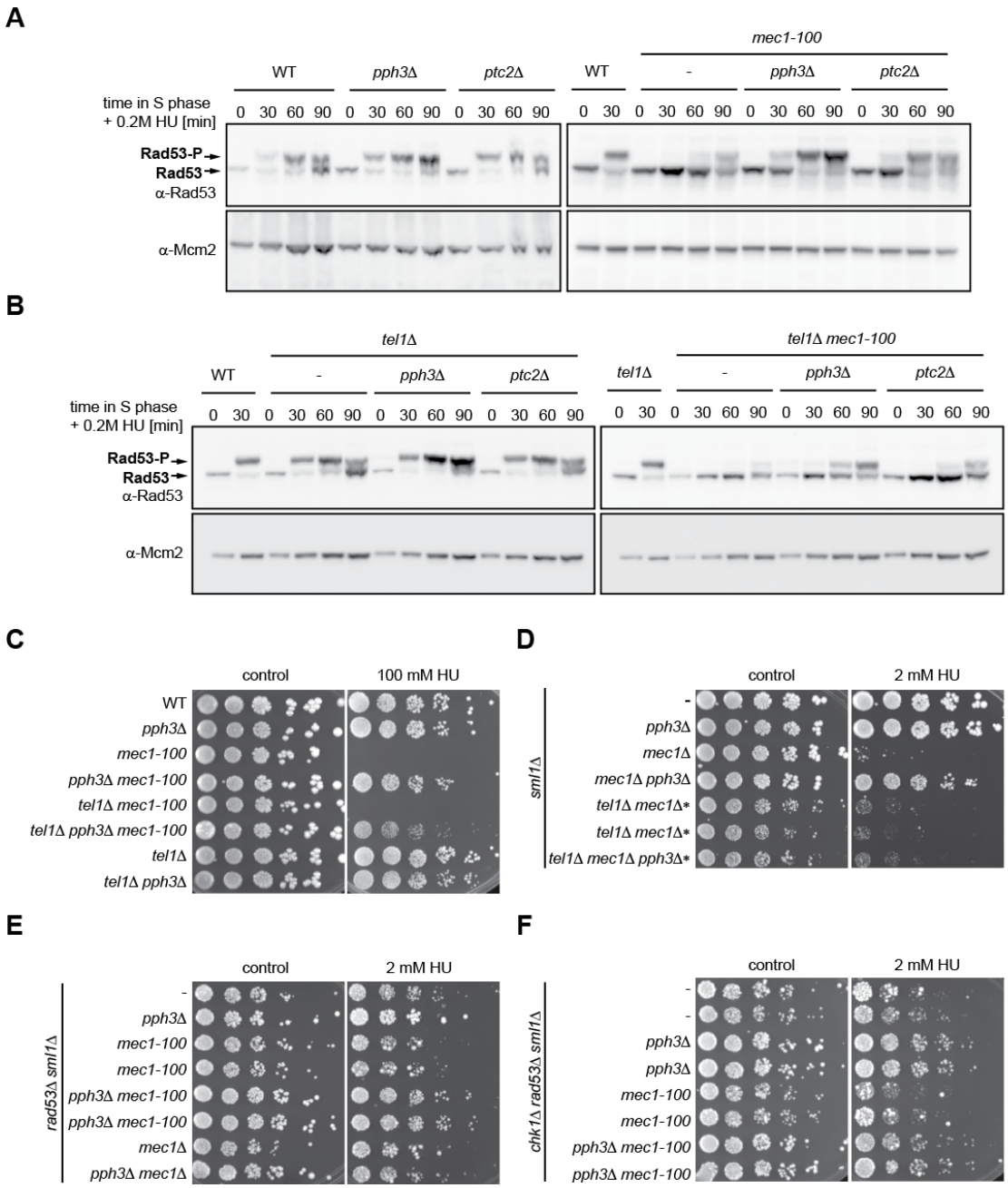


Figure 2.3: Suppression of *mec1-100* correlates with Rad53 activation. (A) Rad53 phosphorylation was monitored by synchronizing cells in G1 (α-factor) and releasing them for the indicated times into 0.2 M HU, before denatured extract preparation and Western blot analysis. Relevant genotypes are indicated in the figure for the following isogenic strains: GA-1981, GA-7049, GA-7273, GA-6582, GA-7086 and GA-7329. **(B)** Cells were treated as in (A). Isogenic strains were GA-1981, GA-6912, GA-6913, GA-7734, GA-7955, GA-7732 and GA-7953. **(C)** Serial 5-fold dilutions of cultures were plated on YPAD ± 100 mM HU. Relevant genotypes are indicated in the figure. Isogenic strains were: GA-1981, GA-7049, GA-6582, GA-7086, GA-6913, GA-7734, GA-6912 and GA-7732. **(D)** Serial 5-fold dilutions of cultures were plated on YPAD ± 2 mM HU. Relevant genotypes are indicated in the figure. Isogenic strains were: GA-4533, GA-7294, GA-5286, GA-7650, GA-7724, GA-7725, GA-7707 and GA-7708. Asterisk: 10x more cells plated **(E)** Cells were treated as in (D). Isogenic strains used were GA-7373, GA-7375, GA-7401, GA-7377 (two colonies of each) and GA-7709 and GA-7711. **(F)** Cells were treated as in (D). Isogenic strains were GA-7656, GA-7657, GA-7658, GA-7659, GA-7660, GA-7661, GA-7662 and GA-7663. Full genotypes of strains in Table S2.5 (see also Fig.S2.3).

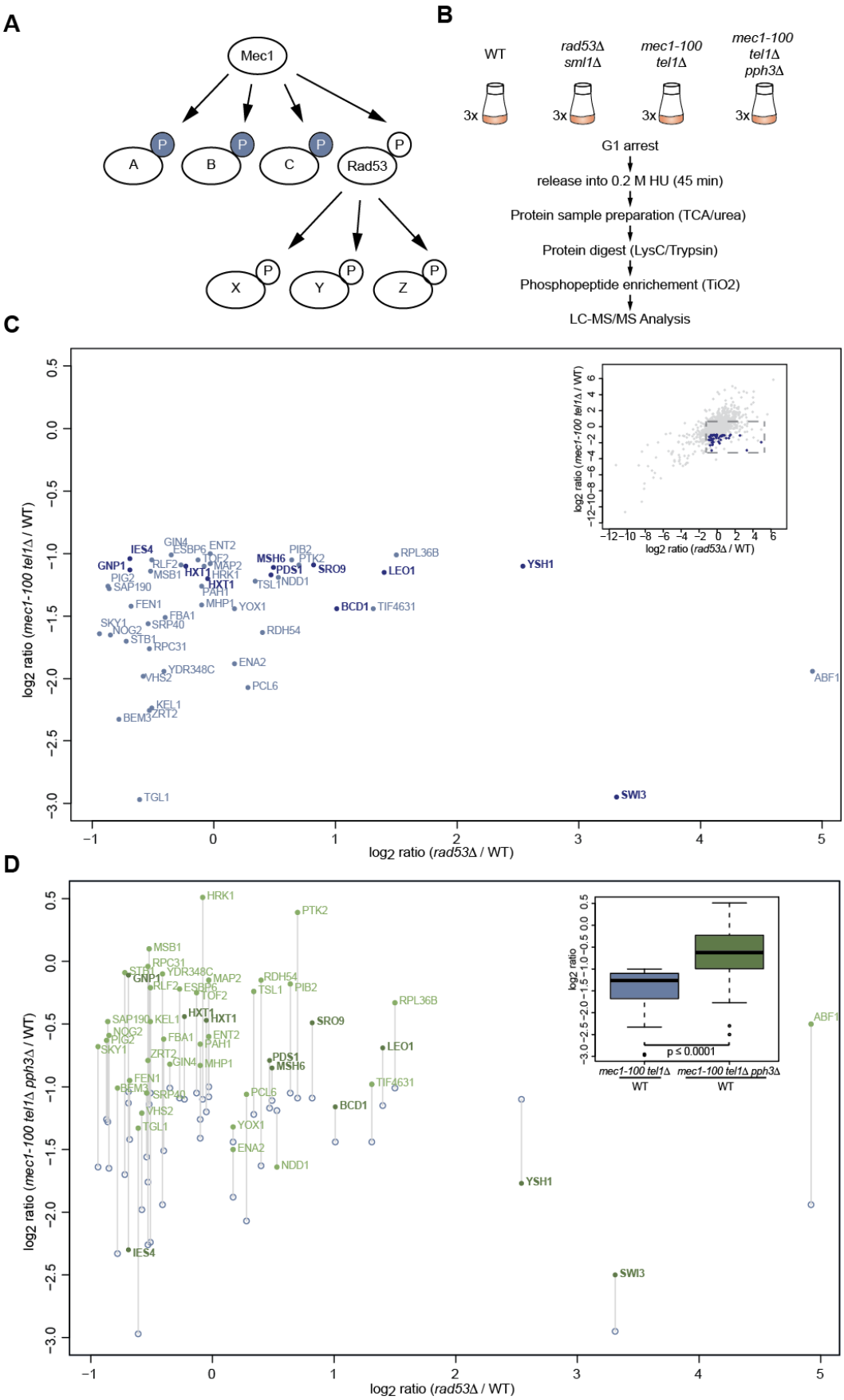
In order to exclude that the more rapid Rad53 phosphorylation observed in *mec1-100 pph3*Δ stems from compensation by Tel1, all assays were concurrently performed in a *tel1*Δ background (Figure 2.3B), but the effects of Pph3 or Psy2 on Rad53 activation were comparable in *tel1*Δ (Figures 2.3AB, S2.2A). Finally, we note that Rad53 remained more robustly phosphorylated at 90 min or after HU washout in *pph3*Δ cells, something only weakly affected by *ptc2*Δ (Figures 2.3AB, S2.3AB). This delay in Rad53 dephosphorylation during recovery from HU treatment did not correlate with survival defects, possibly because with sufficient time cells dephosphorylate Rad53 eventually (Figures 2.2EF; S2.2BC). In a complete *mec1* deletion, unlike *mec1-100, pph3*Δ only conferred HU-suppression in the presence of Tel1, indicating that specifically Mec1/Tel1 activity (no other kinases except those downstream of Mec1/Tel1) is needed for *pph3*Δ to exert its effect (Figure 2.3CD). We note that *ptc2*Δ had similar, but significantly less pronounced effects than *pph3*Δ in restoration of the Rad53 upshift on HU, consistent with its weaker responses in functional assays (Figures 2, 3). In sum, the correlation between Rad53 activation kinetics and the suppression of HU sensitivity argues that at least part of the mechanism through which *pph3*Δ and *psy2*Δ suppresses *mec1-100*, reflects Rad53 activation.

PP4 TARGETS RAD53 AND OTHER FACTORS TO MEDIATE *MEC1-100* SUPPRESSION

It is well established that *mec1-100* cells activate Rad53 weakly on HU (Figure 2.3A) and that Rad53 initiates many of the downstream checkpoint responses (e.g. cell cycle arrest and late origin firing). Nonetheless, there is extensive evidence that Mec1 has unique roles in the replication checkpoint that are independent of Rad53 (Cobb et al., 2005; Segurado and Diffley, 2008). Moreover, there are targets at the replication fork that are modified uniquely by Mec1 (Chen et al., 2010; Smolka et al., 2007) (M. Smolka, pers. communication). To see if the suppression of *mec1-100* phenotypes by *pph3*Δ involves targets other than Rad53, we checked whether *pph3*Δ can suppress *mec1-100* sensitivity to HU, in the absence of Rad53.

Because *RAD53* deletion is lethal, we coupled it with a bypass mutation (*sml1*Δ) (Zhao et al., 1998). The resulting *rad53*Δ *sml1*Δ strain is extremely sensitive to HU, yet the effect of *pph3*Δ on *mec1-100* coupled with *rad53*Δ *sml1*Δ, can be tested at low concentrations of this inhibitor. Serial dilution assays detected a mild, but highly reproducible suppression of *mec1-100* by *pph3*Δ even in the absence of Rad53 (Figure 2.3E). This suggests that while Rad53 is important, it is not the only target through which the phosphatase mutant rescues *mec1-100* defects. This residual suppression was not observed in *rad53*Δ *mec1*Δ *sml1*Δ cells, again suggesting that the residual kinase activity of *mec1-100* is required for the suppressive effect and that Tel1 coupled with *pph3*Δ is not sufficient to suppress the lethal effects of HU in the absence of Rad53 and Mec1. Again this underscores the crucial role of Mec1 in HU survival.

Interestingly, even in the absence of *mec1-100, PPH3* deletion suppressed the HU-sensitivity of *rad53*Δ *sml1*Δ, in contrast to a previous report that scored colony formation on MMS (O'Neill et al., 2007). Our result again suggests that the phosphorylation status of proteins other than Rad53 is beneficial for survival on HU. One candidate for this was the second checkpoint effector kinase, Chk1. However, deletion of *CHK1* had no effect on suppression by *pph3*Δ (Figure 2.3F). We conclude that activation of the downstream checkpoint kinase Rad53 is important, but is not the only Mec1-mediated phosphorylation event that is enhanced by loss of PP4, to ensure *mec1-100* survival on HU.


A
Mec1
A
B
C
Rad53
X
Y
Z
P
B
WT
rad53Δ sml1Δ
mec1-100 tel1Δ
mec1-100 tel1Δ pph3Δ
3x
G1 arrest
release into 0.2 M HU (45 min)
Protein sample preparation (TCA/urea)
Protein digest (LysC/Trypsin)
Phosphopeptide enrichement (TiO2)
LC-MS/MS Analysis
C
log2 ratio (mec1-100 tel1Δ / WT)
log2 ratio (rad53Δ / WT)
IES4
GNP1
HXT1
MSH6
PDS1
SRO9
LEO1
YSH1
BCD1
SWI3
ABF1
D
log2 ratio (mec1-100 tel1Δ pph3Δ / WT)
log2 ratio (rad53Δ / WT)
p ≤ 0.0001
mec1-100 tel1Δ
mec1-100 tel1Δ pph3Δ
WT

RESTORATION OF H2A PHOSPHORYLATION DOES NOT CORRELATE WITH SUPPRESSION

A further target of Pph3 (PP4) during the DNA damage response in both yeast and mammals is histone H2A (Chowdhury et al., 2008; Keogh et al., 2006; Nakada et al., 2008). Yeast H2A is phosphorylated on Serine 129 by Mec1 and/or Tel1 at DSBs and stalled replication forks, fulfilling the role of the mammalian γH2AX (Cobb et al., 2005; Downs et al., 2000; van Attikum et al., 2004).We confirmed that H2A phosphorylation levels were increased by *PPH3* or *PSY2* deletion in both WT and *mec1-100* backgrounds after treating S-phase cells with HU (Figure S2.3D). However, unlike Rad53, phospho-H2A regulation is not only dependent on Pph3 and Psy2, but also on Psy4, a variable third subunit of the complex (Keogh et al., 2006; O'Neill et al., 2007). Consistently *psy4*Δ also led to increased H2A phosphorylation (Figure S2.3D). On the other hand, loss of Psy4 did not rescue *mec1-100* HU sensitivity in WT or *rad53*Δ *sml1*Δ backgrounds (Figures 2.2B, S2.3C). Thus, H2A phosphorylation does not strictly correlate with the rescue of *mec1-100* on HU.

PHOSPHOPEPTIDES DOWNREGULATED IN *MEC1-100* CELLS ARE UPREGULATED BY *PPH3* DELETION

Given that Rad53 activation correlates with the rescue of *mec1-100* HU-sensitivity, yet is not the only relevant target, we performed a quantitative phosphoproteomic study. Specifically, we screened for modifications that are downregulated in *mec1-100*, compensated by *pph3*Δ and left unaffected by *rad53* deletion (Figures 2.4A). Since Tel1 may compensate for *mec1-100* defects (Figures 2.2EF, 2.3B), we further used a *tel1*Δ *mec1-100* double mutant. Prior to extraction of proteins, the cultures were arrested in G1 by α-factor and released into S phase in the presence of HU (Figure 2.4B).

2396 phosphopeptides could be quantified (Table S2.2), of which 47 were specifically reduced in *mec1-100 tel1*Δ, but not in *rad53*Δ *sml1*Δ, cells (Figure 2.4C, Table S2.3). Among them were the repair factor Rdh54, chromatin remodeler INO80 subunit Ies4, the mismatch repair protein Msh6, and transcription regulators like Swi3 and Leo1, the latter being a component of the PAF1 complex (Figure 2.4C). Unexpectedly, we did not find any proteins that were involved directly in DNA replication. Remarkably, however, when the abundance of these phosphopeptides was scored after deletion of *PPH3*, almost all (94%) were upregulated (i.e. restored in *mec1-100 tel1*Δ *pph3*Δ vs *mec1-100 tel1*Δ; Figure 2.4D).

Figure 2.4: Most mec1-100-regulated phosphopeptides are upregulated by loss of Pph3. (A) Scheme of Mec1-dependent, Rad53-independent phosphorylation sites. **(B)** Setup of phosphoproteomics experiment. Three cultures of wild-type (GA-1981), *rad53*Δ *sml1*Δ (GA-7373), *mec1-100 tel1*Δ (GA-6913) and *mec1-100 tel1*Δ*pph3*Δ (GA-7734) were synchronized in G1 and released into 0.2 M HU for 45 min. Samples were processed for phosphoproteomics analysis as described in supplemental material. **(C)** Phosphopeptide abundances (log2 ratio (mutant/WT)) in *mec1-100 tel1*Δ cells were plotted against abundances in *rad53*Δ *sml1*Δ. Shown are phosphopetides which have a log2 ratio ≤ −1 for *mec1-100 tel1*Δ / WT ($p \leq 0.05$, Student's paired t-test over three replicates) and log2 ratio ≥-1 for *rad53*Δ *sml1*Δ / WT. These were considered mec1-100/tel1-specific. Full list in Table S2.3. Phosphopeptides modified on [pS/pT]Q consenses are marked in dark blue and bold. Labels indicate names of proteins. Inlay: Indicated ratios of all quantified phosphopeptides (Table S2.2) were plotted. Phosphopeptides specific for the *mec1-100 tel1* strain in blue. **(D)** Phosphopeptide abundances (log2 ratio (mutant/WT)) in *mec1-100 tel1*Δ *pph3*Δ cells were plotted against phosphopeptide abundances in *rad53*Δ *sml1*Δ cells. Blue circles indicate position in previous plot of peptides selected in (C) to illustrate shift between *mec1-100 tel1*Δ and *mec1-100 tel1*Δ*pph3*Δ cells. Grey lines connect data points of the same phosphopeptides. Inlay: Boxplot showing indicated ratios of mec1-100/tel1-specific phosphopeptides. p-values calculated by one-tailed Wilcoxon signed rank test. See also Figure S2.4.

This increase was averaged over mec1-100/tel1-dependent peptides and is both highly significant (Figure 2.4D inlay) and specific, because it was not observed among the whole population of quantified phosphopeptides (Figure S2.4A). We conclude that the loss of Pph3 balances out most if not all of the phosphorylation defects that we detect in *mec1-100* cells on HU. This beautifully supports our genetic results which showed opposing functions for these two mutations (Figure 2.1).

S/TQ PHOSPHOPEPTIDES ARE UPREGULATED IN *RAD53*Δ BUT ARE UNAFFECTED BY *MEC1-100*

Among the 47 phosphopeptides that were specifically downregulated in the *mec1-100 tel1*Δ mutant, only a few (11 phosphopeptides) fit the generally assumed ATR/ATM consensus p[S/T]Q (Kim et al., 1999). This could mean either that S/TQ sites are also hit by Rad53, that we failed for technical reasons to recover S/TQ sites, or simply that S/TQ containing peptides did not match to the stringent criteria that we had applied to define *mec1-100 tel1*Δ-dependent phosphopeptides. We therefore scanned for phosphopeptides that were less abundant in *mec1-100 tel1*Δ cells as compared to *rad53*Δ *sml1*Δ cells ($\log_2$ ratio ≤-1, p-value ≤0.05), regardless of their abundance in WT cells, and screened independently for known Mec1/Tel1 targets (Chen et al., 2010). Using this approach we identified many p[S/T]Q phosphopeptides including known fork-associated Mec1/Tel1 targets such as Rfa2, (Brush et al., 1996) and H2A (Downs et al., 2000), in our phosphoproteomic dataset (Figure S2.4BC, Table S2.4). They did not appear in the first analysis because they were not downregulated in *mec1-100 tel1*Δ cells when compared to WT. This indicates that the mutant Mec1 kinase (mec1-100) is actually proficient for phosphorylating many S/TQ Mec1 targets on HU, consistent with its robust kinase activity in the pull-down assay (Figure S2.1A). Therefore we conclude that these targets are most likely not responsible for the lethality of *mec1-100* cells on HU.

Intriguingly, the majority of p[S/T]Q phosphopeptides that we recovered in the second analysis were more abundant in the *rad53*Δ *sml1*Δ mutant than in WT cells, and they were not further affected by loss of Pph3 (Figure S2.4CD). We confirmed that H2A phosphorylation is strongly elevated in *rad53*Δ *sml1*Δ cells compared to WT by Western blotting (Figure S2.4E). This may indicate that in *rad53*Δ *sml1*Δ cells on HU, Mec1 and/or Tel1 become hyperactivated, either because the cells accumulate additional DNA damage at the fork, or because there might be a negative feedback of Rad53 on Mec1 activity.

MEC1-DDC2 AND PSY2-PPH3 PHYSICALLY INTERACT IN A DNA DAMAGE INDEPENDENT MANNER

From our phosphoproteome analysis we conclude that almost every phosphopeptides that was uniquely reduced due to the *mec1-100 tel1*Δ mutantions, was restored by elimination of Pph3. How could this robust coordination be guaranteed? We speculated that the kinase and phosphatase might bind each other, to ensure their coordinated action. To test this, we created yeast strains that expressed epitope-tagged versions of the kinase or phosphatase subunits from their native genomic loci. We confirmed that the tagging of Psy2 and Ddc2 did not render the cells sensitive to MMS or HU (Figure S2.5AD), whereas the same tags on Mec1 or Pph3 compromised their function (Figure S2.5BC). Since Ddc2 is known to form a stable complex with Mec1 (Paciotti et al., 2000), as does Psy2 with Pph3 (Gingras et al., 2005), we could use the functional tagged versions of Psy2 or Ddc2 in subsequent assays. For positive and negative controls, we tested Rfa1 and Ptc2 interactions (Figure S2.5EF).

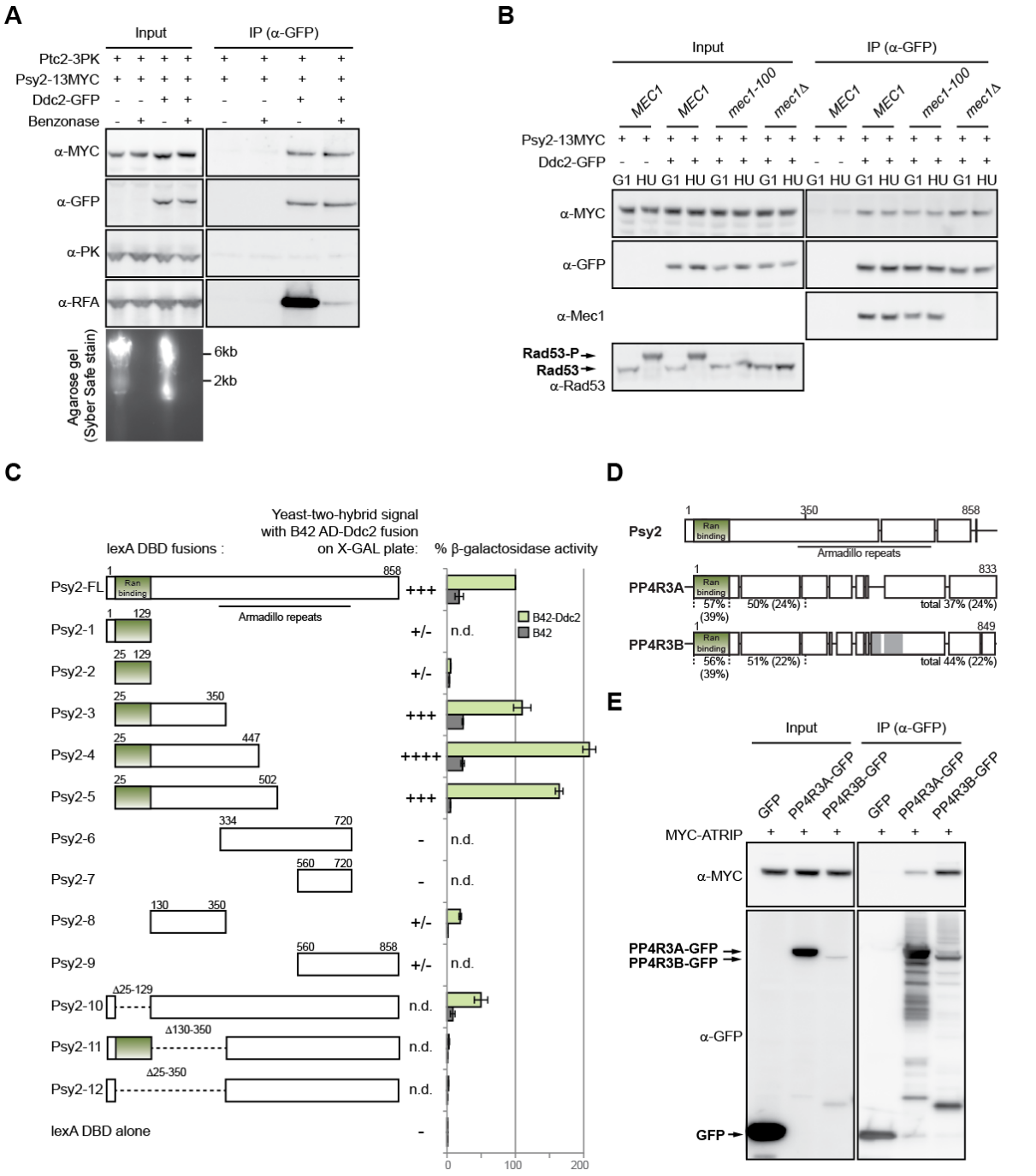


Figure 2.5: Ddc2 and Psy2 physically interact. (A) Native extracts from cycling *Psy2-13MYC Ptc2-3PK* (GA-7972) and *Psy2-13MYC Ptc2-3PK Ddc2-GFP* (GA-7975) cells were treated or not with RNAseA and benzonase. Ddc2-GFP was immunoprecipitated (IP) and analysed by Western blotting with indicated antibodies. DNA isolated from GFP-depleted extracts after IP was analysed by agarose gel to control for nucleic acid digestion. **(B)** *Psy2-13MYC* (GA-7799), *Psy2-13MYC Ddc2-GFP* (GA-7824), *Psy2-13MYC Ddc2-GFP mec1-100* (GA-7835) and *Psy2-13MYC Ddc2-GFP mec1*Δ *sml1*Δ (GA-7827) cells were arrested in G1 by α-factor and held or released into + 0.2 M HU for 30 min. Native and denatured extracts were subjected to α -GFP IP and Western blotting with indicated antibodies. Denatured extracts were blotted for Rad53 phosphorylation. **(C)** Y2H analysis of *DDC2* fused to B42-AD and *PSY2* fragments fused to lexA-DBD. Bars indicate β-galactosidase activity, symbols indicate color on X-GAL plate (raw data in Figure S2.5C). +/- indicates dubious interaction. n.d. not determined. **(D)** Schematic of Clustal Omega multiple sequence alignment of Psy2 (P40164), PP4R3A (Q6IN85-1) and PP4R3B (Q5MIZ7-1) Vertical lines: Alignment gaps (≥ 5 amino acids); grey: region missing in Q5MIZ7-3, which was used in (E). % Sequence similarity (in brackets % sequence identity) was calculated based on Psy2 sequence length or length of indicated Psy2 fragments. **(E)** HEK293T cells were transfected with plasmids expressing MYC-ATRIP (#3525) and GFP (#3493), PP4R3A-GFP (#3518) or PP4R3B-GFP (#3588). Native extracts were prepared at 48h post transfection, and were subjected to IP with α-GFP. Samples were probed with indicated antibodies. See also Figs. S2.5, 2.6.

Immunoprecipitation experiments showed efficient recovery of Psy2-MYC with Ddc2-GFP, while Ptc2 (Ptc2-PK) did not co-precipitate (Figure 2.5A). The Psy2-Ddc2 interaction is unlikely to reflect nonspecific contact through nucleic acids, since combined DNA/RNA digestions using benzonase and RNaseA did not affect recovery. In contrast, most of the detected Ddc2-GFP-Rfa1 interaction that we detected was sensitive to this treatment (Figure 2.5A). The Ddc2-GFP Psy2-MYC interaction did not require HU-induced arrest, since it was detected in G1-phase cells, as well as in an HU-treated S-phase population (Figure 2.5B). Remarkably, the robust Ddc2-Psy2 interaction was independent of Mec1, being detected in *mec1*Δ as well as in the *mec1-100* mutant. Pph3 was also not required for the Psy2-Ddc2 interaction (Figure S2.6A). Finally, when precipitation occurred through Psy2-GFP, Ddc2-MYC could be specifically recovered (Figure S2.6B). The interaction was further mapped by yeast-two hybrid, through which we could define the minimal Psy2 domain that robustly binds Ddc2 (Psy2 amino acids 25-350) (Figures 2.5C, S2.6C). Although a smaller Psy2 fragment (amino acids 130-350) only weakly bound Ddc2, its deletion fully abolished the interaction. Another Psy2 fragment (amino acids 25-129), although robustly expressed (Figure S2.6D), failed to interact significantly and its deletion only reduced the interaction by about 50%. Expression of *psy2*Δ130-350 from its endogenous locus rendered cells as sensitive to MMS as *psy2*Δ cells (Figure 2.S6E), indicating that deletion of amino acids 130-350 impairs protein expression and/or function.

DDC2- PSY2 HOMOLOGUES INTERACT IN MAMMALIAN CELL EXTRACTS

Psy2 has two human homologs, PP4R3A and PP4R3B, which share an overall sequence similarity with Psy2 of 37% and 44% and an identity of 24% and 22%, respectively. Intriguingly, the interaction domain within Psy2 (aa 130-350) has 50% and 51% sequence similarity with PP4R3A and PP4R3B, respectively (Figure 2.5D). This high level of sequence conservation led us to test whether these regulatory phosphatase subunits bind ATRIP in human cells. Following transient transfection of HEK293T cells with plasmids encoding for MYC-tagged ATRIP and either PP4R3A-GFP, PP4R3B GFP or GFP alone, we performed immunoprecipitation with anti-GFP antibody and probed for MYC-tagged ATRIP. ATRIP precipitated efficiently with PP4R3B-GFP, but not with GFP alone and only weakly with PP4R3A-GFP (Figure 2.5E) even though PP4R3A expression levels were much higher. This suggests that the PP4R3B-ATRIP interaction is preferred. We conclude that in yeast the kinase subunit Ddc2 and the phosphatase subunit Psy2 interact in a HU-, Mec1- and Pph3-independent manner that involves a conserved region in Psy2. The ATRIP-PP4R3B interaction thus appears to be conserved in mammalian cells, suggesting a functional relevance of this interaction.

DDC2 AND PSY2 INTERACT AND COLOCALIZE IN NUCLEAR FOCI *IN VIVO*

Although the genetic and biochemical evidence for interaction was strong, it was unclear whether the Mec1/Ddc2 – Psy2/Pph3 interaction occurs at the right place and the right time; that is, at stalled replication forks or other sites of DNA damage. To localize the putative complex in living cells, we fused Psy2 and Ddc2 with distinct fluorescent proteins (RFP and GFP, respectively) and Rfa1 with ECFP. All fusions were expressed from their endogenous loci under the native promoter and were fully functional, as the cells behaved like WT cells when exposed to HU or MMS (Figure S2.5ADF). As expected, Rfa1-CFP has a punctate nuclear signal in S-phase cells, consistent with the existence of replication foci (Pasero et al., 1997)(Figure 2.6AB). The abundance of Rfa1 and the limited resolution of spinning disk (SD) confocal microscopy renders replication foci difficult to analyse in yeast. On the other hand, both Ddc2-GFP and Psy2-RFP foci were larger and less numerous, even in untreated S-phase cells (Figure 2.6B). Finally, consistent with previous reports, rare Rfa1/Ddc2 foci were detected in G1-phase cells (Figure S2.7A) (Lisby et al., 2004).

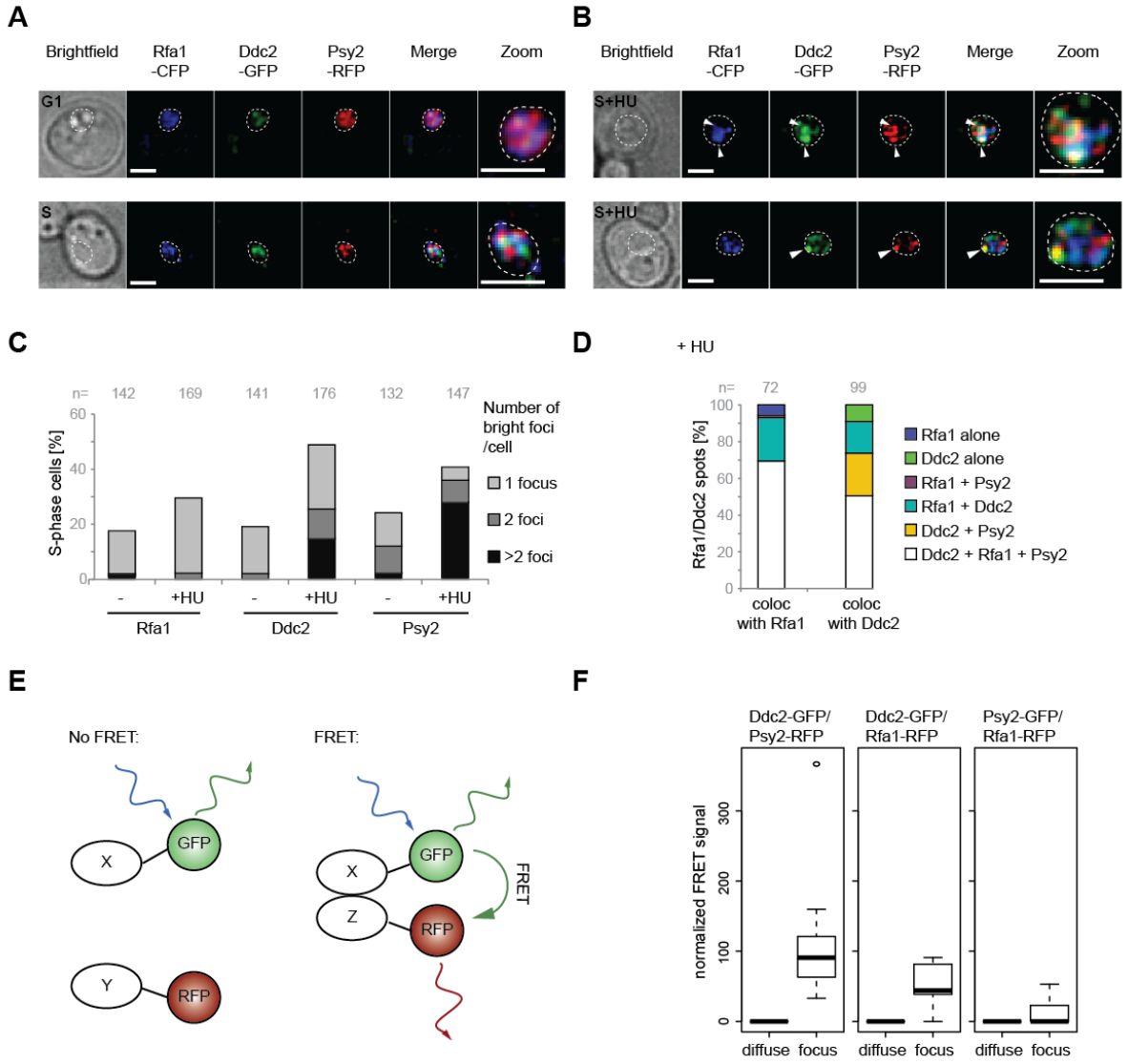


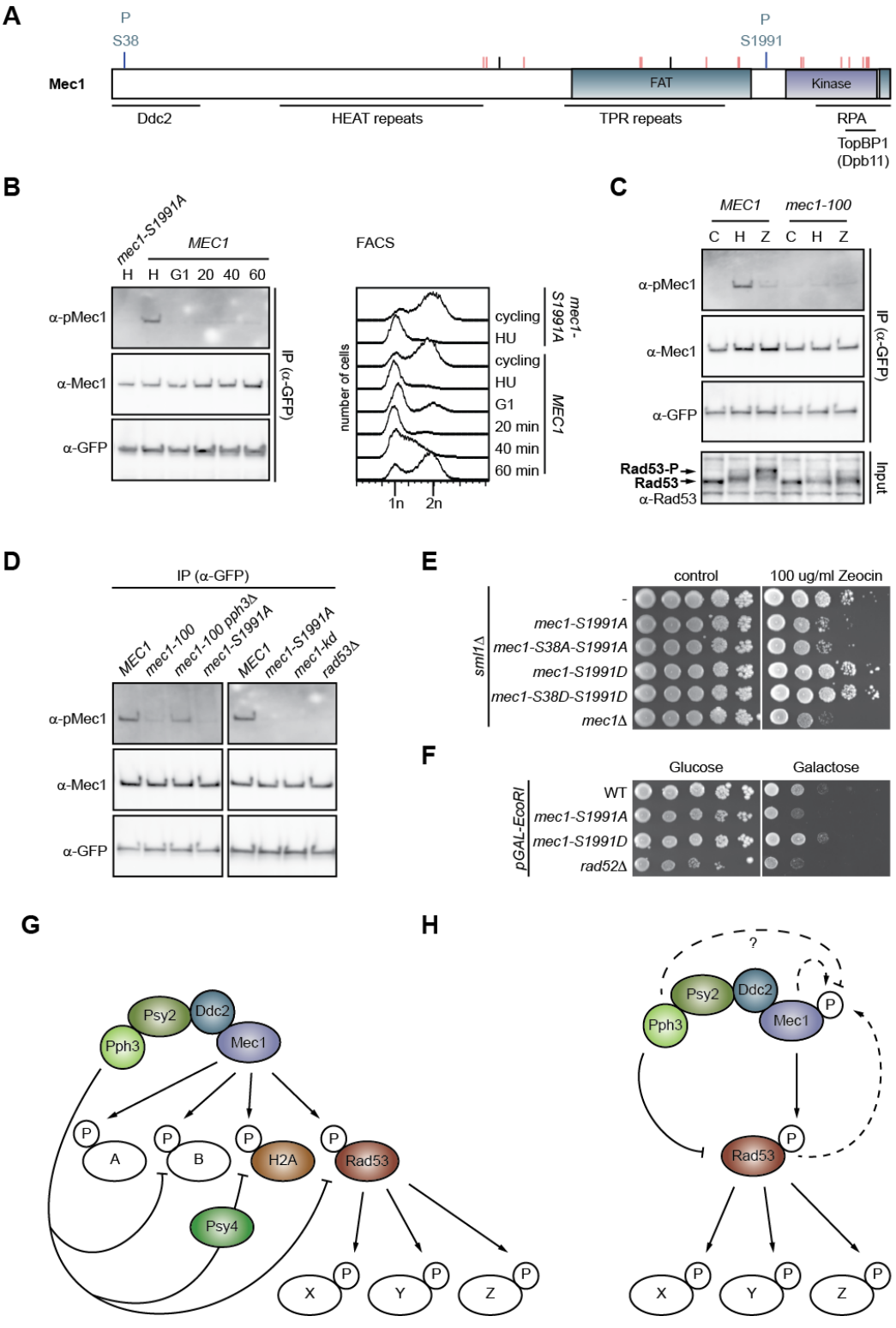
Figure 2.6: Ddc2-GFP and Psy2-RFP foci colocalize and show FRET signals. (A-D) *RFA1-RFP DDC2-GFP PSY2-RFP* (GA-8695) cells were incubated +/- 0.2M HU for 1h prior to fixation for microscopy. **(A)** Shown are images of untreated G1 and S phase cells, with indicated channels shown. Bar = 2 µm. White dashed line: outline of cell nucleus. **(B)** Shown are examples of HU-treated cells. Upper panel: cell showing colocalization of all three proteins in two foci. Lower panel: Cell showing colocalization of Ddc2 and Psy2 only. Arrowheads indicate foci. **(C)** Quantification of bright foci number per S-phase cell. **(D)** Colocalization of Rfa1 and Ddc2 spots with other proteins was quantified after HU treatment. **(E)** Schematic of FRET principle: GFP and RFP must be within 10 nm for RFP emission. **(F)** DDC2-GFP PSY2-RFP (GA-8656) , *DDC2-GFP RFA1-RFP* (GA-8705) and *PSY2-GFP RFA1-RFP* (GA-8702) cells were treated with 0.2 M HU for 1 h before fixation. Fixed samples were analyzed for FRET-induced RFP signals at either bright GFP foci ("focus") or in the nucleus of cells that did not show a focus ("diffuse"). See also Fig. S2.7.

Following incubation with HU, all three tagged proteins, Rfa1, Ddc2 and Psy2, concentrated in intense nuclear foci (Figure 2.6B). We scored the number of bright foci in untreated and treated cells for each protein (Figures 2.6B, S2.7C). Approximately 15% of untreated cells in S phase contain single bright foci of Rfa1 and Ddc2, likely indicative of spontaneous damage, while a few cells contained more than one focus. These foci were not completely coextensive with Psy2-RFP foci, because 10% of cells had one Psy2-RFP focus, and another 10% had two or more bright spots (Figure 2.6C). After treatment with HU, however, the number of cells containing multiple foci of either Ddc2 or Psy2 increased strikingly (Figure 2.6C).

Since the test strain carries all three tagged proteins, we could monitor colocalization of the bright foci. On HU, 70% of the Rfa1 foci coincided with both Ddc2 and Psy2, while an additional 20% contained only Rfa1 and Ddc2 (Figure 2.6D). Almost no foci harbored only Rfa1 and Psy2. Importantly, by scoring colocalization with Ddc2 we found that over 70% of the Ddc2 foci also contained Psy2 (with or without Rfa1; Figure 2.6D). In cells treated with 400 μg/ml Zeocin, a radiomimetic drug that induces both double- and single-stranded breaks, a small number of even larger Rfa1/Ddc2 foci were scored (Figure S2.7B-E), yet Psy2 colocalized with Rfa1 only when Ddc2 was present (roughly 50% of the bright foci, Figure S2.6F). We conclude that Psy2 and Ddc2 colocalize preferentially at HU-induced S-phase foci that contain Rfa1 (i.e. ssDNA at stalled forks), although they also bind coordinately at Zeocin-induced breaks.

Given the limited of resolution of confocal microscopy we sought to confirm contact between these proteins by sensitized emission Förster resonance energy transfer (FRET). This method measures the energy transfer between a donor fluorescent protein (GFP) and an acceptor protein (RFP), and requires that the two are less than 10 nm apart (Figure 2.6E) (Piston and Kremers, 2007). Four FRET pairs were used in our study: Ddc2-GFP/Psy2-RFP; Ddc2-GFP/Rfa1-RFP; Psy2-GFP/Rfa1-RFP and Rfa2-GFP/Psy2-RFP. We find that there is no observable FRET between the non-focal nuclear fractions of any pairs. This does not rule out that they interact outside of foci, but rather suggests that any interaction outside of repair foci is below a detectable level (Piston and Kremers, 2007). Significant FRET signal was observed, however, at bright S-phase foci between Ddc2-GFP and Psy2-RFP after HU treatment, indicating that these proteins are in very close contact with each other (Figure 2.6F). The interaction between Ddc2 and Rfa1 is also substantial, while Psy2 -Rfa1 contact is on average 10-fold lower than the other two pairs (Figure 2.6F). Thus we propose that Ddc2- Psy2 interact at stalled or collapsed fork foci, as does Ddc2-Rfa1.

Figure 2.7: Mec1 phosphoserine 1991 is regulated by Rad53 and Pph3. (A) Mec1 scheme: phosphosites in blue, vertical black lines = *mec1-100* mutations; vertical red lines = suppressor mutations (Fig.2.1). Interaction domains indicated below. **(B)** *Ddc2-GFP* (GA-7824) and *Ddc2-GFP mec1-S1991A* (GA-8232) cells were treated with 0.2 M HU for 1h or arrested in G1 and released into YPAD at 25 °C for indicated times. Fluorescence activated cell sorting (FACS) was performed on samples from which native extracts were prepared for IP with α-GFP. Western blotting used indicated antibodies, including α-pMec1 (Mec1 phosphoserine 1991).**(C)** Exponentially growing cultures of *Ddc2-GFP* (GA-7824) and *Ddc2-GFP mec1-100* (GA-7835) were untreated, or treated with 0.2 M HU or 400 μg/ml Zeocin for 1h. Native extracts were subjected to IP by α-GFP and blots were probed with indicated antibodies. Input samples were probed with α-Rad53 to monitor Rad53 phosphorylation. **(D)** *Ddc2-GFP* (GA-7268), *Ddc2-GFP mec1-100* (GA-7327*), Ddc2-GFP mec1-100 pph3*Δ (GA-7945) *Ddc2 mec1-S1991A* (GA-8232) *Ddc2-GFP mec1-kd sml1*Δ (GA-8484) and *Ddc2-GFP rad53*Δ *sml1*Δ (GA-8486) cells + 0.2M HU for 1h prior to native extract preparation, α-GFP IP and Western blotting with indicated antibodies. **(E)** Serial 10-fold dilutions of cultures were plated on YPAD ± 100 μg/ml Zeocin. Relevant genotypes are indicated. Isogenic strains were GA-4533, GA-8242, GA-8246, GA-8243, GA-8247 and GA-5286. See Fig.S2.8, Table S2.5. **(F)** GA-1981, GA-8338, GA-8342 and GA-5975 (see Table S2.5) cells were transformed with pGAL-EcoRI (#2745) and grown in selective medium to ensure plasmid retention. Serial 10-fold dilutions were plated on selective medium containing 2% glucose or 2% galactose supplemented with 2% raffinose. **(G)** Model showing Ddc2-Psy2 interaction and coordinated action of Ddc2-Mec1 and Psy2-Pph3. Both target Rad53 and Histone H2A and other proteins. Histone H2A dephosphorylation alone requires Psy4. Most mec1-100/Tel1-specific phosphosites are also regulated by Psy2-Pph3 ("B") while a few are not ("A"). **(H)** Mec1 phosphoserine 1991 requires Rad53 and Mec1 kinase activity. Reduced phosphorylation in *mec1-100* cells is rescued by Psy2-Pph3. Regulation of Mec1 may be indirect, potentially through Psy2-Pph3 regulation of Rad53. See also Fig. S2.8


A
P
S38
P
S1991
Mec1
FAT
Kinase
Ddc2
HEAT repeats
TPR repeats
RPA
TopBP1
(Dpb11)
B
mec1-S1991A
MEC1
H H G1 20 40 60
α-pMec1
α-Mec1
α-GFP
IP (α-GFP)
FACS
number of cells
cycling
HU
cycling
HU
G1
20 min
40 min
60 min
mec1-S1991A
MEC1
1n
2n
C
MEC1
mec1-100
C H Z C H Z
α-pMec1
α-Mec1
α-GFP
IP (α-GFP)
Rad53-P
Rad53
α-Rad53
Input
D
IP (α-GFP)
MEC1
mec1-100
mec1-100 pph3Δ
mec1-S1991A
MEC1
mec1-S1991A
mec1-kd
rad53Δ
α-pMec1
α-Mec1
α-GFP
E
control
100 ug/ml Zeocin
sml1Δ
-
mec1-S1991A
mec1-S38A-S1991A
mec1-S1991D
mec1-S38D-S1991D
mec1Δ
F
Glucose
Galactose
pGAL-EcoRI
WT
mec1-S1991A
mec1-S1991D
rad52Δ
G
Psy2
Ddc2
Pph3
Mec1
P
A
B
H2A
Rad53
Psy4
X
Y
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H
?
Psy2
Ddc2
Pph3
Mec1
P
Rad53
X
Y
Z

We observed the same FRET result after treatment with Zeocin and by scoring spontaneous bright foci in untreated cells (Figure .S2.7G). Because Rfa1-RFP cells showed a slight sensitivity to MMS (Figure S2.5F), we also confirmed the reduced Psy2-RPA interaction signal with a second FRET pair, Rfa2-GFP/Psy2-RFP. In agreement with the results for Rfa1-RFP, the Psy2-Rfa2 FRET signal is very low, while Psy2/Ddc2 and Ddc2/Rfa1 gave robust interactions (Figure S2.7G). Thus, the FRET data argue for tight interactions in living cells between the kinase cofactor Ddc2 and the phosphatase cofactor Psy2. We also confirm that Ddc2 contacts Rfa1 at stalled replication forks or collapsed fork foci. The scored colocalization at rare G1-phase foci may account for the cross recovery of Ddc2 and Psy2 in G1 phase extracts (Figure 2.5).

MEC1 PHOSPHORYLATION ON SERINE 1991 IS REGULATED IN A PPH3-DEPENDENT MANNER

Several Pph3/PP4 targets interact stably with the phosphatase (Keogh et al., 2006; Lee et al., 2010; Ma et al., 2014; O'Neill et al., 2007). Thus, we hypothesized that Pph3 might regulate Mec1, and not only counterbalance the enzyme by dephosphorylating its targets. To test this, we looked for phosphorylation sites in Ddc2 and Mec1 that are substrates for Psy2-Pph3. After 1h on HU, *mec1-100* or *MEC1+* cells expressing Ddc2-GFP were lysed, Mec1-Ddc2-GFP complexes were immunoprecipitated, and phosphopeptides analyzed by mass spectrometry. We identified two residues in Mec1 that were robustly phosphorylated in WT, but not in *mec1-100* strains, namely Mec1 Serine 38 and Mec1 Serine 1991 (Ser38, Ser1991, Figure 2.7A). While Ser38 has been described previously as a potential autophosphorylation site (Chen et al., 2010; Smolka et al., 2007), phosphorylation at Ser1991 has not been reported. Ser1991 sits between Mec1's conserved FAT and kinase domains and is well placed to be involved in Mec1 regulation. Indeed, a number of intragenic suppressor mutations in *mec1-100* map to this region (Figures 2.1, 2.7A). The mammalian ATR has an auto-phosphorylation site at the nearby residue Thr1989 (Liu et al., 2011; Nam et al., 2011).

We raised a specific antibody against the phosphorylated Ser1991; the antibody detected Mec1 after precipitation with Ddc2-GFP from HU treated cells, but did not react with a non-phosphorylatable mec1-S1991A form (Figure 2.7B). Using the antibody, we could show that Ser1991 phosphorylation is induced by HU, and is not detected in an unperturbed S phase (Figure 2.7B). Treatment with Zeocin induced Ser1991 phosphorylation to a weaker extent. In the *mec1-100* strain, Ser1991 phosphorylation was virtually absent in all conditions tested (Figure 2.7C). Thus loss of Ser1991 phosphorylation correlates with the *mec1-100* mutation. Importantly, Ser1991 phosphorylation could be restored in *mec1-100* cells by *pph3*Δ, indicating that Psy2-Pph3 indeed regulates Mec1 phosphorylation, compensating for the *mec1-100*-associated loss of Ser1991 modification (Figure 2.7D).

Using the phosphorylation specific antibody, we tested whether Mec1 Ser1991 is a site of autophosphorylation. Indeed, phospho-Ser1991 was absent in a catalytic-dead *mec1* mutant protein, yet we also failed to detect it in a *rad53*Δ mutant (Figure 2.7D). Ser1991 thus seems to require both Mec1 and Rad53 activity for its phosphorylation, although it remains unclear whether the *rad53*Δ effect is direct (Figure 2.7D). We attempted to demonstrate direct dephosphorylation of Ser1991 *in vitro* using Psy2-Pph3 isolated from cells expressing Psy2-Halo. Whereas the precipitated Psy2-Pph3 could dephosphorylate a control target, Cdc13 (Zhang and Durocher, 2010), it did not show reactivity with the phosphorylated Mec1 peptide (Figure S2.8A). In contrast, a nonspecific enzyme, calf intestinal alkaline phosphatase, could dephosphorylate both Cdc13 and Mec1 *in vitro* (Figure S2.8A). While we cannot exclude that our conditions were inappropriate for dephosphorylation it appears that Ser1991 is not a preferred substrate of Psy2-Pph3 *in vitro*.

To see whether loss of Mec1 Ser1991 phosphorylation leads to a phenotype, we scored the S1991A and S1991D mutants for growth in the presence HU, MMS, or Zeocin, and scored recovery after UV or γ-irradiation (IR) (Figures 2.7E, S2.8B). The acceptor-site mutant S1991A renders cells sensitive to the radiomimetic drug Zeocin (Figures 2.7E, S2.8B), independent of Ser38. We further confirmed that *mec1-S1991A* cells are strongly sensitive to induced DSBs by ectopically expressing *Eco*RI in all strains. Indeed, the *mec1-S1991A* mutant shows *Eco*RI-sensitivity (Figure 2.7F), while *mec1-S1991D* has a slight resistance.

DISCUSSION

Our key finding is that the central checkpoint kinase Mec1-Ddc2 (human ATR-ATRIP) forms a stable complex with the PP4 (Pph3-Psy2) phosphatase, and that they regulate, in an opposing manner, a large number of substrates. The modification of these latter targets is compromised in the S-phase-specific Mec1 mutant, *mec1-100*, which confers hypersensitivity to replication stress. We confirm this crosstalk genetically (by suppressor and EMAP analysis) and biochemically (by phosphoproteomics and a phosphospecific antibody for phospho-S1991). We further propose that the opposing action of Mec1 and PP4 and the direct interaction through Psy2-Ddc2 binding, are physiologically relevant, as they occur at sites of replication fork-induced damage in S phase cells and at induced DSBs (Figure 2.6) In an attempt to demonstrate the relevance of the interaction directly, we deleted the Ddc2 interaction domain in Psy2. The mutation showed the same sensitivity to MMS as a *psy2*Δ strain. This suggests either that the deletion inactivates the protein or destabilizes it.

Since about 70% of Ddc2 foci colocalize with Psy2, the majority of Mec1-Ddc2 appears to be associated with PP4, at least as judged by microscopy. IP/Western blot experiments, on the other hand, do not allow us to estimate the stoichiometry of the complex. Indeed, we cannot rule out that the Psy2-Ddc2 interaction also occurs outside of repair foci, given that they coimmunoprecipitate in the absence of damage.

Whereas the mechanisms that lead to checkpoint activation by Mec1-Ddc2 are well characterized, there is little information about what regulates or restricts the kinase complex. The *mec1-100* mutant was informative in this context. This mutant does not impair Mec1-Ddc2 recruitment to stalled forks (Cobb et al., 2005), nor does it attenuate kinase activity on a test peptide (Figure S2.1A). Rather, the mutation appears to alter the affinity of *mec1-100* towards a subset of targets that is particularly crucial for the survival of S-phase replication stress. Intriguingly, this same subset of targets is specifically upregulated by loss of Psy2 or Pph3 activity, which, importantly, suppresses the defects associated with the *mec1-100* mutation. The *mec1-100* deficiency also renders cells profoundly sensitive to HU, especially upon loss of the Sgs1 helicase or other S-phase checkpoint activating signals, as confirmed by our EMAP data.

This complex of phosphatase and kinase may allow the fine-tuning of ATR-ATRIP (Mec1-Ddc2) for different functions through the cell cycle. The fact that there seems to be a higher threshold for damage-induced checkpoint activation in S phase, as opposed to G2 phase, suggests that this may be an important regulatory event in the cell cycle (Shimada et al., 2002; Tercero et al., 2003). Finally, Mec1 not only has to react appropriately to ssDNA, but it must also switch off rapidly to allow efficient replication and cell cycle resumption. This may be a role for the closely associated Pph3-Psy2 complex. Indeed, Rad53 dephosphorylation during recovery from HU treatment is delayed in *pph3*Δ cells, although this did not result in detectable colony formation defects (Figures 2.2EF, S2.2BC, S2.3B). Presumably other phosphatases (Ptc2, Ptc3 or Glc7) eventually compensate for loss of Pph3 with time, as was reported for recovery from MMS treatment and repair of a double strand break (Kim et al., 2011; Szyjka et al., 2008). We note that *pph3*Δ shows synthetic sickness with loss of *dia2*Δ, *sae2*Δ and *ptc2*Δ on HU, which might contribute to recovery (Clerici et al., 2006; Fong et al., 2013; Kim et al., 2011; Leroy et al., 2003; Marsolier et al., 2000; Szyjka et al., 2008). However, in the presence of Pph3, a Ptc2 deletion showed significantly milder effects and did not physically interact with Mec1-Ddc2 (Figures 2.2; 2.3; 2.5)

The copurification of opposing enzymatic activities is not unique. We note that the human RAP80 complex contains both ubiquitin ligase and deubiquitinase enzymes (Sobhian et al., 2007) and histone acetyltransferases and deacetylases have been shown to not only create a dynamic balance of

acetylation of target proteins but also be physically associated with each other, sometimes even regulating each other's activity (Yamagoe et al., 2003). Relevant to this, we find that Pph3-Psy2 regulates a phosphorylation site within the Mec1 kinase, Ser1991, mutation of which compromises survival in face of DSBs. The Ser1991 modification is sensitive to loss of Mec1 activity, but also to *rad53*Δ (Figure 2.7). This suggests that it may be a target of Rad53, although we cannot rule out that it is an autophosphorylation site with an indirect dependence on Rad53 (Figure 2.7G,H). One might speculate that Ser1991 phosphorylation alters the specificity of Mec1 and/or triggers its downregulation, contributing to the attenuation of Mec1-Ddc2 activity during normal lagging strand DNA synthesis, or its inactivation at the end of a checkpoint response. Finally, based on our phosphoproteomic analysis one might speculate that Rad53 feeds back to downregulate Mec1-Ddc2, since we detected a large set of S/TQ phosphoacceptor peptides (Mec1 targets) that are upregulated in the *rad53* deletion strain (Figure S2.4CDE).

How does the checkpoint activation occur if an antagonizing activity is associated with the activating kinase? The phosphorylation of any given protein at any given time is always the result of competing kinase and phosphatase activities. Obviously, when checkpoint activation occurs, the catalytic rate of phosphorylation becomes stronger, because phosphorylated proteins accumulate. If it is stronger, it does not matter how much stronger it is (i.e. whether Pph3 is present or not). This may explain, why Pph3 does not affect phosphorylation in Mec1+ cells, but does in *mec1-100,* which may have a lower catalytic rate towards some substrates *in vivo*. The balance between the opposing activities can only be flipped by altering their specific activity. The recruitment of Rad53 by Sgs1 or Mrc1 (Alcasabas et al., 2001; Hegnauer et al., 2012) may induce a change in the specific activity of Mec1 towards Rad53, triggering checkpoint activation. Alternatively it is also possible that the kinase alters activity of the phosphatase, inhibiting it once a specific level of damage has occurred, and releasing it once damage is repaired. Although we did not detect phosphopeptides from either Psy2 or Pph3 in our *mec1-100* mass spectroscopic analysis of phosphorylation, we cannot exclude that PP4 is a target of Rad53 or Mec1.

The close association of Pph3-Psy2 with the checkpoint kinase may not only downregulate checkpoint by dephosphorylating Rad53, but also H2A-P. H2A dephosphorylation, however, requires a third factor, Psy4, which does not contribute to the suppression of *mec1-100* sensitivity to HU. Other phosphoproteomic studies have identified additional DNA damage-related PP4 targets, both in yeast and in mammals, among them RPA2, KAP-1, 53BP1, CHD4 and Cbf1, even though these studies were performed under non-damaging conditions (Bandyopadhyay et al., 2010; Lee et al., 2012; Lee et al., 2010). Those additional targets and the 47 targets hit by both Mec-Ddc2 and Psy2-Pph3 identified here, is most a likely non-exhaustive list, given that phosphopeptide coverage is rarely complete. We note that the Mec1/PP4 target Cbf1 was not significantly downregulated in *mec1-100* cells after HU treatment (Figure S2.4C).

It is remarkable that 94% of the 47 phosphopeptides that show reduced phosphorylation levels in *mec1-100* responded to a deletion of *PPH3*. Combined with our genetic data, which showed suppression if *mec1-100* by *pph3*Δ and a strong anticorrelation of their genetic interaction profiles, we conclude that these two activities directly counteract each other. Among many other interesting genetic interactions scored for *mec1-100*, we found several subunits of the chromatin remodeling complexes INO80, SWI/SNF, ISW and Chd1, which show synthetic lethality with *mec1-100* (Figures 2.1C,S2.1D). Interestingly, subunits of these chromatin remodelers were also among the *mec1-100* downregulated phosphopeptides (e.g. Ies4 and Swi3). This reflects the close relationship of remodelers such as INO80 and fork recovery (Papamichos-Chronakis and Peterson, 2008; Shimada et al., 2008).

A parallel study indicated two different modes of Mec1 activity, one working during unchallenged DNA replication and one in response to damage (M. Smolka, personal communication). It is tempting to suggest that the association of Ddc2-Mec1 with Psy2-Pph3 might be involved in regulating the switch between these two functions. Further work will delineate the underlying molecular mechanisms of such a switch.

EXPERIMENTAL PROCEDURES

YEAST STRAINS, PLASMIDS, ANTIBODIES, MICROSCOPY, PHOSPHOPROTEOMICS, PHOSPHATASE ASSAY, AND EMAP

Yeast strains and plasmids are described in Table S2.5. If not stated otherwise cells were cultured at 30°C in YPAD medium using standard procedures. For Y2H analysis, fragments of *PSY2* were fused to the lexA DNA binding domain (#3616 - #3623, #3629,#3630) and *DDC2* was fused to the B42 transcription activation domain of pJG4-6 (#993), resulting in pJG4-6-DDC2 (#3308). WT cells (EGY48) containing the lacZ reporter pSH18-34 (#359), the bait and the prey were streaked on X-GAL plates (Golemis et al., 2011) and incubated 1-2 days at 30°C. β–galactosidase assays were performed as previously described (Hegnauer et al., 2012) using pGAL-lexA Psy2 constructs (#3307, #3592-#3595, #3649-#3651, #3653). Details concerning antibodies, microscopy, phosphoproteomics, and the EMAP assay are found in Supplemental Methods.

MAMMALIAN CELL CULTURE

HEK293T cells were cultured in DMEM medium containing 10% fetal bovine serum. Transfections were carried out using jetPEI (Polyplus) transfection reagent according to manufacturer's instructions.

SPONTANEOUS SUPPRESSOR SCREENING

mec1-100 (GA-4978) and *mec1-100 exo1*Δ (GA-6356) cells were plated on YPAD + 50 mM HU and incubated for 3 days. Colonies were picked and backcrossed 2-3 times with WT (GA-1982) cells. Strains yielding no HU sensitive *LEU+HIS+ (mec1-100*) spores were considered to have intragenic suppressors and the *MEC1* locus was sequenced. Strains yielding both HU sensitive and insensitive *LEU+HIS+ (mec1-100*) spores were deep sequenced to find extragenic mutations. Details are in Supplemental Methods.

KINASE AND PHOSPHATASE ASSAYS, RECOVERY AND DROP ASSAY, RAD53 AND H2A PHOSPHORYLATION, FACS

Mec1 kinase assay was performed as described (Hustedt and Shimada, 2014). A recombinant domain of Sgs1 (Sgs1 aa404-604) was used as substrate (Hegnauer et al., 2012). Recovery and drop assays, FACS analysis and Rad53 and H2A phosphorylation reactions were done as described previously (Hustedt and Shimada, 2014). Phosphatase assays are found in Supplemental Methods.

IMMUNOPRECIPITATION (IP)

Anti-GFP IP was carried out as described for kinase assays, except that the lysis buffer was supplemented with protease and phosphatase inhibitors (Complete protease inhibitors (Roche), 1mM phenylmethylsulfonyl fluoride, PhosSTOP phosphatase inhibitors (Roche), 0.1 mM Na_3VO_4, 1 mM NaF and 10 mM NaPP) and bead-bound protein complexes were washed three times with lysis buffer prior elution with 0.2 M glycine. Eluates were neutralized with Tris-HCl and analysed by Western blotting. Immunoprecipitation for mammalian cells was essentially performed the same, except that cells were harvested 48h post transfection by scraping off the plate into PBS, and washed once in PBS before snap-freezing pellets in liquid nitrogen. A modified lysis buffer (50 mM HEPES pH 8.0, 150 mM NaCl, 1 mM $MgCl_2$ and 0.5% NP-40) supplemented with protease and phosphatase inhibitors was used for nuclease treatment. Cleared lysates were incubated with 5 µl RNAseA (Sigma) and 5 µl benzonase (Invitrogen) for 30 min on ice prior to immunoprecipitation. After 1h incubation at 4°C

with antibody-coupled beads, lysates were recovered, DNA was isolated by phenol/chloroform extraction and analyzed by agarose gel electrophoresis and SYBR SAFE (Invitrogen) staining. Bead-bound protein complexes were analyzed as described above.

AUTHOR CONTRIBUTIONS

NH planned and performed most experiments, evaluated results, made all figures and wrote the paper, AS planned, performed and evaluated the FRET studies, KS supervised NH, performed experiments and helped in interpretations, RS performed all mass spectroscopy analyses, MT performed β-galactosidase assays, BB performed genome-wide sequencing of yeast mutants, HV and FvL supervised and hosted NH for the EMAP analysis, AG and HvA provided strains and know-how for the EMAP analysis, TI and RS helped analyse the EMAP results and SMG supervised NH and KS; evaluated and planned experiments, and helped write the paper.

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SUPPLEMENTAL MATERIAL TO CHAPTER 2

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Antibodies for Western blotting

Antibodies used were: Monoclonal α-Rad53 antibody (custom made by Genscript), goat αMcm2 antibody (Santa Cruz) and rabbit αH2A phospho-serine 129 antibody (custom made by Sigma Genosys), mouse α-GFP (Roche), rabbit α-GFP, (Invitrogen), rabbit α-MYC (Santa Cruz), rabbit α-Rfa1 (Agrisera), rabbit α-PK (Novus Biologicals), rabbit α-Mec1 (custom made by SDIX), rabbit α Mec1 phospho-serine 1991 (custom made by Genscript), rat α-HA (Roche), rabbit α–lexA (Santa Cruz)

Sequencing of extragenic suppressors

Genomic DNA was isolated using Qiagen Genomic Tip100 (Qiagen) or phenol chorloform extraction and NucleoSpin PCR clean-up kit (Macherey-Nagel) in case of GA-6610 and quantified using a Nanodrop 3000 (Thermo Scientific) PicoGreen Assay. 50 ng of each individual sample were processed for library generation using Illumina's Nextera DNA sample preparation protocol, and barcoded as described for Illumina's TruSeq Dual Index Sequencing primers (Illumina). The samples were pooled at equimolar concentrations and sequenced using a single-end 75-base reads (50-base reads for GA-6610) on the Illumina's HiSeq2000 platform. The sequence data had >95% alignment, using BWA, to a reference S288C genome (genome build S288C_reference_genome_R62-1-1_20090218, obtained from Saccharomyces Genome Database, www.yeastgenome.org). A sequence of progenitor strains used in the experiment was done for *mec1-100* (GA-4978 and GA-6336) and *mec1-100 exo1*Δ (GA-6356 and GA-6335). By comparison to the progenitor strain sequence, the SNP and indel calls were made in the sequence of the various derived sub-strains. In addition, large regions (>0.1 Megabase) of chromosome amplifications and deletions were assessed in each strain by comparison across all of the strains using read depth information.

High throughput genetic interaction screening

All query strains and the library are described in Table S6. For *mec1-100*, *sgs1-r1* and *rfa1-t11* query strains a NAT resistance cassette was integrated approximately 150 bp downstream of the gene. Subsequently, *mec1-100* and *sgs1-r1* mutations were introduced by pop-in/pop-out (Reid et al., 2002)with linear DNA fragments engineered by PCR using genomic DNA from already mutated strains (Hegnauer et al., 2012; Paciotti et al., 2001) as a template. *rfa1-t11* was created by transforming NheI-linearized plasmid #2221.

Double mutants of query strains and library strains were created as described (Hegnauer et al., 2012). Colony sizes were quantified using HT Colony Grid Analyzer (version 1.1) and genetic interaction scores were computed using the E-MAP toolkit (version 2.0) as previously described (Collins et al., 2006). A stringent QA/QC pipeline was employed to identify and remove (i) strains with a high error of measurement, and (ii) incorrectly deleted strains as identified through linkage analysis (Collins et al., 2010; Collins et al., 2006). In addition, all 1525 array mutants were pooled, genomic DNA extracted, and finally hybridized to a microarray containing probes covering tag sequences from the yeast deletion collection as described (Hegnauer et al., 2012). Strains with an intensity of <800 arbitrary fluorescent units were excluded from further analysis. In total, 214 array strains were dropped for further analysis. This included *ufo1*Δ, for which a genetic interaction with *mec1-100* could not be confirmed despite recreating the mutation.

Mec1 phosphorylation

Immunoprecipitation to map phosphorylation sites in Ddc2-Mec1 was carried out starting from 1 liter cultures treated with 0.2M HU for 1h. Cells were harvested and washed once with PBS. Pellets were weighed, resuspended in 1ml /g PBS and dropped into liquid nitrogen. Droplets were subjected to three rounds of bead-milling using Mixer Mill MM 400 (Retsch). The frozen cell powder was resuspended in an equal volume of cold lysis buffer and IP was performed as described above in Experimental Procedures.

Eluted protein samples were treated with trypsin overnight at 37 °C after reduction and alkylation with tris(2-carboxyethyl)phosphine (TCEP) and iodoacetic acedic acid. The TFA acidified tryptic peptides (final concentration 0.1%) were separated on an Agilent 1100 nanoLC system (Agilent Technologies) coupled to an LTQ Orbitrap Velos hybrid mass spectrometer (Thermo Scientific). The LC system was equipped with a Peptide CapTrap column (Michrom BioResources, Inc.) and a capillary column with integrated nanospray tip (75 µm i.d. x 100 mm, Swiss BioAnalytics AG) filled with MagicC18 (5 µm, Michrom Bioresources, Inc.). Elution was performed with a gradient starting with 2% solvent B and continued with 2 to 10% solvent B in 3 min and 10 to 40% solvent B in 80 min at a flow rate of 400 nL/ min. Solvent A consisted of 0.1% formic acid/ 2% acetonitrile, solvent B was composed of 0.1% formic acid/ 80% acetonitrile. The mass spectrometer operated in positive mode using the top 15 DDA method. MS scans were acquired at a resolution of 60, 000 over a range of m/z 350 to 1200. Singly charged ions were rejected from MSMS fragmentation. Peptides were identified searching SwissProt (version 2011-08) using Mascot Distiller 2.3 and Mascot 2.3.0.2 (Matrix Science) considering acetylation at protein N-terms, deamidation at asparagine and glutamine, oxidation at methionine and phosphorylation at serine as well as at threonine. Two missed cleavage sites were allowed. Results were compiled in Scaffold 3.0 (Proteome Software).

Microscopy

Fluorescence microscopy used an Olympus IX81 microscope equiped with a Yokogawa CSU-X1 scan head, a Evolve 512 Delta EMCCD camera, a ASI MS-2000 Z-piezo stage and a PlanApo x1000 NA 1.45 total internal fluorescence microscope oil objective. Cells where grown from an overnight culture in synthetic complete media complemented with all amino acids until they reached approximately 5 x 10^6 cells/ml. They were treated for 1 hour + 400 µg/ml zeocin, + 0.2 M HU or left untreated. Cells where then fixed in 4% PFA for 30 seconds washed three times with PBS and finally resuspended in PBS. Images were acquired on 2% agarose pads. The lasers used to excite the different fluorophores are as follows: 445 nm for CFP (eCFP), 491 nm for GFP and 561 nm for RFP.

For foci number quantification 4 color Z-stacks were obtained taking 20 slices at 200 nm intervals. Exposure times were: 50 ms GFP, 100 ms CFP, 150 ms RFP, 10 ms brightfield. The EMCCD gain was set to approximately 600 in all cases except for the brightfield where it was set to 50. Images were deconvolved using Huygens Remote Manager v3.0.3. The deconvolution algorithm used was classic maximum likelihood estimate with a signal/noise ratio of 5, automatic background estimation and 30 iterations. “Bright foci” were counted and defined as foci that have clear borders. Thresholding was applied to help see foci over background nuclear signal and done with Fiji. We note that in the case of Ddc2 many smaller less bright foci were present.

For colocalization analysis single slice 4 channel images were acquired and processed as above except the exposure of CFP was increased to 150 ms and RFP to 250 ms. CFP, GFP and RFP were channel aligned using Huygens Pro software. Colocalization was scored when foci either completely overlapped or partially overlapped.

For FRET, the donor GFP was excited by light at 488 nm and the emission signals are collected using filters that allow selective detection of either donor or acceptor signals. Fluorescence bleed-through of the donor signal into the acceptor channel, or the reverse, is quantified by imaging strains that contain only donor or acceptor proteins. Automated subtraction of bleed-through signal, yields the significant FRET value.

Sensitized emission FRET images for each series where acquired on the same day. Four channel images were acquired: GFP channel, FRET channel, RFP channel as well as brightfield, even for donor only (GFP) and acceptor only strains. FRET was calculated using the PixFRET Fiji plugin (Feige et al., 2005). Spectral bleed through was calculated on using donor only (*DDC2-GFP* (GA-7268), *PSY2-GFP* (GA-8033), *RFA2-GFP* (GA-6022)) and acceptor only strains (*PSY2-RFP* (GA-8659), *RFA1-RFP*(GA-8687)). The PixFRET parameters used where 1.0 Gaussian blur, 1.0 Threshold and Output of FRET/sqrt(Donor*Acceptor). The donor only and acceptor only parameters for PixFRET are as follows and were acquired by a montage of 10 donor only or 10 acceptor only images: Ddc2-GFP, a = 2.328, b = 0.00047, linear; Psy2-RFP, a = 0.48385, -b = 0.00004 linear; rfa1-RFP, a= 1.27947, b = -0.00011, linear; Psy2-GFP, a = 0.03595, constant; Rfa2-GFP, a = 0.31318, constant. FRET values were calculated from the mean intensity of the NFRET image of each focus.

Phosphoproteomics

Cells were grown in synthetic medium. 50 ml cultures were grown to an OD_{600}=0.75, arrested in G1 using α-factor, and released into 75 ml synthetic medium containing 0.2M HU until the appearance of small buds (45 min). Proteins were extracted as previously described (Bodenmiller and Aebersold). In brief, proteins were denatured and precipitated by adding a final 6% trichloracetic acid to the cultures and incubating on ice for 30 min. Precipitates were collected by centrifugation and washed three times with ice-cold acetone. Pellets were resuspended in 800 µl urea buffer (8M Urea, 50 mM ammonium bicarbonate, 5 mM EDTA and PhosSTOP phosphatase inhibitors (Roche)) and a corresponding volume of silica beads was added. Extracts were prepared by five round of bead beating. Supernatant was collected, another 800 µl urea buffer added to beads followed by five rounds of bead beating and pooling of supernatants.

Peptide generation and phosphopeptide enrichment

Extracts in 8 M urea, 50 mM ammonium bicarbonate, and 5 mM EDTA had a protein concentration of about 5.2 mg/ mL. 150 µL 200 mM HEPES were added to 1.5 mL of each of the twelve extracts. Reduction and alkylation of cysteines were performed by adding of 160 µL 45 mM DTT for 30 min followed by adding of 180 µL 100 mM iodoacetamide for another 30 min (in the dark), both at room temperature. Before adding of 20 µL 1 mg/ mL LysC (Wako, Japan) the extracts were twofold diluted to keep a final HEPES concentration of 20 mM. First digest was performed overnight at 25 °C. After further twofold diluting of the extracts 100 µL of 0.5 mg/ mL trypsin were added and the second digest was performed at 37 °C overnight. Before phosphopeptide enrichment the digests were desalted using SepPak C18 columns (Waters). The eluates were dried down in a SpeedVac (Thermo Scientific).

The digests were reconstituted in 150 µL 2.5% triflouroacetic acid (TFA)/ 80% acetonitrile, saturated with phthalic acid and 30 min incubated with 1.5 mg TiO2 beads (Inertsil Titansphere 5µm, GL Science, Japan) using Mobitec tubes (MoBiTec, Germany). The beads were thoroughly washed four times with 200 µL 2.5% TFA/ 80% acetonitrile. Phospho-peptides were eluted with 100 µL 0.3 M NH4OH and 100 µL 0.3 M NH4OH/ 30% acetonitrile. The pH of the eluates was lowered to about 3 by adding 4 µL TFA before drying down in a SpeedVac. The final desalting step was performed on Oligo R3 media (Life technologies) immobilized on C18 GELoader pipette tips (Proxeon).

LC/MS/MS analyses of enriched phosphopeptides

The LC/MS/MS analyses were performed on an Easy-nLC 1000 pump coupled to an LTQ Orbitrap Velos mass spectrometer (Thermo Scientific) using a Digital PicoView ion source (New Objective). The peptides were separated on a New Objective analytical column (75 µm x 25 cm, Reprosil, 3 µm) with a gradient from 2 to 30% solvent B in 110 min, 30 to 50% solvent B in 30 min and 50 to 80% solvent B in 5 min. Solvent A consisted of 0.1% formic acid in water, solvent B of 0.1% formic acid in acetonitrile. The flow rate was 200 nL/ min. The dried TiO2 eluates were dissolved in 40 µL 0.1% TFA/ 2% acetonitrile and the peptide concentrations determined with a Qubit fluorometer and the Qubit protein assay kit (Life technologies). The injection volumes were adapted accordingly for 1 µg peptides on column.

Data were acquired in a Top25 data dependent analysis mode using three different charge (z) rejection settings: positive charged ions are considered for MSMS scans with either $z > 1$, $z = 2$ or with $z > 2$. A different charge selection mode was deployed for each of the replicates. MS scans were acquired at a resolution of 60, 000 over a range of m/z 350 to 1200.

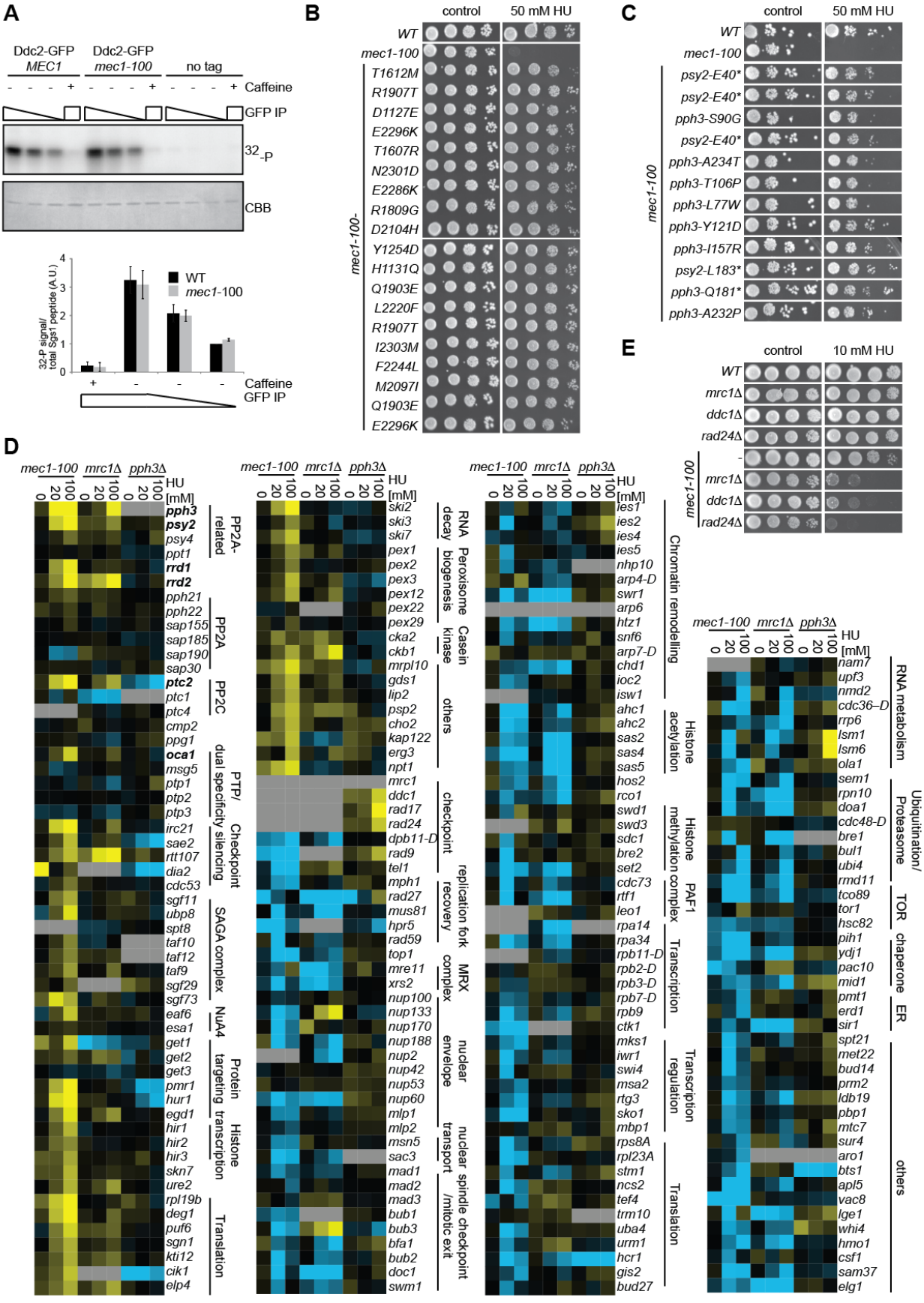
Data evaluation with Progenesis-LC

The twelve raw files were loaded into Progenesis-LC and automatically aligned. The alignments were manually corrected were needed. Finally, the alignment scores were 82.5% and better. Features with two charges and more than two isotopes, features with three to six charges having more than three isotopes and spectra with a limit fragment count of 150 were considered for a database search using MASCOT 2.3. Peptides were identified searching the Saccharomyces Genome Database (SGD), version Sept. 2011) considering the following settings: Carbamidomethylation at cysteines as fixed modifixcation, deamidation at asparagine and glutamine, oxidation at methionine, acetylation at the protein N-terms and phosphorylation at serine as well as at threonine as variable modifications, two missed cleavage sites, a peptide mass tolerance of 7 ppm and a fragment mass tolerance of 0.6 Da, trypsin as enzyme, allowing the cleavage after arginine and lysine also if followed by a proline. Finally, in Progenesis-LC features were kept if they had a MASCOT ion score greater than 15 and were identified as phosphopeptides without any other modifications except acetylation at protein N-terminals. The normalization was performed considering only those phosphopeptides. The final feature data list was exported into Excel. Ratios “mutant versus wild type” were calculated from the average of the normalized abundances of the three replicates and the probability of a Student’s t-test was determined accordingly. Only phosphopeptides with a probability of 0.95 were considered for further evaluation. All SQ/ TQ containing peptides were checked for the phosphosite probability with MaxQuant (version 1.4.1.2, (Cox and Mann, 2008)) and Proteome Discoverer (version 1.4.1.14, Thermo Fisher Scientific) and kept only, if the site probability was higher than 75% in any of the two programs.

Phosphatase Assay

1L of late-log phase WT cells (GA-1981) or *PSY2-HALO* (GA-8179) cells were harvested and washed once with PBS. Pellets were weighed, resuspended in 1ml /g buffer 1 without NP-40 (50 mM Hepes pH7.5, 150 mM NaCl, 2mM EDTA) and dropped into liquid nitrogen. Droplets were subjected to three rounds of bead-milling using Mixer Mill MM 400 (Retsch). The frozen cell powder was resuspended in an equal volume of cold buffer 2 (50 mM Hepes pH7.5, 150 mM NaCl, 1mM DTT, 0.01% NP-40, and protease inhibitors: 1 mM PMSF, 300 µg/mL benzamidine, 1 µg/mL pepstatin, 0.5 µg/mL leupeptin, 40µg/mL bestatin, 2µM E64 and 50 µg/mL TLCK), and cleared by centrifugation. HALO-link resin (Promega) was washed five times with buffer 2, 1ml resin was added to 7 mL cleared lysates and incubated at 4°C overnight. Resin-bound protein complexes were washed once

with buffer 3 (buffer 2 + 1mM EDTA), four times with buffer 3 lacking protease inhibitors and 2 times with phosphatase buffer (25mM Tris pH7.5, 100 mM NaCl, 0.1 mM EDTA, 1 mM DTT, 0.01% Brij-35). Resin-bound protein complexes were finally resuspended in 250 µl Phosphatase buffer + TEV protease and incubated at 4°C overnight. Eluates were separated from resin by centrifuging through micro spin columns (Biorad). 35 µL of eluates were incubated with 10 µM of peptide (positive control: RRA(pT)VA (provided with Assay kit), Cdc13-p: Biotin-GGGKSYIQ(pS)QTPERK-amide, Cdc13: Biotin-GGGKSYIQSQTPERK-amide (both gifts from D. Durocher), Mec1-p: VK(pS)ITSRSGKSLEKC and Mec1: VKSITSRSGKSLEKC (both synthesized by Genscript)) in phosphatase buffer. Reactions also contained a final 5 mM manganese chloride. Release of phosphate was measured using a colorimetric Ser/Thr phosphatase assay kit (Promega). Phosphate leads to the proportional accumulation of a green dye, measured quantitatively as light absorption at 600 nm.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R1907T
D1127E
E2296K
T1607R
N2301D
E2286K
R1809G
D2104H
Y1254D
H1131Q
Q1903E
L2220F
R1907T
I2303M
F2244L
M2097I
Q1903E
E2296K
C
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WT
mec1-100
mec1-100
psy2-E40*
psy2-E40*
pph3-S90G
psy2-E40*
pph3-A234T
pph3-T106P
pph3-L77W
pph3-Y121D
pph3-I157R
psy2-L183*
pph3-Q181*
pph3-A232P
E
control
10 mM HU
WT
mrc1Δ
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rad24Δ
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psy2
psy4
ppt1
rrd1
rrd2
pph21
pph22
sap155
sap185
sap190
sap30
ptc2
ptc1
ptc4
cmp2
ppg1
oca1
msg5
ptp1
ptp2
ptp3
irc21
sae2
rtt107
dia2
cdc53
sgf11
ubp8
spt8
taf10
taf12
taf9
sgf29
sgf73
eaf6
esa1
get1
get2
get3
pmr1
hur1
egd1
hir1
hir2
hir3
skn7
ure2
rpl19b
deg1
puf6
sgn1
kti12
cik1
elp4
PP2A-related
PP2A
PP2C
PTP/dual specificity
Checkpoint silencing
SAGA complex
NuA4
Protein targeting
Histone transcription
Translation
ski2
ski3
ski7
pex1
pex2
pex3
pex12
pex22
pex29
cka2
ckb1
mrpl10
gds1
lip2
psp2
cho2
kap122
erg3
npt1
mrc1
ddc1
rad17
rad24
dpb11-D
rad9
tel1
mph1
rad27
mus81
hpr5
rad59
top1
mre11
xrs2
nup100
nup133
nup170
nup188
nup2
nup42
nup53
nup60
mlp1
mlp2
msn5
sac3
mad1
mad2
mad3
bub1
bub3
bfa1
bub2
doc1
swm1
RNA decay
Peroxisome biogenesis
Casein kinase
others
checkpoint
replication fork recovery
MRX complex
nuclear envelope
nuclear transport
spindle checkpoint /mitotic exit
ies1
ies2
ies4
ies5
nhp10
arp4-D
swr1
arp6
htz1
snf6
arp7-D
chd1
ioc2
isw1
ahc1
ahc2
sas2
sas4
sas5
hos2
rco1
swd1
swd3
sdc1
bre2
set2
cdc73
rtf1
leo1
rpa14
rpa34
rpb11-D
rpb2-D
rpb3-D
rpb7-D
rpb9
ctk1
mks1
iwr1
swi4
msa2
rtg3
sko1
mbp1
rps8A
rpl23A
stm1
ncs2
tef4
trm10
uba4
urm1
hcr1
gis2
bud27
Chromatin remodelling
Histone acetylation
Histone methylation
PAF1 complex
Transcription
Transcription regulation
Translation
nam7
upf3
nmd2
cdc36–D
rrp6
lsm1
lsm6
ola1
sem1
rpn10
doa1
cdc48-D
bre1
bul1
ubi4
rmd11
tco89
tor1
hsc82
pih1
ydj1
pac10
mid1
pmt1
erd1
sir1
spt21
met22
bud14
prm2
ldb19
pbp1
mtc7
sur4
aro1
bts1
apl5
vac8
lge1
whi4
hmo1
csf1
sam37
elg1
RNA metabolism
Ubiquitination/ Proteasome
TOR
chaperone
ER
others

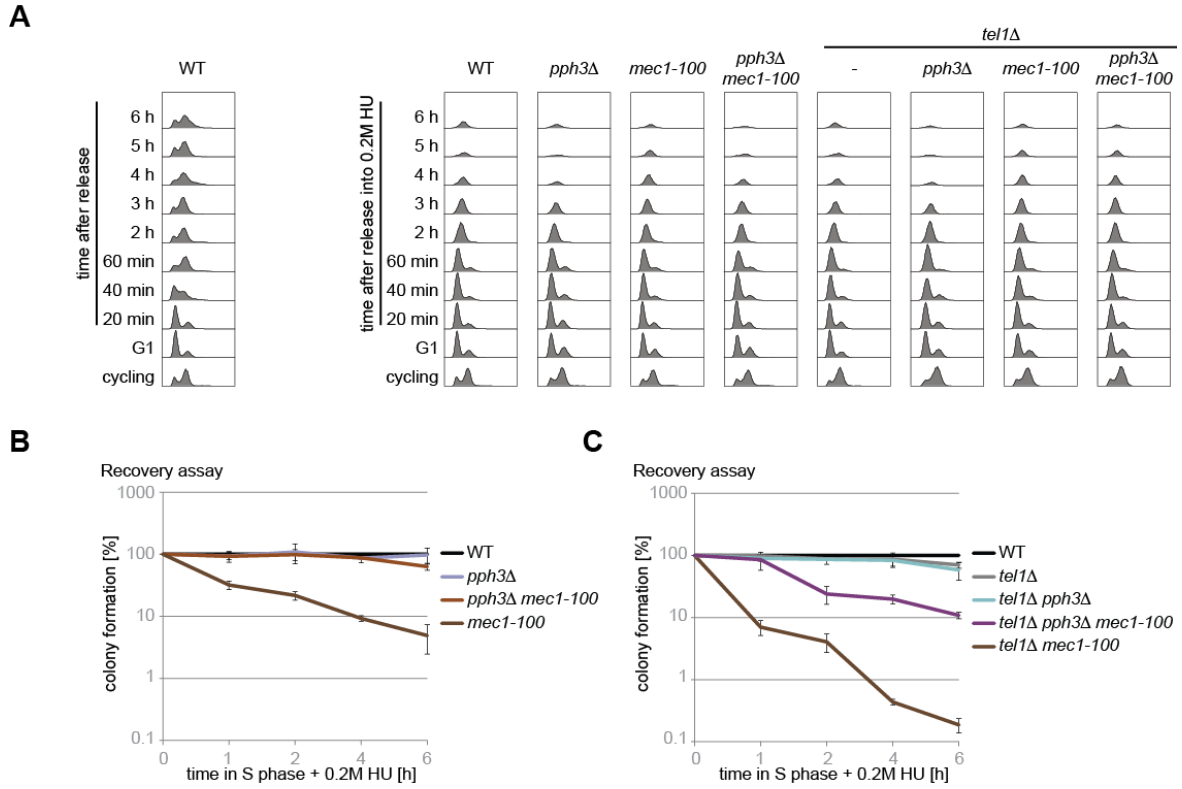

Figure S2.2: *pph3*Δ suppresses *mec1-100* recovery defects after HU treatment at early timepoints; related to Figure 2-2 (A) DNA content was monitored by FACS analysis after synchronization in G1 by α-factor arrest and release into S phase ± 0.2 M HU for the indicated times. Isogenic strains used were: GA-1981, GA-6582, GA-7049, GA-7086, GA-6912, GA-6913, GA-7953 and GA-7955. **(B)** Recovery from replication fork stalling was monitored as colony outgrowth of cells after synchronization in G1 by α-factor arrest and release into S phase with 0.2 M HU for the indicated times. Isogenic strains used were GA-1981, GA-6582, GA-7049 and GA-7086. Error bars indicate standard deviation. **(C)** Cells were treated as in (B). Isogenic strains used were GA-1981, GA-6912, GA-6913, GA-7953 and GA-7955. Relevant genotypes are indicated in the figure and listed in Table S2.5.

Figure S2.1: The mec1-100/Ddc2 kinase shows robust activity, yet genetic interactions implicate its deficiency in replication checkpoint and fork recovery; related to Figure 2.1. (A) Kinase assay using α-GFP IP from *DDC2-GFP* (GA-7268), *DDC2-GFP mec1-100* (GA-7327) or WT (GA-1981) cell extracts. An Sgs1 peptide (aa 404–604, Hegnauer et al., 2010) was used as a substrate in the presence of γ-32P-ATP and was analysed by gel electrophoresis and autoradiography. Where indicated, 30mM caffeine was added to inhibit Mec1. ^{32}P autoradiography and Coomassie Brilliant Blue (CBB) staining are shown. Lower panel shows quantification of ^{32}P signal over CBB signal. Error bars indicate standard deviation of three independent experiments. **(B)** Drop assay of intragenic suppressors. Serial ten-fold dilutions of cultures were plated on YPAD ± 50 mM HU. Relevant genotypes are indicated in the figure. Isogenic strains used were: GA-1981, GA-6583, GA-6769, GA-6410, GA-6412, GA-6416, GA-6418, GA-6422, GA-6466, GA-6468, GA-6470, GA-6472, GA-6480, GA-6510, GA-6514, GA-6518, GA-6522, GA-6529, GA-6533, GA-6537 and GA-6539. **(C)** Drop assay of extragenic suppressors. Cells were treated as in (B). Isogenic strains used were: GA-1981, GA-6583, GA-6575, GA-6596, GA-6577, GA-6598, GA-6600, GA-6601, GA-6603, GA-6605, GA-6606, GA-6610, GA-6608 and GA-6572. Genotypes indicted in figure and in Table S2.5. **(D)** Genetic interactions with *mec1-100* (genetic interaction score ≤-2 or ≥+2) are shown. Interactions of *mec1-100* with mutants of other phosphatase classes. Mutations of additional subunits of multisubunit complexes were included. Interactions of *mrc1*Δ and *pph3*Δ with the same mutants are shown for comparison. **(E)** Serial ten-fold dilutions of cultures were plated on YPAD ± 10 mM HU. Relevant genotypes are indicated in the figure and in Table S2.5. Isogenic strains used were: GA-1981, GA-6826, GA-7907, GA-5321, GA-6582, GA-7964 and GA-7209.

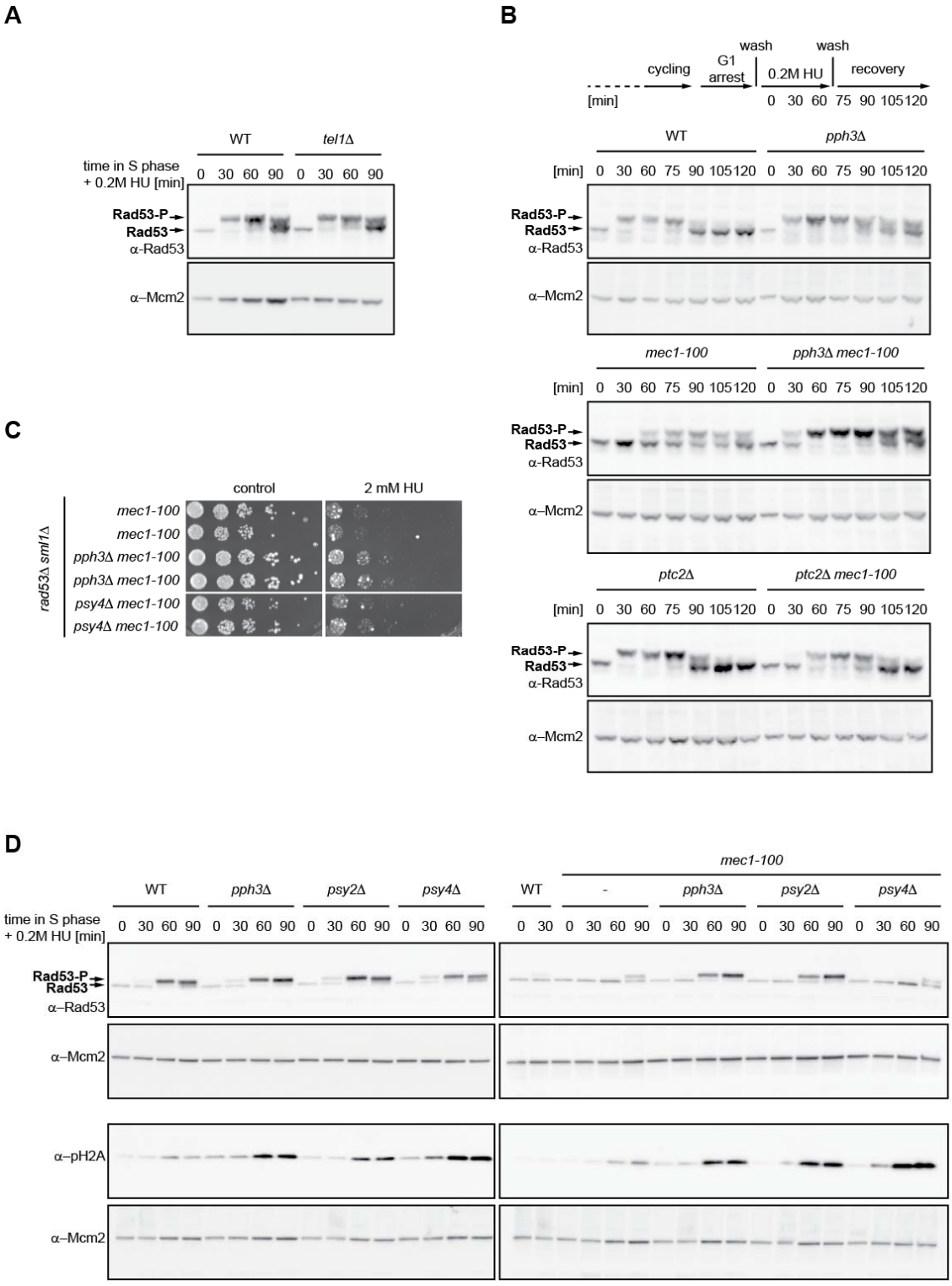

Figure S2.3: Psy4 dephosphorylates H2A, but does not suppress *mec1-100* HU sensitivity; related to Figure 2.3. (A) Rad53 activation was monitored in WT (GA-1981) and *tel1*Δ (GA-6912) cells. Cells were synchronized in G1 by α-factor arrest and released for indicated times into 0.2 M HU before denatured extract preparation and Western blot analysis. **(B)** Cells were treated as in (A) except that HU was washed out after 60 minutes. Samples were taken at indicated timepoints and analysed for Rad53 phosphorylation. **(C)** Serial five-fold dilutions of *rad53*Δ *sml1*Δ *mec1-100* (GA-7401), *rad53*Δ, *sml1*Δ *mec1-100 pph3*Δ (GA-7377), *rad53*Δ *sml1*Δ *mec1-100 psy4*Δ (GA-8581) cultures (2 colonies each) were plated on YPAD ± 2 mM HU. **(D)** Rad53 and H2A serine 129 phosphorylation was monitored by treating cells as in (A) and blotting with indicated antibodies. Isogenic strains used GA-1981, GA-7049, GA-7391, GA-7383, GA-6582, GA-7086, GA-7393 and GA-7385 cells. Relevant genotypes are indicated in the figure and are listed in Table S2.5.

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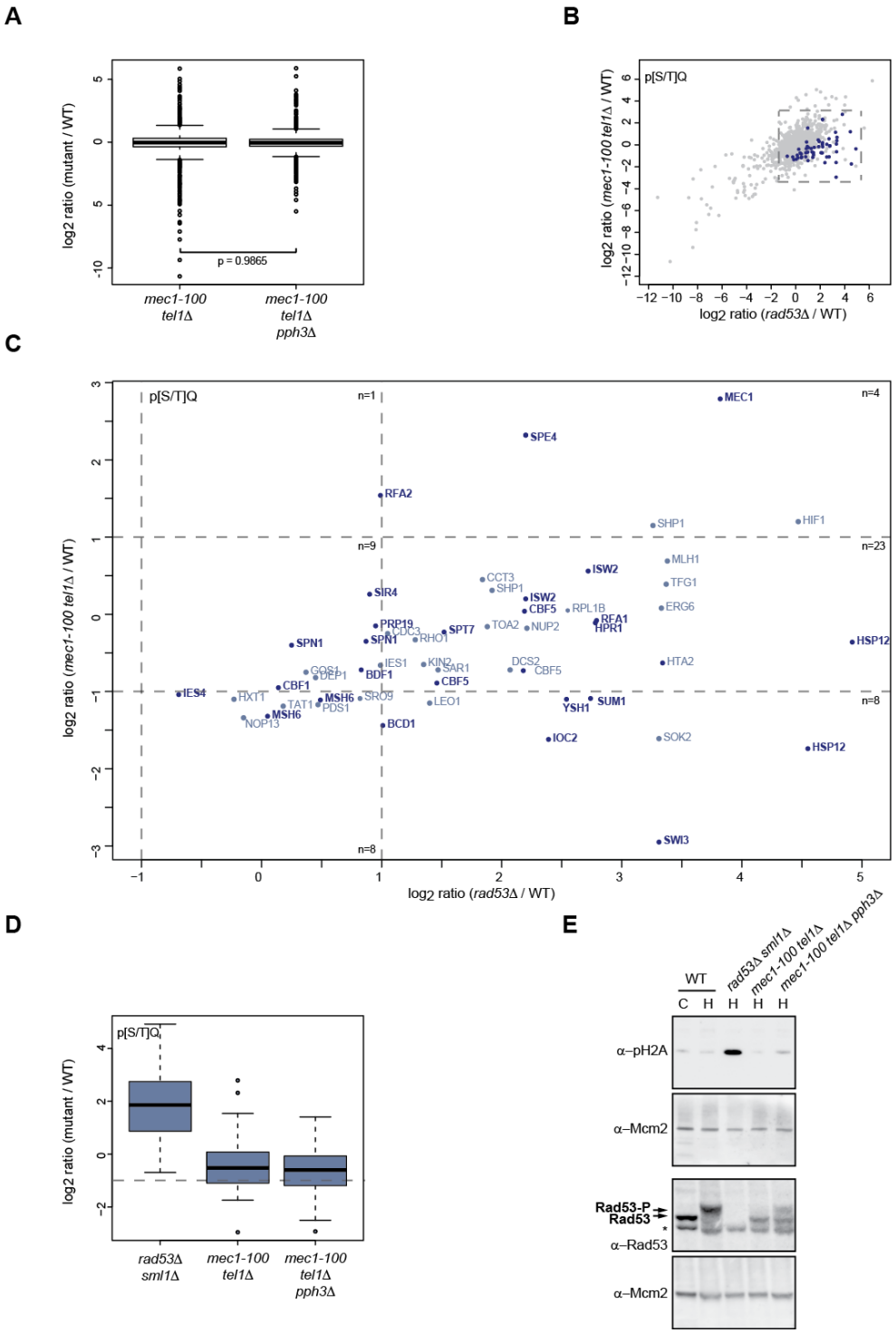


Figure S2.4: Most S/TQ phosphopeptides are not reduced in *mec1-100* cells on HU; related to Figure 2.4. **(A)** Boxplot of indicated abundance ratios of all quantified phosphopeptides. P-value was calculated by one-tailed Wilcoxon signed rank test**. (B)** Abundances (log2 ratio (mutant/WT)) of all quantified phosphopeptides in *mec1-100 tel1*Δ cells were plotted against abundances in *rad53*Δ *sml1*Δ. Blue marked peptides are phosphorylated on [pS/pT]Q consenses and are (1) mec1-100/tel1-specific (see Figure 4) and/or (2) were at least two-fold more abundant in *rad53*Δ compared to *mec1-100 tel1*Δ samples ($\log_2$ ratio ≥ 1, p≤0.05, Student's paired t-test) regardless of the levels in WT sample and/or (3) were previously described as Mec1/Tel1-dependent (Chen et al., 2010) (full list in Table S4). Dotted lines indicate area enlarged in (D). **(C)** Enlarged area of plot shown in (B). Displayed are selected phosphopeptides marked blue in (B). Labels indicated protein names. Bold: phosphopeptides previously described as Mec1/Tel1 specific (Chen et al., 2010). Dotted lines indicate thresholds for up/downregulation. n= number of phosphopeptides that fall between dotted lines. **(D)** Boxplot of indicated ratios of phosphopeptides that match the [pS/pT]Q consensus and were marked blue in (B). **(E)** Samples taken before synchronization (C) and prior protein extraction (H) (Fig. 2.4B) were analyzed by Western blotting with indicated antibodies

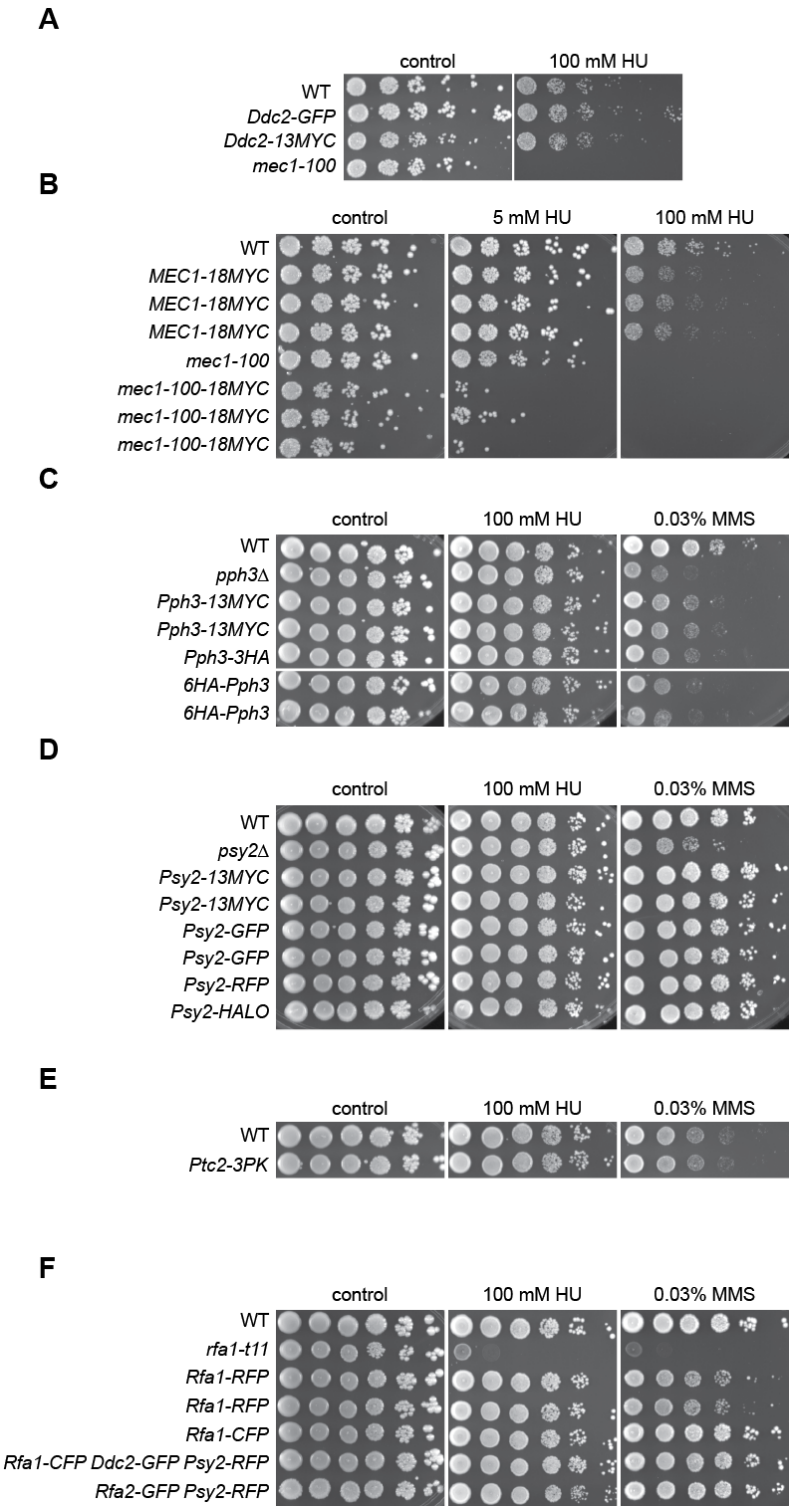


Figure S2.5. Functionality of tagged strains used in this study; Related to Figure 2.5. (A) Serial 5-fold dilutions of cultures were plated on YPAD ± 100 mM HU. Relevant genotypes are indicated in the figure. Strains used were GA-1981, GA-7268, GA-7337 and GA-6582. **(B)** Serial 5-fold dilutions of cultures were plated on YPAD, YPAD + 5 mM HU and YPAD + 100 mM HU. Strains used were GA-1981, GA-7353, GA-7354, GA-7355, GA-6582, GA-7366, GA-7367 and GA7368. **(C)** Serial ten-fold dilutions of cultures were plated on YPAD, YPAD + 100 mM HU and YPAD + 0.03% methyl methanesulfonate (MMS). Strains used were GA-1981, GA-7049, GA-7852, GA-7853, GA-7865, GA-7966 and GA-7967. **(D)** Cells were treated as in (C). Strains used were GA-1981, GA-7391, GA-7798, GA-7799, GA-8033, GA-8021, GA-8659 and GA-8179 **(E)** Cells were treated as in (C). Strains used were GA-1981 and GA-7923. **(F)** Cells were treated as in (C). Strains used were GA-1981, GA-8396, GA-8687, GA-8688, GA-8694, GA-8695 and GA-8676. Relevant genotypes are indicated and are listed in Table S2.5.

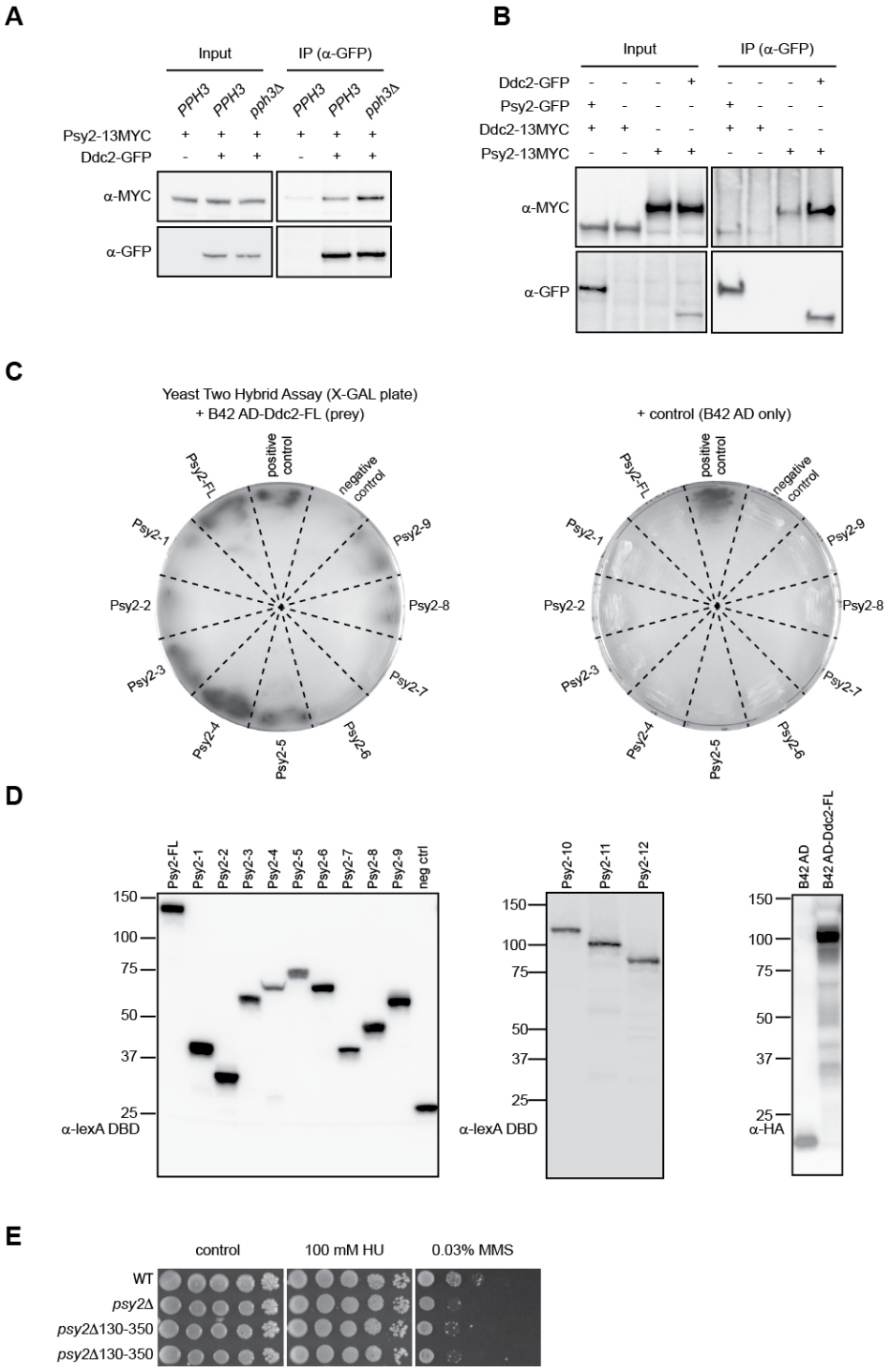


Figure S2.6. Ddc2-GFP and Psy2-MYC interaction does not require Pph3, and is detected when tags are swapped and in Y2H experiments; Related to Figure 2.5. (A) Native extracts were prepared from cycling *Psy2-13MYC* (GA-7798), *Psy2-13MYC DDC2-GFP* (GA-7824) and *Psy2-13MYC DDC2-GFP pph3*Δ (GA-7939) cells, subjected to IP with anti-GFP and analysis by blotting with indicated antibodies. **(B)** Cells were treated as in (A). Strains used were *PSY2-13MYC* (GA-7972), PSY2-13MYC DDC2-GFP (GA-7975), DDC2-13MYC (GA-7337) and *DDC2-13MYC PSY2-GFP* (GA-8034). **(C)** Yeast two hybrid (Y2H) analysis between full length Ddc2 fused with the B42 transcription activation domain (B42 AD) and an HA-tag and Psy2 fragments fused with the lexA DNA binding domain (DBD) was performed by observing β-galactosidase expression on X-GAL plates. Negative control: empty lexA-DBD plasmid; positive control: LexA-DBD fused with B42-AD. **(D)** Yeast Two Hybrid construct expression. Cells were grown in 2% raffinose-containing selective medium to ensure plasmid retention and expression was induced with 2% galactose for 4h prior to denatured extract preparation and Western blot analysis with indicated antibodies. **(E)** Serial ten-fold dilution of cultures were plated on YPAD, YPAD + 100 mM HU and YPAD + 0.03% MMS. Isogenic strains used were GA-1981, GA-7391, GA-8821 and GA-8822. Relevant genotypes are indicated and listed in Table S2.5

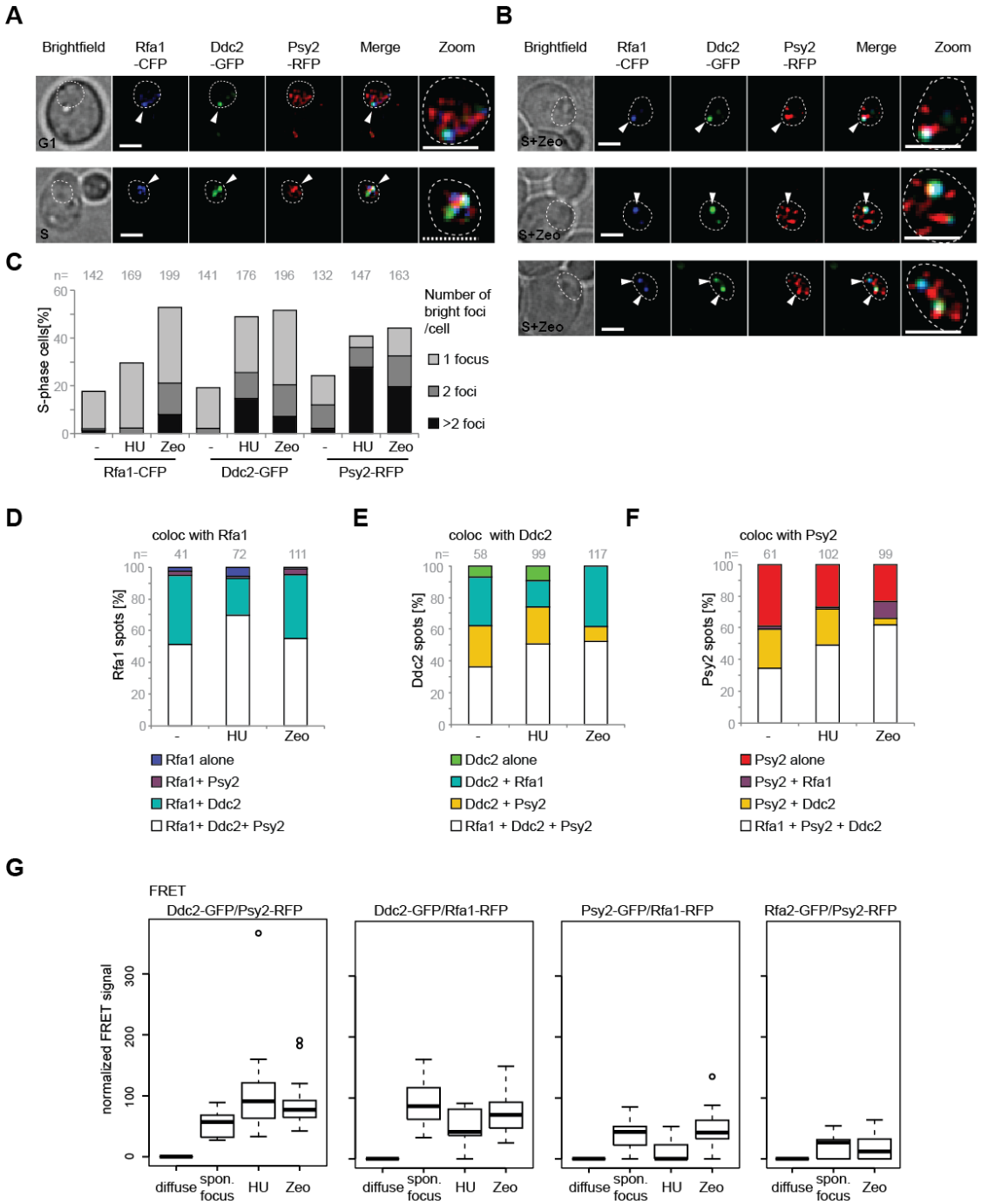
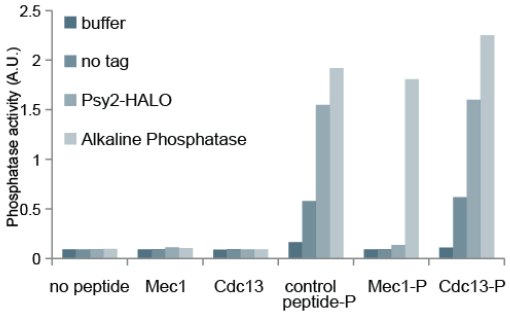


Figure S2.7. Ddc2 and Psy2 colocalize and show FRET at spontaneous and Zeocin induced foci; related to Figure 2.6. (A) Upper panel: Example of a G1-phase cell with a Ddc2/Rfa1 spot. Lower panel: Example of an S-phase cell with a spontaneous Rfa1/Ddc2/Psy2 focus. Strain used bears *RFA1-RFP DDC2-GFP PSY2-RFP* (GA-8695). Arrowheads indicate spots. Scale Bar = 2 µm. White dashed line: outline of cell nucleus. **(B)** Example images of Zeocin-treated cells, which frequently leads to a few bright foci per cell. Upper and middle panel: example in which foci of all three fluorophores colocalize. Lower panel: Example of cell in which Ddc2 and Rfa1 colocalize, with partial colocalization of Rfa1/Ddc2/Psy2 in a second spot. The same strain was used as in (A). Arrowheads indicate foci. **(C)** Cells were treated +/- 0.2 M HU or 400 ug/ml Zeocin for 1h prior to fixation. Bright spots per cell were quantified for S-phase cells. The same strain was used as in (A). **(D)** Cells were treated the same as in (C). Colocalization of Ddc2-GFP and/or Psy2-RFP spots with Rfa1-CFP spots was quantified. The same strain was used as in (A). **(E)** Colocalization of Rfa1-CFP and/or Psy2-RFP spots with Ddc2-GFP spots was quantified in the same experiment as (D). **(F)** Colocalization of Rfa1-CFP and/or Ddc2-GFP spots with Psy2-RFP spots was quantified in the same experiment as (D). **(G)** *DDC2-GFP PSY2-RFP* (GA-8656), *DDC2-GFP RFA1-RFP* (GA-8705), *PSY2-GFP RFA1-RFP* (GA-8702) and *RFA2-GFP PSY2-RFP* (GA-8676) cells were treated with 0.2M HU or 400 ug/ml Zeocin or left untreated for 1 h before fixation. Fixed samples were analyzed for FRET-induced RFP signals at either bright GFP foci ("focus", "HU", "Zeo") or in the nuclear background ("diffuse").

A



B

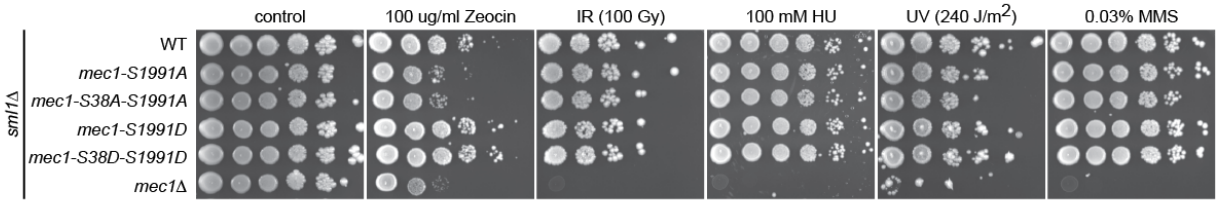


Figure S2.8. Damage sensitivity of the non-phosphorylatable mutant *mec1-S1991A*; related to Figure 2.7. **(A)** Phosphatase Assay to test dephosphorylation of Mec1 serine 1991 and Cdc13 serine 306 by Psy2-Pph3. Psy2-Pph3 was purified from *PSY2-HALO* cells (GA-8179) and WT cells (GA-1981, "no tag") served as a negative control. Purifications were incubated with indicated phosphopeptides for 60 min at 30 °C prior measurement of phosphatase activity by release of phosphate. Results are representative of two independent experiments. **(B)** Serial ten-fold dilutions of cultures were plated on YPAD, YPAD + 100 µg/ml Zeocin, YPAD + 100 mM HU, YPAD + 0.03% MMS and on YPAD plates and subsequently treated with γ-irradiation (100 Gy) or UV light (240 J/m^2). Relevant genotypes are indicated in the figure. Isogenic strains (see Table S2.5) used were: GA-4533, GA-8242, GA-8246, GA-8243, GA-8247 and GA-5286

SUPPLEMENTAL TABLES

Table S2.1: Genetic interaction data

see Appendix

Table S2.2: All quantified phosphopeptides

see Appendix

Table S2.3: Mec1-100 dependent phosphopeptides

see Appendix

Table S2.4: Selected SQ/TQ phosphopeptides

see Appendix

Table S2.6: Query strains and library used for EMAP

see Appendix

Table S2.5: Yeast strains and plasmids used in this study

strain	genotype	source
GA-181	*MATa, ade2-1, trp1-1, his3-11, -15, ura3-1, leu2-3, -112, can1-100 (W303)*	R. Rothstein
GA-338	*MATa, trp1, his3, ura3, leu2::(pLEU2-lexAop6)(EGY48)*	R. Brent
GA-1981	*MATa, ade2-1 ,trp1-1 ,his3-11 , -15, ura3-1, leu2-3, -112, can1-100* (W303), RAD5+	H.L. Klein
GA-1982	*MATα, ade2-1 ,trp1-1 ,his3-11 , -15, ura3-1, leu2-3, -112, can1-100* (W303), RAD5+	H.L. Klein
GA-2529	GA-181 with *mec1::HIS3, sml1::KanMX*	this study
GA-4533	GA-1981 with *sml1::HIS3*	this study
GA-4978	GA-1981 with *mec1-100::LEU2(HIS3)*	(Hegnauer et al., 2012)
GA-5286	GA-1981 with *mec1::TRP1, sml1::HIS3*	this study
GA-5321	GA-1981 with *rad24::TRP1*	(Hegnauer et al., 2012)
GA-5975	GA-1981 with *rad52::TRP1*	this study
GA-6022	*MATa, his3-D1, leu2D0, met15D0, ura3D0, rfa2::RFA2-GFP-HIS3 (BY4741)*	I.Filipuzzi
GA-6635	GA-1982 with *mec1-100::LEU2(HIS3) exo1::kanMX*	this study
GA-6636	GA-1982 with *mec1-100::LEU2(HIS3)*	this study
GA-6356	GA-1981 with *mec1-100::LEU2(HIS3) exo1::kanMX*	this study
GA-6410	GA-1981 with *mec1-100-R1907T::LEU2(HIS3)*	this study
GA-6412	GA-1981 with *mec1-100-D1127E::LEU2(HIS3)*	this study
GA-6416	GA-1981 with *mec1-100-E2296K::LEU2(HIS3)*	this study
GA-6418	GA-1981 with *mec1-100-T1607R::LEU2(HIS3)*	this study
GA-6422	GA-1981 with *mec1-100-N2301D::LEU2(HIS3)*	this study
GA-6466	GA-1981 with *mec1-100-E2286K::LEU2(HIS3)*	this study
GA-6468	GA-1981 with *mec1-100-R1809G::LEU2(HIS3)*	this study
GA-6470	GA-1981 with *mec1-100-D2104H::LEU2(HIS3)*	this study
GA-6472	GA-1981 with *mec1-100-Y1254D::LEU2(HIS3)*	this study
GA-6480	GA-1981 with *mec1-100-H1131Q::LEU2(HIS3)*	this study
GA-6510	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3)*	this study
GA-6514	GA-1981 with *mec1-100-L2220F::LEU2(HIS3)*	this study
GA-6518	GA-1981 with *mec1-100-R1907T::LEU2(HIS3)*	this study
GA-6522	GA-1981 with *mec1-100-I2303M::LEU2(HIS3)*	this study
GA-6529	GA-1981 with *mec1-100-F2244L::LEU2(HIS3)*	this study
GA-6533	GA-1981 with *mec1-100-M2097I::LEU2(HIS3)*	this study
GA-6537	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3)*	this study
GA-6539	GA-1981 with *mec1-100-E2296K::LEU2(HIS3)*	this study
GA-6572	GA-1981 with *mec1-100::LEU2(HIS3), pph3-A232P*	this study
GA-6575	GA-1981 with *mec1-100::LEU2(HIS3), psy2-E40**	this study
GA-6577	GA-1981 with *mec1-100::LEU2(HIS3), psy2-E40**	this study
GA-6582	GA-1981 with *mec1-100::natMX*	this study
GA-6583	GA-1982 with *mec1-100::natMX*	this study
GA-6596	GA-1981 with *mec1-100::LEU2(HIS3), psy2-E40**	this study
GA-6598	GA-1981 with *mec1-100::LEU2(HIS3), pph3-S90G*	this study
GA-6600	GA-1981 with *mec1-100::LEU2(HIS3), pph3-A234T*	this study
GA-6601	GA-1981 with *mec1-100::LEU2(HIS3), pph3-T106P*	this study
GA-6603	GA-1981 with *mec1-100::LEU2(HIS3), pph3-L77W*	this study
GA-6605	GA-1981 with *mec1-100::LEU2(HIS3), pph3-Y121D*	this study
GA-6606	GA-1981 with *mec1-100::LEU2(HIS3), pph3-I157R*	this study
GA-6608	GA-1981 with *mec1-100::LEU2(HIS3), pph3-Q181**	this study
GA-6610	GA-1981 with *mec1-100::LEU2(HIS3), psy2-L183**	this study
GA-6769	GA-1981 with *mec1-100-T1612M::LEU2(HIS3)*	this study
GA-6826	GA-1981 with *mrc1::TRP1*	this study
GA-6828	GA-1981 with *mec1-100::natMX, mrc1::TRP1*	this study
GA-6912	GA-1981 with *tel1::URA3*	this study
GA-6913	GA-1981 with *tel1::URA3, mec1-100::natMX*	this study
GA-7049	GA-1981 with *pph3::HIS3*	this study
GA-7086	GA-1981 with *mec1-100::natMX, pph3::HIS3*	this study
GA-7209	GA-1981 with *mec1-100::natMX, rad24::TRP1*	this study
GA-7268	GA-1981 with *ddc2::DDC2-GFP-kanMX*	this study
GA-7273	GA-1981 with *ptc2::URA3*	this study
GA-7276	GA-1981 with *ptc3::HIS3, mec1-100::natMX*	this study
GA-7294	GA-1981 with *pph3::kanMX, sml1::HIS3*	this study
GA-7327	GA-1981 with *ddc2::DDC2-GFP-kanMX, mec1-100::natMX*	this study
GA-7329	GA-1981 with *ptc2::URA3, mec1-100::natMX*	this study
GA-7337	GA-1981 with *ddc2::DDC2-13MYC-URA3*	this study
GA-7353	GA-1981 with *mec1::LEU2-18MYC-MEC1*	this study

GA-7354	GA-1981 with *mec1::LEU2-18MYC-MEC1*	this study
GA-7355	GA-1981 with *mec1::LEU2-18MYC-MEC1*	this study
GA-7366	GA-1981 with *mec1::LEU2-18MYC-mec1-100::natMX*	this study
GA-7367	GA-1981 with *mec1::LEU2-18MYC-mec1-100::natMX*	this study
GA-7368	GA-1981 with *mec1::LEU2-18MYC-mec1-100::natMX*	this study
GA-7373	GA-1981 with *rad53::URA3, sml1::kanMX*	this study
GA-7375	GA-1981 with *rad53::URA3, sml1::kanMX, pph3::HIS3*	this study
GA-7377	GA-1981 with *rad53::URA3, sml1::kanMX, pph3::HIS3, mec1-100::natMX*	this study
GA-7383	GA-1981 with *psy4::hphMX*	this study
GA-7385	GA-1981 with *psy4::hphMX, mec1-100::natMX*	this study
GA-7391	GA-1981 with *psy2::URA3*	this study
GA-7393	GA-1981 with *psy2::URA3, mec1-100::natMX*	this study
GA-7395	GA-1981 with *psy2::URA3, mec1-100::natMX, pph3::HIS3*	this study
GA-7398	GA-1982 with *psy2::URA3, pph3::HIS3*	this study
GA-7401	GA-1981 with *rad53::URA3, sml1::kanMX, mec1-100::natMX*	this study
GA-7650	GA-1981 with *mec1::TRP1, sml1::HIS3, pph3::kanMX*	this study
GA-7656	GA-1981 with *rad53::URA3, sml1::kanMX, chk1::TRP1*	this study
GA-7657	GA-1982 with *rad53::URA3, sml1::kanMX, chk1::TRP1*	this study
GA-7658	GA-1981 with *rad53::URA3, sml1::kanMX, chk1::TRP1, pph3::HIS3*	this study
GA-7659	GA-1982 with *rad53::URA3, sml1::kanMX, chk1::TRP1, pph3::HIS3*	this study
GA-7660	GA-1981 with *rad53::URA3, sml1::kanMX, chk1::TRP1, mec1-100::natMX*	this study
GA-7661	GA-1982 with *rad53::URA3, sml1::kanMX, chk1::TRP1, mec1-100::natMX*	this study
GA-7662	GA-1981 with *rad53::URA3, sml1::kanMX, chk1::TRP1, mec1-100::natMX, pph3::HIS3*	this study
GA-7663	GA-1982 with *rad53::URA3, sml1::kanMX, chk1::TRP1, mec1-100::natMX, pph3::HIS3*	this study
GA-7707	GA-1981 with *mec1::TRP1, tel1::URA3, sml1::HIS3, pph3::kanMX*	this study
GA-7708	GA-1982 with *mec1::TRP1, tel1::URA3, sml1::HIS3, pph3::kanMX*	this study
GA-7709	GA-1981 with *mec1::TRP1, rad53::URA3, sml1::kanMX*	this study
GA-7711	GA-1981 with *mec1::TRP1, rad53::URA3, sml1::kanMX, pph3::HIS3*	this study
GA-7724	GA-1981 with *mec1::TRP1, tel1::URA3, sml1::HIS3*	this study
GA-7725	GA-1982 with *mec1::TRP1, tel1::URA3, sml1::HIS3*	this study
GA-7732	GA-1981 with *tel1::URA3, pph3::HIS3*	this study
GA-7734	GA-1981 with *tel1::URA3, pph3::HIS3, mec1-100::natMX*	this study
GA-7799	GA-1981 with *psy2::PSY2-13MYC-URA3*	this study
GA-7824	GA-1981 with *ddc2::DDC2-GFP-kanMX, psy2::PSY2-13MYC-URA3*	this study
GA-7827	GA-1981 with *ddc2::DDC2-GFP-kanMX, psy2::PSY2-13MYC-URA3, mec1::TRP1, sml1::HIS3*	this study
GA-7835	GA-1981 with *ddc2::DDC2-GFP-kanMX, psy2::PSY2-13MYC-URA3, mec1-100::natMX*	this study
GA-7852	GA-1981 with *pph3::PPH3-13MYC-URA3*	this study
GA-7853	GA-1981 with *pph3::PPH3-13MYC-URA3*	this study
GA-7865	GA-1981 with *pph3::PPH3-3HA-URA3*	this study
GA-7907	GA-1981 with *ddc1::URA3*	this study
GA-7908	GA-1981 with *rrd1::HIS3*	this study
GA-7923	GA-1981 with *ptc2::PTC2-3PK-LEU2*	this study
GA-7929	GA-1981 with *rrd1::HIS3, mec1-100::natMX*	this study
GA-7932	GA-1981 with *rrd2::kanMX, mec1-100::natMX*	this study
GA-7935	GA-1981 with *oca1::URA3, mec1-100::natMX*	this study
GA-7939	GA-1981 with *DDC2-GFP-kanMX, psy2::PSY2-13MYC-URA3, pph3::HIS3*	this study
GA-7945	GA-1981 with *DDC2-GFP-kanMX, mec1-100::natMX, pph3::HIS3*	this study
GA-7953	GA-1981 with *tel1::URA3, ptc2::HIS3*	this study
GA-7955	GA-1981 with *tel1::URA3, ptc2::HIS3, mec1-100::natMX*	this study
GA-7964	GA-1981 with *mec1-100::natMX, ddc1::URA3*	this study
GA-7966	GA-1981 with *pph3::6HA-PPH3*	this study
GA-7967	GA-1981 with *pph3::6HA-PPH3*	this study
GA-7972	GA-1981 with *psy2::PSY2-13MYC-URA3, ptc2::PTC2-3PK-LEU2*	this study
GA-7975	GA-1981 with *psy2::PSY2-13MYC-URA3, ptc2::PTC2-3PK-LEU2, ddc2::DDC2-GFP-kanMX*	this study
GA-7977	GA-1981 with *ptc2::URA3, pph3::HIS3*	this study
GA-7979	GA-1981 with *ptc2::URA3, pph3::HIS3, mec1-100::natMX*	this study
GA-7981	GA-1981 with *rrd1::HIS3, pph3::HIS3*	this study
GA-7982	GA-1981 with *rrd1::HIS3, pph3::HIS3, mec1-100::natMX*	this study
GA-8021	GA-1982 with *psy2::PSY2-GFP-kanMX*	this study
GA-8033	GA-1981 with *psy2::PSY2-GFP-kanMX*	this study
GA-8034	GA-1981 with *psy2::PSY2-GFP-kanMX, ddc2::DDC2-13MYC-URA3*	this study

GA-8052	GA-1981 with *rrd1::HIS3, psy2::URA3*	this study
GA-8054	GA-1981 with *rrd1::HIS3, psy2::URA3, mec1-100::natMX*	this study
GA-8079	GA-1981 with *glc7-132, mec1-100::natMX*	this study
GA-8179	GA-1981 with *psy2::PSY2-TEV-HALO-kanMX*	this study
GA-8232	GA-1981 with *DDC2-GFP-kanMX, psy2::PSY2-13MYC-URA3, mec1-S1991A::natMX*	this study
GA-8242	GA-1981 with *mec1-S38A::natMX, sml1::HIS3*	this study
GA-8243	GA-1981 with *mec1-S38D::natMX, sml1::HIS3*	this study
GA-8246	GA-1981 with *mec1-S38A-S1991A::natMX, sml1::HIS3*	this study
GA-8247	GA-1981 with *mec1-S38D-S1991D::natMX, sml1::HIS3*	this study
GA-8338	GA-1981 with *mec1-S1991A::natMX*	this study
GA-8342	GA-1981 with *mec1-S1991D::natMX*	this study
GA-8396	GA-1981 with *rfa1-t11*	this study
GA-8484	GA-1981 with *ddc2::DDC2-GFP-kanMX, mec1-D2243E(kd1), sml1::kanMX*	this study
GA-8486	GA-1981 with *ddc2::DDC2-GFP-kanMX, rad53::URA3, sml1::HIS3*	this study
GA-8659	GA-1981 with *psy2::PSY2-RFP-URA3*	this study
GA-8676	GA-1981 with *psy2::PSY2-RFP-URA3, rfa2::RFA2-GFP-HIS3*	this study
GA-8687	GA-1981 with *rfa1::RFA1-RFP-HIS3*	this study
GA-8688	GA-1981 with *rfa1::RFA1-RFP-HIS3*	this study
GA-8694	GA-1981 with *rfa1::RFA1-eCFP-hphMX*	this study
GA-8695	GA-1981 with *psy2::PSY2-RFP-URA3, ddc2-DDC2-GFP-kanMX, rfa1::RFA1-eCFP-hphMX*	this study
GA-8702	GA-1981 with *rfa1::RFA1-RFP-HIS3, psy2::PSY2-GFP-kanMX*	this study
GA-8705	GA-1981 with *rfa1::RFA1-RFP-HIS3, ddc2::DDC2-GFP-kanMX*	this study
GA-8821	GA-1981 with *psy2Δ130-350*	this study
GA-8822	GA-1982 with *psy2Δ130-350*	this study

plasmid No.	plasmid name	source
#286	*pRS416*	(Mumberg et al., 1995)
#359	*pSH18-34*	(Golemis et al., 2011)
#361	*pSH17-4*	(Golemis et al., 2011)
#965	*pGAL-lexA*	(Bjergbaek et al., 2005)
#993	*pJG4-6*	(Golemis et al., 2011)
#2221	*pKU2-rfa1-t11*	(Soustelle et al., 2002)
#2745	*pGAL-EcoRI*	(Schar et al., 2004)
#2842	*pEG203+NLS*	this study
#3307	*pGAL-lexA-PSY2*	this study
#3308	*pJG4-6-DDC2*	this study
#3367	*Yeplac195+PPH3*	(O'Neill et al., 2007)
#3368	*Yeplac195+pph3-H112N*	(O'Neill et al., 2007)
#3493	*pcDNA3.1-GFP*	Antoine Peters
#3518	*pcDNA3.1-PP4R3A-GFP*	this study
#3525	*pDEST12.2-MYC-ATRIP*	this study
#3588	*pcDNA3.1-PP4R3B-GFP*	this study
#3592	*pGAL-lexA-PSY2-2(aa25-129)*	this study
#3593	*pGAL-lexA-PSY2-3(aa25-350)*	this study
#3594	*pGAL-lexA-PSY2-4(aa25-447)*	this study
#3595	*pGAL-lexA-PSY2-5(aa25-502)*	this study
#3616	*pEG203+NLS+PSY2*	this study
#3617	*pEG203+NLS+PSY2-1(aa1-129)*	this study
#3618	*pEG203+NLS+PSY2-2(aa25-129)*	this study
#3619	*pEG203+NLS+PSY2-3(aa25-350)*	this study
#3620	*pEG203+NLS+PSY2-4(aa25-447)*	this study
#3621	*pEG203+NLS+PSY2-5(aa-25-502)*	this study
#3622	*pEG203+NLS+PSY2-6(aa-334-720)*	this study
#3623	*pEG203+NLS+PSY2-7(aa560-720)*	this study
#3629	*pEG203+NLS+PSY2-8(aa130-350)*	this study
#3630	*pEG203+NLS+PSY2-9(aa560-end)*	this study
#3649	*pGAL-lexA-PSY2-10(Δ aa25-129)*	this study
#3650	*pGAL-lexA-PSY2-11(Δ aa130-350)*	this study
#3651	*pGAL-lexA-PSY2-12(Δ aa25-350)*	this study
#3563	*pGAL-lexA-PSY2-8(aa130-350)*	this study

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CHAPTER 3: CHARACTERIZATION OF *MEC1-100*, AN S-PHASE DEFECTIVE ALLELE OF *MEC1*

This chapter provides additional data, which is unpublished.

Nicole Hustedt planned all and performed most experiments, evaluated results, made figures and wrote the chapter, Heinz Gut performed structure modeling and analysis, Ragna Sack performed mass spectroscopy analyses and Kenji Shimada performed cell fractionation.

SUMMARY

In an attempt to understand the causes for the S-phase specific defect in *mec1-100*, which carries two point mutations that result in N1700S and F1179S, we further characterized this mutant. We show that both mutations are required for full *mec1-100* HU sensitivity. Ddc2-Mec1 interaction, enzymatic activity, Ddc2-Ddc2-oligomerization and chromatin association are not altered compared to the wild-type protein complex. When testing genetic interactions with other checkpoint proteins we did not find clear epistasis between any of these mutants and *mec1-100*. Rather most of the double mutants were additive, indicating that *mec1-100* phenotypes cannot be explained by loss of interaction with any of these factors. In a screen for spontaneous suppressor mutations, in addition to extragenic suppressors in *PSY2* or *PPH3* (Chapter 2), we identified 16 additional mutations in *mec1-100,* each of which suppresses *mec1-100* HU sensitivity (Chapter 2). Here, we characterize some of those intragenic suppressors further and find that a subset of mutations are completely dependent on Rad24 for suppression of lethality on HU, while others act independently of Rad24. Those dependent on Rad24 are surface mutations that may alter protein-protein interactions while the others are buried in the catalytic domain of a modeled Mec1 structure. Once actual structural data of Ddc2-Mec1 together with its activators is available, these data may help dissect Rad24-dependent Mec1 activation on a molecular level.

INTRODUCTION

Ddc2-Mec1 is a central player in the replication and DNA damage checkpoint. While DNA damage leads to cell cycle arrest in G1 or G2 phases, the replication checkpoint senses and signals stalled replication forks in S phase. Once activated, it slows down replication by inhibiting late origin firing, induces transcription of DNA repair genes and stabilizes stalled forks to prevent their disengagement (Chapter 1). Several proteins promote Mec1 activation *in vitro*, i. e., Dpb11, Ddc1 (both are recruited in a Rad24 dependent manner), and Dna2, and it was suggested that they act in a cell-cycle dependent manner (Kumar and Burgers, 2013; Navadgi-Patil and Burgers, 2011) (Chapter 1). The Mec1 activating function of all three proteins relies on bulky hydrophobic residues embedded in the unstructured N- or C-terminal tails. Point mutants of the critical residues were shown to impair Rad53 activation *in vivo*. The mediator proteins Rad9, Mrc1 and Sgs1 also facilitate Rad53 activation, but rather act downstream of Mec1 (Alcasabas et al., 2001; Bjergbaek et al., 2005; Sweeney et al., 2005) (Chapter 4), although Sgs1, through its helicase function, could also act upstream by providing single stranded DNA. Rad9 and Sgs1 were both shown to bind and recruit Rad53 after their phosphorylation by Mec1 (Sun et al., 1998; Sweeney et al., 2005) (Chapter 4). Similarly, *in vitro* experiments showed that Mrc1 stimulates Mec1-enzyme-Rad53-substrate interaction rather than enhancing Mec1 catalytic activity (Chen and Zhou, 2009).While Rad9 is important for the response to DNA damage which results in a cell cycle arrest in G1 or G2, before mitosis, Mrc1 and Sgs1 are localized at stalled replication forks and promote Rad53 activation in response to HU (Chapter 1). Interestingly, *mec1-100* shows strong synergistic lethality with a deletion of *SGS1* on HU (Cobb et al., 2003; Cobb et al., 2005), but not with a *sgs1-r1* mutant lacking the Rad53-recruiting domain (Chapter 4). It could be that lack of Mec1 activity in S phase might create structures at forks that need the Sgs1 helicase activity, rather than its checkpoint function, for their resolution.

Paciotti and colleagues reported the discovery of an S phase defective allele of Mec1, *mec1-100* (Paciotti et al., 2001). *mec1-100* cells show delayed Rad53 phosphorylation in S phase. In contrast, the DNA damage G2 checkpoint is intact and Rad53 phosphorylation in G2 phase shows similar kinetics in WT and *mec1-100* cells. *mec1-100* consists of two point mutations, one in the conserved FAT domain (N1700S) (Bosotti et al., 2000) and one N-terminal of the FAT domain (F1179S) (Figure 3.1). Both are located outside of the catalytic domain and in Chapter 2 we show that mec1-100 catalytic activity measured in an *in vitro* assay in complex with Ddc2, is comparable to the wild-type Mec1-Ddc2 complex. Therefore the mechanism of how the two *mec1-100* mutations impair Mec1 function is unclear.

Here, we aimed at understanding the causes for the S phase specific defect of *mec1-100*. *MEC1*+ and mutant cells were compared for several known features of Ddc1-Mec1 such as its oligomerization and association with chromatin and other proteins. Also, we analyzed some of the intragenic *mec1-100* suppressor mutations identified in Chapter 2 further and found that a subset of presumably surface exposed suppressors require Rad24 for the *mec1-100* survival on HU.

RESULTS AND DISCUSSION

BOTH F1179S AND N1700S MUTATIONS ARE REQUIRED FOR FULL *MEC1-100* PHENOTYPE

mec1-100 has two point mutations, F1179S, which is located at the end of a HEAT (Huntingtin, EF3, PP2A, TOR1) repeat stretch, and N1700S, which is located in the TPR (tetratricopeptide) repeat-forming FAT (FRAP, ATM, TRRAP) domain (Figure 3.1). Since no separation of these mutations had been reported, we created each mutation independently to ask whether either of the two mutations is dispensable for the *mec1-100* phenotype. Single *mec1-F1179S* and *mec1-N1700S* mutants were integrated in the *MEC1* locus under the native promoter. We found that *mec1-N1700S* cells did not show sensitivity to HU in this assay (Figure 3.2A). Cells expressing *mec1-F1179S* were HU sensitive, although less so than *mec1-100* cells. This shows that both mutations act in an additive manner and neither of the single mutation is sufficient for the full *mec1-100* phenotype. Both *mec1-100*-mutated residues are conserved among yeast species, but not in higher eucaryotes (Figure 3.1). However, in human ATR a mutant (3A-ATR) has been described, which also shows S phase but not G2 checkpoint defects (Nam et al., 2011). The responsible mutations mapped to a region immediately N-terminal of the FAT domain and thus are located in between F1179 and N1700 in Mec1 (Figure 3.1). This suggests that this region mediates an important and possibly conserved function of ATR/Mec1 for the replication checkpoint.

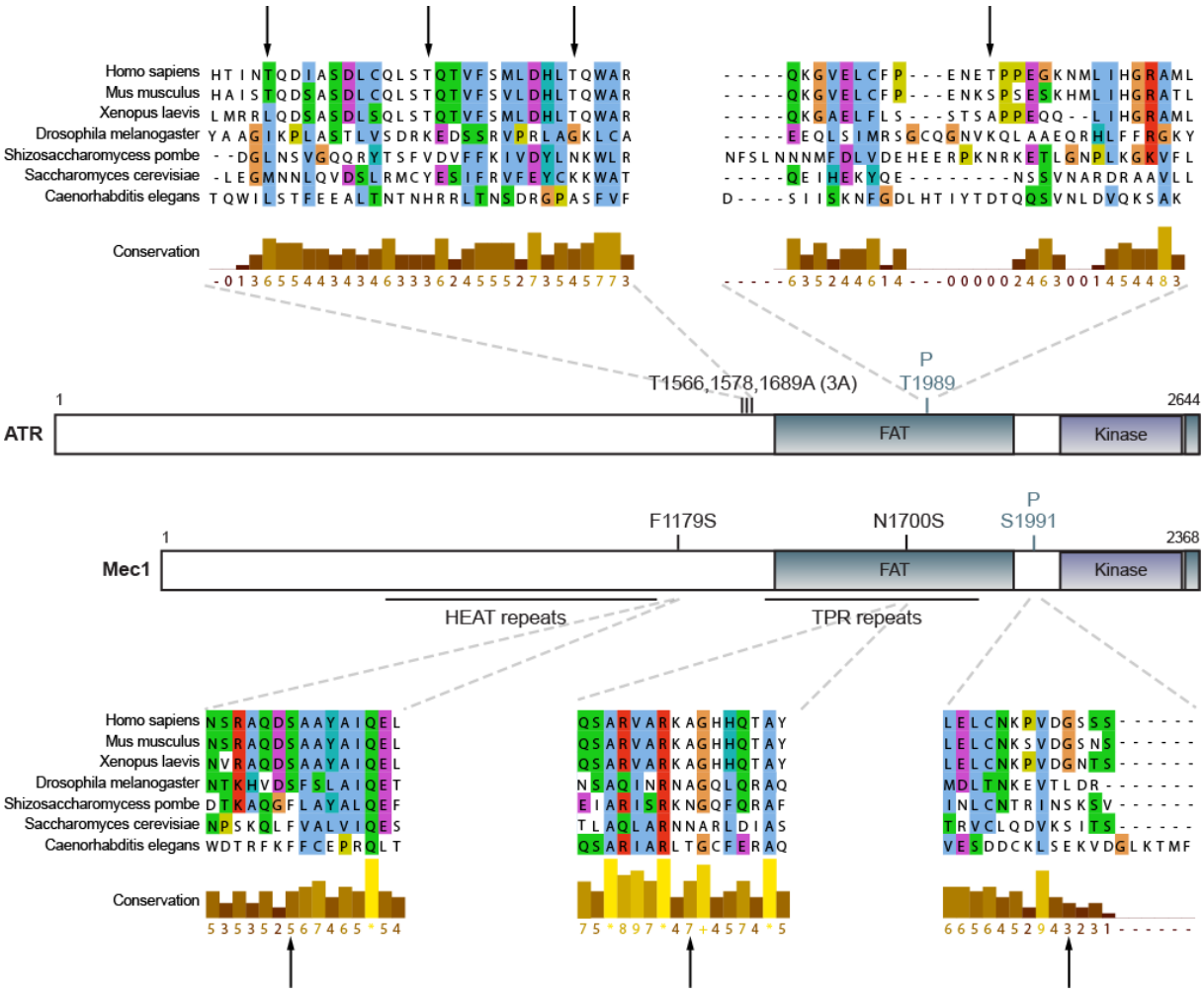


Figure 3.1: *Mec1-100* mutations are in conserved regions. Mec1 protein sequence was aligned with ATR sequences from indicated species using ClustalW and jalview to visualize the alignment. Residues were colored according to ClustalX standard. Shown are alignment sections around *mec1-100* mutations, 3A-ATR mutations and phosphorylated residues (ATR T1989 and Mec1 S1991; see Chapter 2). Relevant residues are marked with arrows.

DDC2-MEC1 OLIGOMERIZATION IS NOT IMPAIRED IN *MEC1-100* CELLS

TPR and HEAT repeats are often involved in protein-protein interactions or oligomerization (Andrade et al., 2001). Indeed, Mec1-Ddc2 and ATR-ATRIP were shown to oligomerize, although the size of the resulting oligomer, as well as the function of oligomerization is still unclear (Chapter 1). Ddc2 contains a predicted coiled coil domain (Figure 2.1B), that could also oligomerize. Consistently, it has been shown that both ATRIP and ATR contribute to oligomerization (Ball and Cortez, 2005). To test whether oligomerization of Mec1-Ddc2 is impaired in *mec1-100* cells, we created diploid yeast strains that had one allele of *DDC2* fused with a GFP and the second fused with a triple HA tag. Immunoprecipitation (IP) with anti-GFP antibody following HU treatment showed efficient recovery of Ddc2-HA from both WT and *mec1-100* cells to the same extent (Figure 3.2D). Thus, mec1-100 is proficient for oligomerization in this assay. We note, however, that much less Ddc2-HA was recovered when the IP was performed from *mec1*Δ cells, indicating that Mec1 contributes to oligomerization in agreement with previous studies on ATR-ATRIP (Ball and Cortez, 2005). Even though the mutated residues of *mec1-100* are not located in the kinase domain, they might nonetheless reduce enzymatic activity of Mec1. In Chapter 2 we show that $Mec1^{+}$ and mec1-100 have comparable enzymatic activity on an Sgs1 target peptide *in vitro*, when recovered in an immunoprecipitate with Ddc2 (Figure S2.1A). Moreover, The Mec1-Ddc2 interaction was not affected by the mutation (Figure. 2.5B) and previous studies reported that both Mec1-Ddc2 and mec1-100-Ddc2 localize to stalled replication forks in a similar manner as revealed by chromatin immunoprecipitation and Ddc2 focus formation (Cobb et al., 2005; Tercero et al., 2003). Thus, we did not find any evidence that *mec1-100* defects are caused by reduced enzymatic activity, Ddc2 interaction, oligomerization or defective localization.

MEC1-100 IS ADDITIVE WITH OTHER CHECKPOINT MUTANTS

We then hypothesized that the mutated region might constitute a binding platform for another factor important for Mec1 *in vivo* activity. We first addressed this question using a genetic approach. If the *mec1-100* mutations disrupted a specific protein-protein interaction that is crucial for *mec1-100 in vivo* activity, mutation of this factor should be epistatic with *mec1-100*. Therefore we tested genetic interactions of *mec1-100* with several candidates that are known to either activate Mec1 or mediate Rad53 activation just downstream of Mec1 in the checkpoint pathway and thus might be Mec1 binding partners. Dpb11, Ddc1 and Dna2 were shown to enhance Mec1 catalytic activity *in vitro* through critical residues in their N-or C-terminal unstructured tails (Kumar and Burgers, 2013; Navadgi-Patil and Burgers, 2009; Navadgi-Patil et al., 2011). Mutation of these residues also affected Mec1 activation *in vivo.* Thus, we considered Dpb11, Ddc1 and Dna2 as good candidates for upstream activators that might directly bind to Ddc2-Mec1. Dpb11 and Ddc1 are both recruited in a Rad24-dependent manner; therefore *rad24*Δ affects Mec1 activation through both proteins. Other than kinase activation, a protein-protein interaction could serve to bridge between Mec1 and one or several of its substrates. Mrc1, Sgs1 and Rad9 can recruit Rad53 for phosphorylation by Mec1 (Chapter 1). Thus, loss of a potential protein-protein interaction between Mec1 and Rad9, Sgs1 or Mrc1 could result in Rad53 activation defects. Additional checkpoint mutants that rather act in parallel to the Mec1-Rad53 checkpoint branch (i.e. *tel1*Δ and *chk1*Δ) were also included, although we did not expect an epistatic genetic relationship between *tel1*Δ or *chk1*Δ and *mec1-100*.

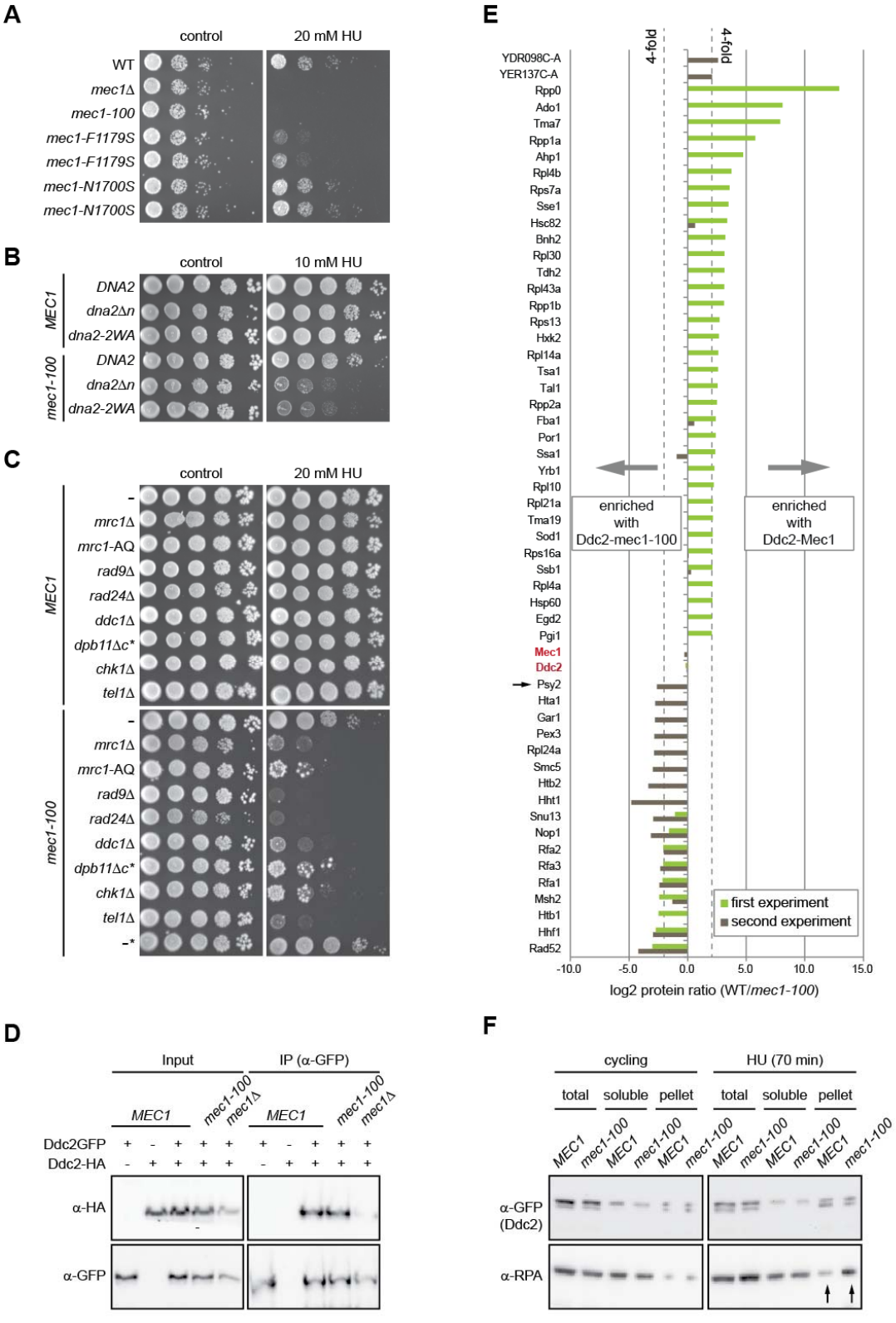
We created checkpoint protein double mutants with *mec1-100* and compared HU sensitivity of both single and double mutants (Figures 3.2B, C). As expected, mutations of checkpoint proteins that act in parallel to Mec1-Rad53 signaling (*chk1*Δ and *tel1*Δ) were found to be additive with *mec1-100* on HU. To assess the genetic interaction of *mec1-100* with the upstream activator Dna2, two mutants of *dna2* were used. A deletion of the N-terminus (*dna2*Δ*n*) that contains two residues important for its function in Mec1 activation, as well as point mutations of the respective residues (*dna2-2WA*) (Kumar and Burgers, 2013), were additive with *mec1-100* rather than epistatic (Figure 3.1B). Similarly, *ddc1*Δ and a deletion of the C-terminal Mec1 activation domain in Dpb11, as well as *rad24*Δ were additive with *mec1-100*, rather than epistatic. Regarding the downstream factors, Mrc1 is not only involved in the replication checkpoint but also in normal replication. A separation of function mutant, *mrc1-AQ*, that is impaired for checkpoint signaling, but shows normal S phase progression and replication (Osborn and Elledge, 2003), was used in addition to *mrc1*Δ. However, both *mrc1* mutants were found additive with *mec1-100* rather than epistatic (Figure 3.2C). The same was observed when we combined *mec1-100* with *rad9*Δ. An Sgs1 mutant that disrupts Rad53 binding, did not show detectable HU sensitivity on its own, arguing that it is redundant with other factors (Chapter 4). Thus, it might be necessary to assess a genetic interaction between *sgs1-r1* and *mec1-100* in a sensitizing background, e.g. *rad24*Δ which was previously shown to be on a parallel pathway with Sgs1 for checkpoint activation (Bjergbaek et al., 2005)

This additive sensitivity of *mec1-100* with checkpoint mutants indicates that *mec1-100* and any of the checkpoint mutants are not epistatic. Thus, *mec1-100* defects cannot simply explained by impaired interaction with one of these factors. Besides the canonical checkpoint proteins tested here there are other factors (e.g. the alternative clamp loader containing Ctf18, Ctf8 and Dcc1) involved in replication checkpoint activation or maintenance, although their exact role remains enigmatic (Crabbe et al., 2010). Further experiments would be needed to test whether *mec1-100* behaves epistatic with and consequently might impair checkpoint function of any of these factors.

Analysis of Mec1/mec1-100 differentially interacting proteins identified exclusively factors with increased binding to mec1-100

None of the canonical checkpoint proteins was epistatic with *mec1-100*. Thus, we reasoned that an unknown factor might bind the regulatory region spanning F1179 and N1700 and that this interaction would be impaired when the two residues were mutated. To identify this unrevealed factor we first tried a proteomics approach. We immunoprecipitated Mec1-Ddc2 and mec1-100-Ddc2 complexes after HU treatment and identified co-precipitating proteins by mass spectrometry. Protein abundance ratios (Mec1/mec1-100) were calculated. Figure 3.2E shows protein abundance ratios for all differentially interacting proteins that were at least four times enriched with either WT Mec1-Ddc2 or mec1-100-Ddc2 ($\log_2 \geq 2$ or $\log_2 \leq -2$, respectively). Table 3.3 shows a full list of all co-precipitating proteins. We did not detect any proteins that were reproducibly enriched in WT Mec1-Ddc2 pull-down in two independent experiments. However, we found several proteins reproducibly enriched with mutant mec1-100-Ddc2. Among them were all three RPA subunits (Rfa1, Rfa2, Rfa3), Rad52 and Histone H4. All of these bind to DNA, and since we did not digest DNA with nucleases prior IP we cannot rule out that proteins were co-precipitated due to unspecific DNA binding. In fact, in Figure 2.5A we show that most of the Ddc2-RPA interaction is lost when extracts are pretreated with benzonase/RNaseA. Impaired replication fork stabilization in *mec1-100* cells could result in a higher level of ssDNA, thus leading to elevated RPA accumulation on DNA, which might be nonspecifically pulled down together with mec1-100-Ddc2.

Importantly, in one of the two experiments we identified Psy2 (Figure 3.2E, arrow), confirming the interaction described in Chapter 2. Here, Psy2 was found enriched with mec1-100-Ddc2 compared to Mec1^{+}-Ddc2 This enrichment with mec1-100, however, was not reproduced by IP and subsequent Western blotting (Chapter 2).

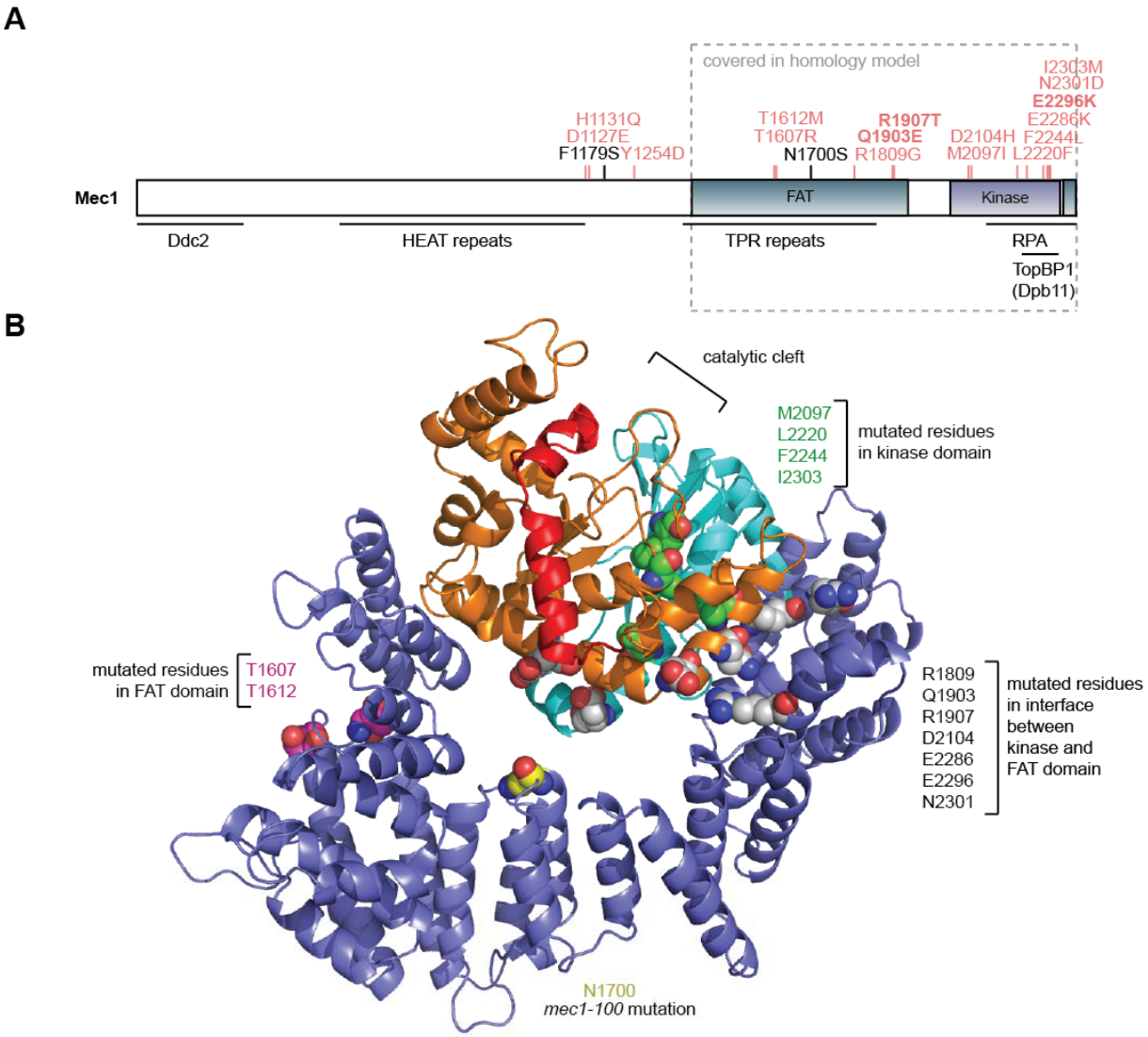


To test whether *mec1-100* cells generally showed higher levels of RPA accumulation on DNA, we isolated chromatin fractions from HU-treated WT and *mec1-100* cells and analyzed them by

western blotting. While Ddc2 association with Chromatin was comparable in WT and mutant cells, RPA was more enriched in chromatin fractions of mutant cells compared to WT after HU treatment (Figure 3.2F, arrows). We note that in this experiment we detected two Ddc2-GFP species by Western blot, with the faster migrating form being absent from non-chromatin bound fractions. These two species were not detected in other extracts of Ddc2-GFP expressing cells (Figure 2.5). It is unclear whether one of them is a degradation product due to the spheroplast preparation or the result of a posttranslational modification. Indeed, Ddc2 was shown to be phosphorylated in a Mec1-dependent manner after MMS or UV treatment but also in an unperturbed S phase (Paciotti et al., 2000). In our Ddc2 IP combined with mass spectrometry experiments (Figure 3.2E) we found multiple phosphorylation sites in Ddc2 (serine 10, serine 11, threonine 159, serine 162, serine 163, and serine 182), although we did not detect any Ddc2 phosphopeptide in our phosphoproteomics experiment (Chapter 2).

From these experiments we cannot absolutely rule out that mec1-100-Ddc2 indeed binds more RPA than WT Mec1-Ddc2 directly, which might somehow impair mec1-100 S-phase function. Yet, this seems unlikely, since the major site of RPA interaction in Mec1-Ddc2 was mapped to the N-terminus of Ddc2 (Ball et al., 2005), rather than the mutated domain of mec1-100. Although the C-terminus of Mec1 might contribute to RPA interaction (Nakada et al., 2005), *mec1-100* mutations are far from the C-terminus. Instead, it is more conceivable that *mec1-100* cells accumulate more ssDNA after HU treatment, reflecting an inability of mec1-100 to preserve replication fork structures. This would result in enhanced RPA binding to chromatin and elevated RPA levels in mec1-100-Ddc2 IPs due to co-precipitation of chromatin. Thus, we hypothesize that the elevated coprecipitation of RPA with mec1-100-Ddc2 is a consequence rather than a cause of the *mec1-100* defects. Similarly, elevated Rad52 coprecipitation could reflect a stronger association of Rad52 with chromatin broken forks in *mec1-100* cells. It is currently unclear why more histones were pulled down with mec1-100-Ddc2, even though Ddc2 association with chromatin was not altered in WT compared to mutant cells (Figure 3.2F). This result could, however, reflect a different chromatin structure. Indeed, several chromatin remodeling complexes were shown to be phosphorylated by Mec1 (Chapter 2). Further experiments, especially IPs combined with prior treatment of extracts with benzonase/RNase would be needed to differentiate between protein-protein interactions and co-precipitation due to protein-DNA interactions.

Figure 3.2: Characterization of *mec1-100* **(A)** Serial 10-fold dilutions of cultures were plated on YPAD ± 20 mM HU. Relevant genotypes are indicated in the figure. Strains used were GA-1981, GA-2529, GA-4978, GA-6330, GA-6331, GA-6332 and GA-6333. **(B)** Cells were treated as in (A). Strains used were GA-8605, GA-8606, GA-8607, GA-8608, GA-8609 and GA-8610. **(C)** Serial 10-fold dilutions of cultures were plated on YPAD ± 10 mM HU. Relevant genotypes are indicated in the figure. Asterisk indicates *rad5-535* background. Strains used were GA-1981, GA-6826, GA-6574, GA-6625, GA-5321, GA-7907, GA-7795, GA-7062, GA-6912, GA-6582, GA-6828, GA-6663, GA-6624, GA-7209, GA-7964, GA-7764, 7064, GA-7064, GA-6913 and GA-2474. **(D)** Exponentially growing cultures were treated with 0.2 M HU for 1h. Native extracts were subjected to IP by α-GFP and blots were probed with indicated antibodies. Diploid strains used were GA-7760, GA-7668, GA-7761, GA-7762 and GA-7763. **(E)** Exponentially growing cultures of Ddc2-GFP (GA-7268) and Ddc2-GFP mec1-100 (GA-7327) were treated with 0.2 M HU for 1h. Native extracts were subjected to IP by α-GFP and isolated protein complexes were digested with Trypsin for LC-MS/MS analysis. Shown are protein abundance ratios (WT/mec1-100) of differentially ($\log_2 \leq -2$ or $\log_2 \geq 2$) interacting proteins, in addition to ratios for Ddc2 and Mec1 as controls (red). Arrow indicates Psy2, which was found as an interactor with mec1-100 in one of the two experiments. **(F)** Ddc2-GFP (GA-7268) and Ddc2-GFP mec1-100 (GA-7327) cells were untreated or treated with 0.2 M HU for 70 min prior cell fractionation. Samples of cells fractions were subjected to western blot analysis using indicated antibodies. total: total protein extracts; pellet: Chromatin - bound fraction; soluble: non-Chromatin bound, soluble fraction. Arrows indicate Rfa1 bands to compare (see text).


A
covered in homology model
I2303M
N2301D
E2296K
H1131Q
D1127E
F1179S Y1254D
T1612M
T1607R
N1700S
R1907T
Q1903E
R1809G
D2104H
M2097I
E2286K
F2244L
L2220F
Mec1
FAT
Kinase
Ddc2
HEAT repeats
TPR repeats
RPA
TopBP1
(Dpb11)
B
catalytic cleft
M2097
L2220
F2244
I2303
mutated residues
in kinase domain
mutated residues
in FAT domain
T1607
T1612
R1809
Q1903
R1907
D2104
E2286
E2296
N2301
mutated residues
in interface
between
kinase and
FAT domain
N1700
mec1-100 mutation
C
control
5 mM HU
20 mM HU
WT
rad24Δ
mec1-100
mec1-100 rad24Δ
mec1-100-D1127E
mec1-100-D1127E rad24Δ
mec1-100-D1127E rad24Δ
mec1-100-T1612M
mec1-100-T1612M rad24Δ
mec1-100-T1612M rad24Δ
mec1-100-R1809G
mec1-100-R1809G rad24Δ
mec1-100-R1809G rad24Δ
mec1-100-D2104H
mec1-100-D2104H rad24Δ
mec1-100-D2104H rad24Δ
mec1-100-F2244L
mec1-100-F2244L rad24Δ
mec1-100-F2244L rad24Δ
mec1-100-Q1903E
mec1-100-Q1903E rad24Δ
mec1-100-Q1903E rad24Δ

SOME, BUT NOT ALL MEC1-100 INTRAGENIC SUPPRESSORS REQUIRE RAD24 FOR SUPPRESSION OF HU SENSITIVITY

To identify novel, potentially regulating, factors in the Mec1 checkpoint pathway we conducted a screen in the *mec1-100* background for spontaneous suppressors of HU sensitivity (Figure 2.1AB). We found both additional mutations in *mec1-100* (intragenic suppressors) and mutations in Psy2-Pph3 (extragenic suppressors). For intratenic suppressor mutations outside the catalytic domain we used secondary structure prediction to locate the mutated residues relative to the alpha helices of HEAT and TPR repeats or non-repeat helices. Both D1127 and H1131 reside in loop regions between helices and should not affect the overall protein fold. In contrast, Y1254 is at the beginning of a helix and the impact of its mutation is unclear. For mutations in FAT and kinase domains a homology model was built based on the resolved structure of the PI3K-like kinase mTOR (Yang et al., 2013). T1612 and T1607 were located in turns between helices of TPR repeats in the FAT domain, and therefore unlikely disturb the fold, similar to N1700. Rather, these residues could be involved in protein-protein interactions. The FAT domain wraps around the kinase domain and although N1700 is located far away from the kinase domain in this model, small differences in the actual Mec1 structure could result in a different curvature of the FAT domain. Thus, we cannot absolutely exclude that N1700 might be involved in intra-molecular interactions with residues in the kinase domain. M2097, L2220 and I2303 residues were found to be buried in the helical core that attaches N-terminal and C-terminal kinase lobe and therefore might impact folding or protein stability (Figure 3.3A). It is noteworthy that F2244, which is highly conserved, resides at the beginning of the activation loop and could position both catalytic and activation loops, thereby influencing kinase activity. Importantly, the neighboring residue, D2243, is mutated in an activity-dead allele of Mec1 (Paciotti et al., 2001). Another group of mutated residues (R1809G, Q1903, R1907, D2104, E2286, E2296 and N2301) is located at the interface between kinase and FAT domain, either on kinase or FAT domain. Some of them seem surface exposed (R1809, D2104), while the others might stabilize the position of the FAT relative to the kinase domain and therefore could influence enzymatic activity.

Figure 3.3: Some intragenic suppressors require *RAD24* for HU sensitivity suppression. (A) Mec1 domain architecture with *mec1-100* mutations indicated in black and *mec1-100* suppressor mutations in red. Bold: mutations found twice independently. Box indicates region that is covered by homology model in (B). **(B)** Homology model of Mec1 kinase domain based on crystal structure of mTOR. dark blue: FAT domain, light blue: N-terminal kinase lobe; orange: C-terminal kinase lobe; red: FATC domain, pink: mutated residues located within FAT domain, yellow: mec1-100 –mutated residue N1700, grey: mutated residues located in interface between kinase and FAT domain, green: mutated residues in kinase lobes. **(C)** Serial 5-fold dilutions of cultures were plated on YPAD, YPAD + 5 mM HU and YPAD + 20 mM HU. Relevant genotypes are indicated in the figure. Strains used were GA-1981, GA-5321, GA-6582, GA-7209, GA-6412, GA-7220, GA-7221, GA-6341, GA-7218, GA-7219, GA-6468, GA-7201, GA-7202, GA-6470, GA-7193, GA-7194, GA-6529, GA-7191, GA-7192, GA-6510, GA-7199 and GA-7200.

To see if the suppressors act through specific cofactors of Mec1-Ddc2, we further studied a subset of these intragenic suppressor mutations by genetic interactions. Mutations that are predicted to influence kinase activity (i.e. Q1903E and F2244L) and others that seem surface exposed and might be involved in protein-protein interactions (i.e. D1127E, T1612M, R1809G and D2104H) were used. We asked whether the suppression required Mec1 activation through the Rad24 pathway. Interestingly, in the absence of Rad24 some intragenic suppressors (T1612M, R1809G and D2104H) became as HU sensitive as the *mec1-100 rad24*Δ double mutant, indicating that Rad24 was absolutely required for their mechanism of suppression (Figure 3.3C). Others (D1127E and Q1903E) showed some residual suppression of *mec1-100* HU sensitivity in a *rad24*Δ background. Interestingly, F2244L was found to act independently of Rad24. It is reasonable to speculate that this residue would enhance Mec1 kinase activity independent of Rad24, thereby balancing *mec1-100* S phase defects. Further experiments, e.g. *in vitro* kinase assays with a *mec1-F2244L* single mutant would be required to test this hypothesis. Interestingly, several attempts to generate a *mec1-F2244L* single mutant failed, indicating that this mutation might result in cell lethality.

Table 3.1: Growth of *mec1-100* intragenic suppressors in combination with checkpoint mutants on HU.

	*rad24*Δ	*dpb11*Δc	*mrc1*Δ	*rad9*Δ	*tel1Δ*	*chk1Δ*	position of suppressor mutation
-	++++	++++	++++	++++	++++	++++	
mec1-100	-	++	-	-	-	++	
mec1-100-D1127E	++	+++	++	+++	++++	++++	unclear
mec1-100-T1612M	-	++	+	+	++++	++++	surface
mec1-100-R1809G	-	+++	++	++	++++	++++	surface
mec1-100-Q1903E	+++	++++	++	++++	++++	++++	buried
mec1-100-D2104H	-	+++	++	++	++++	++++	surface
mec1-100-F2244L	++++	++++	++	++++	++++	++++	buried

We further combined the selected subset of intragenic suppressors with other checkpoint mutants (i.e. *mrc1*Δ, *rad9*Δ, *dpb11*Δ*c*, *tel1*Δ, *chk1*Δ) and tested their growth on HU by Drop Assays. The results are summarized in Table 3.1. Combination of the intragenic suppressors with *rad9*Δ or *dpb11*Δ*c* showed a similar tendency as with *rad24*Δ, but the effects on HU sensitivity were not as strong. On the other hand, neither Tel1 nor Chk1 were required for the suppression of HU sensitivity , indicating that the mutations do not rely on signaling through Tel1 or Chk1. Interestingly, deletion of Mrc1 rendered all suppressors slightly HU sensitive again, thus all of the suppressors require Mrc1 for the full suppression. The strong dependency of some intragenic suppressors on Rad24 might indicate that they enhance Mec1 activation through Ddc1 and/or Dpb11 which are recruited in a Rad24-dependent manner (Chapter 1). Again, further *in vitro* assays are necessary to address this hypothesis. However, once there is actual structural data of the Ddc2-Mec1 complex available, possibly together with Mec1 activators Dna2, Ddc1 or Dpb11, these data on Mec1 mutations could help to elucidate the molecular mechanism of Mec1 activation.

EXPERIMENTAL PROCEDURES

YEAST STRAINS, DROP ASSAYS AND IMMUNOPRECIPITATION

Yeast strains used in this chapter are described in Table 3.2. Cells were cultured at 30°C in YPAD medium using standard procedures. Drop assays were performed as previously described (Hustedt and Shimada, 2014). IP experiments, mass spectrometry sample preparation and analysis were performed as described in Chapter 2. The identification and relative quantification of proteins was performed with Progenesis-LC (Nonlinear Dynamics Ltd) using Mascot 2.3.0.2 (Matrix Science) for databases search. Protein abundances were normalized to Ddc2 and Mec1 within Progenesis-LC. Finally data were exported to Excel and protein ratios were calculated from the normalized abundances.

CELL FRACTIONATION

Cells were centrifuged and resuspended in YPAD containing 1 M sorbitol, 0.05M EDTA-KOH, 10mM DTT, 20mM K-phosphate pH7.0. 0.2 M HU was further supplemented to the buffer for HU-treated cells. Cells were spheroplasted with zymolyase (0.4 mg/ml) and lyticase (50 U/ml) for 15 min at 30°C. Spheroplasts were recovered by centrifugation and washed once in wash buffer (50mM HEPES-KOH pH7.5, 20mM KCl, 2mM K-EDTA,0.125 mM spermidine, 0.05 mM spermine, 0.4 M sorbitol, 1% Trasylol, and 0.5 mM PMSF). A total of 100 µl of the cell pellet was resuspended in 500 µl of EB buffer (100 mM KCl, 50 mM HEPES-KOH pH7.5, 2.5 mM MgCl2, 1% Trasylol and COMPLETE protease inhibitors (Roche)) and cells were lysed on ice by adding a final concentration of 0.25% TritonX-100. An aliquot was kept as total protein extract. The remaining cells were sedimented through 30% sucrose in EB buffer. Supernatant was kept as non-chromatin bound fraction. The cell pellet (chromatin bound fraction) was resuspended in EB buffer with 0.25% Triton X-100. Total protein extracts, non-chromatin bound and chromatin bound fractions were analyzed by western blotting.

HOMOLOGY MODELING OF MEC1

The amino acid sequence of *S. cerevisiae* Mec1 (Uniprot P38111, residues 1400-2368) was submitted to the HHPRED server for homology detection and structure prediction (Hildebrand et al., 2009). The structure of H. sapiens mTOR (PDB 4JSN) (Yang et al., 2013) was the top hit resulting in very high scores (Score=1498, E-value=1.9e-145, 23% sequence identity). The HHPRED Mec1 mTOR sequence alignment was sent to the HHPRED MODELLER pipeline for homology modeling. Structural figures were prepared using PyMOL (www.pymol.org).

Table 3.2: Yeast strain used in this chapter

strain	genotype	source
GA-181	*MATa, ade2-1, trp1-1, his3-11, -15, ura3-1, leu2-3, -112, can1-100 (W303)*	R. Rothstein
GA-1981	*MATa, ade2-1 ,trp1-1 ,his3-11 , -15, ura3-1, leu2-3, -112, can1-100 (W303), RAD5+*	H.L. Klein
GA-1982	*MATα, ade2-1 ,trp1-1 ,his3-11 , -15, ura3-1, leu2-3, -112, can1-100 (W303), RAD5+*	H.L. Klein
GA-2474	GA-181 with *mec1-100::LEU2(HIS3)*	(Cobb et al., 2005)
GA-2529	GA-181 with *mec1::HIS3, sml1::KanMX*	this study
GA-4978	GA-1981 with *mec1-100::LEU2(HIS3)*	(Hegnauer et al., 2012)
GA-5321	GA-1981 with *rad24::TRP1*	(Hegnauer et al., 2012)
GA-6330	GA-1981 with *mec1-F1179S sml1::HIS3*	this study
GA-6331	GA-1981 with *mec1-F1179S sml1::HIS3*	this study
GA-6332	GA-1981 with *mec1-N1700S sml1::HIS3*	this study
GA-6333	GA-1981 with *mec1-F1179S sml1::HIS3*	this study
GA-6341	GA-1982 with *mec1-100-T1612M::LEU2(HIS3)*	this study
GA-6412	GA-1981 with *mec1-100-D1127E::LEU2(HIS3)*	this study
GA-6468	GA-1981 with *mec1-100-R1809G::LEU2(HIS3)*	this study
GA-6470	GA-1981 with *mec1-100-D2104H::LEU2(HIS3)*	this study
GA-6510	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3)*	this study
GA-6529	GA-1981 with *mec1-100-F2244L::LEU2(HIS3)*	this study
GA-6574	GA-1981 with *mrc1::HIS3, pRS405-mrc1-AQ (LEU2) URA3::GPD-TK* (PP676)	P. Pasero
GA-6582	GA-1981 with *mec1-100::natMX*	this study
GA-6624	GA-1981 with *mec1-100::natMX, rad9::TRP1*	this study
GA-6625	GA-1981 with *rad9::TRP1*	this study
GA-6663	GA-1981 with *mec1-100::natMX, mrc1::HIS3, pRS405-mrc1-AQ (LEU2) URA3::GPD-TK*	this study
GA-6723	GA-1981 with *mec1-100-D1127E::LEU2(HIS3), rad9::TRP1*	this study
GA-6725	GA-1981 with *mec1-100-T1612M::LEU2(HIS3), rad9::TRP1*	this study
GA-6727	GA-1981 with *mec1-100-R1809G::LEU2(HIS3), rad9::TRP1*	this study
GA-6730	GA-1981 with *mec1-100-F2244L::LEU2(HIS3), rad9::TRP1*	this study
GA-6732	GA-1981 with *mec1-100-D2104H::LEU2(HIS3), rad9::TRP1*	this study
GA-6815	GA-1981 with *mec1-100-D1127E::LEU2(HIS3), mrc1::TRP*	this study
GA-6817	GA-1981 with *mec1-100-T1612M::LEU2(HIS3), mrc1::TRP*	this study
GA-6819	GA-1981 with *mec1-100-D2104H::LEU2(HIS3), mrc1::TRP*	this study
GA-6821	GA-1981 with *mec1-100-R1809G::LEU2(HIS3), mrc1::TRP*	this study
GA-6823	GA-1981 with *mec1-100-F2244L::LEU2(HIS3), mrc1::TRP*	this study
GA-6826	GA-1981 with *mrc1::TRP*	this study
GA-6828	GA-1981 with *mec1-100::natMX, mrc1::TRP*	this study
GA-6912	GA-1981 with *tel1::URA*	this study
GA-6913	GA-1981 with *mec1-100::natMX, tel1::URA*	this study
GA-6920	GA-1981 with *mec1-100-D1127E::LEU2(HIS3), tel1::URA*	this study
GA-6922	GA-1981 with *mec1-100-T1612M::LEU2(HIS3), tel1::URA*	this study
GA-6924	GA-1981 with *mec1-100-R1809G::LEU2(HIS3), tel1::URA*	this study
GA-6926	GA-1981 with *mec1-100-D2104H::LEU2(HIS3), tel1::URA*	this study
GA-6928	GA-1981 with *mec1-100-F2244L::LEU2(HIS3), tel1::URA*	this study
GA-7062	GA-1981 with *chk1::TRP1*	this study
GA-7064	GA-1981 with *mec1-100::natMX, chk1::TRP1*	this study
GA-7069	GA-1981 with *mec1-100-D1127E::LEU2(HIS3), chk1::TRP1*	this study
GA-7071	GA-1981 with *mec1-100-T1612M::LEU2(HIS3), chk1::TRP1*	this study
GA-7073	GA-1981 with *mec1-100-R1809G::LEU2(HIS3), chk1::TRP1*	this study
GA-7075	GA-1981 with *mec1-100-D2104H::LEU2(HIS3), chk1::TRP1*	this study
GA-7077	GA-1981 with *mec1-100-F2244L::LEU2(HIS3), chk1::TRP1*	this study
GA-7183	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3), mrc1::TRP*	this study
GA-7185	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3), rad9::TRP1*	this study
GA-7187	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3), chk1::TRP1*	this study
GA-7189	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3), tel1::URA*	this study
GA-7191	GA-1981 with *mec1-100-F2244L::LEU2(HIS3), rad24::TRP1*	this study
GA-7192	GA-1982 with *mec1-100-F2244L::LEU2(HIS3), rad24::TRP1*	this study
GA-7193	GA-1981 with *mec1-100-D2104H::LEU2(HIS3), rad24::TRP1*	this study
GA-7194	GA-1982 with *mec1-100-D2104H::LEU2(HIS3), rad24::TRP1*	this study
GA-7199	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3), rad24::TRP1*	this study
GA-7200	GA-1982 with *mec1-100-Q1903E::LEU2(HIS3), rad24::TRP1*	this study
GA-7201	GA-1981 with *mec1-100-R1809G::LEU2(HIS3), rad24::TRP1*	this study
GA-7202	GA-1982 with *mec1-100-R1809G::LEU2(HIS3), rad24::TRP1*	this study
GA-7209	GA-1981 with *mec1-100::natMX, rad24::TRP1*	this study
GA-7218	GA-1981 with *mec1-100-T1612M::LEU2(HIS3), rad24::TRP1*	this study
GA-7219	GA-1982 with *mec1-100-T1612M::LEU2(HIS3), rad24::TRP1*	this study
GA-7220	GA-1981 with *mec1-100-D1127E::LEU2(HIS3), rad24::TRP1*	this study
GA-7221	GA-1982 with *mec1-100-D1127E::LEU2(HIS3), rad24::TRP1*	this study
GA-7268	GA-1981 with *ddc2::DDC2-GFP-kanMX*	this study
GA-7327	GA-1981 with *ddc2::DDC2-GFP-kanMX, mec1-100::natMX*	this study
W303 diploid	*MATa/MATα, ade2-1/ade2-1, trp1-1/trp1-1, his3-11/his3-11, his3-15/his3-15, ura3-1/ura3-1, leu2-3/leu2-3, leu2-112/leu2-112, can1-100/can1-100*	

GA-7668	W303 diploid with *ddc2::DDC2-3HA-URA3/DDC2, sml1::HIS3/SML1, RAD5/rad5-535*	this study
GA-7760	W303 diploid with *ddc2::DDC2-GFP-KanMX/DDC2, sml1::HIS3/SML1, RAD5+/RAD5+*	this study
GA-7761	W303 diploid with *ddc2::DDC2-3HA-URA3/ddc2::DDC2-GFP-KanMX, RAD5+/rad5-535*	this study
GA-7762	W303 diploid with *ddc2::DDC2-3HA-URA3/ddc2::DDC2-GFP-KanMX, mec1-100::LEU2(HIS3)/mec1-100::natMX, sml1::KanMX/SML1, RAD5+/rad5-535*	this study
GA-7763	W303 diploid with *ddc2::DDC2-3HA-URA3/ddc2::DDC2-GFP-KanMX, mec1::HIS3/mec1::TRP1, sml1::KanMX4/sml1::His3 RAD5+/rad5-535*	this study
GA-7764	GA-1981 with *mec1-100::natMX, dpb11Δc::hphMX*	this study
GA-7767	GA-1982 with *mec1-100-D2104H::LEU2(HIS3), , dpb11Δc::hphMX*	this study
GA-7768	GA-181 with *mec1-100-D1127E::LEU2(HIS3), dpb11Δc::hphMX*	this study
GA-7770	GA-1981 with *mec1-100-T1612M::LEU2(HIS3), dpb11Δc::hphMX*	this study
GA-7774	GA-1981 with *mec1-100-F2244L::LEU2(HIS3), dpb11Δc::hphMX*	this study
GA-7776	GA-1981 with *mec1-100-R1809G::LEU2(HIS3), dpb11Δc::hphMX*	this study
GA-7795	GA-181 with *dpb11Δc::hphMX*	this study
GA-7797	GA-1981 with *mec1-100-Q1903E::LEU2(HIS3), dpb11Δc::hphMX*	this study
GA-7907	GA-1981 with *ddc1::URA3*	this study
GA-7964	GA-1981 with *mec1-100::natMX, ddc1::URA3*	this study
GA-8605	GA-1981 with *dna2::Hyg, pBL584-DNA2(TRP1)*	this study
GA-8606	GA-1981 with *dna2::Hyg, pBL584-dna2-ΔN (TRP1)*	this study
GA-8607	GA-1981 with *dna2::Hyg, pBL584-dna2-2WA(TRP1)*	this study
GA-8608	GA-1981 with *mec1-100::natMX, dna2::Hyg, pBL584-DNA2(TRP1)*	this study
GA-8609	GA-1981 with *mec1-100::natMX, dna2::Hyg, pBL584-dna2-ΔN (TRP1)*	this study
GA-8610	GA-1981 with *mec1-100::natMX, dna2::Hyg, pBL584-dna2-2WA(TRP1)*	this study

Table 3.3: Mec1-Ddc2 co-precipitating proteins

Accession (UNIPROT/SGD)	log_2 protein ratio (wt/ mec100)		Description
	first expeirment	second experiment	
RAD52_YEAST/Rad52	-3.00	-4.22	DNA repair and recombination protein RAD52
H4_YEAST/Hhf1	-2.71	-2.97	Histone H4
H2B1_YEAST/Htb1	-2.48		Histone H2B.1
MSH2_YEAST/Msh2	-2.43	-1.30	DNA mismatch repair protein MSH2
RFA1_YEAST/Rfa1	-2.15	-2.40	Replication factor A protein 1
RFA3_YEAST/Rfa3	-2.09	-2.33	Replication factor A protein 3
RFA2_YEAST/Rfa2	-2.08	-2.04	Replication factor A protein 2
YO086_YEAST/YOL086W-A	-1.68	-1.38	Uncharacterized protein YOL086W-A
FBRL_YEAST/Nop1	-1.60	-3.14	rRNA 2'-O-methyltransferase fibrillarin
YG1T_YEAST/YGR042W	-1.46	-1.22	Uncharacterized protein YGR042W
ABF2_YEAST/Abf2	-1.15		ARS-binding factor 2, mitochondrial
SNU13_YEAST/Snu13	-1.08	-2.93	13 kDa ribonucleoprotein-associated protein
RL28_YEAST/Rpl28	-0.76		60S ribosomal protein L28
ACS2_YEAST/Acs2	-0.43	0.44	Acetyl-coenzyme A synthetase 2
LCD1_YEAST/Ddc2	-0.17	-0.08	DNA damage checkpoint protein LCD1
RL39_YEAST/Rpl39	-0.08	0.06	60S ribosomal protein L39
ATR_YEAST/Mec1	0.01	-0.27	Serine/threonine-protein kinase MEC1
RL9A_YEAST/Rpl9a	0.07	0.01	60S ribosomal protein L9-A
PMA1_YEAST/Pma1	0.19		Plasma membrane ATPase 1
RS7B_YEAST/Rpl26a	0.33		40S ribosomal protein S7-B
RL26A_YEAST/Rps7b	0.44	0.31	60S ribosomal protein L26-A
RL38_YEAST/Rpl38	0.46	0.29	60S ribosomal protein L38
HSP72_YEAST/Ssa2	0.47	-0.36	Heat shock protein SSA2
RL9B_YEAST/Rpl9b	0.51	0.09	60S ribosomal protein L9-B
RL2A_YEAST/Rpl2a	0.59		60S ribosomal protein L2-A
RS11A_YEAST/Rps11a	0.61	0.26	40S ribosomal protein S11-A
RS28A_YEAST/Rps28a	0.63		40S ribosomal protein S28-A
RL34A_YEAST/Rpl34a	0.73	-0.15	60S ribosomal protein L34-A
RS19A_YEAST/Rps19a	0.81		40S ribosomal protein S19-A
RL23A_YEAST/Rpl23a	0.82	-0.01	60S ribosomal protein L23-A
RS20_YEAST/Rps20	0.88	0.18	40S ribosomal protein S20
RS17A_YEAST/Rps17a	0.93	-1.62	40S ribosomal protein S17-A
RL36A_YEAST/Rpl36a	0.93		60S ribosomal protein L36-A
KPYK1_YEAST/Cdc19	1.05	0.53	Pyruvate kinase 1
RS29A_YEAST/Rps29a	1.05	0.79	40S ribosomal protein S29-A
RL13A_YEAST/Rpl13a	1.07	-0.02	60S ribosomal protein L13-A
G3P3_YEAST/Tdh3	1.08	0.15	Glyceraldehyde-3-phosphate dehydrogenase 3
RS14A_YEAST/Rps14a	1.08	-0.02	40S ribosomal protein S14-A
RS15_YEAST/Rps15	1.13	-0.12	40S ribosomal protein S15
PMG1_YEAST/Gpm1	1.14	0.22	Phosphoglycerate mutase 1
RS9B_YEAST/Rps9b	1.20	-0.03	40S ribosomal protein S9-B
RS25A_YEAST/Rps25a	1.21		40S ribosomal protein S25-A
RS3_YEAST/Rps3	1.25	0.40	40S ribosomal protein S3
RL19A_YEAST/Rpl19a	1.25		60S ribosomal protein L19-A
RL32_YEAST/Rpl32	1.25	-0.01	60S ribosomal protein L32
HSP77_YEAST/Ssc1	1.28		Heat shock protein SSC1, mitochondrial
RL17A_YEAST/Rpl17a	1.29	-0.41	60S ribosomal protein L17-A
ATPA_YEAST/Atp1	1.30		ATP synthase subunit alpha, mitochondrial
EF1A_YEAST/Tef1	1.32	0.09	Elongation factor 1-alpha
RS5_YEAST/Rps5	1.37		40S ribosomal protein S5
RL31A_YEAST/Rpl31a	1.38		60S ribosomal protein L31-A

ENO2_YEAST/Eno2	1.44	0.00	Enolase 2
RS12_YEAST/Rps12	1.45	-0.30	40S ribosomal protein S12
RS2_YEAST/Rps2	1.48	-0.18	40S ribosomal protein S2
FHP_YEAST/Yhb1	1.50		Flavohemoprotein
RS21A_YEAST/Rps21a	1.56	0.42	40S ribosomal protein S21-A
IF5A1_YEAST/Hyp2	1.60		Eukaryotic translation initiation factor 5A-1
RL12A_YEAST/Rpl12a	1.64	-0.33	60S ribosomal protein L12-A
RS26A_YEAST/Rps26a	1.66		40S ribosomal protein S26-A
RS27B_YEAST/Rps27b	1.66	0.04	40S ribosomal protein S27-B
RS18A_YEAST/Rps18a	1.66	0.17	40S ribosomal protein S18-A
ENO1_YEAST/Eno1	1.72		Enolase 1
EF3A_YEAST/Yef3	1.73	0.25	Elongation factor 3A
RL22A_YEAST/Rpl22a	1.74		60S ribosomal protein L22-A
ADH1_YEAST/Adh1	1.80	0.56	Alcohol dehydrogenase 1
PGK_YEAST/Pgk1	1.82	-0.25	Phosphoglycerate kinase
EF1B_YEAST/Efb1	1.82		Elongation factor 1-beta
CYS3_YEAST/Cys3	1.83		Cystathionine gamma-lyase
RL8A_YEAST/Rpl8a	1.83		60S ribosomal protein L8-A
CYPH_YEAST/Cpr1	1.84		Peptidyl-prolyl cis-trans isomerase
PDC1_YEAST/Pdc1	1.86	-1.29	Pyruvate decarboxylase isozyme 1
TPIS_YEAST/Tpi1	1.88		Triosephosphate isomerase
RL35A_YEAST/Rpl35a	1.91	-0.02	60S ribosomal protein L35-A
RL1A_YEAST/Rpl1a	1.94		60S ribosomal protein L1-A
RS24A_YEAST/Rps24a	1.97		40S ribosomal protein S24-A
STM1_YEAST/Stm1	1.97		Suppressor protein STM1
G6PI_YEAST/Pgi1	2.05		Glucose-6-phosphate isomerase
NACA_YEAST/Egd2	2.06		Nascent polypeptide-associated complex subunit alpha
HSP60_YEAST/Hsp60	2.10		Heat shock protein 60, mitochondrial
RL4A_YEAST/Rpl4a	2.11		60S ribosomal protein L4-A
HSP75_YEAST/Ssb1	2.11	0.29	Heat shock protein SSB1
RS16A_YEAST/Rps16a	2.12	0.07	40S ribosomal protein S16-A
SODC_YEAST/Sod1	2.14		Superoxide dismutase [Cu-Zn]
TCTP_YEAST/Tma19	2.14		Translationally-controlled tumor protein homolog
RL21A_YEAST/Rpl21a	2.15		60S ribosomal protein L21-A
RL10_YEAST/Rpl10	2.23		60S ribosomal protein L10
YRB1_YEAST/Yrb1	2.29		Ran-specific GTPase-activating protein 1
HSP71_YEAST/Hsp71	2.35	-0.93	Heat shock protein SSA1
VDAC1_YEAST/Por1	2.39		Mitochondrial outer membrane protein porin 1
ALF_YEAST/Fba1	2.39	0.55	Fructose-bisphosphate aldolase
RLA2_YEAST/Rpp2a	2.50		60S acidic ribosomal protein P2-alpha
TAL1_YEAST/Tal1	2.55		Transaldolase
TSA1_YEAST/Tsa1	2.58		Peroxiredoxin TSA1
RL14A_YEAST/Rpl14a	2.61		60S ribosomal protein L14-A
HXKB_YEAST/Hxk2	2.65		Hexokinase-2
RS13_YEAST/Rpl43a	2.72		40S ribosomal protein S13
RLA3_YEAST/Tdh2	3.10		60S acidic ribosomal protein P1-beta
RL43A_YEAST/Rpl43a	3.11		60S ribosomal protein L43-A
G3P2_YEAST/Tdh2	3.13	0.01	Glyceraldehyde-3-phosphate dehydrogenase 2
RL30_YEAST/Rpl30	3.13		60S ribosomal protein L30
BMH2_YEAST/Bmh2	3.21		Protein BMH2
HSC82_YEAST/Hsc82	3.37	0.62	ATP-dependent molecular chaperone HSC82
HSP7F_YEAST/Sse1	3.49		Heat shock protein homolog SSE1
RS7A_YEAST/Rps7a	3.57		40S ribosomal protein S7-A
RL4B_YEAST/Rpl4b	3.72		60S ribosomal protein L4-B
AHP1_YEAST/Ahp1	4.73		Peroxiredoxin type-2
RLA1_YEAST/Rpp1a	5.77		60S acidic ribosomal protein P1-alpha

TMA7_YEAST/Tma7	7.89		Translation machinery-associated protein 7
ADK_YEAST/Ado1	8.08		Adenosine kinase
RLA0_YEAST/Rpp0	12.92		60S acidic ribosomal protein P0
CAF17_YEAST/Iba57		0.47	Putative transferase CAF17, mitochondrial
EF2_YEAST/Eft1		0.32	Elongation factor 2
GAR1_YEAST/Gar1		-2.80	H/ACA ribonucleoprotein complex subunit 1
GAT1_YEAST/Gat1		0.97	Transcriptional regulatory protein GAT1
GDE_YEAST/Gdb1		0.75	Glycogen debranching enzyme
H2A1_YEAST/Hta1		-2.77	Histone H2A.1
H2B2_YEAST/Thb2		-3.36	Histone H2B.2
H3_YEAST/Hht1		-4.80	Histone H3
MAL31_YEAST/Mal31		1.00	Maltose permease MAL31
MSB1_YEAST/Msb1		1.10	Morphogenesis-related protein MSB1
MSH6_YEAST/Msh6		-0.84	DNA mismatch repair protein MSH6
NOP56_YEAST/Nop56		-0.85	(Q12460) Nucleolar protein 56
PEX3_YEAST/Pex3		-2.84	Peroxisomal biogenesis factor 3
PP4R3_YEAST/Psy2		-2.63	Serine/threonine-protein phosphatase 4 regulatory subunit 3
RIM1_YEAST/Rim1		-1.24	Single-stranded DNA-binding protein RIM1, mitochondrial
RL24A_YEAST/Rpl24a		-2.86	60S ribosomal protein L24-A
RL3_YEAST/Rpl3		0.38	60S ribosomal protein L3
RL8B_YEAST/Rpl8b		-0.07	60S ribosomal protein L8-B
RTF1_YEAST/Rtf1		0.02	RNA polymerase-associated protein RTF1
SGS1_YEAST/Sgs1		-1.30	ATP-dependent helicase SGS1
SMC5_YEAST/Smc5		-2.97	Structural maintenance of chromosomes protein 5
SMY2_YEAST/Smy2		0.29	Protein SMY2
SPO13_YEAST/Spo13		0.17	Meiosis-specific protein SPO13
SPT5_YEAST/Spt5		-0.17	Transcription elongation factor SPT5
SWR1_YEAST/Swr1		0.26	Helicase SWR1
UAP1_YEAST/Qri1		0.23	UDP-N-acetylglucosamine pyrophosphorylase
YB21A_YEAST/Ty2a-b		1.82	Transposon Ty2-B Gag polyprotein
YD11A_YEAST/YDL160C-A		2.58	Transposon Ty1-DR1 Gag polyprotein
YD160_YEAST/YDL160C-A		-0.89	Uncharacterized protein YDL160C-A
YE11A_YEAST/Ty1a-ER1		2.08	Transposon Ty1-ER1 Gag polyprotein

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CHAPTER 4: AN N-TERMINAL ACIDIC REGION OF SGS1 INTERACTS WITH RPA70 AND RECRUITS RAD53 KINASE TO STALLED FORKS

Anna Maria Hegnauer[1,2,6], Nicole Hustedt[1,2,6], Kenji Shimada[1], Brietta L Pike[1], Markus Vogel[1], Philipp Amsler[1,2], Seth M Rubin[3], Fred van Leeuwen[4], Aude Guéolé[5], Haico van Attikum[5], Nicolas H Thomä[1] and Susan M Gasser[1,2,*]

1. Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland, 2. Faculty of Sciences, University of Basel, Basel, Switzerland, 3. Department of Chemistry and Biochemistry, University of California, Santa Cruz, CA, USA, 4. Division of Gene Regulation, Netherlands Cancer Institute, Amsterdam, The Netherlands, 5. Department of Toxicogenetics, Leiden University Medical Center, Leiden, The Netherlands, 6. These authors contributed equally to this work

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AUTHOR CONTRIBUTIONS:

AMH performed yeast two hybrid, ChIP, recovery assay and Sgs1-RPA co-IP experiments, contributed to writing and assembled figures; NH performed E-MAP screen, western blots (Sgs1 *in vivo* phosphorylation, Rad53 phosphorylation and Sgs1 expression), Sgs1-Rad53 Co-IP and additional ChIP and recovery assay experiments, contributed to writing and assembled figures; KS advised, performed in *vitro kinase* assay experiments, contributed to writing and figures; BLP advised and contributed to writing; PA and MV purified proteins and cooperated on biochemical analyses; SMR performed and analysed ITC experiments; NHT advised MV, PA, and contributed to writing; HvA advised AG who generated strains used in the E-MAP analysis, and FvL hosted NH for same; SMG advised, interpreted results, planned experiments, contributed to writing, figures and funding of the project.

SUMMARY

DNA replication fork stalling poses a major threat to genome stability. This is counteracted in part by the intra-S phase checkpoint, which stabilizes arrested replication machinery, prevents cell-cycle progression and promotes DNA repair. The checkpoint kinase Mec1/ATR and RecQ helicase Sgs1/BLM contribute synergistically to fork maintenance on hydroxyurea (HU). Both enzymes interact with replication protein A (RPA). We identified and deleted the major interaction sites on Sgs1 for Rpa70, generating a mutant called sgs1-r1. In contrast to a helicase-dead mutant of Sgs1, sgs1-r1 did not significantly reduce recovery of DNA polymerase alpha at HU-arrested replication forks. However, the Sgs1 R1 domain is a target of Mec1 kinase, deletion of which compromises Rad53 activation on HU. Full activation of Rad53 is achieved through phosphorylation of the Sgs1 R1 domain by Mec1, which promotes Sgs1 binding to the FHA1 domain of Rad53 with high affinity. We propose that the recruitment of Rad53 by phosphorylated Sgs1 promotes the replication checkpoint response on HU. Loss of the R1 domain increases lethality selectively in cells lacking Mus81, Slx4, Slx5 or Slx8.

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An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks

Anna Maria Hegnauer[1,2,6], Nicole Hustedt[1,2,6], Kenji Shimada[1], Brietta L Pike[1], Markus Vogel[1], Philipp Amsler[1,2], Seth M Rubin[3], Fred van Leeuwen[4], Aude Guénolé[5], Haico van Attikum[5], Nicolas H Thomä[1] and Susan M Gasser[1,2,*]

[1]Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland, [2]Faculty of Sciences, University of Basel, Basel, Switzerland, [3]Department of Chemistry and Biochemistry, University of California, Santa Cruz, CA, USA, [4]Division of Gene Regulation, Netherlands Cancer Institute, Amsterdam, The Netherlands and [5]Department of Toxicogenetics, Leiden University Medical Center, Leiden, The Netherlands

DNA replication fork stalling poses a major threat to genome stability. This is counteracted in part by the intra-S phase checkpoint, which stabilizes arrested replication machinery, prevents cell-cycle progression and promotes DNA repair. The checkpoint kinase Mec1/ATR and RecQ helicase Sgs1/BLM contribute synergistically to fork maintenance on hydroxyurea (HU). Both enzymes interact with replication protein A (RPA). We identified and deleted the major interaction sites on Sgs1 for Rpa70, generating a mutant called *sgs1*-r1. In contrast to a helicase-dead mutant of Sgs1, *sgs1*-r1 did not significantly reduce recovery of DNA polymerase α at HU-arrested replication forks. However, the Sgs1 R1 domain is a target of Mec1 kinase, deletion of which compromises Rad53 activation on HU. Full activation of Rad53 is achieved through phosphorylation of the Sgs1 R1 domain by Mec1, which promotes Sgs1 binding to the FHA1 domain of Rad53 with high affinity. We propose that the recruitment of Rad53 by phosphorylated Sgs1 promotes the replication checkpoint response on HU. Loss of the R1 domain increases lethality selectively in cells lacking Mus81, Slx4, Slx5 or Slx8.

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Introduction

The accurate replication of DNA and its segregation into daughter cells is aided by the intra-S checkpoint, which is triggered by the single-stranded DNA (ssDNA) that accumulates when DNA polymerases pause, either due to reduced nucleotide concentration or due to the presence of adducts that impair fork progression. Avoidance of fork collapse is mediated both by the Mec1/ATR kinase and by the action of a RecQ helicase, which reverses fold-back structures and resolves strand exchange to suppress inappropriate recombination events. Resumption of replication generally requires that engaged DNA polymerases remain associated with paused forks, which in wild-type yeast cells can persist for many hours (reviewed in Cobb and Bjergbaek, 2006; Tourriere and Pasero, 2007 and Aguilera and Gomez-Gonzalez, 2008).

The checkpoint kinase Mec1-Ddc2 in *S. cerevisiae* (ATR-ATRIP in humans) plays two critical roles in this event (reviewed in Cimprich and Cortez, 2008 and Friedel *et al*, 2009). First, Mec1-Ddc2 regulates replisome function and enables the stable retention of replicative polymerases at very early origins like ARS607 (Cobb *et al*, 2003, 2005; De Piccoli *et al*, 2012). Second, it modifies and activates Rad53, the downstream checkpoint kinase that in turn retards cell-cycle progression, regulates levels of dNTPs and repair enzymes, represses the firing of late origins, and prevents fork collapse through poorly identified pathways (reviewed in Tourriere and Pasero, 2007; Segurado and Diffley, 2008).

The activation of Mec1/Ddc2 kinase under restricted nucleotide conditions (0.2 M hydroxyurea, HU) most likely stems from the stalling of leading and/or lagging strand DNA polymerases, which generates stretches of ssDNA. These become coated by replication protein A (RPA; Aparicio *et al*, 1999), which signals the recruitment and activation of Mec1-Ddc2 checkpoint kinase (Zou and Elledge, 2003), not unlike the situation at resected double-strand breaks (Dubrana *et al*, 2007). In both budding yeast and mammals, RPA contributes to the recruitment of Mec1/ATR to stalled or damaged replication forks, through its cofactor, Ddc2/ATRIP (Melo *et al*, 2001; Rouse and Jackson, 2002). Intriguingly, RPA is itself a target of Mec1/ATR phosphorylation (Brush *et al*, 1996; Zou and Elledge, 2003).

Besides RPA, fork-associated activators of the intra-S phase checkpoint include the 9-1-1 checkpoint clamp and Dbp11/TOPBP1 (Majka *et al*, 2006; Mordes *et al*, 2008; Navadgi-Patil and Burgers, 2008), while additional, unidentified co-activators are postulated to exist (Navadgi-Patil and Burgers, 2011). Once recruited Mec1/ATR phosphorylates Mrc1/Claspin, which helps activate the downstream effector kinases Rad53/CHK2, or CHK1 in mammalian cells (reviewed in Tourriere and Pasero, 2007), possibly by facilitating the contact between Mec1 and its target Rad53 (Chen and Zhou, 2009). In mammals, the RecQ helicase BLM was also reported to be a target of ATR/ATM phosphorylation, and to contribute to recovery from replicative stress (Davies *et al*, 2004; Rao *et al*, 2005).

Whereas the Rad53 kinase mediates crucial downstream events in the yeast checkpoint response, Mec1/ATR has a distinct role in stabilizing replicative polymerases, particu-

*Corresponding author. Friedrich Miescher Institute for Biomedical Research, Maulbeerstrasse 66, Basel 4058, Switzerland.
Tel.: +41 61 697 7255; Fax: +41 61 697 3976;
E-mail: susan.gasser@fmi.ch
[6]These authors contributed equally to this work

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larly at early firing origins, such as the budding yeast ARS607 or ARS305. This was demonstrated by chromatin immunoprecipitation (ChIP) from cells synchronously arrested in S phase: the recovery of DNA polymerases α and ε bound to the replication fork dropped rapidly in cells lacking Mec1, but not in cells lacking Rad53 (Cobb *et al*, 2003, 2005). Similar separation of function was demonstrated in a study of *exo1* deletion effects on viability in *rad53* versus *mec1* mutants (Segurado and Diffley, 2008). Nonetheless, a loss of Rad53 triggers an accumulation of both ssDNA (Sogo *et al*, 2002; Tourriere and Pasero, 2007) and recombination intermediates (Lucca *et al*, 2004). Surprisingly, and in contrast to the situation at early firing origins, it was recently reported that the replisome can be recovered largely intact and associated with later firing origins upon replication stress, in cells lacking either Mec1 or Rad53 (De Piccoli *et al*, 2012). These checkpoint kinases were proposed to regulate replication fork progression through multiple targets, including Psf1, a component of the replicative Cdc45-MCM-GINS helicase (De Piccoli *et al*, 2012).

RecQ helicases have also been shown to be important for the stable binding of DNA polymerases at stalled replication forks and for efficient fork restart after exposure to HU or aphidicolin (Cobb *et al*, 2005; Davies *et al*, 2007; Bachrati and Hickson, 2008; Pirzio *et al*, 2008). Loss of Sgs1, the unique RecQ helicase in budding yeast, leads to a reduced recovery of DNA polymerases at early firing origins, a lower survival rate after exposure to HU (Cobb *et al*, 2003, 2005), and the accumulation of aberrant recombination structures after exposure to MMS (Liberi *et al*, 2005). Indeed, *sgs1* deficient cells display abnormally high levels of recombination (Watt *et al*, 1996) and spontaneous gross chromosomal rearrangements (GCRs), particularly on HU (Myung and Kolodner, 2002; Schmidt and Kolodner, 2006). The role of RecQ helicases in resistance to replicative stress is conserved: mutations in three human RecQ helicases (BLM, Bloom's; WRN; Werner's, and RECQ4) cause syndromes associated with a predisposition to cancer and/or genome instability (reviewed by Bachrati and Hickson, 2008 and Ashton and Hickson, 2010).

Genetic studies argue that Sgs1 acts both in complex with Top3 and Rmi1 (Gangloff *et al*, 1994; Chang *et al*, 2005; Mullen *et al*, 2005) and alone (reviewed in Bernstein *et al*, 2010). Sgs1 requires Top3 for dissolution of Holliday junctions and for enhancing DNA polymerase at stalled forks (Liberi *et al*, 2005; Mankouri *et al*, 2011), while it acts independently of Top3 to activate Rad53 in the presence of HU (Bjergbaek *et al*, 2005). Sgs1, like BLM and WRN, also binds Rad51 and RPA, and acts both upstream and downstream of Rad51-mediated strand invasion, to prevent and to resolve recombination intermediates. Finally, synthetic lethal screens link Sgs1 not only to recombination enzymes, but also to enzymes and proteins essential for lagging strand synthesis, such as Pol32, RNase H2 and FEN1/Rad27 (Ooi *et al*, 2003; Tong *et al*, 2004; Ii and Brill, 2005).

Here, we focus on the role of Sgs1 at replication forks stalled by HU, which seems to mimic the situation that ensues when forks encounter tight DNA–protein complexes (reviewed in Aguilera and Gomez-Gonzalez, 2008). Double mutants in budding yeast have been particularly helpful in elucidating this pathway. Whereas the effects of *sgs1*Δ are relatively mild (Cobb *et al*, 2003), its combination with *mec1*-100, an S phase-specific mutation in Mec1, causes extensive fork collapse and a failure of nucleotide incorporation after recovery from acute exposure to HU (Cobb *et al*, 2005). The *mec1*-100 mutation compromises the intra-S phase checkpoint response, but is able to modify and activate Rad53, triggering the G2/M checkpoint (Paciotti *et al*, 2001). Importantly, and in contrast to the effects of *mec1*-100, deletion of *rad53* is not additive with *sgs1*Δ in GCR or polymerase stability assays. Indeed, neither the loss of checkpoint activity in the *rad53*-11 mutant nor *rad53* deletion coupled with *sml1*Δ affects polymerase recovery by ChIP at early firing origins (Cobb *et al*, 2003, 2005).

The fact that Sgs1, Mec1-Ddc2 and DNA pol α all bind RPA, led us to test the hypothesis that Sgs1 influences the association of lagging strand polymerases at stalled forks through its interaction with the ssDNA binding complex. To this end, we mapped the region of Sgs1 that binds RPA and generated a mutant lacking the interaction domain, which we call *sgs1*-r1. We monitored the status of DNA pol α at stalled forks in mutants lacking the main RPA-interaction domain, with and without Sgs1 helicase activity. We found that the Sgs1 helicase activity and not its RPA interacting domain contributes to the stabilization of engaged DNA pol α/primase at the HU-stalled replication fork. Moreover, we show that Mec1-Ddc2 modifies Sgs1 within the RPA-interaction domain, and that once phosphorylated, Sgs1 has a significant affinity for the FHA1 phospho-threonine binding module of the downstream checkpoint kinase Rad53. We propose that the interaction of Sgs1 and Rad53 contributes to checkpoint kinase activation during replicative stress, independent of the role of Sgs1 helicase activity in stabilizing polymerases at the fork.

Results

Sgs1 interacts with Rpa70 through an acidic region N-terminal of the helicase domain

To analyse the role of Sgs1 in stabilizing lagging strand polymerases at stalled forks, we first mapped the Sgs1–RPA interaction site. Sgs1 contains three conserved domains that are characteristic of RecQ helicases: an SF2-type helicase domain, an RQC (RecQ C-terminal) motif and an HRDC (helicase and RNase D C-terminal) domain (Figure 1A). In addition, a region of unknown structure in the N-terminus of Sgs1 (first 158 aa) has been shown to interact with Top3/Rmi1 (Bennett *et al*, 2000; Fricke *et al*, 2001; Chen and Brill, 2007; Weinstein and Rothstein, 2008). There is both an acidic block at aa 664 and a larger acidic region located N-terminal of the helicase domain. Although structure prediction suggests that this region is intrinsically disordered in solution, it has been proposed to help prevent or resolve aberrant recombination structures at MMS-treated forks (Bernstein *et al*, 2009). To see which domain is responsible for binding to RPA, we fused fragments containing the functional domains of Sgs1 to a B42 transactivation domain (B42-AD) and performed yeast two-hybrid (Y2H) analysis with RPA (Figure 1A).

RPA is an evolutionarily conserved heterotrimeric protein, consisting of Rpa70, Rpa32 and Rpa14 (names based on molecular weight, or Rpa1, Rpa2 and Rpa3, based on gene names). The smallest subunit, Rpa14, is believed to mediate protein–protein interaction only within the RPA complex, while Rpa70 and Rpa32 were shown to bind other proteins

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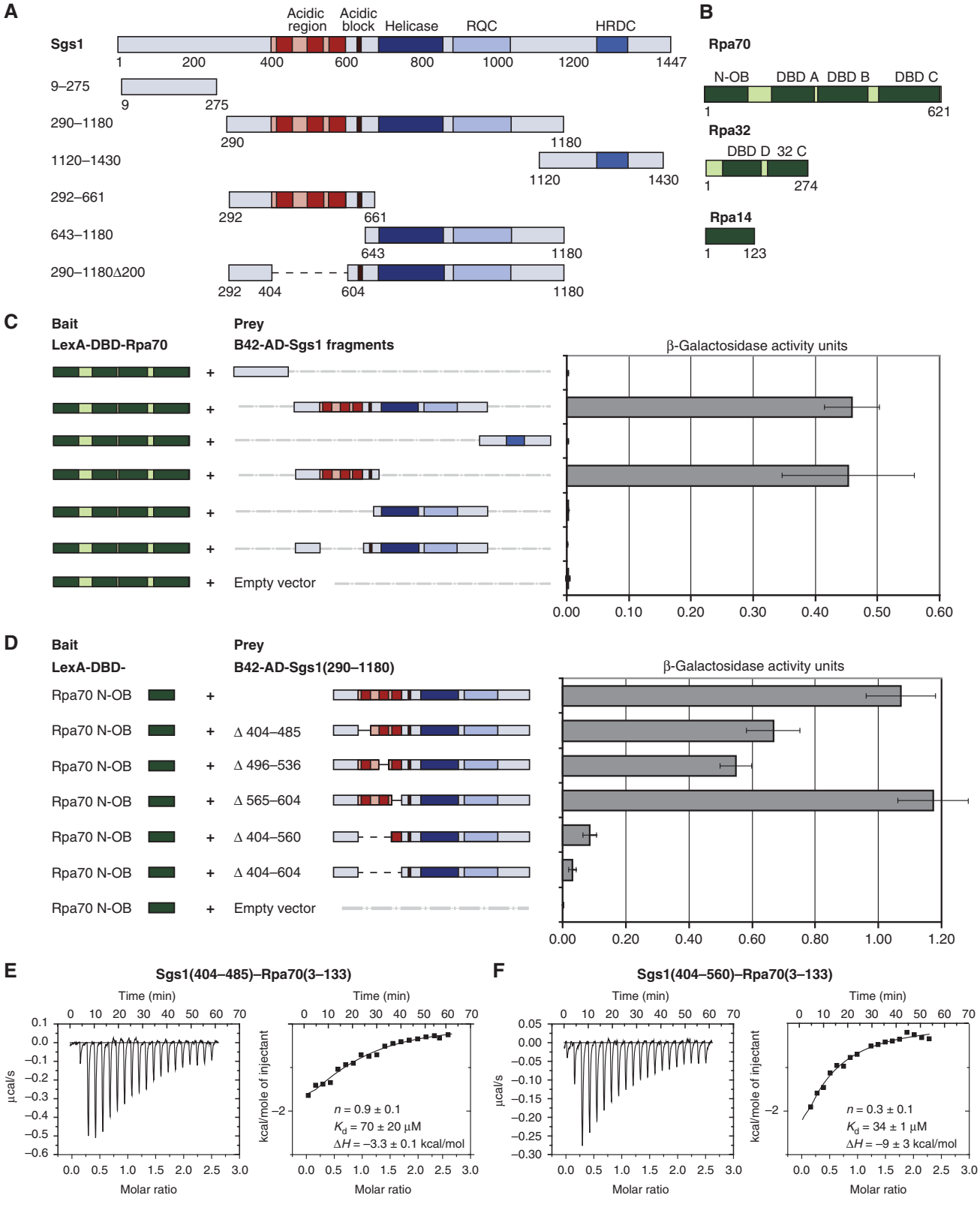
(Binz *et al*, 2004; Zou *et al*, 2006). We therefore expressed full-length Rpa70 and Rpa32 fused to the LexA-DNA binding domain (LexA-DBD) under control of a galactose inducible promoter, as bait in the Y2H assay (Figure 1B). Strong interactions were scored between the largest subunit Rpa70 and the large core of the Sgs1 enzyme (aa 290–1180; Figure 1C; Supplementary Figure S1A), while Rpa32 showed a very weak β-galactosidase signal in the Y2H assay with Sgs1 (Supplementary Figure S1B). A 400-aa fragment containing only the acidic region N-terminal of the Sgs1 helicase domain bound Rpa70 as efficiently as a larger fragment (Figure 1C). Within this region, we identified three sequences of 35–41 aa



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by BLAST and Quick2D analysis, which are conserved among close homologues of the *S. cerevisiae* enzyme (dark red boxes, Figure 1; aa 404–485, aa 496–536 and aa 565–604). To test the importance of these conserved sequences for the Sgs1–Rpa70 interaction, we removed them by deleting aa 404–604 in the Sgs1-B42-AD construct. Consistently, this deletion abolished Y2H interaction between Rpa70 and Sgs1 (Figure 1C). Similarly, we mapped the interaction site on Rpa70 by fusing Rpa70 subdomains to the LexA-DBD and monitoring their interaction with the Sgs1(290–1180)-B42-AD fusion. The highest β-galactosidase activity was measured for the N-terminal oligonucleotide binding fold (N-OB) of Rpa70 without the linker region (Supplementary Figure S1A).

Sgs1 bears multiple interaction sites for the Rpa70 N-OB fold

To see if each conserved repeat within the Sgs1 acidic domain contributed equally to the interaction, we created three Sgs1-B42-AD deletion constructs each lacking only one of the three conserved sequences (Sgs1(290–1180, Δ404–485), Sgs1(290–1180, Δ496–536) and Sgs1(290–1180, Δ565–604)). These constructs were tested for interaction with the Rpa70 N-OB fold (Rpa70(1–133)) by Y2H analysis (Figure 1D). Deletion of the first or second conserved sequence (Sgs1(290–1180, Δ404–485) or Sgs1(290–1180, Δ496–536)) cut the β-galactosidase signal in half, while deletion of the third conserved sequence (Sgs1(290–1180, Δ565–604)) had no effect. This suggests that Sgs1 binds the RPA70 N-OB fold through two sites, aa 404–485 and aa 496–536. Indeed, deletion of the first two of the three motifs (aa 404–560 in Sgs1-B42-AD), abolished the interaction with the N-OB fold of Rpa70 almost as efficiently as deleting the entire 200 aa region, arguing that two related motifs spanning from aa 404 to 485 and aa 496 to 536, mediate the interaction with Rpa70.

We confirmed that these regions of Sgs1 and Rpa70 interact directly by performing an isothermal titration calorimetry (ITC) assay with purified recombinant proteins (Figure 1E and F). We found that both Sgs1(404–485) and Sgs1(404–560) bound RPA70(3–133) with similar affinity ($K_d = 70 \pm 20\,\mu M$ and $K_d = 34 \pm 1\,\mu M$, respectively). The ITC data suggested differences in the complex stoichiometry (n) and molar enthalpy (ΔH) between the two Sgs1 fragments: it appears that the more N-terminal motif of Sgs1 (aa 404–485) binds one molecule of the RPA70 N-OB fold, while the larger domain (aa 404–560) is able to bind two. This suggests that Sgs1 might be able to bind multiple RPA complexes, possibly leading to RPA delivery and/or removal as Sgs1 unwinds duplex DNA.

The Sgs1–RPA interaction site is structurally isolated from the helicase domain and its deletion does not affect protein stability

To determine whether this region of Sgs1 is also important for interaction with RPA *in vivo*, we deleted amino acids 404–604 within the *SGS1* chromosomal locus using a PCR-based allele-replacement technique. The resulting allele (*sgs1*-r1; Figure 2A), C-terminally tagged by 13Myc, is expressed when tested by western blot analysis on whole cell extracts (Figure 2B and C, inputs). The signal for sgs1-r1–13Myc is slightly stronger than for wild-type Sgs1–13Myc, which may either reflect a better blotting efficiency or slightly improved stability. This deletion leaves intact the aa 664 shown to be important for resolving recombination intermediates, and is distinct from the previously published AR2 deletion, which reduced Sgs1 levels (Bernstein *et al*, 2009).

To monitor the interaction of the sgs1-r1 mutant protein with RPA *in vivo*, we performed co-immunoprecipitation (co-IP) experiments with appropriately tagged proteins. Strains expressing Rpa70–3HA and either 13Myc-tagged Sgs1 or sgs1-r1 were released from G1 phase for 20 min to allow cells to accumulate in S phase. Rpa70–3HA and Sgs1-13Myc were efficiently precipitated as a complex using either anti-Myc antibody (Figure 2C) or anti-HA (Supplementary Figure S2). In the sgs1-r1–13Myc precipitation, the efficiency of Rpa70 recovery was reduced roughly two-fold (Figure 2C), as was the reciprocal recovery (sgs1-r1 by Rpa70, Supplementary Figure S2). This suggests that the deleted domain indeed mediates Sgs1–RPA interaction *in vivo*, although other contacts may support interactions in the context of the holo-RPA complex. Indeed, residual binding could be explained by the interaction detected between Sgs1 and Rpa32 (Supplementary Figure S1B), through a site unaffected by the *sgs1*-r1 mutation, or by an indirect interaction of sgs1-r1–13Myc and Rpa70–3HA to DNA.

To ensure that the sgs1-r1 protein retained helicase activity, despite the reduced interaction with RPA, we tested the ability of *sgs1*-r1 to support growth in a *srs2* null background. Rothstein and colleagues have shown that the helicase activity of Sgs1 is essential for growth in the absence of the Srs2 helicase (Weinstein and Rothstein, 2008). Tetrad analysis confirms that spores containing helicase-dead Sgs1 (K706R or *sgs1*-hd) in combination with *srs2*Δ showed almost no growth, while the *sgs1*-r1 *srs2*Δ double mutant spores grew normally (Figure 2D). We conclude that *sgs1*-r1 retains helicase activity, consistent with its weak suppression of *top3*Δ slow growth (Supplementary Figure S3).

We next tested whether the *sgs1*-r1 allele yields the same levels of sensitivity to DNA damage as *sgs1*Δ in drop assays. This assay monitors the capacity of cells to repair DNA

Figure 1 Mapping the interaction site between Sgs1 and Rpa70. (**A**) Schematic representation of Sgs1 and its functional domains. Dark and light red—largely disordered acidic region, dark red—sequences that are conserved in close homologues of *S. cerevisiae*; other domains labelled in figure. RQC = RecQ C-terminal motif, HRDC = helicase and RNase D C-terminal. Below are the Sgs1 domains used in Y2H experiments, which were fused to the B42 activation domain (B42-AD) in pJG46 and expressed under a galactose-inducible promoter. Numbers indicate the boundaries of the Sgs1 domains in aa. (**B**) Scheme of the RPA subunits with their functional domains. Rpa70 and Rpa32 were fused to the lexA-DNA binding domain (lexA-DBD) in pGAL-lexA, expressed under a galactose-inducible promoter and subjected to Y2H analysis. N-OB = N-terminal OB fold, DBD = DNA binding domain, 32 C = Rpa32 C-terminus. (**C**) Y2H analysis between Rpa70 fused to lexA-DBD and Sgs1 fragments fused to B42-AD was performed using a quantitative β-galactosidase assay as described in Materials and methods. Error bars indicate standard error of four or more independent transformants. (**D**) Y2H analysis between Rpa70 N-OB fused to lexA-DBD and Sgs1 fragments fused to B42-AD with different deletions of the three conserved regions within the RPA binding site. (**E**, **F**) Isothermal titration calorimetry (ITC) experiment of Rpa70(3–133) with Sgs1(aa 404–485) and Sgs1(aa 404–560). The dissociation constant (K_d), stoichiometry (n) and molar enthalpy (ΔH) are indicated within the figure.

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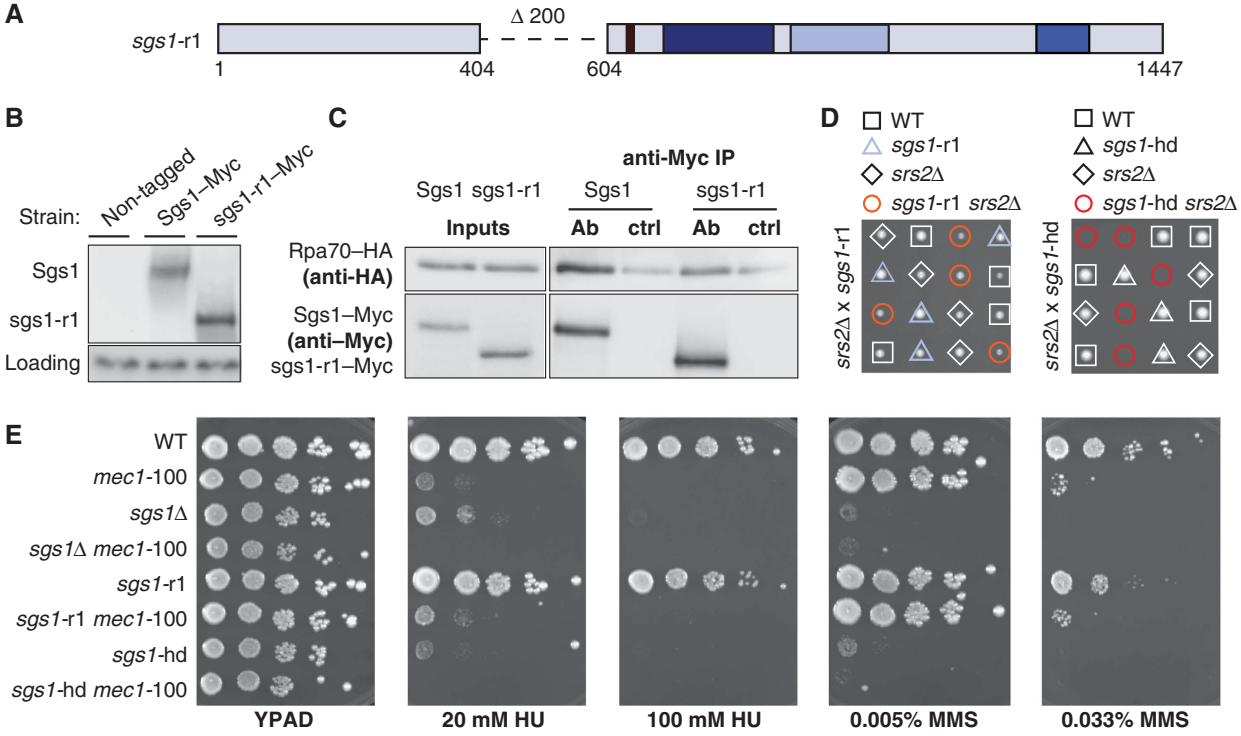

Figure 2 Loss of the acidic region in Sgs1 impairs Sgs1–RPA interaction *in vivo*. (**A**) Schematic representation of *sgs1*-r1: a new allele generated by deleting the acidic region (aa 404–604) at the endogenous *SGS1* locus. The deleted region is indicated by a dashed line. Black = acidic block, dark blue = helicase domain, light blue = RQC domain, blue = HRDC domain. (**B**) Wild type and sgs1-r1 were C-terminally fused to 13Myc epitopes at the endogenous *SGS1* locus (Sgs1–13Myc; GA-5311, sgs1-r1–13Myc; GA-5313) and expression levels were analysed by western blot with anti-Myc antibody. Non-tagged strain (GA-7249) was used as a negative control. Anti-actin was used to detect Act1 as a loading control. (**C**) Co-IP of exponentially growing 13Myc-tagged Sgs1 (GA-1759) or sgs1-r1 (GA-5316) with 3HA-tagged Rpa70. Exponentially growing cells were collected for IP using Dynabeads either coupled to monoclonal anti-Myc (AB) or not (ctrl). Western blots were probed with anti-Myc (9E10) for Sgs1 or sgs1-r1 and anti-HA (F-7) for Rpa70. (**D**) *sgs1*-r1 (GA-4848) and *srs2*Δ (GA-1805), as well as *sgs1*-hd (GA-5445) and *srs2*Δ (GA-5334) mutants were crossed and sporulated and tetrad analysis was performed. (**E**) Ten-fold serial dilutions of the following strains were plated onto YPAD, ± 20 mM or 100 mM HU, 0.005% or 0.033% MMS: GA-1981 (WT), GA-4978 (*mec1*-100), GA-5457 (*sgs1*Δ), GA-4967 (*sgs1*Δ *mec1*-100), GA-5076 (*sgs1*-r1), GA-5077 (*sgs1*-r1 *mec1*-100), GA-5445 (*sgs1*-hd) and GA-5447 (*sgs1*-hd *mec1*-100).

damage induced by different genotoxic drugs. Previous work has shown that *sgs1*Δ is sensitive to low concentrations of the replication fork inhibitor HU and the alkylating agent MMS, and that this phenotype is dramatically enhanced when *sgs1*Δ is coupled to the S phase-specific Mec1 mutant, *mec1*-100 (Cobb *et al*, 2005). As described previously, we observed that both *sgs1*Δ and the helicase-dead mutant *sgs1*-hd are sensitive to HU and MMS, and show synthetic sensitivity when combined with the *mec1*-100 allele (Figure 2E). This was not observed for the *sgs1*-r1 mutant, although it did show a mild sensitivity to high concentrations of MMS (0.033% MMS, Figure 2E). Surprisingly, no additive effects were seen when *sgs1*-r1 *mec1*-100 cells were compared with the single *mec1*-100 mutant, suggesting that either *sgs1*-r1 acts on the same pathway as *mec1*-100 or it simply does not affect survival during persistent replicative stress (Figure 2E).

The Sgs1 helicase function, but not its R1 domain, stabilizes DNA pol α on HU

Given that fork restart after prolonged exposure to HU requires different activities than does growth under persistent damage, we next arrested S-phase cells in 0.2 M HU for 2–6 h, and quantitatively measured cell survival after plating on HU-free YPAD (Figure 3A). Similar to the lack of sensitivity observed on HU-containing plates, we found that *sgs1*-r1 did not confer sensitivity to this acute HU treatment. Unlike the *sgs1*Δ *mec1*-100 or *sgs1*-hd *mec1*-100 double mutants (Figure 3A), the *sgs1*-r1 *mec1*-100 combination showed no additive or synergistic effects. This suggested that strong RPA-Sgs1 binding is not crucial for fork recovery after HU-induced replication fork arrest.

We next tested the effects of *sgs1*-r1 on DNA pol α association at replication forks arrested on HU. We performed ChIP for DNA pol α after synchronizing single and double mutants in G1 and releasing them into S phase in the presence of 0.2 M HU. Over 1 h, the abundance of DNA-bound DNA pol α was quantified by real-time PCR analysis of the recovered DNA, using primers that amplify the early firing origin ARS607 and the late firing origin ARS522 (formerly ARS501; Figure 3E). As a negative control, a primer set placed 14 kb away from ARS607 was analysed and used to normalize the absolute enrichment at ARS607 or ARS522. As previously reported (Cobb *et al*, 2005), *sgs1*Δ or *mec1*-100 cells yield lower recoveries of DNA pol α at HU-arrested replication forks (Figure 3B, black solid and stippled lines). This effect is additive when both mutations are combined, resulting in complete loss of DNA pol α from the stalled fork (Figure 3B, blue stippled line). The *sgs1*-r1 mutant showed a much weaker displacement of DNA pol α than *sgs1*Δ, and was not additive when combined with the *mec1*-100 mutation (Figure 3B, second panel). Similar results were obtained, when we scored DNA pol α association at two other early

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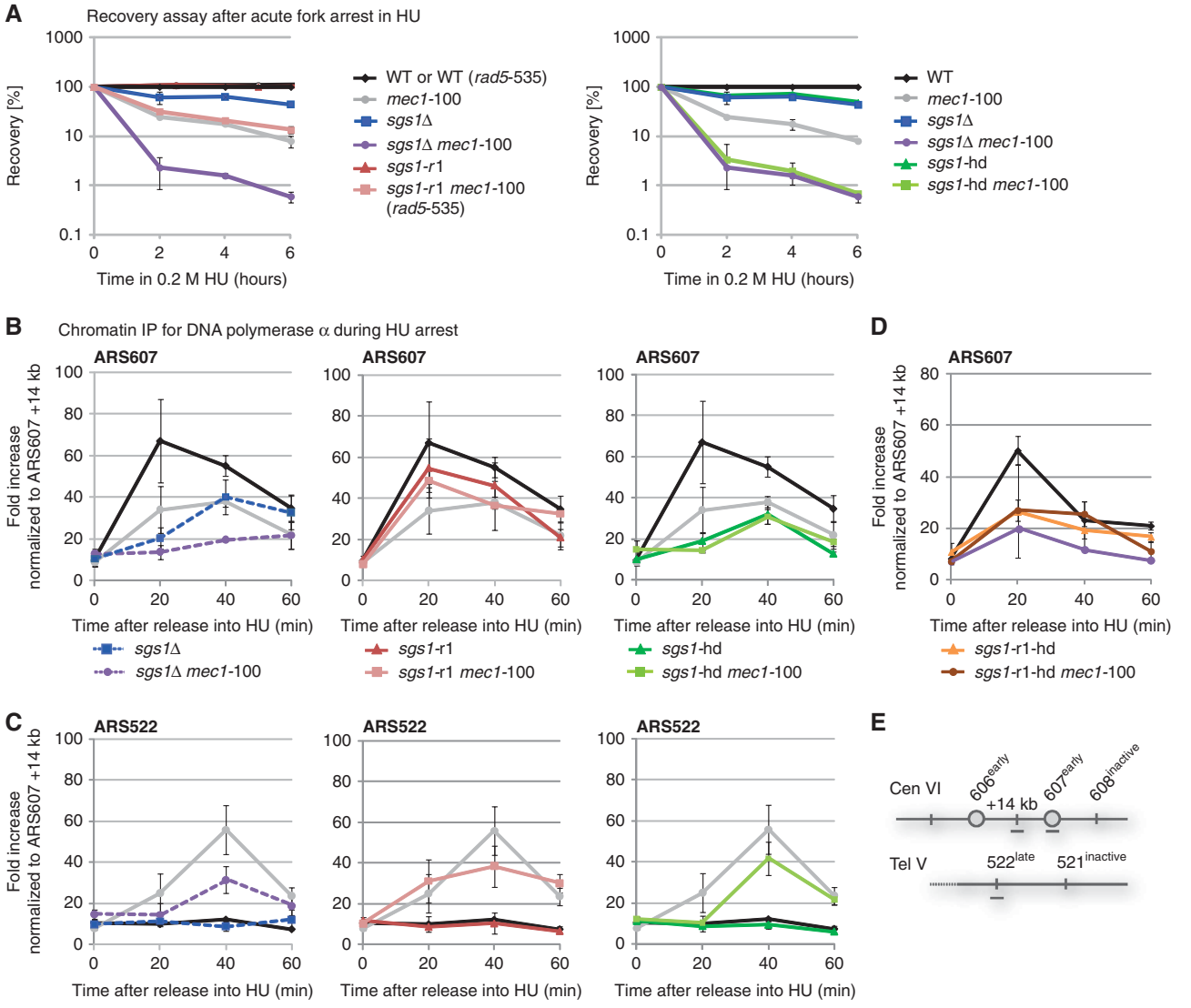

Figure 3 *sgs1*-r1 does not destabilize DNA pol α from HU-stalled replication forks in contrast to a helicase-deficient *sgs1* mutant. (**A**) Recovery from replication fork stalling was monitored as colony outgrowth of cells which were synchronized in G1 by α-factor arrest and released into S phase in the presence of 0.2 M HU for the indicated times. Strains used were GA-1981 (WT), GA-180 (WT *rad5*-535), GA-5457 (*sgs1*Δ), GA-4978 (*mec1*-100), GA-4967 (*sgs1*Δ *mec1*-100), GA-5076 (*sgs1*-r1), GA-4504 (*sgs1*-r1 *mec1*-100 rad5-*535*), GA-5445 (*sgs1*-hd) and GA-5447 (*sgs1*-hd *mec1*-100). 0 min after release indicates G1 phase. (**B**, **C**) ChIP was performed on synchronized cultures released into S phase in the presence of 0.2 M HU. 3HA-tagged DNA pol α was precipitated with monoclonal anti-HA antibody (F-7) coupled to Dynabeads. Strains used were GA-4973 (WT), GA-4974 (*mec1*-100), GA-5055 (*sgs1*-r1), GA-5075 (*sgs1*-r1 *mec1*-100), GA-5449 (*sgs1*-hd) and GA-5451 (*sgs1*-hd *mec1*-100). The ChIP data for *sgs1*Δ and *sgs1*Δ *mec1*-100 from Cobb *et al* (2005) are shown for comparison (indicated by the dashed lines). The relative enrichment for ARS607 or ARS522 was obtained by normalizing the absolute enrichment at ARS607 or ARS522 for each time point to the absolute enrichment at a locus 14 kb away from ARS607. Mutant strains are indicated using the same colour code as in (**A**). (**D**) ChIP was performed as described above using strains GA-4973 (WT), GA-6266 (*sgs1*-r1-hd), GA-6260 (*sgs1*-r1-hd *mec1*-100) and GA-4975 (*sgs1*Δ *mec1*-100). (**E**) Primers (grey bars) used for ChIP that amplify the genomic regions corresponding to the early firing origin ARS607, a region 14 kb away from ARS607 (+14 kb) and the late firing origin ARS522 are shown.

firing origins, ARS306 and ARS606, while ARS603.5, which fires in mid-S phase, displayed a pattern similar to the late origin ARS522 (Supplementary Figure S4).

Because HU treatment activates the intra-S phase checkpoint response, late firing origins like ARS522 are repressed, and show no DNA pol α in wild-type cells (Figure 3C, black line). However, due to the compromised intra-S-phase checkpoint in *mec1*-100 cells, DNA pol α is detected at the late firing origin ARS522, by 40 min on HU (Figure 3C, grey line). Interestingly, loss of Sgs1 combined with *mec1*-100 reduces polymerase recovery at this late origin firing, or else partially maintains repression. However, the *sgs1*-r1 mutation alone did not promote late origin firing, and was largely epistatic with *mec1*-100 for late origin activation (Figure 3C, second panel). Similar effects were observed at the mid-to-late firing origin ARS603.5 (Supplementary Figure S4). We conclude that deletion of a major Sgs1–RPA interaction domain has little or no effect on DNA pol α binding at HU-arrested forks, consistent with the colony outgrowth assay in Figure 3A.

Given that the R1 deletion did not affect polymerase binding, nor act synergistically with *mec1*-100 like *sgs1*Δ, we examined if Sgs1 helicase activity is responsible for these functions. By performing ChIP in the *sgs1*-hd (K706R) and the *sgs1*-hd *mec1*-100 double mutant (Figure 3B and C,

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third panel), we scored a significant destabilization of DNA pol α at the HU-stalled fork, comparable to *sgs1*Δ. This shows that the enzymatic activity of Sgs1 helicase is indeed critical for DNA pol α stabilization. However, the *sgs1*-hd mutation was not additive with *mec1*-100; the double mutant showed the same level of residual DNA pol α recovery as *sgs1*-hd alone (Figure 3B). Thus, whereas *sgs1*-hd and *mec1*-100 are synergistic in the recovery assay (Figure 3A), they are not with respect to polymerase stability. The *sgs1*Δ and *mec1*-100 defects, on the other hand, are additive in both assays (Cobb *et al*, 2005).

To see if a strain that carries both the R1 deletion and helicase deficiency in Sgs1 (*sgs1*-r1-hd) shows even stronger polymerase destabilization, we tested this strain alone and in combination with *mec1*-100. However, *sgs1*-r1-hd *mec1*-100 cells resemble *sgs1*-r1-hd for polymerase ChIP, with neither completely displacing DNA pol α from ARS607 (Figure 3D). We conclude that the helicase function of Sgs1, and not its interaction with RPA, is crucial for stabilizing DNA pol α at stalled replication forks. We note that other Sgs1 functions may contribute to lagging strand replisome retention, given that *sgs1*-r1-hd *mec1*-100 cells still retain low levels of polymerase on HU-stalled forks. Consistently, *sgs1*-r1-hd mutants grew better than *sgs1*Δ cells on 10 mM HU, although both display synergistic lethality with *mec1*-100 (Supplementary Figure S5).

The sgs1-r1 mutant is a separation-of-function mutant that does not cause synthetic defects with replication mutants

To shed light on the function of the R1 domain within Sgs1, we next compared the behaviour of *sgs1*Δ and *sgs1*-r1 in a synthetic lethal screen against a sublibrary of yeast deletion strains. Previously, Collins *et al* (2007) had sorted 743 *S. cerevisiae* genes using hierarchical clustering according to the similarity of their genetic interaction profiles, which allowed them to distinguish functionally multi-protein complexes and to group different protein complexes into pathways. We performed a similar epistasis analysis (epistasis miniarray profile, E-MAP), comparing the interaction profiles of *sgs1*Δ and *sgs1*-r1 cells with 1536 genes involved in various chromatin functions (Guénole *et al*, under review). For this, we created four sets of double mutants in two independent experiments using a high-throughput setup (Schuldiner *et al*, 2006). Genetic interactions were quantified by calculating scores based on colony sizes of double mutants (Collins *et al*, 2006). Threshold levels of genetic interaction scores equal or lower than -2 and equal or higher than $+2$ were used to define negative (synthetically sick, blue) or positive (epistatic or suppressive, yellow) genetic interactors. In Figure 4A, we list genes showing genetic interaction with either *sgs1*Δ or *sgs1*-r1 in two independent experiments (bold), and genes that were previously shown to be synthetically lethal with *sgs1*Δ (in red; Ooi *et al*, 2003; Tong *et al*, 2004), along with other genes falling within the relevant functional clusters (Collins *et al*, 2007).

In the E-MAP, the *sgs1*-r1 mutant displayed a distinct interaction profile from either that of *sgs1*Δ or wild-type cells (Figure 4A). There are a few clear conclusions from this analysis. Importantly, *sgs1*-r1 did not display negative interaction with replication mutants. In particular, *sgs1*-r1 shows mildly improved growth with strains that lack enzymes involved in lagging strand synthesis, such as Rad27, Pol32 and RNAseH2 (Qiu *et al*, 1999; Arudchandran *et al*, 2000; Ii and Brill, 2005), whereas the *sgs1*Δ mutant showed synthetic sickness with these strains, even under non-damaging conditions. Neither query strain scored negatively with genes involved in homologous recombination, perhaps because the screen was performed under non-damaging conditions. Nonetheless, several interactions stand out as having negative synthetic effects with *sgs1*-r1, namely *mus81*Δ and *wss1*Δ. Mus81 works together with Mms4 as a Holliday junction resolvase that is thought to work together with Sgs1–Top3–Rmi1 to process homologous recombination repair (HRR) intermediates that occur behind replication forks (for review, Hickson and Mankouri, 2011). Wss1 is a SUMO peptidase associated with Slx5/Slx8, the SUMO-dependent Ubiquitin ligase required for telomere-telomere recombination and recovery from fork collapse (Mullen *et al*, 2010; Nagai *et al*, 2011).

We confirmed the strongly negative interaction of *sgs1*-r1 with *mus81*Δ by generating the double mutant independently. The slow growth phenotype persisted and cells were hypersensitive to HU (Figure 4B), while the *mus81*Δ *sgs1*Δ strain was synthetic lethal (data not shown and Tong *et al*, 2001). This implicates the R1 domain of Sgs1 in the resolution of, or recovery from, recombination events at the fork, particularly those that might form in the absence of Mus81-Mms4. We note, however, that *sgs1*-r1 does not aggravate the HRR pathway *per se* (Figure 4A, including *rad51*Δ, Supplementary Figure S6B). Based on the E-MAP data, we suspected that *slx4*Δ, *slx5*Δ, *slx8*Δ and *mre11*Δ might also be synthetic lethal with *sgs1*-r1, since they failed to yield E-MAP results. We crossed strains bearing these null alleles with *sgs1*-r1 and again tested synthetic lethality. We confirmed that *slx4*Δ, *slx5*Δ and *slx8*Δ are synthetic lethal with *sgs1*-r1, whereas *mre11*Δ is not (Figure 4A; data not shown). This result suggests that the R1 domain of Sgs1 confers an essential function when cells lack the activity for Slx5/Slx8 SUMO-dependent ubiquitin ligase or the Slx4-Slx1 structure-specific endonuclease. These results are fully consistent with the synthetic lethality observed in the absence of Wss1, which forms a complex with Slx5/Slx8, or of Mus81, which together with Mms4 helps resolve strand-exchange events, in parallel to the Slx4-Slx1 complex (Muñoz-Galván *et al*, 2012). In contrast, even though the loss of topoisomerase I should enhance torsional stress and promote strand exchange, we saw only a minor negative interaction between *sgs1*-r1 and *top1*Δ, by E-MAP or in drop assays on HU (Supplementary Figure S6A).

We extended the E-MAP observations to conditions of replicative stress by testing different mutant combinations with *sgs1*-r1 or *sgs1*Δ on plates containing HU (Figure 4B). Consistently, we saw that combinations of *sgs1*-r1 with genes that function in lagging strand synthesis (*pol32*Δ, *rad27*Δ) do not show negative interactions even on HU, while the corresponding double mutants with *sgs1*Δ showed either synthetic lethality or synthetic slow growth (Figure 4A and B). Similarly, there was no synthetic defect when *sgs1*-r1 was combined with the deletion mutant of the origin and replication fork associated F-box protein Dia2 (Mimura *et al*, 2009; Morohashi *et al*, 2009), either with or without HU (Figure 4A and B). Consistent with the ChIP data, we conclude that the *sgs1*-r1 mutation does not destabilize the stalled replication

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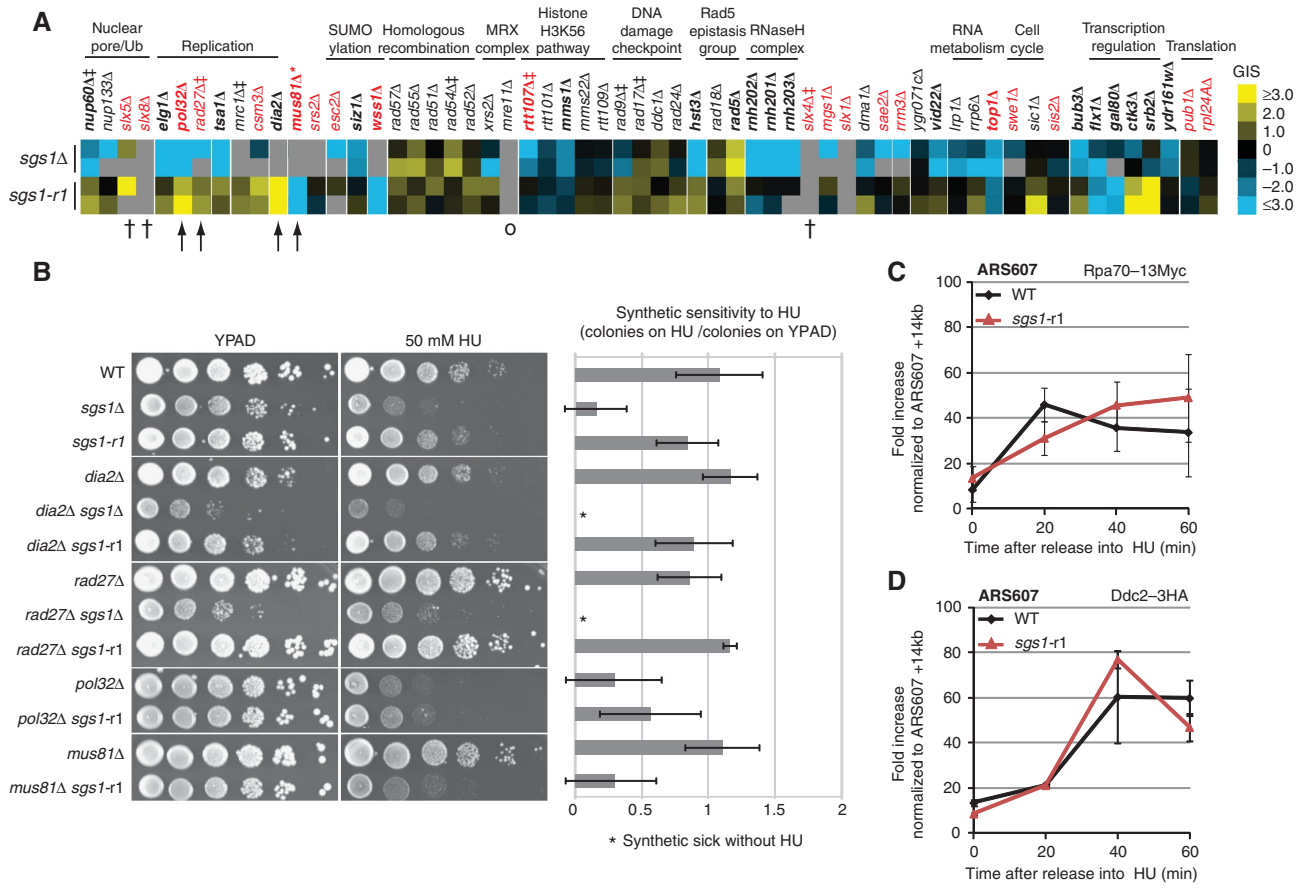

Figure 4 *sgs1*-r1 does not interact genetically with lagging strand replication machinery. (**A**) Genetic interaction profiles of *sgs1*Δ and *sgs1*-r1 were determined by crossing with a strain library comprising 1536 knockout alleles (Guénole *et al*, under review) and measuring growth of resulting double mutants as described in Materials and methods. Genetic interaction scores (GIS) of selected double mutants obtained from two independent experiments are depicted by colour (positive (yellow) = epistatic/suppressive, negative (blue) = synthetically sick). Genes were sorted into functional groups as performed earlier (Collins *et al*, 2007). Bold represents the mutant genes with GIS above threshold (− 2 for negative or + 2 for positive interactions) for double mutants with *sgs1*Δ and/or *sgs1*-r1 in two independent screens. Red represents gene deletions previously reported as synthetically lethal with *sgs1*Δ (Tong *et al*, 2001). Genes marked with ‡ were previously reported to be a target of checkpoint kinases (Chen *et al*, 2010). Mus81 (*) was reported to be a target of *S. pombe* Cds1 (*S. cerevisiae* Rad53) (Kai *et al*, 2005). The † indicates genes that showed synthetic lethality with *sgs1*-r1, while o indicates no synthetic lethal interaction. Arrows indicated mutants further analysed in (**B**). (**B**) Left: a representative picture of 10-fold serial dilutions of the following strains plated onto YPAD and YPAD with 50 mM HU: GA-1981 (WT), GA-5457 (*sgs1*Δ), GA-5076 (*sgs1*-r1), GA-7549 (*dia2*Δ), GA-7540 (*dia2*Δ *sgs1*Δ), GA-7542 (*dia2*Δ *sgs1*-r1), GA-7548 (*rad27*Δ), GA-7530 (*rad27*Δ *sgs1*Δ), GA-7532 (*rad27*Δ *sgs1*-r1), GA-7498 (*pol32*Δ), GA-7499 (*pol32*Δ *sgs1*-r1) GA-7494 (*mus81*Δ) and GA-6326 (*mus81*Δ *sgs1*-r1). Right: the number of colonies scored on 50 mM HU plates normalized by colony number on YPAD plates. Error bars indicate standard deviation of three independent experiments. (**C**, **D**) ChIP of 13Myc-tagged RPA or 3HA-tagged Ddc2 using strains GA-5525 (WT) and GA-5365 (*sgs1*-r1) as described in Figure 3.

fork. However, *sgs1*-r1 is important when cells are deficient for functional complexes that promote replication fork recovery through exchange or invasion of the sister chromatid.

Given that the R1 domain of Sgs1 binds RPA, we asked whether the RPA levels at the stalled replication fork might be altered in the *sgs1*-r1 mutant. However, levels of Myc-tagged RPA at the early origin ARS607 were not changed in *sgs1*-r1 cells synchronously arrested in S phase by 0.2 M HU (Figure 4C). RPA was undetectable at the late firing origin ARS522 (Supplementary Figure S7A). This argues that although RPA–Sgs1 interaction is diminished in *sgs1*-r1 cells, it neither affects RPA deposition at stalled replication forks, nor the amount of ssDNA generated. Synthetic lethality might also arise through an inability to recruit or activate Mec1-Ddc2. To test this, we performed ChIP for the essential Mec1 cofactor, Ddc2, in both wild-type and *sgs1*-r1 cells (Figure 4D; Supplementary Figure S7B). Again, we detected no change in the level of Mec1-Ddc2 recruitment in the R1 mutant. We conclude that the R1 domain functions, but on a pathway that is essential in the absence of Mus81, Slx4/Slx1 or the Slx5/Slx8/Wss1 ubiquitin conjugating complex.

The Sgs1 R1 domain is phosphorylated by Mec1 in vitro and in vivo

Earlier work had implicated a function of Sgs1 in intra-S phase checkpoint activation, independent of its enzymatic activity (Frei and Gasser, 2000; Bjergbaek *et al*, 2005). We therefore investigated whether the R1 domain of Sgs1 might be implicated in checkpoint activation, or be a target of Mec1-Ddc2 phosphorylation. Activation of the intra-S phase checkpoint by Mec1 occurs through the phosphorylation of numerous targets containing SQ/TQ motifs. Previous studies report that Mec1 substrates often contain several closely spaced motifs, which are also referred to as SQ/TQ cluster domains (SCDs; Traven and Heierhorst, 2005). Such SCDs are

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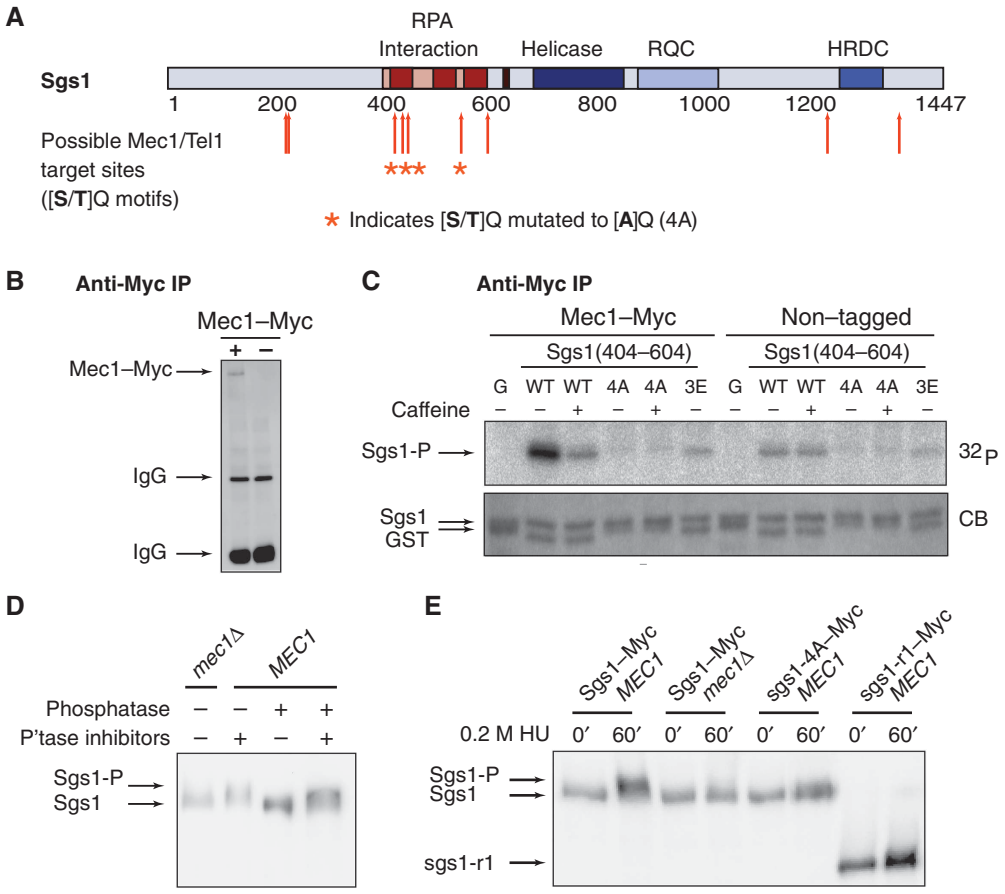

Figure 5 Mec1 targets the RPA-interacting site on Sgs1 *in vitro* and *in vivo*. (**A**) Schematic representation of Sgs1 with its functional domains. Mec1/Tel1 consensus target sites are indicated by red arrows, while asterisks tag phospho-acceptor sites mutated to A or E. (**B**) Exponentially growing GA-1456 (Mec1–18Myc) and GA-426 (non-tagged) cells were exposed for 1 h to 0.1% MMS. After cell lysis, Mec1–18Myc was precipitated using anti-Myc coupled Sepharose beads and analysed by western blot. (**C**) Kinase assay using Mec1–18Myc or control immunoprecipitates (non-tagged lysates). Sgs1 peptides (aa 404–604) were used as substrates in the presence of γ-^{32}P-ATP and analysed by gel electrophoresis and autoradiography. Where indicated, 30 mM caffeine was added to the reaction to inhibit Mec1. Mutant Sgs1 peptides were as follows: 4A = Sgs1(404–604-T451A-S470A-S482A-T585A) or 3E = Sgs1(404–604-T451E-S470E-S482E) ^{32}P autoradiography and Coomassie Brilliant Blue (CB) staining are shown. (**D**) Exponentially growing GA-6402 (Sgs1–13Myc) cells were exposed for 2 h to 0.2 M HU. Native extracts were treated with phosphatase and/or phosphatase inhibitors as described in Materials and methods and subjected to western blot analysis using anti-Myc antibody. A denatured extract of GA-6403 (Sgs1–13Myc *mec1*Δ) cells treated as described in (**E**) was loaded as a control. (**E**) Cells were synchronized in G1 by α-factor arrest and released into S phase in the presence of 0.2 M HU for 60 min. Protein extracts were analysed by western blot using anti-Myc antibody. Strains used were GA-6402 (Sgs1–13Myc), GA-6403 (Sgs1–13Myc *mec1*Δ), GA-7485 (sgs1-4A–13Myc) and GA-5313 (sgs1-r1–13Myc).

defined by at least three SQ/TQ motifs within 100 aa with additional sites within another 100 aa. The human Sgs1 homologues BLM and WRN contain such clusters and are phosphorylated by ATR/ATRIP (Pichierri *et al*, 2003; Davies *et al*, 2004; Rao *et al*, 2005), the human homologue of Mec1-Ddc2.

Sequence analysis revealed nine SQ or TQ sites within Sgs1, of which four are clustered in the R1 region ($T_{451}Q_{452}$, $S_{470}Q_{471}$, $S_{482}Q_{483}$, $T_{585}Q_{586}$) with a fifth nearby ($S_{628}Q_{629}$; Figure 5A). To test if this domain of Sgs1 was indeed a target for Mec1 *in vitro*, we expressed Sgs1 aa 404–604 in bacteria and challenged it with kinase immunoprecipitated from a yeast strain expressing an epitope-tagged Mec1. A parallel precipitate from a yeast strain lacking the 18Myc tag was used as a control (Figure 5B and C). The Sgs1(404–604) domain is a robust substrate for Mec1–Myc phosphorylation (Figure 5C). We could significantly reduce the phosphate incorporation into the domain by adding the Mec1/Tel1 inhibitor caffeine to the *in-vitro* reaction, while the background phosphorylation in a non-tagged strain was not caffeine sensitive.

We next mutated the SQ/TQ motifs in this region and purified substrates with either alanine or glutamate substitutions at the relevant phospho-acceptor sites, generating *sgs1-4A* (Sgs1(404–604-T451A-S470A-S482A-T585A)) and *sgs1-3E* (Sgs1(404–604-T451E-S470E-S482E). These mutations efficiently abolished the modification of Sgs1 by precipitated Mec1–18Myc (Figure 5C). As the *sgs1*-3E mutant was also sufficient to abrogate Sgs1 phosphorylation *in vitro*, it is likely that Mec1-Ddc2 targets T_{451}, S_{470} and/or S_{482}.

To investigate whether Sgs1 is phosphorylated *in vivo*, we examined extracts from both wild-type and *mec1*Δ *sml1*Δ strains expressing Sgs1–13Myc, after growth for 2 h in 0.2 M HU. Indeed, in wild-type cells a diffuse and more slowly migrating form of Sgs1–13Myc was observed, that was not detected in cells lacking Mec1 (Figure 5D), or in wild-type cells not treated with HU (data not shown). Treatment of the cell lysate with phosphatase eliminated the presence of the

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slower migrating band, while the addition of both phosphatase and phosphatase inhibitors restored the signal. We conclude that the slower migrating band of Sgs1 reflects a phosphorylated form, generation of which requires Mec1 kinase.

We next asked whether Mec1 indeed targets the R1 region of Sgs1, by expressing Myc-tagged versions of wild-type Sgs1, and mutant forms bearing either the four S/T mutations (sgs1-4A–13Myc) or a deletion of the entire R1 domain (sgs1-r1–13Myc). We examined the shift in mobility in cells that were first synchronized in G1 and released into medium containing 0.2 M HU. A strain lacking Mec1 kinase (*mec1*Δ *sml1*Δ) was used as a control (Figure 5E). Sgs1–13Myc did not show a shift in G1-arrested *MEC1* cells, while the slower migrating, phosphorylated form was evident in cells exposed to HU (Figure 5E). The phosphorylation of Sgs1 was lost in *mec1*Δ *sml1*Δ cells exposed to HU, and importantly, also greatly diminished in both the *sgs1*-4A–13Myc and *sgs1*-r1–13Myc mutants (Figure 5E). We detected a residual shift in the sgs1-4A–13Myc and sgs1-r1–13Myc, which may be explained by phosphorylation outside of the R1 domain. Indeed, our own LC-MS/MS data and data of (Bodenmiller *et al*, 2008, 2010) indicate that Sgs1 may be phosphorylated either on residue 1221/1222/1223 (Supplementary Table S2) or on residues 348, 1268 or in peptide aa 605–619. These Sgs1 phospho-acceptor sites are not typical Mec1 target sites as they lack the SQ/TQ consensus, and they may reflect phosphorylation by a kinase downstream of Mec1. Important to note is that the confirmed *in-vitro* Mec1 target sites within the R1 domain (T_{451} and/or S_{470}) are found within a large tryptic cleavage fragment that could not be detected in our MS analysis (47 aa; see Supplementary Table S2), even when combined chymotryptic and tryptic digestions were used (data not shown). In contrast, S_{482} is in a smaller peptide that is not phosphorylated *in vivo*.

Earlier work from our laboratory showed that Sgs1 interacts directly with the FHA1 domain of the major Mec1 target and checkpoint kinase, Rad53 (Bjergbaek *et al*, 2005). The FHA1 domain of Rad53 is a phosphopeptide binding module that has a key role for both intra-S checkpoint activation and late origin control (Pike *et al*, 2004a). To determine whether the Mec1-modified R1 domain of Sgs1 is the site of Rad53 interaction, we first employed Y2H assays. We detect a strong interaction between the core Sgs1 fragment (290–1180) and the FHA1 domain of Rad53, which is entirely lost upon deletion of aa 404–604 (*sgs1*-r1; Figure 6A). The Sgs1 subdomain aa 292–661 was sufficient to mediate binding to the Rad53 FHA1 domain, and again, deletion of aa 404–604 ablated interaction with Rad53 FHA1 (Figure 6A). We also tested a non-phosphorylatable *sgs1*-4A substitution within the smaller Sgs1 fragment, which gave a 50% drop in β-galactosidase signal, suggesting that phosphorylation is important for high binding affinity, although contacts to flanking residues may contribute to the interaction (Figure 6A). Given that Y2H assays can detect indirect interactions, we decided to turn to a more quantitative binding assay to evaluate the importance of the Mec1 phosphorylation sites on the Sgs1-Rad53 interaction.

Using ITC with the FHA1 domain and short Sgs1 peptides that encompass phosphorylated T_{451}, S_{470} or S_{482} (Sgs1(446–456), Sgs1(466–475) and Sgs1(478–487) respectively), we analysed the interaction between these peptides and the minimal FHA1 domain (aa 22–162) comparing phosphorylated and non-phosphorylated acceptor sites. Remarkably, only the Sgs1(446–456) peptide carrying a phosphorylated $T_{451}Q_{452}$, and not its unphosphorylated counterpart, bound the FHA1 domain of Rad53 (Rad53(22–162) significantly (Figure 6B). The phosphorylated Sgs1(446–456) peptide had a dissociation constant $K_D = 21 \pm 0.2\,\mu M$ for the FHA1 domain, a value that is similar to that observed between Rpa70(3–133) and Sgs1(404–560) (Figure 1F). Two other peptides bearing phosphor-serine (S_{470} in Sgs1(466–475) and S_{482} in Sgs1(478–487)) did not show significant binding to the Rad53 FHA1 domain by ITC (Supplementary Figure S8), consistent with the demonstrated preference of FHA1 for p-Thr over p-Ser (Durocher *et al*, 2000; Pennell *et al*, 2010).

To determine if the phosphorylation of Sgs1 by Mec1 on these residues also mediates Rad53 interaction *in vivo*, we performed co-IP experiments with strains expressing Rad53-9PK and either Sgs1–13Myc or sgs1-4A–13Myc. A strain lacking the Sgs1–Myc tag was used as a control. Cells were synchronized in G1 and released into 0.2 M HU for 60 min, prior to lysis in buffer with phosphatase inhibitors. Precipitation by anti-Myc antibody, and subsequent western blotting with anti-PK or anti-Myc antibodies, showed that Rad53-9PK and Sgs1–13Myc precipitate efficiently as a complex (Figure 6C and D). The amount of Rad53-9PK recovered with sgs1-4A–13Myc was >2-fold less than with wild-type Sgs1 (Figure 6C and D). We conclude that Sgs1 interacts with Rad53 in a phosphorylation-dependent manner, requiring modification on SQ/TQ acceptor sites within its R1 domain. The RPA-interaction site on Sgs1 would thus be targeted by Mec1 after HU-induced replication fork stalling, enabling phospho-T_{451} interaction with Rad53.

sgs1-r1 cells display a defect in Rad53 activation in a rad24 background

Previous studies have shown that Sgs1 and Rad24 act on parallel pathways to activate Rad53 when cells are exposed to HU during S phase (Frei and Gasser, 2000; Bjergbaek *et al*, 2005), yet how Sgs1 leads to Rad53 activation is unclear. Since both the helicase activity of Sgs1 and its interaction with Top3 are dispensable for Rad53 activation (Bjergbaek *et al*, 2005), we next examined whether the *sgs1*-r1 and/or *sgs1*-4A mutations, which lack the Mec1-dependent phosphorylation sites and show reduced binding to Rad53 in Y2H, ITC and *in-vivo* assays, have an effect on checkpoint activation.

We released G1-synchronized cells into HU-containing media for 30 or 60 min and monitored Rad53 activation on SDS–PAGE. The hyper-phosphorylated, activated form of Rad53 was visualized on western blots as a band with delayed migration (Figure 6E). We tested the impact of either *sgs1*-r1 or *sgs1*-4A in both wild-type and *rad24* mutant backgrounds, since Rad24/9-1-1 contributes to checkpoint activation through an alternative pathway in response to fork stalling (Frei and Gasser, 2000). Upon release from α factor arrest into HU, Rad53 became phosphorylated, not only in wild-type cells, but also in *rad24*Δ, *sgs1*-r1 or *sgs1*-4A single mutant cells, as well (Figure 6E). In the *sgs1*-r1 *rad24*Δ double mutant, however, the upshift of Rad53 was significantly reduced, as observed in the *sgs1*Δ *rad24*Δ mutant. Similarly, the *sgs1*-4A in combination with *rad24*Δ showed a

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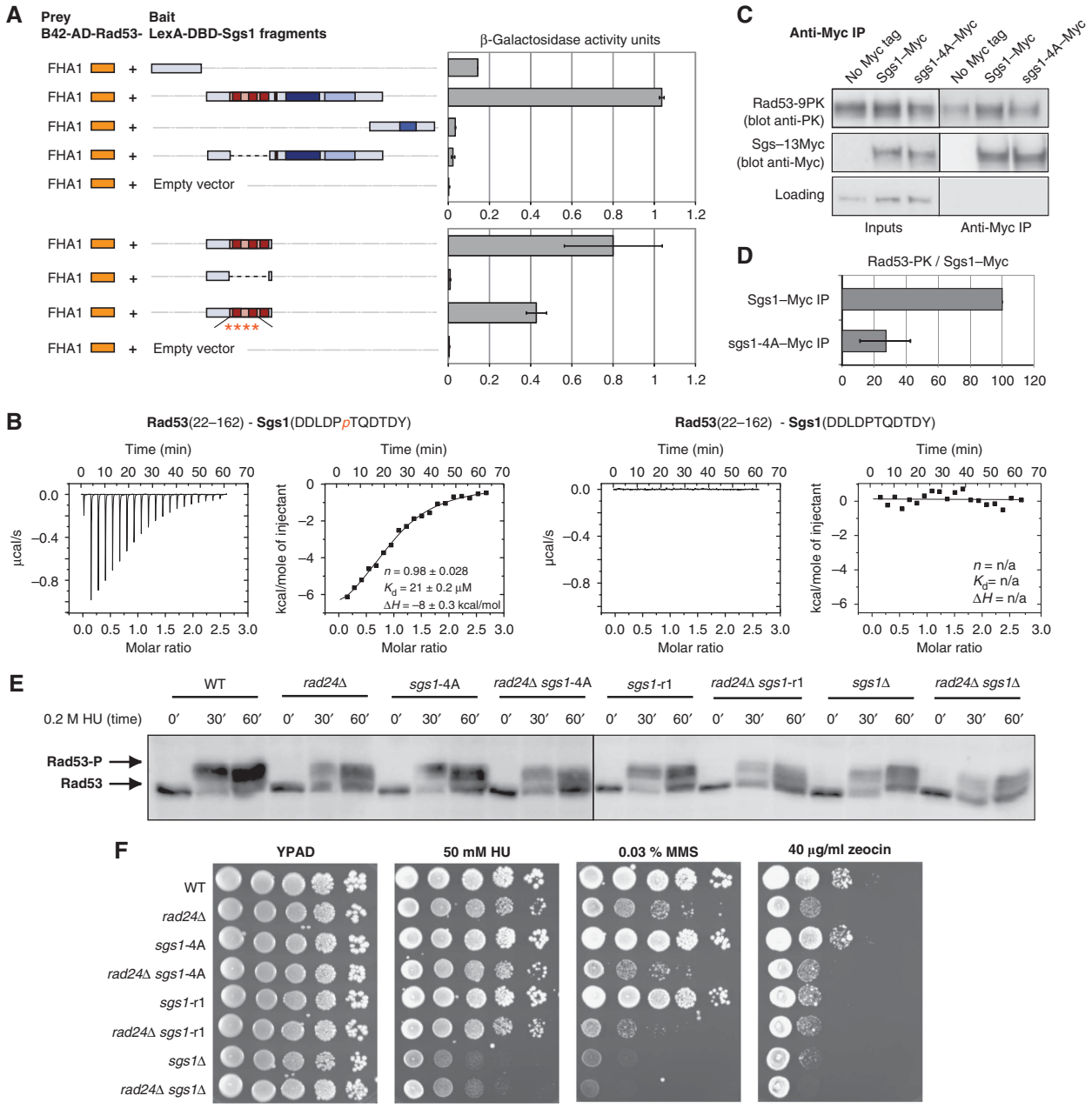

Figure 6 Sgs1 phosphorylation promotes Sgs1-Rad53 interaction. (**A**) Y2H analysis of Rad53-FHA1 fused to the B42-AD and Sgs1 fragments fused to LexA-DBD, as in Figure 1. Asterisks indicate phospho-acceptor sites mutated to alanine. (**B**) ITC assay of the FHA1 domain of Rad53, Rad53(22–162), and two Sgs1(446–456) peptides, Sgs1 (DDLDPTQDTDY), encompassing either phosphorylated $T_{451}Q_{452}$ (left panel) or non-phosphorylated $T_{451}Q_{452}$ (right panel). Parameters as in Figure 1E. (**C**) Co-IP of 13Myc-tagged Sgs1 (GA-7487), sgs1-4A (GA-7483) or non-tagged Sgs1 (GA-7467) with 9PK-tagged Rad53. Cells were released from G1 (α-factor arrest) for 60 min in the presence of 0.2 M HU and lysed for Dynabead-IP using monoclonal anti-Myc. Western blots were probed with anti-Myc for Sgs1 or sgs1-r1 and anti-PK for Rad53. An anti-PK-cross-reacting 250 kDa protein served as loading control. (**D**) Quantification of three independent Sgs1-Rad53 co-IP experiments. The unspecific binding (no tag control) signal was subtracted from Rad53-9PK signals in Sgs1- and sgs1-4A IPs, and normalized to Sgs1–13Myc or sgs1-4A–13Myc signals in the IP fractions. Error bars indicate standard deviation. (**E**) Rad53 activation in GA-1981 (WT), GA-5321 (*rad24*Δ), GA-5932 (*sgs1*-4A), GA-5934 (*sgs1*-4A *rad24*Δ), GA-5076 (*sgs1*-r1), GA-5324 (*sgs1*-r1 *rad24*Δ), GA-1761 (*sgs1*Δ) and GA-2056 (*sgs1*Δ *rad24*Δ). Cells were synchronized in G1 by α-factor arrest and released for 60 min into 0.2 M HU before denatured extract preparation as done previously (Pike *et al*, 2003). Rad53 phosphorylation (Rad53-P) was monitored by western blot with anti-Rad53. (**F**) Ten-fold serial dilutions of (WT), GA-5321 (*rad24*Δ), GA-5932 (*sgs1*-4A), GA-5934 (*sgs1*-4A *rad24*Δ), GA-5076 (*sgs1*-r1), GA-5324 (*sgs1*-r1 *rad24*Δ), GA-5457 (*sgs1*Δ) and GA-2056 (*sgs1*Δ *rad24*Δ) on YPAD ± 50 mM HU, 0.03% MMS, or 40 µg/ml Zeocin.

strongly impaired upshift of Rad53. Since Mec1-Ddc2 recruitment is not altered in *sgs1*-r1 cells (Figure 4D), we conclude that the drop in Rad53 activation likely stems from impaired Rad53 recruitment by Sgs1.

Finally, we checked the effect of the Mec1 target sites in Sgs1 by combining the *sgs1*-4A mutant with *mec1*-100 or *rad24*Δ. In a drop assay on media containing HU, cells expressing a non-phosphorylatable sgs1-4A protein, behaved like *sgs1*-r1 cells: both showed wild-type sensitivity to HU and both were epistatic with *mec1*-100 (Figure 2E; Supplementary Figure S9A). Indeed, when we scored recovery from HU-induced arrest in S phase, the *sgs1*-4A mutant cells behaved

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like wild-type cells, even though the synergy of *sgs1*Δ with *mec1*-100 was readily reproducible (Supplementary Figure S9B). This was also true, when we combined *sgs1*-r1 and *sgs1*-4A mutant cells with *rad24*Δ cells in survival assays on HU (Figure 6F). However, when double mutants were scored on MMS, we found that *sgs1*-r1 is slightly additive with *rad24*Δ, and, both alone and in combination with *rad24*Δ, *sgs1*-r1 was as sensitive as either *rad24*Δ or *sgs1*Δ to Zeocin (Figure 6F). Surprisingly, *sgs1*-4A was not, suggesting that the R1 domain contributes more than just assisting checkpoint activation, which was reduced identically in *sgs1*-r1 and *sgs1*-4A mutants (Figure 6E). This is consistent with the E-MAP data which implicated the R1 domain in the resolution of strand-exchange intermediates that might arise as a result of double-strand breaks. The sensitivity of the *sgs1*-r1 mutation to Zeocin may reflect both Rad53 recruitment and a downstream function that is partially redundant with Mus81-Mms4 or Slx4-Slx1 (Figure 4A and B).

Discussion

RecQ helicases have been implicated in the maintenance of genome stability in multiple pathways, some of which involve the double cross-over resolving activity of Top3, while others do not (Cobb and Bjergbaek, 2006). Here, we show that the role of Sgs1 in preserving DNA pol α on the lagging strand at stalled replication forks is largely due to its helicase activity (Figure 3). Despite the strong affinity shown by Sgs1 for RPA, deletion of a major interaction site within Sgs1 for Rpa70 did not destabilize DNA pol α during HU arrest. On the other hand, we found that the Rpa70-binding domain also mediates interaction with the downstream checkpoint kinase Rad53 (Figure 5). Given that both *in vitro* and *in vivo* this interaction requires the phosphorylation of Sgs1 by the ATR homologue, Mec1, we propose that the Sgs1 phospho-R1-Rad53 interaction occurs only under conditions that activate Mec1-Ddc2, for example, at stalled replication forks.

Functional studies confirm the relevance of the interaction between the phosphorylated Sgs1 R1 domain with Rad53 FHA1, a domain of demonstrated importance for intra-S phase checkpoint activation (Boddy *et al*, 2000; Pike *et al*, 2004b; Smolka *et al*, 2006). Using appropriate mutants, we show that the R1 domain and the Mec1 phosphorylation sites within this domain contribute to Rad53 activation during fork arrest. This is most obvious in a *rad24*Δ background. Whether loss of Rad24 leads to a particular type of damage that requires Sgs1-mediated Rad53 recruitment, or whether it simply unmasks the dependence of the event on Sgs1, is unknown. However, our results suggest that the *sgs1*-r1 mutation neither impairs the generation of ssDNA nor Mec1-Ddc2 recruitment (Figure 4C and D); nonetheless, it affects Rad53 activation during fork arrest on HU (Figure 6E). We therefore suggest that the R1 domain of Sgs1, once modified by Mec1, recruits Rad53 to the complex of ssDNA, RPA, Ddc2-Mec1, to facilitate its activation. This demonstrates a non-enzymatic role of Sgs1 in the DNA damage response at stalled forks (Figure 7). Sgs1 clearly plays other roles in the pathways leading to replication fork recovery, namely, the helicase-dependent reversal of fold-back structures and the resolution of unproductive strand exchange events behind the fork (reviewed in Bernstein *et al*, 2010).

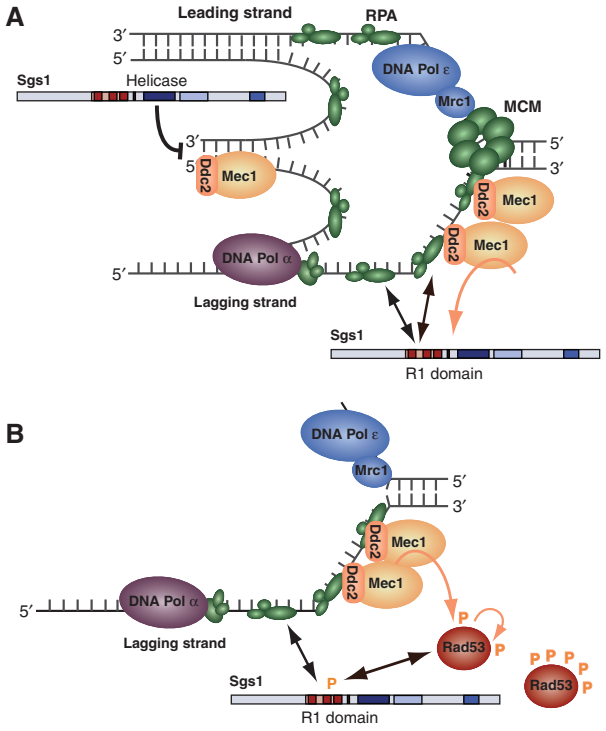

Figure 7 Multiple roles for Sgs1 helicase at stalled replication forks: reversal of fold-back structures, polymerase stabilization and Rad53 recruitment. (**A**) Sgs1 helicase activity contributes to the retention of DNA polymerases at stalled replication forks possibly by reversal of fold-back or strand invasion structures between nascent or template strands. The checkpoint kinase Mec1-Ddc2 is recruited to ssDNA coated by RPA and phosphorylates Sgs1 in the R1 domain. The green hexameric ring is the MCM helicase. (**B**) Sgs1 phosphorylation may shift Sgs1 binding preference from RPA to the Rad53 FHA1 domain. This could recruit Rad53 into close proximity of Mec1-Ddc2 which is associated with stalled forks. Mec1-Ddc2 then phosphorylates Rad53, to activate it and initiate the intra-S phase checkpoint response.

Multiple binding sites in a domain upstream of the Sgs1 helicase domain

The domain we identify here in Sgs1 as both an RPA and Rad53 binding site is upstream of the helicase domain and overlaps partially with an acidic domain (aa 502–648) implicated in replication fork stability on MMS (Bernstein *et al*, 2009). We define both an RPA-binding region (aa 404–560) and a Rad53-binding motif (aa 446–456), and show by ITC, Y2H interaction and co-IP that the latter interaction is phosphorylation dependent, while the former is not.

Both the interaction sites and the Mec1 acceptor sites that we have mapped are distinct from the *sgs1*-D664Δ point mutant studied by Bernstein *et al* (2009), which partially mimics the larger deletion. Their AR2 deletion does not eliminate the Sgs1-FHA1 interaction site, but may have indirect effects, given that the mutant protein appeared to be unstable. Both the RPA and Rad53 binding activities of Sgs1 are also independent of the Siz1/Siz2 sumoylation site K621 in Sgs1, which remains intact in our mutants, but was removed by the AR2 deletion (SC Teng, personal communication). Nonetheless, the *sgs1*-r1 mutant shows similar phenotypes as *sgs1*-AR2Δ or *sgs1*-D664Δ with respect to HU and MMS sensitivity during continuous growth on plates. Both sets of mutations suppress *top3*Δ slow growth (Supplementary Figure S3), and thus retain Sgs1 helicase activity (Bernstein *et al*, 2009).

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sgs1-hd mutants fail to stabilize the replisome at stalled forks

In our attempt to explore the importance of Sgs1–RPA interaction on lagging strand polymerases, we found instead that Sgs1 helicase activity is essential for the maintenance of DNA pol α at ARS607 (Figure 3). Additional removal of the R1 domain in the *sgs1*-r1-hd mutant did not aggravate this effect. This result supports earlier findings from our laboratory suggesting that *sgs1*-hd expression cannot complement *sgs1*Δ for DNA pol ε stability on HU (Cobb *et al*, 2003). We show by epistasis analysis that *sgs1*-r1 is a separation of function mutant, because *sgs1*-r1, unlike *sgs1*Δ, does not exhibit negative synthetic interaction when combined with replication mutants. Nonetheless, the R1 domain contributes to Rad53 activation on HU, and shows strong synergistic lethality with deletions of *mus81*, *slx4*, or with *slx5* and/or *slx8* (Figure 4).

These results argue that Sgs1 probably contributes to replication polymerase stability by a dissolution of fold-back structures (i.e., upstream of Mec1 activation) and/or resolution of strand exchange behind the fork (Bennett *et al*, 1999; Bjergbaek *et al*, 2005; Ashton and Hickson, 2010). Holliday junction dissolution is especially important for restart of a collapsed fork after DNA damage, which occurs after persistent exposure with MMS or HU in drop assays. Consistently, both Sgs1 helicase activity and its Top3 interaction contribute to DNA repair and survival during prolonged exposure to HU or MMS. This may explain the synthetic lethality observed between *sgs1*-r1 and *mus81*Δ and *slx4*Δ in the E-MAP analysis, since strand exchange is thought to enable the fork restart that is necessary when lesions block leading or lagging strand elongation (Lambert *et al*, 2010; Muñoz-Galván *et al*, 2012). Given that these pathways may be controlled by Slx5-Slx8 ubiquitination and subsequent degradation of a factor blocking strand exchange, all E-MAP results are consistent with a contribution of the R1 domain of Sgs1 to this pathway.

What, then, is the importance of the Sgs1–RPA interaction? Whereas RPA has been shown to stimulate RecQ helicase activity in human cells (Shen *et al*, 2003; Machwe *et al*, 2006; Sowd *et al*, 2009; Yodh *et al*, 2009), it is not clear that RPA truly promotes unwinding. Direct interaction of RPA with RecQ helicases may alter enzymatic activity through a conformational change or switch in the oligomeric state of the RecQ helicase. It is noteworthy that RPA also counteracts the annealing activity of the RecQ helicase by stabilizing the ssDNA that occurs from unwinding (Bachrati and Hickson, 2008). Different Sgs1–RPA disruption mutants or further analysis of the relevant Rpa70 OB fold will be necessary to identify the exact role of Sgs1–RPA interaction for helicase activity and replication fork integrity.

Sgs1 R1 domain phosphorylation by Mec1-Ddc2 aids Rad53 activation

The most novel aspect of our study is to show how Sgs1 contributes to Rad53 activation during conditions that arrest replication forks. We propose that phosphorylated Sgs1 interacts with the FHA1 domain of Rad53 to promote Rad53 recruitment to sites of damage. We found that Sgs1 is a target of Mec1 *in vitro* and *in vivo* and we map the phosphorylation sites to the Rad53-interaction domain. Importantly, ITC studies show that the binding of Sgs1(446–456) to Rad53 FHA1 is phospho-threonine dependent, while Sgs1 binding to RPA through the same domain is not. We confirm that mutation of the key Mec1 acceptor sites alters Rad53 activation, Sgs1–Rad53 interaction, and deletion of the domain confers sensitivity to Zeocin. We do not know if phosphorylation of the Sgs1 R1 domain also facilitates Rad53 recruitment to DSBs, but we consider it likely.

An additional fork-associated adaptor protein, Mrc1, has been implicated as a bridge between Mec1-Ddc2 and Rad53 activation at stalled replication forks (Alcasabas *et al*, 2001; Osborn and Elledge, 2003; Crabbé *et al*, 2010). Indeed, *in-vitro* checkpoint reconstitution assays have shown that Mrc1 can facilitate the phosphorylation and activation of Rad53 probably by promoting Mec1–Rad53 interaction (Chen and Zhou, 2009). A recent study demonstrated that Mec1- but not Rad53-dependent phosphorylation of Mrc1 is necessary for the establishment of a positive feedback loop that leads to Mec1 stabilization at stalled replication forks (Naylor *et al*, 2009). Thus, Mrc1 may act prior to Sgs1 function ensuring Mec1-Ddc2 recruitment to stalled replication forks, which in turn is necessary for Sgs1 phosphorylation (Naylor *et al*, 2009). While Mrc1 and Sgs1 are epistatic for Rad53 activation on HU, they nonetheless show strong synergistic defects for stalled fork recovery and DNA polymerase stability on HU (Bjergbaek *et al*, 2005). This argues that Mrc1, like Sgs1, serves multiple roles at stalled forks. One possible scenario for the synergy observed between Sgs1 and Mrc1 would be that they act preferentially on different strands (the leading versus the lagging strand). Indeed, Mrc1 has been shown to function together with leading strand polymerase pol ε (Lou *et al*, 2008).

As in yeast, the human RecQ helicase BLM has been shown to be a target of ATR in a region N-terminal of its helicase domain (Davies *et al*, 2004; Rao *et al*, 2005). Interestingly, the N-terminal region of BLM (aa 1–477) including the ATR-target sites ($T_{99}Q_{100}$, $T_{122}Q_{123}$) binds hRPA *in vitro* (Davies *et al*, 2004, 2007). In contrast to Sgs1, BLM is not a constitutive component of the replisome, but is recruited from PML bodies to sites of stalled replication forks in response to HU (Sengupta *et al*, 2003). This re-localization requires ATR-dependent phosphorylation of BLM (Davalos *et al*, 2004). It has been suggested that ATR phosphorylation of BLM is required for recovery from HU-mediated replication fork stalling, but not for the recruitment of BLM to damaged forks nor for the suppression of sister chromatid exchanges with hTOPO IIIα-hRMI1-hRMI2 (Davies *et al*, 2004; Wu, 2007). Davies *et al* (2007) demonstrated that ATR-dependent phosphorylation of BLM is required for efficient replication fork resumption and repression of new origin firing after aphidicolin treatment. Furthermore, and similar to our findings, the presence of BLM at stalled replication forks is required for robust intra-S phase checkpoint activation in human cells (Franchitto and Pichierri, 2002; Davalos and Campisi, 2003). Nonetheless, the mechanisms through which mammalian ATR and BLM work together to maintain replisomes at stalled replication forks and activate the intra-S phase checkpoint are unknown. A conserved, damage-specific assembly of a RecQ homologue (BLM and/or WRN) with a downstream checkpoint kinase is an attractive hypothesis.

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Materials and methods

Yeast strains and plasmids

S. cerevisiae strains (Supplementary Table S1) were derived from W303-1A (*MAT***a** *ade2*-1 *ura3*-1 *his3*-11,*15 trp1*-1 *leu2*-3,*112 can1*-100). If not stated otherwise, all strains were cultured at 30°C in YPAD media. The *sgs1*-r1 allele was generated using pop-in/pop-out mutagenesis as previously described (Tam *et al*, 2007). For Y2H analyses, fragments of Sgs1, Rpa70 and Rpa32 were fused in frame to the B42 activator domain in the pJG46 or the lexA DNA binding domain in the pGAL-lexA vector (Bjergbaek *et al*, 2005). Y2H was performed as described (Bjergbaek *et al*, 2005), except that both bait and prey were under GAL_{UAS} control. EGY191 cells (GA-1211) containing the lacZ reporter pSH18-34, the bait and the prey were glucose depleted, then 2% galactose added to the exponentially growing culture to induce expression of the fusion proteins. The quantitative β-galactosidase assay for permeabilized cells (Adams *et al*, 1997) was performed on four independent transformants in at least two independent experiments for each data point. Expression of the fusion proteins was confirmed by western blot analysis (data not shown). β-Galactosidase units are defined as $OD_{420}/(OD_{600} \times \text{dilution} \times \text{time(min)})$.

Survival and drop assays

For liquid survival assays, overnight cultures were diluted to $OD_{600} = 0.15$ and grown for 3 h, then synchronized with α-factor in G1 and released into YPAD containing 0.2 M HU. At the indicated time points, relevant dilutions were plated onto fresh YPAD plates and colonies were counted after 3–4 days. Survival is defined as the fraction of colonies compared to the untreated control (0 h) normalized to the survival of WT cells for each time point. Drop tests used overnight cultures diluted to $OD_{600} = 0.5$ with 2 μl drops of 10-fold dilutions plated on YPAD or the appropriate selective medium with indicated concentrations of damaging agents.

ChIP analysis, co-IP and kinase assays

ChIP experiments were performed as described (Cobb *et al*, 2005) using monoclonal anti-HA (F-7, Santa Cruz) to precipitate HA-tagged DNA pol α or Ddc2, and anti-Myc (9E10) to precipitate Myc-tagged Rpa70. Details are in Supplementary Methods. For each time point, the relative enrichment for ARS607 or ARS522 was obtained by normalizing the absolute enrichment at ARS607 or ARS522 to the absolute enrichment 14 kb away from ARS607.

Co-IP was performed essentially as described in Bjergbaek *et al* (2005), except that two additional rounds of washing with 100 mM Tris pH 8.0, 500 mM NaCl, 1 mM EDTA, 0.5% NP-40 and 0.5% sodium deoxycholate were performed. Note that the use of more stringent washing conditions most probably explains why the Sgs1-Rad53 interaction was not dependent on checkpoint induction in the previous study (Bjergbaek *et al*, 2005). Mec1 immunoprecipitation and kinase assays are described in Supplementary Methods.

Rad53 and Sgs1 phosphorylation and mass spectroscopic analysis

Conditions used to monitor Rad53 or Sgs1 phosphorylation by western blot and by semi-quantitative mass spectroscopy are described in Supplementary Methods. In brief, peptides were separated by nano-HPLC (Agilent 1100 nanoLC system, Agilent Technologies) coupled to an LTQ Orbitrap Velos hybrid mass spectrometer (Thermo Scientific) using a top 15 DDA method and an LC-MSMS method containing *m/z* values of predicted phosphopeptides. Peptides were identified by searching SwissProt database (version 2010-09) with Mascot 2.3.0 (Matrix Science). Data were compiled and evaluated with Scaffold 3.4.3 and Scaffold PTM 1.1.3 (Proteome Software).

Protein purification and ITC

The Rad53(22–162) and Rpa70(1–133) and Rpa70(3–133) constructs inserted into a pET15 derived vector, containing a TEV protease cleavable His_6-tag, and Sgs1 constructs (404–485, 404–560) were amplified and inserted into a pET15 derived vector, containing a thrombin protease cleavable His_6 tag. All were expressed in *E. coli* BL21 cells and purified by metal chelate affinity (His-Select Nickel Affinity Gel, Sigma-Aldrich), anion-exchange (Resource 15 Q, GE Healthcare), and gel-filtration chromatography (Superdex S-200, GE Healthcare). ITC experiments were conducted with a MicroCal VP-ITC calorimeter as described in Supplementary Methods.

Genetic interactions and sequence analysis

GA-6998 (*sgs1*-r1) and yHA429 (*sgs1*Δ) cells together with 33 other query strains (data to be published elsewhere) were crossed with a library of 1536 mutants (Guénole *et al*, under review) as described (Schuldiner *et al*, 2006), except that four sets of double mutants were created in two independent experiments. Results and the analysis of the library by pooled TAG amplification are described in Supplementary Methods. Genetic interaction scores (S scores) were calculated using the E-MAP toolbox (Collins *et al*, 2006). The analysis of sequence motifs in Sgs1 is described in Supplementary Methods.

Supplementary data

Supplementary data are available at *The EMBO Journal* Online (http://www.embojournal.org).

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Conflict of interest

The authors declare that they have no conflict of interest.

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CHAPTER 5: CONCLUDING REMARKS AND FUTURE PROSPECTS

This work contributes to our understanding of Mec1 signaling. Specifically, in Chapter 2, I have revealed an intimate and unexpected relationship between the checkpoint kinase complex Mec1-Ddc2 and the PP4 phosphatase Pph3-Psy2. We identify PP4 as a major regulator of Mec1 signaling. In two independent genetic screens we found that mutants lacking *PPH3* or its regulatory subunit *PSY2* suppress *mec1-100* defects on HU. We further show that both complexes physically interact and co-regulate many phosphorylation sites including a previously unidentified acceptor site in Mec1, S1991. In the mutant *mec1-100* the replication checkpoint is compromised, but the G2 DNA damage checkpoint remains intact (Paciotti et al., 2001). In Chapter 3, I extended my analysis of *mec1-100* by characterizing intragenic suppressors and I further investigate the molecular nature of the *mec1-100* defects. In a third project, I studied the role of the RecQ helicase Sgs1 in checkpoint signaling and replication fork stabilization in collaboration with a previous graduate student. The main conclusions drawn from these three projects are summarized and areas of potential future research are discussed here.

MEC1-DDC2 AND PSY2-PPH3 PHYSICALLY INTERACT

In Chapter 2 we show that Ddc2 and Psy2 subunits physically interact by yeast two-hybrid assays, IP combined with western blotting and FRET. We also provide evidence that the Ddc2-Psy2 interaction may be conserved. Two different, but not mutually exclusive scenarios regarding the function of such a complex can be envisioned.

First, the two opposing enzymes might interact to regulate steady-state phosphorylation of overlapping targets. Even though at first glance this seems to be a waste of energy, other examples of association of antagonizing enzymes exist in nature: The deubiquitinating enzyme BRCC3 associates with the ubiquitin ligase BRCA1 within the RAP80 complex (Sobhian et al., 2007) Also, histone acetyltransferases and deacetylases have been reported to bind each other and are often found in single transcription-regulatory complexes (Yamagoe et al., 2003). Finally, histone methylating and demethylating enzymes are also found linked together, notably in conserved versions of the Trithorax and Polycomb group complexes, originally described in flies. The Trx complex contains both the H3K4me3 methyltransferase MLL/KMT2 and the H3K27 demethylase UTX/KDM6A, while the PcG complex PRC2, contains the H3K27 methyltransferase subcomplex PRC2/KMT6 and the H3K4me3 demethylase RBP2/KDM5A (reviewed in (Nottke et al., 2009)).

Systems biology studies revealed that antagonizing enzymatic functions in the same complex can confer robustness to enzyme or substrate perturbations in order to preserve steady-state levels (Russo and Silhavy, 1993). However, it was argued that this can only be achieved if the antagonizing functions are found exclusively together in one complex and share the same targets (reviewed in (Hart and Alon, 2013)). Psy2 is about ten times more abundant in cells (about 7000 molecules/cell on average) than Ddc2 (about 600 molecules/cell on average) (Ghaemmaghami et al., 2003). Although we do not know the stoichiometry of the complex, we observed by microscopy that a fraction of Psy2 foci did not colocalize with Ddc2 foci (Figure 2.6). Both observations suggest that a population of Psy2-Pph3 exists in yeast cells that does not bind Ddc2. Thus it seems unlikely that the function of this complex is to provide robustness, although we cannot exclude that the non-Ddc2 bound fraction might be inactive or otherwise sequestered. On the other hand, our microscopy data suggests that most of Ddc2 colocalizes with Psy2 (Chapter 2). Thus, it is tempting to speculate that the association of the kinase with the counteracting phosphatase could serve to keep target phosphorylation levels low until kinase activation overcomes phosphatase activity.

We sought to study the function of the Psy2-Ddc2 interaction by mapping and disrupting the interaction domain on Psy2. We found that a region within amino acids 25 – 350 of Psy2 interacted

with Ddc2 by yeast two hybrid and deleting amino acids 130-350 within Psy2 disrupted the interaction (Chapter 2). However, cells expressing *psy2Δ130-350* from the endogenous promoter were as MMS sensitive as *psy2*Δ cells, indicating that deleting amino acids 130-350 turned Psy2 dysfunctional. It is unclear at present whether this renders Psy2 unstable, interferes with its binding to Pph3, or whether the Psy2-Ddc2 interaction is essential for survival on MMS. Future research will aim at better defining the interaction domain and possibly generating point mutants that disrupt the Psy2-Ddc2 interaction, rather than deleting a large domain. Alternatively, the interaction site within Ddc2 could be mapped and mutated. Unfortunately, initial yeast two hybrid experiments to map the interaction on the Ddc2 side were inconclusive, although it should be possible to map the interaction site by GST pull-down experiments.

A second scenario for the function of the Mec1-Ddc2/Psy2-Pph3 complex is that the two might not only regulate overlapping targets, but also may regulate the other's activity. In this context other regulatory interactions between checkpoint kinases and phosphatases have been described previously: ATM has been shown to associate with and be regulated by PP1, PP2A and the PP2C phosphatase Wip1. Similarly, CHK1 and CHK2 interact with and are regulated by PP2A and Wip1 (reviewed by (Shimada and Nakanishi, 2013)). ATR is reported to associate with PP5, although PP5 rather seems to positively influence ATR signaling (Zhang et al., 2005). In all other cases, the phosphatase negatively regulates kinase function, thereby preventing untimely activation and/or promoting checkpoint recovery. Often the phosphatase was shown to achieve this through targeting of a phosphorylation site within the kinase that is crucial for kinase activity (e.g. PP2A dephosphorylates ATM serine 1981 and CHK1 serine 317 and 345) (Goodarzi et al., 2004; Leung-Pineda et al., 2006). Relevant to this, we also find a phosphorylation site in Mec1 that is regulated by Pph3, although this regulation may be indirect. Important to this scenario of cross-control is that the association between checkpoint kinase and phosphatase in mammalian cells often seems to be disrupted in response to DNA damage (Freeman et al., 2010; Goodarzi et al., 2004). Dissociation relieves the inhibition of the kinase by the phosphatase, allowing kinase activation.

In our study, we did not observe a detectable difference in the interaction of Ddc2 with Psy2 before or after HU treatment, following IP or western blot analysis. Interestingly, a similar, constitutive interaction was reported for the PP2C phosphatase Wip1 and ATM (Shreeram et al., 2006). A second study showed, however, that Wip1 protein levels are regulated in a cell-cycle and DNA damage-dependent manner (Macurek et al., 2013), thereby providing an explanation how Wip1-mediated ATM inhibition might be relieved upon DNA damage. Currently, it remains unclear whether or not Mec1 is directly inhibited by Psy2-Pph3. Nor do we know how the potential inhibition of Mec1 is overcome during the process of checkpoint activation. Psy2 or Pph3 mRNAs do not show cell-cycle or damage-induced variations in levels (Benton et al., 2006; Cho et al., 1998; Lee et al., 2000; Pramila et al., 2006; Spellman et al., 1998; van Attikum et al., 2004). Similarly, protein abundance is not reported to change upon HU or MMS treatment, nor is protein localization (Mazumder et al., 2013; Tkach et al., 2012). Accordingly, genome-wide studies did not report any posttranslational modifications (i.e. acetylation, ubiquitination, sumoylation or phosphorylation) on either Psy2 or Pph3 (Bodenmiller et al., 2008; Henriksen et al., 2012; Peng et al., 2003; Wohlschlegel et al., 2004) Thus, we have no evidence for cell-cycle and/or damage-induced regulation of Psy2-Pph3. Another possibility is that the association between Psy2 and Pph3 is regulated. Unfortunately, several attempts to fuse Pph3 to epitope tags have resulted in dysfunctional proteins and MMS-sensitive cells (Figure S2.4), and thus we have not been able to address directly whether Psy2-Pph3 interaction is regulated. Raising an antibody against Pph3 would allow us to address this question.

PPH3 TARGETS PHOSPHOPEPTIDES THAT ARE DOWNREGULATED IN *MEC1-100* CELLS

In support of the hypothesis that Pph3 might negatively regulate Mec1 function, I was able to show that most of the phosphopeptides that are downregulated in the *mec1-100* mutant are restored to their wild-type levels by the deletion of *PPH3* (Chapter 2). Interestingly, only few of the *mec1-100* dependent downregulated phosphotarget sites match the reported S/TQ consensus sequence (Kim et al., 1999). Several explanations for this phenomenon are plausible. First, the original consensus was determined by using peptides in ATM *in vitro* kinase assays (Kim et al., 1999). Regarding *in vivo* targets, one yeast phosphoproteomics study found that only 51% of all Mec1/Tel1-dependent (and Rad53-independent) targets matched to the consensus (Chen et al., 2010). A rather prominent example for non-consensus targeting is ATR autophosphorylation at threonine 1989, which is followed by a proline (Liu et al., 2011; Nam et al., 2011b). Similarly, the S1991 phosphoacceptor site in Mec1 is also not an S/TQ consensus site (Figure 3.1). Thus, the S/TQ consensus might be not as strict as generally assumed.

Alternatively, non-S/TQ phosphorylation sites might represent targets that are indirectly regulated by Mec1, that is, be targets of another kinase that is activated by Mec1. Rad53 can be ruled out, since we specifically filtered our data for Rad53-independent phosphorylation sites. Chk1 could be a candidate for this pathway. On the other hand our genetic data shows that Chk1 is not involved in suppression of *mec1-100* HU sensitivity by loss of Pph3. This does not rule out, however, that Chk1 might be regulated by Pph3, without functional significance for survival on HU.

Besides the two checkpoint signaling kinases, other kinase candidates were found in the list of *mec1-100* targets. Namely, Hrk1, Vhs2, Gin4, Sky1, Ptk2, Pcl6 are all kinases that showed reduced phosphorylation in *mec1-100* cells after HU treatment in our phosphoproteomics dataset. Pcl6, a kinase mainly involved in glycogen metabolism (Wang et al., 2001) shows partial nuclear localization, while all others are exclusively cytoplasmic. Interestingly, it hast been reported that a small fraction of Ddc2 is also localized in the cytoplasm, providing an explanation how phosphorylation of these cytoplasmic kinases could be targeted by Mec1-Ddc2 (Huh et al., 2003). The sole link of these kinases to the replication checkpoint or to replication stress signaling is Hrk1, which regulates trans-membrane transport (Goossens et al., 2000). Its protein level was found affected after replication stress (Tkach et al., 2012), although the functional significance of this remains unclear. While we cannot exclude that another kinase might be responsible for non-S/TQ consensus site modification that shows *mec1-100* sensitivity, there is no obvious mediator for this modification other than Mec1.

To confirm that the detected phosphoacceptor sites are indeed direct Mec1 phosphorylation sites, we must perform *in vitro* kinase assays, even though this is often inconclusive, as kinases can show promiscuous phosphorylation *in vitro*. Nonetheless, our work shows strikingly that most Mec1-100-dependent phosphorylation sites are also targeted by Psy2-Pph3, whether directly or indirectly. This confirms the intimate functional relationship between both kinase and phosphatase as found in our two independent genetic screens (Figure 2.1).

MEC1 IS PHOSPHORYLATED AT SERINE 1991

Not only does this work show that the kinase Mec1-Ddc2 and the PP4 phosphatase Psy2-Pph3 interact and balance each other's functions, we also report a phosphorylation site in Mec1, serine 1991, that is regulated in a Pph3-dependent manner. Similarly, human ATR autophosphorylates at a site in its FAT domain (T1989, Figure 3.1), (Liu et al., 2011; Nam et al., 2011b). and phosphorylation correlates with ATR activation. We show that Mec1 kinase activity but also the Rad53 protein is required for serine 1991 phosphorylation (Figure 2.7). At this stage we do not know whether Rad53 regulates Mec1 phosphorylation directly or indirectly. Even though it is unlikely, we cannot rule out

that Rad53 presence contributes in a manner independent of its kinase activity. It is intriguing that although Rad53 is required for Mec1 phosphorylation, S1991 modification does not strictly correlate with Rad53 phosphorylation, which is often taken as a measure for Rad53 activity. Specifically, Mec1 S1991 phosphorylation after Zeocin treatment is barely detectable compared to after HU treatment, yet Rad53 phosphorylation due to Zeocin is much stronger than on HU (Figure 2.7). Thus, additional unknown mechanisms seem to influence the Mec1 phosphorylation status. HU treatment leads to accumulation in S phase due to replication checkpoint activation, while the radiomimetic drug Zeocin rather triggers G1 or G2 checkpoints. Thus, the cell cycle stage might somehow influence Mec1 phosphorylation. Finally, it remains possible that Mec1 autophosphorylates in a manner dependent on Rad53.

Phosphorylation can regulate proteins on different levels. It can affect protein stability, enzymatic activity or association with binding partners, or it can occur without any detectable function. We were unable to directly measure protein levels of a non-phosphorylatable mec1-S1991A or phosphomimicking mec1-S1991D mutant, because all Mec1 antibodies that we tested so far, were too weak to detect Mec1 in extract samples by western blot. However, the amount of mec1-S1991A that is pulled down with Ddc2 is comparable to $Mec1^{+}$ (Figure 2.7). This indicates that expression and Mec1-Ddc2 interaction are not affected due to S1991 mutation, although we have not ruled out that the phosphomimicking mec1-S1991D mutant might be impaired for Ddc2 binding. We further find that mutating S1991A renders cells sensitive to double strand breaks, indicating that S1991 phosphorylation does have a function in survival of DNA damage. Since S1991 is localized close to the catalytic domain, in a helical area that might fold back onto the kinase domain (Figure 3.3), it is reasonable to speculate that it might regulate enzymatic activity. Similarly, we identified *mec1-100* intragenic suppressor mutations around that same area (e.g. Q1903E, R1907T, D2104H). Further genetic analysis showed that a surface exposed subset of mutations required Rad24 for *mec1-100* suppression while others act independently of Rad24 (Chapter 3). We speculate that these may enhance Mec1 enzymatic activity possibly through a similar mechanism as Mec1 S1991 phosphorylation.

The phosphorylation of S1991 after HU treatment is reduced in *mec1-100* cells, due to the reduced activity of the mec1-100 protein *in vivo* after HU treatment. Phosphorylation is rescued by loss of Pph3, which also rescues the majority of mec1-100 targets. By this criteria, S1991 phosphorylation correlates with Mec1 activity. However, even though Mec1 is activated and Mec1 S1991 phosphorylation is strongly induced after HU treatment, cells expressing the non-phosphorylatable *mec1-S1991A* mutant are not as HU sensitive as *mec1-100* or *mec1*Δ cells by drop assay, although we have not analyzed mec1-S1991A in other assays (e.g. replication fork restart). Thus, S1991 phosphorylation might contribute to, but cannot be crucial for, Mec1 activity. Alternatively, S1991 modification might induce or disrupt binding of an unknown factor or interaction with a subset of substrates, and thus may be important for the survival of double strand breaks. Analysis of genetic interactions of *mec1-S1991A* with mutants defective in specific repair pathways (e.g. *rad9*Δ for DNA damage checkpoint, *mrc1-AQ* for replication checkpoint, *rad52*Δ for homologous recombination or *dnl4*Δ for non-homologous end joining) could result in testable hypotheses regarding the function of this modification. Additionally, *in vitro* kinase assays would contribute to dissect a potential role of S1991 phosphorylation in Mec1 activation.

MEC1-100 – AN S-PHASE DEFECTIVE ALLELE

To study Mec1 function in the replication checkpoint we make use of an S-phase defective allele of Mec1, *mec1-100* (Paciotti et al., 2001). A similar mutant allele of human ATR has been described, with three mutations just N-terminal of the FAT domain (Figure 3.1) (Nam et al., 2011a). Therefore, this region seems to be a conserved regulatory domain important for replication checkpoint function. One part of my work aimed to identify the cause for this S phase defect. In Chapter 3 several hypotheses were developed and tested. Neither kinase activity (Figure S2.1), dimerization, Ddc2 interaction (Figure 2.5) nor localization (Cobb et al., 2005; Tercero et al., 2003) seem to be impaired to a measurable extent in the mutant. Genetic interaction analysis showed that *mec1-100* likely acts on a different pathway than other known canonical checkpoint mutants (Figure 3.2). We could not identify binding partners by IP and mass spectrometry that were lost due to *mec1-100* mutations (Figure 3.2). However, in order to identify binding partners by IP and mass spectrometry, an interaction must be strong and stable enough to be maintained throughout the procedure. Weak and transient interactions may be undetectable by this method, unless crosslinking agents are used.

Some of the other features tested, e.g. oligomerization, could be studied further *in vitro* using purified proteins and more sensitive methods, like size exclusion chromatography. Mec1-Ddc2 is a very large protein complex (Ddc2: 86 kDa, Mec1: 273 kDa) and not very abundant in cells (Ddc2 abundance: about 600 molecules per cell) (Ghaemmaghami et al., 2003). Together with the fact that fusing Mec1 with an epitope tag, even an internal one, impairs its function (Figure S2.4), turns large scale Mec1-Ddc2 complex purification into a great challenge. In order to perform *in vitro* assays, Galactose-inducible overexpression and 500g of yeast for Mec1-Ddc2 purification were used (Majka et al., 2006). On the other hand, resolution of the partial structure of another PI3K-like kinase, mammalian target of Rapamycin (mTOR), covering its FAT, kinase and FATC domain was recently reported (Yang et al., 2013). Thus it seems reasonable to expect that the Mec1-Ddc2 structure could be resolved in the near future as well. Structural data would certainly help to understand the mechanism of Mec1 activation, the function of residues mutated in *mec1-100* and the mechanism of intragenic *mec1-100* suppressor mutations described and modeled in Chapter 3.

SGS1 IS A MEC1 TARGET AND BINDS RAD53 IN A MEC1-DEPENDENT MANNER *IN VIVO*

In a third project I contributed to understanding the role of the yeast RecQ helicase Sgs1 in checkpoint signaling and replication fork stabilization. Genetically, *sgs1*Δ shows synthetic lethality with *mec1-100* on HU and the two mutations destabilize replication forks in a synergistic manner (Cobb et al., 2005). The rate of spontaneous gross chromosomal rearrangements in yeast increases 80-fold in *sgs1*Δ cells, 500-fold when *sgs1*Δ is combined with *mec1-100* and then 160 thousand-fold when the double mutant is exposed to HU (Cobb et al., 2005). The ability of Sgs1 to preserve or stabilize replication forks on HU requires its helicase activity, but not is ability to bind Rad53 (Chapter 4). Finally, it was shown that Sgs1 or other RecQ homologs such as BLM or WRN can unwind some simple double-stranded DNA substrates, although they prefer more complex structures like G4 quartets, three-way junctions, fold-back structures or Holliday junctions *in vitro* (Cejka and Kowalczykowski, 2010; Huber et al., 2002; Mohaghegh et al., 2001; Sun et al., 1998).

The contribution of Sgs1 and BLM to preserve genome stability during DNA double strand break (DSB) repair has been intensively studied: Sgs1 promotes resection together with Dna2 (Cejka et al., 2010; Nimonkar et al., 2011; Zhu et al., 2008), regulates Rad51 filament and D-loop formation (Bachrati et al., 2006; Bugreev et al., 2007; van Brabant et al., 2000). Furthermore, together with Top3 and Rmi1, Sgs1 can resolve double Holliday junctions such that exclusively non-crossover products are generated (Ira et al., 2003; Wu and Hickson, 2003).

On the other hand, Bloom Syndrome cells progress slowly through S phase, accumulate replication intermediates and are sensitive to replication fork stalling agents such as HU (reviewed by (Manthei and Keck, 2013)), indicating an additional role in replication fork stabilization and restart. Indeed, *sgs1* mutants are more sensitive to perturbed replication than to the induction of DSBs. Furthermore, BLM and Sgs1 protein levels peak in S phase (Dutertre et al., 2000; Frei and Gasser, 2000), and BLM was recently shown to be stabilized through an interaction with TopBP1 in S phase, independent of TopBP1 functions in ATR activation and DNA replication (Wang et al., 2013). In budding yeast the stabilization of replicative polymerases at forks stalled on HU, and recovery from HU treatment, depends on Sgs1 helicase activity. Given the preference of Sgs1 and BLM to unwind unusual folded DNA structures, one likely function of the helicase at stalled replication forks is the reversal or elimination of fold-back or reversed forks, which accumulate when forks stall and excessive ssDNA accumulates. This would explain the ability of Sgs1 to promote RPA and Polα binding at stalled forks. Thus, in addition to well-known functions in DSB repair, multiple lines of evidence point to an important role of BLM/Sgs1 in the survival of stalled replication forks.

It has been suggested that BLM/Sgs1 can promote lesion bypass through driving fork regression by its branch migration activity followed by template switching. Subsequently, BLM/Sgs1 could reverse the regressed fork by branch migration. Alternatively, BLM/Sgs1 might regulate recombination events, either to prevent aberrant recombination or in contrast to promote homologous recombination-mediated restart (reviewed by (Manthei and Keck, 2013)). BLM sumoylation was recently proposed to facilitate RPA/Rad51 exchange and Rad51 accumulation after prolonged replication fork stalling (Eladad et al., 2005; Ouyang et al., 2009; Ouyang et al., 2013). WRN and Sgs1 are sumoylated as well (Branzei et al., 2006; Kawabe et al., 2000), but Sgs1 sumoylation seems to be important for telomere recombination only (Lu et al., 2010). Although the exact role of BLM/Sgs1 in restart of stalled replication forks remains to be determined, BLM directly interacts and collaborates with several components of the Fanconi anemia pathway both in intra-strand crosslink repair and replication fork restart (Chaudhury et al., 2013; Deans and West, 2009; Suhasini and Brosh, 2012). The Fanconi anemia pathway is thought not to be conserved as such in yeast, although putative FancM, FancJ and FancP homologs exist (reviewed by (McHugh et al., 2012) Interestingly, the putative FancM homolog Mph1 is also implicated in limiting crossover formations, similar to Sgs1 (Prakash et al., 2009). Further delineating the crosstalk between Fanconi anemia pathway proteins and Sgs1/BLM is an area of ongoing research.

RPA, which is essential for DNA repair and replication, interacts with all RecQ helicases (Croteau et al., 2014). In Chapter 4 we show that an acidic region distinct from the helicase domain in Sgs1 binds RPA. Impaired RPA binding in the *sgs1-r1* mutant, however, did not result in replication fork stabilization defects, unlike disrupting Sgs1 helicase function. Previously, RPA was found to stimulate Sgs1 and other RecQ helicases *in vitro* (Cejka and Kowalczykowski, 2010; Croteau et al., 2014). It was suggested, however, that RPA might stabilize a single stranded reaction intermediate (Cejka and Kowalczykowski, 2010), rather than enhancing catalytic activity through a direct interaction with Sgs1. This is in agreement with our genetic results that show that *sgs1-r1* retains helicase activity *in vivo* (Chapter 4). BLM and WRN were shown to bind RPA through a similar acidic domain as Sgs1 (Doherty et al., 2005). In contrast, a recent study mapped the RPA interaction within the BLM-TopIIIα-RMI1-RMI2 complex to a region in RMI1 (Xue et al., 2013). The discrepancy between both studies remains unresolved, but the respective RMI domain is not conserved in *S. cerevisiae* Rmi1. Thus, the acidic domain in Sgs1 remains the strongest interaction domain for the large subunit of RPA in the yeast Sgs1-Top3-Rmi1 complex.

Apart from its function in resolving complex DNA templates Sgs1 was shown to act in checkpoint signaling independent of its helicase activity (Bjergbaek et al., 2005). It associates with

Rad53 and promotes Mec1-dependent Rad53 phosphorylation (Bjergbaek et al., 2005; Frei and Gasser, 2000). In Chapter 4 we show that the acidic region bound by RPA is also phosphorylated by Mec1. The phosphorylation of Sgs1 allows it to bind Rad53 through the same acidic region both *in vitro* and *in vivo*. Similar to Sgs1, WRN and BLM are phosphorylated by ATM/ATR (Ammazzalorso et al., 2010; Davies et al., 2004; Pichierri et al., 2003). On the other hand, BLM and WRN phosphorylation seems to be important for their recruitment or stable association with stalled replication forks, while Sgs1 is permanently associated with replication forks, also during an unperturbed S phase (Cobb et al., 2003). Recently, it was shown that BLM knockdown did not affect CHK1 phosphorylation, although WRN knockdown does in response to CPT, but not to HU (Patro et al., 2011; Wang et al., 2013) This may indicate that redundant pathways recruit the downstream kinase. Even in yeast, multiple pathways for Rad53 recruitment to stalled or damaged forks exist (Chapter 1).

Whether RPA and Rad53 binding to Sgs1 can occur at the same time or is mutually exclusive remains to be investigated. Sgs1 associates with replication forks and can be recovered from cell lysates tightly bound to RPA even in the absence of DNA damage (Cobb et al., 2003). However, Sgs1 phosphorylation is only detected after HU treatment (Chapter 4). Thus, Sgs1 would only acquire Rad53 binding activity after Mec1 activation. Given that the RPA-Sgs1 interaction seems to be constitutive and is not disrupted by Sgs1 phosphorylation, a trimeric RPA-Sgs1-Rad53 complex is possible. On the other hand, given the size of the acidic stretch (200 aa) it may be unlikely that both bind concurrently. Interestingly, Sgs1 is epistatic with the replication checkpoint mediator Mrc1 with respect to Rad53 activation, but not with respect to fork stabilization (Alcasabas et al., 2001; Bjergbaek et al., 2005). Mrc1 has been suggested to promote Mec1-Rad53 interaction (Chen and Zhou, 2009), but may also play a role in stabilizing recruited Mec1-Ddc2 (Naylor et al., 2009). It could therefore act upstream of Sgs1 in the signaling pathway to Rad53. The broad range of contributions made by Sgs1 at replication forks, renders it difficult to determine the exact interplay of partially redundant pathways, that enable fork restart, checkpoint activation or translesion synthesis.

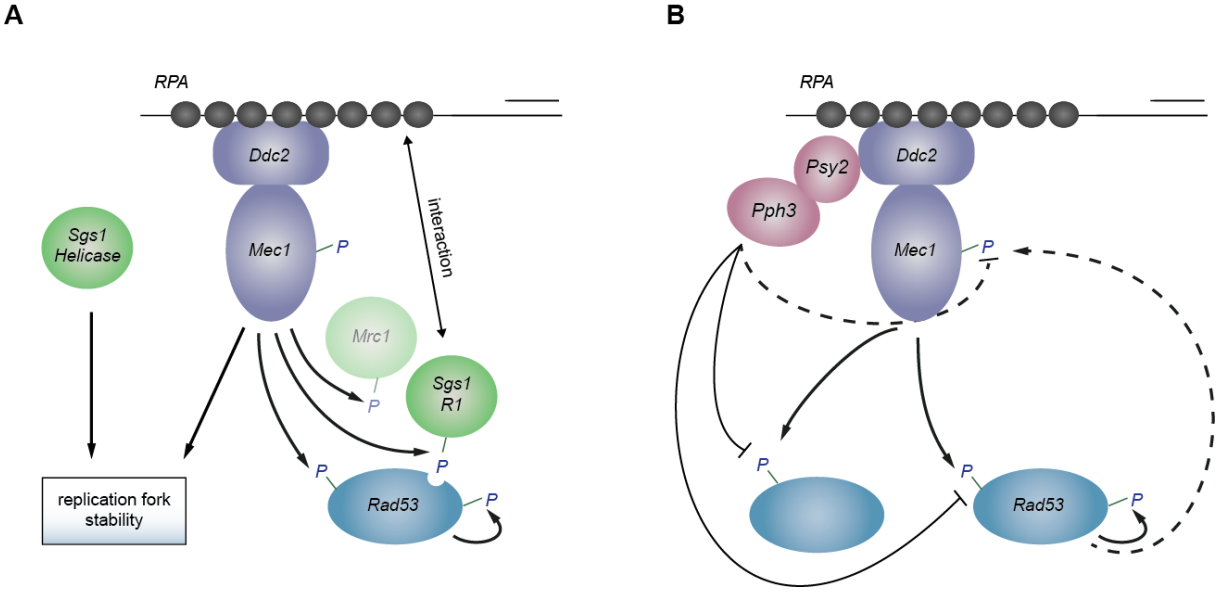

Figure 5.1: Conclusions from this work. (A) While Mec1 and the Sgs1 helicase activity synergistically contribute to replication fork stabilization, the Sgs1 R1 region contributes to checkpoint signaling. R1 both interacts with RPA and binds Rad53, the latter being dependent on phosphorylation by Mec1. Regarding checkpoint signaling Sgs1 is epistatic with the replication checkpoint mediator Mrc1. **(B)** Psy2-Pph3 physically interact with Mec1-Ddc2 and regulates phosphorylation of both Rad53 and other Mec1 targets that were found downregulated in *mec1-100* cells. Pph3 further regulates Mec1 S1991 phosphorylation, although likely indirectly through Rad53.

The relationship between the study of Sgs1 and our insights into the regulation of Mec1-Ddc2 requires comment. Sgs1 is a target of Mec1, both are found at stalled or damage replication forks, and mutation of each leads to a profound sensitivity to replication fork stalling on HU. The combination of *sgs1*Δ with loss of the S-phase function of Mec1 (*mec1-100*) leads to full fork collapse and cell death on even low doses of HU. Such synergism is not observed when *sgs1*Δ is combined with *rad53*Δ, and it places *mec1-100* on a distinct pathway from that of *sgs1*Δ with respect to fork stability (Cobb et al., 2005). This reinforces earlier conclusions that the roles of Mec1 and Rad53 are not equivalent at stalled replication forks: Indeed, whereas *rad53* mutation can be suppressed by *exo1* deletion, *mec1* mutants are not (Segurado and Diffley, 2008). Unlike the synergism observed between *mec1-100* and the loss of Sgs1 helicase activity, there was no synergy with the *sgs1-r1* mutation which deleted the Rad53 binding site. In fact, this mutant was not hypersensitive to HU, although it showed Zeocin sensitivity, indicating that it acts redundantly with other factors in the checkpoint response to HU. My main goal was to understand Mec1 function and regulation by characterizing a specific Mec1 mutant, *mec1-100*, which shows a selective, S-phase specific loss of Rad53 activation ((Paciotti et al., 2001) (Chapter 3). Consistently, in the main part of my work I found that the PP4 phosphatase regulates Mec1 signaling, both by targeting Rad53, but also by regulating a majority (94%) of Rad53-independent targets, and a phosphoacceptor site within Mec1 (Chapter 2). In summary, I found both a new factor acting in the Rad53 branch (the R1 region in Sgs1, Chapter 4) and a major regulatory factor of overall Mec1 signaling (Psy2-Pph3, Chapter 2), that fine-tune Mec1 activity to ensure precise timing and level of target protein phosphorylation (Figure 5.1). These insights significantly expand our knowledge of this central kinase of the DNA damage checkpoint and its impact on genome stability.

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CHAPTER 6: APPENDIX

LIST OF ABBREVIATIONS

4-NQO	4-nitroquinoline 1-oxide
53BP1	p53-binding protein 1
9-1-1	Rad9-Hus1-Rad1
A	alanine
AAD	ATR activation domain
AD	transcription activation domain
AHC	ADA histone acetyltransferase complex
ATM	Ataxia telangiectasia mutated
ATP	adenosine triphosphate
ATR	Ataxia telangiectasia and Rad3 related
ATRIP	ATR interacting protein
BER	base excision repair
Bfa1	Byr-four-alike 1
BLAST	basic local alignment search tool
BLM	Bloom's syndrome protein
BRCA1	Breast cancer type 1 susceptibility protei
BRCT	BRCA1 C-terminal domain
Bre1	brefeldin A sensitivity 1
Bub2*	budding uninhibited by benzimidazole 2
C	cytosine
CAF-1B	chromatin assembly factor 1 subunit B
CCT	chaperonin containing TCP1
Cdc6*	cell division cycle 6
CDK	cyclin dependent kinase
Cds1	checking DNA synthesis 1
Cdt1	Cdc10 dependent transcript 1
Chd1	chromatin organization modifier, helicase, and DNA-binding domains
ChIP	chromatin immunoprecipitation
Chk1*	checkpoint kinase 1
Cin8	chromosome instability 8
CMG	Cdc45, MCM, GINS
Cmp2	calmodulin binding protein 2
Cna1	calcineurin A 1
co-IP	co-immunoprecipitation
COMPASS	complex proteins associated with Set1p
CPT	camptothecin
Crb2	Cut5-repeat binding 2
Crt1	constitutive RNR transcription 1
Csm3	chromosome segregation in meiosis
CTD	C-terminal domain
Ctf4*	chromosome transmission fidelity
CtIP	CtBP-interacting protein
CUL1*	Cullin-1
Cut5	cell untimely torn 5
D	aspartate

DAmP	decreased abundance by mRNA perturbation
DBD	DNA binding domain
Dbf4	dumbbell former 4
Dcc1	defective in sister chromatid cohesion 1
Ddc1*	DNA damage checkpoint 1
DDK	Dbf4-dependent kinase
Dia2	digs into agar
Dis2	defective in sister chromatid disjoining
DMEM	Dulbecco's modified Eagle's medium
DNA	deoxyribonucleic acid
Dna2	DNA synthesis defective 2
dNTP	deoxynucleotide
Dot1	disruptor of telomeric silencing 1
Dpb11*	DNA polymerase B 11
DSB	double strand break
dsDNA	double stranded DNA
DTT	dithiothreitol
Dun1	DNA-damage uninducible 1
E	glutamate
ECFP	enhanced cyan fluorescent protein
EDTA	ethylenediaminetetraacetic acid
EMAP	epistatic miniarray profiling
Eme1	essential meiotic endonuclease 1
Exo1	exonuclease 1
F	phenylalanine
FAT	FRAP, ATM, TRRAP
FATC	FAT C-terminal domain
FCP	TFIIF-associating component of CTD phosphatase
Fen1	Flap endonuclease 1
FHA	forkhead-associated domain
Flp	flippase
Fob1	fork blocking less
FRET	Förster resonance energy transfer
Fun30	function unknown now 30
G	glycine
G1 phase	gap 1 phase
G2 phase	gap 2 phase
GAP	GTPase-activating protein
GCR	gross chromosomal rearrangement
GFP	green fluorescent protein
GINS	go-ichi-ni-san
Glc7	glycogen 7
H	histidine
H2A	histone H2A
H2AX	histone variant H2A.X
H3	histone H3
HAD	haloacid dehalogenase
HEAT	Huntingtin, EF3, PP2A, TOR1
HEK	human embryonic kidney

HELB	DNA helicase B
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HIR	histone regulation
HIS	*HIS3* gene
HPLC	high-performance liquid chromatography
HR	homologous recombination
HRDC	helicase and RNaseD C-terminal
HU	hydroxyurea
HUS1	hydroxyurea sensitive 1
I	isoleucine
IC	Interstrand crosslink
Ies4*	ino eighty subunit 4
Ino80	inositol requiring 80
IP	immunoprecipitation
IR	irradiation
Irc21	increased recombination centers 21
Isw2*	imitation switch subfamily 2
ITC	isothermal calibration
K	lysine
KAP1	KRAB-domain-associated protein 1
kD	kilodalton
L	leucine
lacZ	β-Galactosidase gen
LC	liquid chromatography
Leo1	left open reading frame 1
LEU	*LEU2* gene
M phase	mitosis
M	methionine
MBF	MluI cell-cycle box (MCB) binding factor
MCM	mini-chromosome maintenance
Mcm4*	mini-chromosome maintenance 4
MDC1	mediator of DNA damage checkpoint protein 1
Mec1*	mitosis entry checkpoint 1
Mih1	mitotic inducer homolog 1
Mlp1	myosin-like protein 1
MMS	methyl methanesulfonate
Mrc1	mediator of the replication checkpoint 1
Mre11	meiotic recombination 1
MRN	Mre11, Rad50, Nbs1
MRX	Mre11, Rad50, Xrs2
MS	mass spectrometry
Mus81	MMS and UV sensitive 81
MYH	MutY homolog
N	asparagine
NaPP	sodium pyrophosphate
Nbs1	Nijmegen breakage syndrome 1
Nek1	Never in mitosis A-related kinase 1
N-OB	N-terminal OB fold
NP-40	4-Nonylphenyl-polyethylene glycol

Nrm1	negative regulator of MBF targets 1
Nup84*	nuclear pore 84
OB	oligonucleotide binding
Oca1	oxidant-induced cell-cycle arrest 1
ORC	origin recognition complex
p	phosphorylated
P	proline
PAF1	RNA polymerase II associated factor 1
PBS	phosphate buffered saline
PCR	polymerase chain reaction
Pds1	precocious dissociation of sisters 1
PI3K	phosphoinositide 3-kinase
PIKK	PI3K-related kinase
Plk1	Polo-like kinase 1
Plx1	Xenopus Polo-like kinase 1
PMSF	phenylmethylsulfonyl fluoride,
Pol1*	polymerase 1
PP	protein phosphatase
PP4C	PP4 catalytic subunit
PP4R3*	PP4 regulatory subunit 3
Ppg1	protein phosphatase involved in glycogen accumulation 1
Pph3*	protein phosphatase 3
PPM	phosphatase, metal dependent
PPP	phosphoprotein phosphatase
Ppq1	protein phosphatase Q 1
Ppt1	protein phosphatase T 1
Ppz1*	protein phosphatase Z 1
pre-RC	pre-replicative complex
Psf1*	partner of Sld five
Psy2*	platinum sensitivity
Ptc2*	phosphatase two C 2
PTP	protein tyrosine phosphatase
PTPA	phosphotyrosyl phosphatase activator
Q	glutamine
R	arginine
Rad53*	radiation sensitive 53
RAP80	Receptor-associated protein 80
rDNA	ribosomal DNA
Rfa1*	replication factor A 1
RFC	replication factor C
RFP	red fluorescent protein
Rif1	RAP1-interacting factor 1
Rmi1	RecQ mediated genome instability
RNA	ribonucleic acid
RNR	ribonucleotide reductase
RPA	replication protein A
RQC	RecQ C-terminal motif
Rqh1	RecQ-type DNA helicase 1
Rrd1*	resistant to rapamycin deletion 1

Rts1*	rox three suppressor 1
Rtt107	regulator of Ty1 transposition 107
Rvb1*	RuvB-like 1
S phase	synthesis phase
S	serine
S. c.	*Saccharomyces cerevisiae*
S. cerevisiae	*Saccharomyces cerevisiae*
S. pombe	*Shizosaccharomyces pombe*
Sae2	sporulation in the absence of spo eleven 2
SAGA	Spt-Ada-Gcn5 acetyltransferase
SAP	Sit4 associated protein
Sap155*	Sit4 associated protein 155
SAS	something about silencing
SBF	Swi4-Swi6 cell-cycle box (SCB) binding factor
SC	synthetic complete medium
SCD	SQ/TQ cluster domain
SCF	Skp, Cullin, F-box containing complex
SCP	small CTD phosphatase
SD	spinning disc
Ser	serine
SGD	Saccharomyces genome database
Sgs1	slow growth suppressor 1
Sit4	suppressor of initiation of transcription 4
Siz1*	SAP and MIZ-finger domain
Sld2*	synthetically lethal with *dpb11-1*
Slx4*	synthetic lethal of unknown (X) function 4
SMARCAD1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1
Sml1	suppressor of *mec1* lethality
SNF	sucrose non fermenting
Srs2	suppressor of rad six
ssDNA	single stranded DNA
Ssn6	suppressor of *snf1* 6
SUMO	small ubiquitin-like modifier
SWI	switching defective
Swi3	switching defective 3
T	threonine
Tap42	two A phosphatase associated protein 42
TDG	thymine DNA glycosylase
Tel1	telomere maintenance 1
TFA	trifluoroacetic acid
THO	suppressor of the transcriptional defect of *hpr1* by overexpression
Thr	threonine
THREX-2	transcription/export-2
Tip41	Tap42 interacting protein 41
TIPIN	TIMELESS-interacting protein
TLCK	N-alpha-tosyl-L-lysinyl-chloromethylketone
Tof1	topoisomerase I-interacting factor 1
Top1*	topoisomerase 1

TopBP1	DNA topoisomerase 2-binding protein 1
TOR	target of rapamycin
Tpd3	tRNA processing deficient 3
TPR	tetratricopeptide repeat
Tris	2-amino-2-hydroxymethyl-propane-1,3-diol
tRNA	transfer RNA
TRP	tryptophane
Tup1	dTMP-uptake 1
Ubc13	ubiquitin-conjugating 13
Ubi	ubiquitin
Ulp1	UbL-specific protease 1
USP7*	ubiquitin-specific-processing protease 7
UV	ultraviolet light
V	valine
W	tryptophane
WDHD1	WD repeat and HMG-box DNA-binding protein 1
Wip1	wild-type p53-induced phosphatase 1
WRN	Werner syndrome ATP-dependent helicase
Wss1	weak suppressor of *smt3* 1
WT	wild type
X-GAL	5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside
Xrs2	X-ray sensitive 2
Y	tyrosine
Y2H	yeast two hybrid
Yku70*	yeast KU protein 70 kD
YPAD	Yeast extract-peptone-dextrose medium + adenine
α	anti
γH2AX	Ser 139 phosphorylated mammalian histone H2AX

*= alternative numbers may be possible

TABLES 2.1-2.4 AND 2.6 (RELATED TO CHAPTER 2)

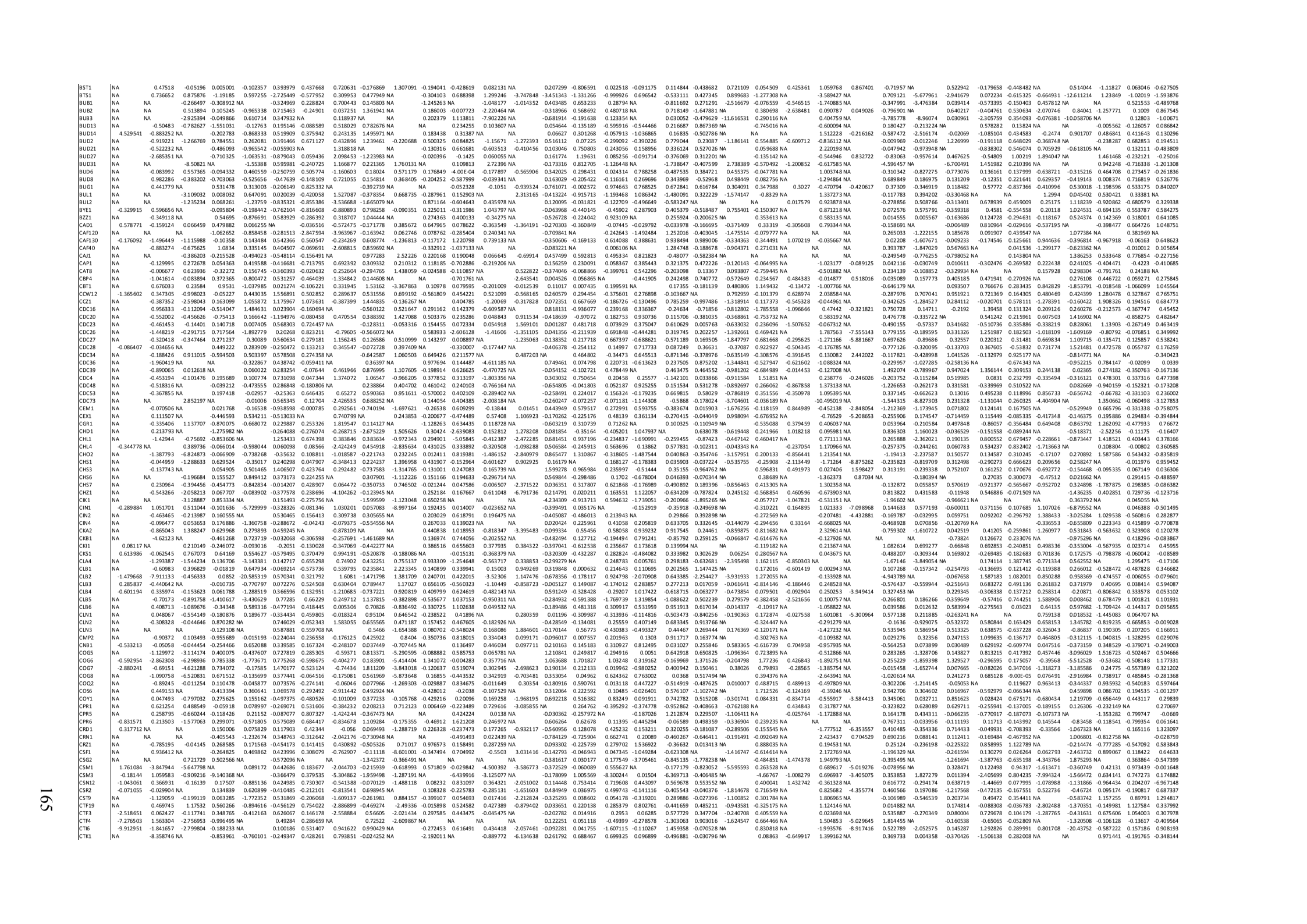
Table 2.1 Genetic interaction data

0 mM HU

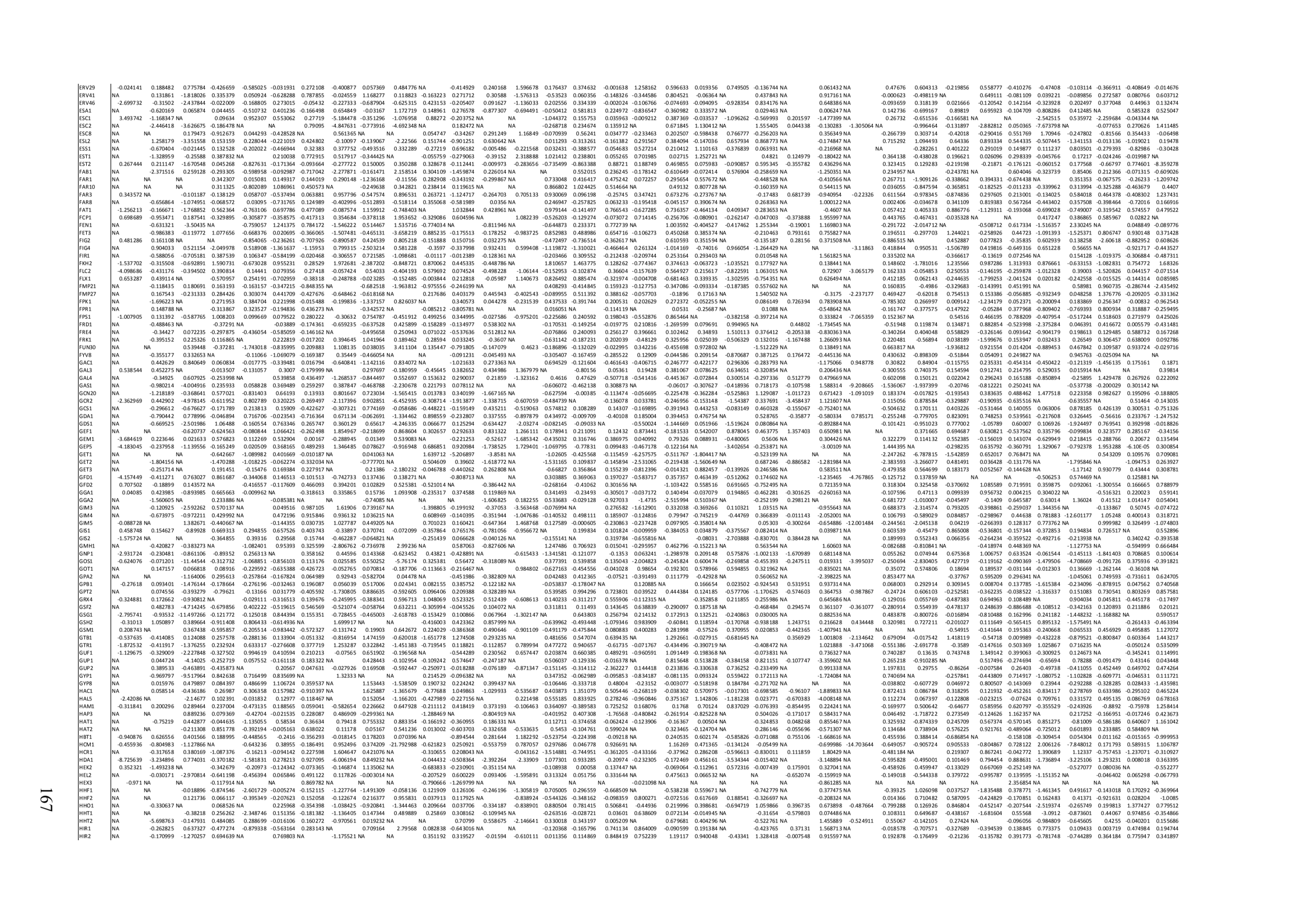
0 mM HU

Gene	ARP8	ASF1	BRE1	DCC1	DDC1	DOT1	EXO1	HEX3	HST3	HTZ1	MEC1	MRC1	MRE11	NUP133	PPH3	PSY2	RAD17	RAD18
AAD4	NA	-0.430467	-0.448914	-0.154058	0.230225	-0.285902	-0.601357	0.11428	0.344855	-1.193244	0.476956	-0.912801	0.055757	1.148938	-0.908442	-0.766851	-0.425614	1.183448
ABP1	NA	NA	0.899776	NA	-0.539383	-0.344974	-0.827616	-0.26132	-0.336558	-0.029241	-0.163223	-0.730468	-0.130564	-1.583749	-0.161321	0.434361	0.381341	NA
ACB1	0.670778	0.760163	-1.359502	0.298289	-0.20366	-0.802075	0.968571	-0.817222	-0.265106	0.313988	0.167206	0.350048	-0.017036	NA	-0.349216	0.053755	-0.186526	-0.192668
ACE2	NA	-0.260213	1.782581	-1.182855	0.135676	-0.117769	0.008055	1.536025	-1.440851	NA	NA	-0.02853	0.356094	NA	-0.448772	0.107653	-0.279814	NA
ACK1	-0.532469	0.611727	NA	-0.925831	-0.086701	-0.571223	-0.502384	0.089654	-0.783036	0.856598	-0.19621	-0.181562	0.842489	-0.860376	-0.161072	-0.401048	0.17214	NA
ADD66	NA	0.107181	0.54373	0.707587	-0.559357	0.658922	-0.349979	0.849759	0.640116	NA	-0.309577	0.201736	-0.199839	NA	-0.193543	-0.002703	-0.194295	0.099056
AGE2	NA	-0.580931	-0.636225	0.459979	0.043358	0.531337	-0.262776	-1.514101	0.344891	-2.136451	0.453092	-0.458357	0.111704	NA	-0.256427	0.222792	-0.179382	-0.400482
AGP2	0.244033	0.015977	0.410697	0.336663	0.973687	-0.558453	0.279786	-0.846827	0.299708	-0.046142	NA	-0.099843	0.618433	-0.106869	-0.004646	-1.247301	0.283481	1.103892
AGX1	NA	0.307293	0.03913	0.145294	-0.019407	-0.41556	-0.409146	NA	0.020825	0.259275	-0.678211	-0.223547	NA	-2.411944	0.881442	0.639059	-0.275824	0.247297
AHC1	NA	NA	-0.774613	-0.606689	0.578437	0.172265	NA	-2.155646	NA	NA	0.202456	0.082606	0.248757	-2.609363	0.175757	-0.017229	0.18506	0.885428
AHC2	-2.383111	0.657219	-1.188669	NA	0.570923	-0.102762	0.070304	-2.206461	0.561226	-0.991594	0.109111	-0.016697	0.566462	-2.128869	0.418399	0.488728	0.08499	NA
AIM21	0.309132	-0.132905	0.204076	0.743834	0.043883	0.320431	0.004153	0.136448	-0.360419	0.89009	-0.280275	0.21911	0.767308	0.706915	-0.673068	-0.455131	-0.007822	0.738264
AIM22	NA	NA	0.433621	-0.578342	0.178064	-0.368246	0.175294	0.851424	0.008445	-0.621655	-0.295032	0.803977	0.802769	-0.374557	0.18673	-0.100832	-0.395315	-0.322421
AIM26	0.183587	-0.061516	-0.684705	-0.585252	0.001001	-0.104954	0.39919	-0.088269	-0.615114	0.235485	0.374926	0.131157	-0.014719	-0.675606	0.263583	0.438699	0.351401	-0.408329
AIM29	-2.133961	0.075779	0.446851	-0.374882	-3.188437	-0.187928	-0.48854	0.499257	-0.299017	-4.365106	0.068026	0.103361	0.061268	NA	0.564654	0.371086	0.002623	-0.166337
AIM3	-0.008469	NA	-0.705364	0.015985	0.535667	-0.468216	0.373285	0.421672	-0.475479	0.869218	NA	-0.075749	NA	0.764015	0.797154	-0.112713	-0.259433	-0.145176
AIM32	NA	-0.272944	-0.266208	-0.547539	-0.30569	0.792347	0.137141	0.718793	-0.401911	1.196074	0.279584	-0.302188	-0.080027	-0.729033	0.884557	0.175828	0.302076	0.140386
AIM34	-0.417626	0.699429	-0.451057	-0.720384	0.25982	-0.055677	0.240528	-0.290701	0.686083	-0.032634	0.404008	0.086953	-0.182124	NA	-0.232071	-0.12302	-0.169824	-0.432629
AIM4	NA	NA	0.820516	-0.752769	0.521974	-0.562635	-0.325006	NA	-1.377805	1.843954	NA	-0.233161	-0.034736	NA	-1.066687	-0.181316	0.101235	1.336167
AIM44	NA	-2.948251	NA	-0.326506	NA	0.043159	-0.298072	-0.48719	-0.195491	2.115866	0.40124	0.011951	-1.729302	0.778123	0.635289	0.802514	-0.727609	-2.661489
AIP1	NA	0.436418	NA	0.209593	-0.0093	-0.303592	-0.030553	-3.193017	-1.424902	NA	-0.110327	-0.418651	NA	NA	0.084596	0.030758	-0.442572	NA
AIR1	NA	0.193472	0.861866	0.191189	-0.332868	-0.625499	-0.45559	0.666546	-0.447577	0.468928	0.157561	0.23918	0.623651	-0.564334	-0.468382	-0.173247	-0.55532	-0.125225
AIR2	-0.564529	0.336464	NA	-0.156162	-0.01857	-0.193778	0.582505	-0.282074	0.388982	0.465917	-0.32175	-0.189655	0.446832	NA	0.434416	0.420217	-0.353563	0.219201
AKR2	NA	-0.647291	NA	0.240466	-0.881576	-0.06382	NA	-0.915668	NA	NA	0.302684	-0.596375	0.108256	-1.783555	0.49289	0.788115	0.502165	-0.533487
ALB1	-0.764755	NA	NA	-0.565668	-0.73456	-0.302123	0.021886	-0.395617	1.306336	-0.29749	-1.218979	1.683627	0.231522	NA	1.172594	0.713414	0.095409	0.611709
ALG12	NA	0.183126	0.827336	0.174102	-0.439803	-0.573549	0.198248	-0.803106	0.575178	0.772304	-0.080938	0.293271	0.266219	0.757068	-0.252513	-0.403211	0.030069	-0.234482
ALG3	NA	-0.207299	1.842586	-0.592053	-0.070194	0.544429	-0.007314	NA	-0.185085	NA	NA	0.55104	NA	NA	0.351945	0.037125	-0.067578	NA
ALG5	-0.602655	0.272163	NA	-0.331428	NA	0.509463	-0.042314	-0.182892	-0.288817	0.547416	-0.24608	-0.560759	0.235966	1.514799	-0.466192	-0.312914	-0.0054	0.26995
ALG6	NA	NA	-1.2134	-0.628008	0.758994	-0.083815	NA	-0.061193	NA	NA	0.554332	-0.087439	NA	1.943083	-0.095923	0.483267	0.080286	-0.409745
ALG8	NA	0.387265	-0.326053	-0.218882	0.084214	-0.937557	NA	-0.244321	NA	NA	-0.138377	-0.608181	0.359673	NA	0.143908	0.342467	0.222613	-0.033847
ALT1	-3.878835	-0.768558	-1.709584	-0.661429	-0.21257	-0.360355	-0.183021	1.742858	-0.561709	-0.089206	0.205	0.464059	0.446972	NA	-0.329806	0.497638	0.128641	0.470946
AMD1	NA	0.376684	0.339513	-0.63356	0.15227	-0.375798	0.617725	0.330927	-0.246492	NA	-0.137361	-0.098902	-0.179366	2.620973	-0.044254	-0.235278	-0.303697	0.912256
APA1	-1.318324	0.971766	-0.252341	NA	-0.009499	-0.228887	0.207133	-0.147817	0.042563	-0.259416	NA	NA	-0.248149	0.227233	0.095063	0.234299	-0.212499	NA
APC1	NA	NA	-0.197285	0.09071	-0.011738	-0.336612	0.720196	0.034054	0.058789	-0.387649	0.231789	-0.157297	-0.208214	NA	0.649895	NA	0.062778	0.502299
APC11	NA	0.029527	NA	0.3242	-0.431225	0.489988	-1.2684	NA	-0.633418	NA	0.058251	-0.696736	-1.489087	0.669639	NA	-0.099891	0.11379	-0.143806
APC4	NA	-0.745555	0.410181	-0.079617	0.486972	0.191763	0.043742	0.730024	0.018924	0.387388	0.095399	0.585023	-0.434755	0.075534	NA	-0.50028	-0.329219	0.010975
APC5	-0.355252	-0.718268	-0.536838	0.314974	0.091287	0.140421	0.109723	0.857913	0.517441	-1.511178	NA	0.128422	-0.864995	-0.495632	-0.011919	-0.554691	-0.100795	0.102482
APC9	NA	0.020173	0.198482	-0.150853	-1.269909	0.402887	0.72352	0.243911	0.247952	-0.041191	NA	0.360949	-0.212099	-2.438128	0.017601	-0.231902	0.240017	-0.97433
APE3	NA	0.115329	NA	0.66756	-0.534909	0.386025	0.02413	0.410315	0.277378	NA	-0.206432	-0.160139	0.218915	2.101236	-0.104228	0.211344	0.302128	-0.311169
APL5	NA	NA	-0.670292	-0.351622	NA	0.248314	0.040373	0.172481	-0.260895	NA	-0.152058	-0.501063	0.006978	0.149436	-0.11116	0.051583	NA	NA
APL6	NA	0.013656	NA	-0.668762	-0.548238	0.219303	0.444894	-1.771848	0.26991	-0.191007	0.203917	-0.430961	0.588054	NA	0.083713	-0.051771	0.416906	NA
APM3	NA	-0.399921	-1.061818	0.228639	-0.5105	-0.022977	0.354684	-0.546715	-0.959546	-0.660973	0.85858	-0.094538	0.030449	-0.310361	0.038104	-0.016079	0.700723	NA
APM4	0.261652	NA	-0.533276	0.027799	-0.282039	0.171362	NA	-0.288072	NA	NA	0.086714	0.132395	0.218601	NA	-0.346557	-0.185501	-0.176096	0.748373
APQ12	3.460118	-0.815918	-5.338925	0.295356	-0.98435	-0.478759	-0.100863	-1.689561	-0.396778	NA	0.675943	-0.073353	-0.537974	NA	-0.060915	0.283674	0.730824	-0.70845
APS3	NA	NA	-0.81203	-0.105625	-0.017875	0.16896	0.218788	-0.882118	0.008197	0.676426	0.228711	0.052195	-0.062279	NA	-0.376178	0.241939	0.056789	0.331706
APT1	NA	NA	NA	-1.013545	-0.347207	0.662935	0.467622	-0.739998	-1.809673	-0.81114	NA	-0.344872	0.077241	0.715753	-0.18038	-0.621925	-1.031177	-0.343313
ARC1	NA	-0.174708	-0.91158	-0.502101	-1.483428	-0.982812	-0.327953	NA	-0.603631	NA	NA	0.803751	NA	1.410427	0.302905	0.075915	0.105045	-0.095875
ARG80	-1.122491	0.062747	NA	0.268224	0.07339	-0.070927	0.458532	0.426667	-0.206222	-1.259526	0.721068	0.737244	-0.514417	-0.681017	-0.165812	0.608972	0.361013	0.186858
ARL1	NA	-0.777003	-3.642221	0.42693	-0.354034	0.668699	-0.008777	-1.120995	-0.755121	NA	NA	-0.18108	0.205662	-5.038856	0.121091	-0.427106	0.478655	0.932511
ARO1	NA	-1.123669	-2.397237	0.624867	-1.480394	0.883621	-2.297845	0.728018	-2.234104	NA	-0.374281	NA	-2.998819	1.087077	NA	0.547655	-0.40312	-0.958795
ARP1	NA	-1.541359	2.263443	-1.005786	1.131857	-0.061971	0.089556	0.348173	-0.118386	NA	-0.749657	1.199735	-0.367917	0.826723	1.036399	1.033414	-0.935655	-0.223847
ARP4	NA	NA	-10.30232	-0.106187	-0.318026	0.589014	0.288664	-3.675054	-1.757343	1.507908	0.931778	-0.398729	-0.304632	-1.717306	0.141241	0.648514	-0.208355	0.355385
ARP6	NA	NA	NA	NA	NA	-0.562948	0.167184	NA	-1.447037	3.186231	NA	NA	NA	NA	NA	-0.734968	-1.054813	-0.457129
ARP7	-0.997147	0.281238	-3.801451	-0.14517	0.188552	-0.269213	-0.169603	NA	-0.039647	NA	1.133445	0.740833	0.243002	NA	0.916217	0.173891	-0.134929	0.232629
ARV1	NA	NA	-4.508914	0.913779	NA	1.10E-05	0.435946	-0.762025	0.111393	-2.729202	0.37865	0.592493	0.109595	NA	-0.196196	-0.170724	0.102526	-0.15787
ARX1	4.255541	0.019822	1.301669	-0.953964	0.077576	-0.678727	0.127607	1.872223	0.491573	1.435872	-0.496974	0.151609	0.167492	NA	NA	0.001191	0.053479	-0.325178
ASF1	NA	NA	-2.208937	0.83307	NA	1.108678	-0.017282	-6.06866	NA	NA	1.04122	1.716922	NA	NA	-0.48879	NA	NA	0.025895
ASH1	NA	-0.351953	0.04331	0.425922	-0.597209	-0.350692	-0.09273	-0.015858	0.005203	0.582895	0.108611	0.587331	0.202528	NA	-1.09451	-0.978914	0.209407	0.586352
ASI1	NA	-0.201244	-0.915298	0.198334	-0.666218	0.65469	0.186025	-0.325169	-0.778974	-0.552629	0.678313	-0.116464	-0.181819	-0.896993	0.116351	0.669081	0.52366	0.026179
ASI3	0.419969	0.064263	NA	-0.373195	0.093651	-0.320354	-0.131076	-0.679079	-0.042704	1.033396	0.096884	-0.26364	0.160105	-0.584263	-0.334703	-0.231108	-0.1487	0.032858
ASK10	0.999238	0.412526	0.014548	-0.361814	-0.084997	0.251945	0.387708	-0.895456	0.651605	-1.477136	0.36794	-0.872414	0.337883	0.313215	-0.167924	-0.298397	-1.111215	-0.148871
ASM4	0.103691	0.176303	NA	0.000789	0.650079	0.417692	0.248912	NA	0.515306	-2.795809	-0.1843	-0.564788	-0.189776	-14.989912	NA	0.063484	0.285215	NA
ASR1	NA	-0.724266	0.305975	0.737469	-0.452109	0.902988	-0.418078	NA	-1.021836	-0.534796	-0.091308	0.112903	NA	NA	0.554568	0.186091	0.690888	0.336051
ATG21	NA	-0.623474	-1.684932	0.420749	NA	0.218245	0.094905	-0.349598	0.722839	-1.035552	0.742658	0.84528	0.30882	NA	0.189148	0.313314	0.226541	0.13348
ATG8	NA	NA	0.071048	-0.148603	0.182877	-0.30225	0.673652	-0.632479	-0.858023	-1.005086	-0.32786	0.344702	0.453444	0.261794	-1.061077	-0.331271	-0.463726	0.538734
ATP23	-0.996653	0.801034	0.616075	-0.811128	0.203486	-0.838899	0.479683	-0.056088	0.292889	-1.189106	-1.187374	0.7738	0.649845	-1.58523	1.316216	0.69404	-1.232643	0.285356
ATS1	NA	-0.333492	-0.728918	-0.378156	0.345559	-0.194302	-0.127513	-0.118963	0.937597	0.745148	0.220065	0.46234	0.031339	0.555116	-0.282156	0.012502	0.215032	-0.045468
AVL9	NA	0.821672	-1.557466	-0.177247	0.47288	-0.675684	-0.128964	-0.503599	0.251235	-0.342945	0.026878	0.301642	0.448225	-1.060002	-0.359048	-0.256484	0.097587	-0.082302
AVO2	NA	0.156485	-0.233171	-0.146677	0.803806	0.544109	0.174398	-0.410836	-0.183212	NA	-0.084535	0.755275	NA	-0.421985	-0.162977	0.016115	0.781681	-0.006149
AZF1	NA	-0.75356	0.645109	-0.025042	-0.844259	0.682108	NA	0.052259	NA	-0.039122	0.638599	-0.351182	-0.591844	-1.122646	0.228598	1.095148	0.605147	0.288213
BAS1	NA	0.595339	0.572161	-0.142592	-0.397108	-0.140375	0.079777	1.014628	0.608521	0.297401	-0.648804	0.439223	-0.319504	NA	-0.683016	-0.731426	0.333004	-0.847912
BBC1	NA	0.082788	-0.279124	0.153268	0.488988	0.779031	0.134432	-0.056026	0.030212	-0.122629	-0.043464	0.16083	0.292311	NA	-0.167738	-0.463964	0.13466	-0.659919
BCK1	0.105088	NA	-0.294	0.301443	-0.913987	-0.462729	0.18305	0.16651	-0.795319	0.423163	0.556776	0.170303	0.162707	0.987992	-0.205371	0.538008	0.357843	-0.020001
BCK2	NA	0.753252	-0.773327	-0.604783	0.838246	-0.53095	-0.341905	0.224154	0.078784	1.211425	0.040321	-0.654351	0.660508	0.162884	-0.607783	0.432062	-0.667763	0.382567
BDF2	-1.887903	NA	NA	0.372132	0.048908	0.091886	0.297108	NA	-0.009305	-4.608338	-0.276708	0.146837	1.227199	NA	0.14129	-0.225309	-0.52013	0.570115
BEM2	NA	-0.864899	0.185007	-0.369445	-0.688706	0.796756	0.216751	0.632115	-0.312222	1.406	0.540475	-0.416998	-0.824638	NA	0.396596	0.213788	-0.186363	0.385711
BEM3	-0.56286	0.05198	-0.112714	-0.429353	NA	0.75451	0.605969	-1.848188	-0.363613	-0.501593	0.645784	0.885725	-0.196545	-1.646247	0.482916	-0.31315	-0.091402	0.684876
BEM4	NA	-0.315587	-2.008195	0.458538	NA	0.323003	-0.031674	1.580752	-0.0907	-2.181306	1.192978	-0.207328	0.144818	2.183333	0.016299	0.337783	-1.054354	-0.923482
BFA1	NA	-3.064958	-0.257545	-0.454701	-1.023388	0.583603	0.646907	-2.025829	0.452673	NA	0.896305	0.088365	-2.291314	-1.509905	0.324548	0.57948	0.599726	-4.111784
BIK1	NA	0.877146	0.270368	NA	-0.281229	-0.753162	0.72167	0.320186	0.664976	-7.146768	-0.392639	NA	0.077703	NA	-1.107717	-0.66758	-0.181344	NA
BIM1	NA	-2.472329	1.405292	-0.320234	NA	0.209836	0.375065	0.320808	0.205789	NA	0.562666	-8.166811	-1.062806	NA	-2.837328	-0.264994	0.520989	-1.030098
BIT2	NA	0.220415	0.619519	-0.169418	0.572793	-0.088702	0.19399	-0.365739	0.749347	NA	-0.376579	0.252638	0.517854	1.014889	-0.033098	0.864775	-0.366807	0.384502
BLM10	NA	0.623084	1.263684	-1.518556	1.514012	-0.094379	-0.541419	-0.172958	-1.226994	NA	NA	-0.345722	0.289009	-1.705372	0.970956	0.776425	-0.711887	0.130486
BMH1	NA	NA	-2.936867	-0.033156	-1.323144	0.239891	0.154022	0.118253	0.014471	-3.85918	-0.874289	-0.517688	0.92212	-0.531398	-0.258469	0.194014	0.505599	-1.490433
BMH2	NA	-0.688871	-0.354657	-0.89558	-0.083435	0.629989	0.249476	-0.010178	0.477132	NA	-0.307811	-0.056716	0.465479	NA	NA	0.659514	-0.598156	-0.259434
BNI5	NA	0.095365	0.751421	-0.23067	0.636111	0.090406	0.79632	-0.258153	-0.379565	0.126733	0.310817	-0.109794	0.376095	-0.044751	0.588843	NA	-0.571476	0.224029
BOI1	-0.278235	-0.236813	0.522536	-0.201991	-1.104693	0.011298	0.037312	0.82478	0.222177	0.772797	NA	0.211299	0.321738	-0.422838	-0.393184	-0.025422	0.001271	-0.33381
BOI2	-1.096746	-0.351292	-0.805383	-0.046138	0.112939	-0.020489	1.293466	-0.214417	1.261461	NA	-0.373844	-0.032763	-0.262029	0.490119	-0.273212	0.010209	0.878085	-0.989728
BOP2	-0.455794	-0.970474	-0.251151	0.463285	-0.601783	0.327187	0.440796	NA	0.109409	-2.004786	0.362073	0.064106	-0.022643	NA	0.030357	0.087151	0.214859	-0.423654
BRE1	4.253741	NA	NA	1.103318	NA	0.295029	0.51418	NA	NA	NA	0.764816	0.227854	NA	NA	NA	NA	NA	0.895704
BRE2	-5.331497	-3.395593	0.564663	-0.150354	0.34784	-0.246274	0.128991	1.195022	0.292525	NA	-0.099532	0.556934	NA	-3.766907	0.165768	-0.202789	0.658678	-1.125248
BRE5	NA	-0.877981	-0.950036	0.133529	0.063371	-0.567041	0.090909	0.277769	-0.354768	NA	0.048356	-0.438501	-0.877803	NA	0.125991	0.068824	0.498387	-0.314853
BRR1	NA	0.468245	NA	-1.139452	-0.049503	-0.094856	-0.459128	-0.870143	-0.670888	-8.829741	0.363914	0.087624	-0.096621	-0.438286	-0.109288	-0.119772	-0.314835	0.3885
BSD2	NA	-0.490686	-2.354568	0.30737	-0.228913	0.246422	-0.041903	-0.106971	-0.483373	-1.297872	0.324586	-0.189488	0.314274	0.535596	0.001143	0.447541	0.224589	0.217739

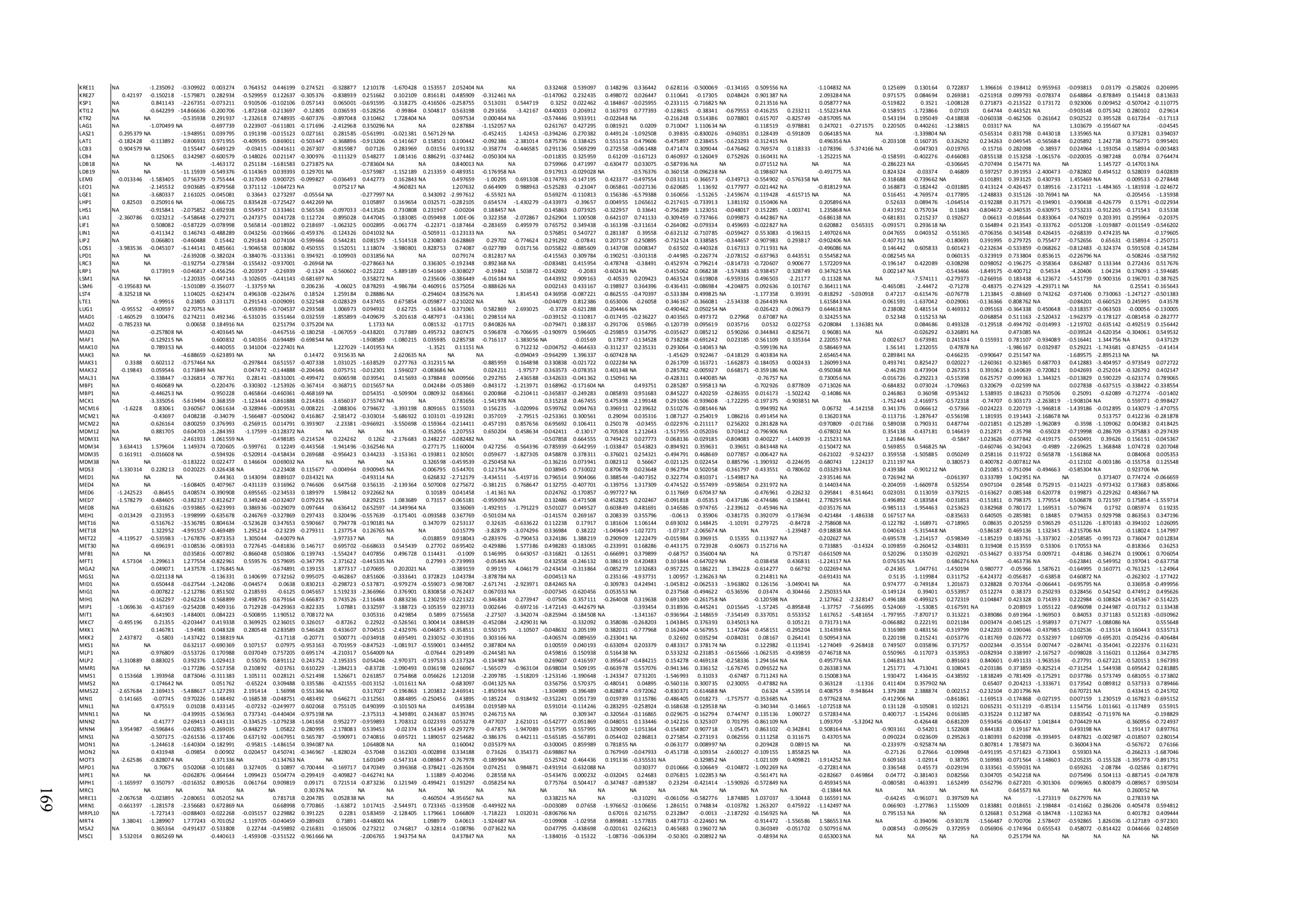
Gene	RAD24	RAD5	RAD52	RAD9	RFA1	RPD3	RSC1	RTT101	RTT109	SAE2	SGS1--NULL	SGS1--PM	SLX8	SWR1	TOF1	UBC13	YKU70
AAD4	-0.00201	0.523409	0.858083	-0.89891	NA	1.585702	-4.671464	-0.143522	0.748758	0.138224	1.448028	-0.133102	0.195244	0.598694	-0.080148	0.259892	-0.401201
ABP1	0.660437	0.384132	0.595788	-0.544316	NA	0.711836	NA	0.130721	0.598325	0.255204	0.80479	0.152642	-0.515442	0.389571	0.518498	-0.047738	-0.490235
ACB1	0.457048	-0.014878	NA	0.90323	NA	0.360346	NA	0.155246	-0.075059	-0.274605	0.493367	0.444317	-0.723177	0.743233	0.727454	-0.592504	-0.893617
ACE2	-0.963149	NA	0.404126	-0.348691	1.801411	0.781673	NA	0.758772	-0.80855	-0.62353	-0.143197	-0.116337	0.522445	-0.345803	-2.14346	-0.049728	-1.120643
ACK1	0.141562	0.468311	0.210163	-0.944469	NA	0.868194	-3.21829	0.60025	0.289767	0.249868	0.26862	-0.287753	0.653462	0.380887	-0.686497	-0.224631	-0.66837
ADD66	-0.078616	0.510971	NA	0.299424	-1.206144	1.087388	NA	-0.241342	-0.172971	-0.641046	-0.299605	0.329157	0.207766	-0.326941	-0.093868	0.174941	0.46218
AGE2	1.130065	0.393602	0.685608	0.612503	-0.009129	-1.240917	NA	-0.070407	-1.282445	-0.108076	0.322394	0.428511	-1.788746	-0.753176	0.347651	-0.144238	0.992346
AGP2	0.135055	0.384371	0.191546	-0.877979	NA	-0.685901	-3.251117	-0.641041	0.102442	0.917021	0.08254	0.103872	NA	0.816489	-0.040522	-0.285712	0.482045
AGX1	-0.362298	-0.583936	0.182906	0.537173	0.455904	-0.969468	NA	0.034797	-0.442363	-0.233588	0.764593	0.274956	NA	-0.218715	-0.613637	-0.309755	-0.687115
AHC1	0.754963	1.042681	0.847101	-0.019584	NA	-0.555311	NA	0.190459	0.469565	0.07823	0.618792	0.15191	-1.480621	-1.059416	-0.839486	-0.150268	0.547805
AHC2	-0.861318	-0.585389	0.694861	0.023624	-0.730252	0.284806	NA	0.376168	1.068151	0.217707	-0.226309	0.121178	-1.311044	-1.848256	0.847494	0.169119	0.216523
AIM21	-0.615353	0.36913	0.423497	0.081856	NA	0.577771	-0.014914	0.030039	0.101212	-0.900769	0.145012	-0.161811	NA	0.306395	-1.280141	-0.697573	1.016503
AIM22	-0.841262	-0.041568	-0.079432	-0.961042	NA	0.095339	NA	NA	-1.550471	-0.22054	0.333172	-0.893396	0.967504	-0.010986	1.203102	-0.814485	-0.574038
AIM26	0.355208	-0.537725	-0.361565	0.373427	-0.041824	-0.201876	NA	-0.70977	-0.280952	-0.395836	0.022188	0.052159	0.427347	-0.03487	0.193452	0.08195	-0.156479
AIM29	-0.543313	0.199148	-0.601098	0.156179	NA	0.329076	NA	0.823924	0.287719	-0.482664	0.180856	-0.227084	0.547797	-1.080457	0.372561	0.095482	-0.425092
AIM3	0.896075	-0.843768	0.118336	0.016406	-0.122678	-0.374562	NA	0.140228	0.596717	-0.049428	0.789257	-0.199796	0.609472	0.035769	-0.737936	-0.378734	0.217702
AIM32	0.40154	-0.182353	NA	0.110569	-0.092894	-0.071379	NA	-0.329042	0.387273	0.76354	0.480564	-0.635965	-1.52258	0.129015	1.266434	0.633107	-0.205285
AIM34	-0.021302	0.858087	NA	-0.349898	-0.390366	-0.050547	-3.36489	0.06485	0.429928	-0.163123	NA	0.111624	0.5743	-0.110431	-1.335155	-0.663154	0.840257
AIM4	-0.479542	-0.033754	NA	-0.744966	0.251548	0.176729	NA	-0.929755	NA	-0.680654	NA	0.058451	NA	0.56513	0.231233	-0.305027	NA
AIM44	0.5233	-0.942415	-1.985815	0.254461	-0.548519	1.864354	-8.536835	-0.126953	-2.520641	-0.476728	-0.018859	0.623423	-1.155924	1.829939	1.436015	1.02044	-0.229506
AIP1	0.574986	0.190946	NA	0.358834	-0.656924	0.104469	NA	NA	-0.14618	-0.910776	NA	NA	NA	0.535238	NA	0.670713	0.277064
AIR1	-0.688207	-0.41868	0.782046	0.315853	NA	0.887348	-2.904112	0.468087	0.398275	-0.144301	0.043363	-0.258255	-0.128837	0.533782	-0.596658	0.137823	0.619565
AIR2	0.448192	0.825072	-0.82079	0.015567	NA	0.741505	NA	-0.067986	-0.502589	-0.175212	0.887874	0.309501	-0.873129	-1.178587	-0.376826	0.012896	0.477145
AKR2	0.563682	0.602985	-0.735468	1.065908	0.287052	0.572274	NA	0.057625	0.502786	0.469836	-0.399284	0.585971	-1.27736	-1.302706	0.542223	0.129394	0.09723
ALB1	0.405942	0.522954	NA	-0.199773	NA	0.13521	NA	NA	-1.03316	-0.099467	0.169742	0.324606	-0.279562	0.289163	0.366541	0.225615	1.067938
ALG12	-0.176443	0.304237	0.080904	-0.270064	-0.206238	-0.694341	0.30218	-0.182703	-0.168499	0.891084	0.367563	0.039882	-1.336395	1.130518	-2.122553	-0.129699	0.430293
ALG3	-0.009552	-0.903202	NA	-0.59451	NA	1.372345	1.002164	-1.117913	NA	0.004832	0.333567	-0.702061	3.377031	0.489461	-0.96911	-0.11164	0.115855
ALG5	0.371756	0.569161	0.183193	0.451871	1.02431	0.24311	-2.128563	-0.044029	0.054624	-0.880034	0.292195	0.820911	0.124008	0.710493	NA	0.000446	0.05353
ALG6	-0.040127	0.741759	0.491695	-0.876994	-0.012129	-0.028263	NA	0.207669	0.583317	0.163471	0.086596	0.117922	-0.800774	-0.005176	NA	0.044344	-0.220339
ALG8	-0.201882	0.819884	0.35889	-0.19418	-0.016637	0.647671	NA	-0.060156	0.34524	-0.555255	1.145871	0.233602	0.280095	0.416272	-0.821058	-0.420945	-1.068916
ALT1	-0.010836	NA	0.38138	-0.063983	-0.11004	0.70586	NA	-0.496123	NA	-0.23315	-0.100464	-0.005365	1.868914	0.068703	-1.093981	-0.067658	-0.396304
AMD1	0.140259	0.134936	NA	-0.267386	-0.01564	0.300663	-1.824426	1.071457	0.278021	-0.420705	-0.223286	0.005892	-0.249124	0.794072	-1.705119	-0.40134	-1.311048
APA1	0.088706	-0.599729	0.492637	0.093016	NA	0.995568	-3.302916	-0.189485	1.138773	0.133202	-0.39287	0.41754	0.25814	-0.224411	0.605888	0.086493	-0.082218
APC1	-0.926953	0.27032	-0.305125	0.179191	-0.127122	-0.305031	NA	0.056941	-1.03323	-0.137887	1.100766	0.035892	0.78661	0.577687	NA	-0.915536	0.080426
APC11	0.211291	0.387482	NA	0.18589	NA	1.495144	NA	0.14912	NA	0.298047	0.076651	0.011479	NA	-0.094004	0.130392	NA	0.303844
APC4	0.701078	1.160351	-0.712822	-0.499058	NA	-0.811699	NA	-0.475417	-0.679043	-0.118112	0.182918	-0.485831	0.675415	0.114383	-0.196732	NA	0.360547
APC5	0.281286	0.3234	NA	-0.040418	NA	-0.051016	NA	-0.44501	-0.195894	0.440045	0.316461	-0.430515	0.376336	0.237495	-1.340896	-0.514059	0.735721
APC9	0.935342	NA	NA	-0.318743	0.95679	0.915872	-1.261433	-0.1665	NA	-0.692346	0.802855	0.394943	-0.502274	0.678264	-1.433802	-0.851434	-0.002496
APE3	-0.023046	-0.192187	-0.374079	0.088804	0.606574	0.488281	NA	-0.293909	-0.075502	0.528577	-0.396365	-0.382657	-1.627396	0.182393	-0.44332	-0.435702	0.322228
APL5	1.245761	0.291229	-0.059839	0.297955	-0.076937	-0.10202	NA	0.16014	0.638321	0.217721	0.446967	-0.347139	-0.939402	0.128122	-1.892002	0.014943	-1.419339
APL6	-0.179625	0.582843	0.363945	0.042127	-0.554981	-0.672295	NA	0.841266	-0.135667	0.753769	NA	0.146847	-0.511986	-0.35647	NA	-0.156999	-0.349901
APM3	0.300214	0.320516	-0.414126	-0.037488	NA	0.705177	NA	0.379507	0.198362	0.0705	-1.201216	-0.26234	-0.530458	-0.284045	0.257177	NA	0.054017
APM4	0.104276	0.102472	NA	0.457695	0.146538	0.358557	NA	-0.767834	-0.127098	0.042431	NA	-0.423505	-0.344541	0.642158	1.051323	-0.391305	0.163923
APQ12	0.112282	-0.272351	-2.715184	0.675985	-0.742367	1.623978	NA	-0.288024	-1.930613	0.312036	-0.841601	0.139015	-0.481787	-5.897979	-0.552598	-0.274051	0.602062
APS3	-0.1327	0.660433	0.266745	0.890189	0.269524	-0.589665	NA	NA	0.170737	-0.131328	0.828006	-0.191907	-0.373951	0.195957	0.385275	0.368521	-0.086311
APT1	1.335834	-0.489725	NA	0.258573	0.70944	-0.811329	NA	-0.423678	-1.790391	NA	0.558287	-0.139263	-0.870616	-0.571246	NA	-0.02168	-0.120127
ARC1	-0.285081	NA	-0.528155	-0.384412	0.537939	NA	NA	-0.42949	-3.04136	NA	-1.183932	0.458279	NA	0.157338	1.235274	-0.057165	-1.915847
ARG80	0.308474	0.780022	NA	0.550579	NA	-0.768476	-3.630875	0.312751	-0.384986	-0.106381	0.032082	-0.239944	-0.270329	0.207557	0.173885	0.035432	1.055207
ARL1	-0.037714	0.332182	0.512515	-0.007053	0.555832	0.541342	NA	0.100966	0.318837	0.241638	0.230547	0.129742	NA	0.351124	NA	0.565354	-0.636065
ARO1	0.767123	0.591458	NA	NA	-1.532135	1.665971	NA	0.595013	1.631708	-0.271773	1.19058	0.831505	-1.391899	-2.61253	NA	NA	0.510948
ARP1	-0.560282	-0.398701	NA	-0.698783	NA	-0.064296	NA	0.041321	-0.393396	-0.048182	0.504863	0.260218	0.270891	-1.632955	1.120625	0.811725	-1.289525
ARP4	0.20332	0.393799	-0.280888	-0.684455	-0.703969	-0.685274	NA	NA	-1.611342	0.302857	0.49425	0.658198	-3.525622	1.013346	1.193927	0.52839	0.242745
ARP6	-0.952104	NA	NA	0.342345	-4.615994	0.367906	NA	-0.448112	NA	-1.398111	0.182926	1.831916	NA	2.464455	0.002866	0.631431	-0.82887
ARP7	-0.416004	-0.409813	NA	-0.231359	0.064181	-1.221289	-0.575876	0.818883	0.270338	0.605169	0.456419	-0.161303	0.218666	-2.013734	0.390013	-0.437131	-0.89761
ARV1	0.397815	0.450164	-0.439284	-0.966916	NA	-3.559784	NA	-1.212428	-0.578485	-0.082418	-0.050165	0.283454	-0.46489	-1.526172	-1.297727	0.377248	-0.599926
ARX1	0.110504	-0.435584	-0.108408	0.158699	NA	1.625661	NA	0.282354	NA	-0.381121	-0.269348	0.356866	NA	-0.000951	-0.104367	NA	-1.2629
ASF1	-0.48727	NA	NA	0.563995	NA	-1.059816	-1.82024	NA	NA	-0.14577	-1.176562	0.218389	-7.5518	-2.122323	1.035707	0.452268	-0.158362
ASH1	0.317442	0.948561	NA	-0.020078	NA	0.319041	NA	0.730468	NA	-0.085603	0.796293	0.278487	0.721486	-0.06638	-2.201342	-0.547801	0.319569
ASI1	0.440563	0.409977	-1.425364	1.301017	-0.397161	0.625417	NA	-0.136407	0.218268	0.532899	NA	NA	-0.767118	0.154331	0.640624	0.291934	1.317727
ASI3	0.383142	-0.622208	0.142636	0.576593	-0.595362	0.017184	NA	0.098732	0.540184	-0.060425	0.556663	-0.3072	-0.388145	0.688428	-0.029227	0.630381	1.085357
ASK10	-0.044035	0.205933	0.849222	1.015876	-0.087243	-0.041629	NA	-0.414814	-0.12694	-0.610431	1.060364	0.33944	-0.066064	-0.062068	-0.242036	-0.333074	-0.39485
ASM4	0.462614	-0.324199	0.199672	0.676754	0.086142	0.623162	NA	0.694414	0.359292	0.309327	NA	0.081014	-0.624063	0.063548	-0.536836	0.107443	0.969269
ASR1	0.390796	0.154395	-1.371457	0.69495	0.295023	0.152806	NA	-0.640136	NA	0.346256	-0.412643	-0.023948	0.300091	-0.546462	-0.905217	0.210208	-0.353388
ATG21	-0.018973	0.225818	NA	0.701552	NA	0.836909	NA	-0.345577	-0.936136	0.264711	0.460985	0.421149	-1.350849	0.258001	0.397828	0.183374	-0.397347
ATG8	-0.414746	0.359913	NA	-0.734486	0.326314	-0.307076	NA	0.837748	-0.776957	-0.585527	0.093943	-0.227344	0.356283	0.569483	0.217879	-0.827845	-0.780608
ATP23	-0.661332	0.130884	1.202591	-1.154031	NA	-0.235265	NA	-0.265304	0.890357	-0.553483	0.432199	0.200469	-0.293987	0.343612	1.455033	-0.402517	-0.640185
ATS1	-0.212563	0.273205	-0.606398	0.492292	NA	0.424737	NA	-0.153655	-0.177612	-0.093013	-0.248905	0.087377	-0.458362	0.124128	0.165229	-0.162461	0.038578
AVL9	0.447397	NA	0.137223	-0.183218	0.483935	0.544001	NA	-0.042556	NA	-0.627099	-0.082799	0.438561	-0.564419	0.218723	0.485966	-0.005511	0.032911
AVO2	0.591339	0.809957	NA	-0.274549	0.220984	-1.170631	NA	1.129228	0.995316	-0.458872	0.143105	-0.119517	-0.396285	-0.088573	-0.402899	-0.406581	-0.899836
AZF1	-0.209326	0.595839	-0.489027	0.672287	0.337352	1.522373	NA	-0.13343	-0.032483	0.337055	-0.473001	0.380078	-0.577729	-1.521183	-0.225553	0.413418	0.13858
BAS1	-0.117472	-0.220271	0.545284	-1.153393	NA	-0.179905	NA	0.599561	-0.470327	0.466908	-0.360149	-0.079272	0.684396	1.363042	0.552152	0.634144	-0.654006
BBC1	-0.435794	0.204355	-0.077766	0.696421	NA	-0.012281	NA	NA	0.2715	0.307602	0.357847	0.307051	0.239777	0.302037	-0.454444	0.214154	-0.17039
BCK1	0.316321	0.148026	-0.958242	-0.238223	-0.012376	2.132854	NA	NA	-1.548352	-0.535212	0.068674	0.046062	0.121078	0.281089	0.139185	0.084571	-0.840257
BCK2	NA	-0.843332	0.514568	-1.380758	NA	-0.195396	-3.134089	0.036589	0.710375	-1.513272	0.477662	0.171735	NA	0.75692	-0.062072	-0.573759	-1.175191
BDF2	-0.168766	-0.161388	0.974639	-0.376558	NA	-1.550247	-3.291706	0.896941	1.231391	-0.118044	-0.255876	-0.220147	0.391621	-0.663443	0.087687	-0.726917	-0.816714
BEM2	NA	-0.758531	-2.579758	0.594052	NA	1.747739	NA	-0.78014	-0.402829	-0.227916	0.208892	0.876384	NA	0.400385	-0.238396	0.552977	-0.711397
BEM3	0.73733	0.578492	-0.758888	-0.348374	0.862475	1.048986	NA	-0.678845	-0.931562	1.012211	-0.191246	0.348059	-0.892611	0.007366	0.578501	0.923	0.462404
BEM4	0.897616	0.157081	0.466394	0.142571	0.126718	-1.081008	NA	-1.186159	-0.614031	0.374831	0.693181	0.357193	1.838264	0.265389	-0.58626	0.322401	0.118248
BFA1	0.444084	-2.444505	-4.906739	-0.524454	-1.689115	0.156334	NA	NA	-5.163037	0.331298	0.01983	0.42537	NA	0.040702	-0.008375	1.269277	0.51947
BIK1	-0.191369	0.459749	0.76348	-0.821557	-0.16878	-0.722047	NA	0.520942	1.117277	-0.18772	0.231477	-0.502848	0.831599	-0.491376	-0.553782	0.239671	0.223874
BIM1	0.327922	-0.527208	-2.242781	-0.183025	NA	0.16134	NA	0.004366	-1.838946	0.124847	0.995372	-0.018024	-0.462656	-4.3562	NA	0.295931	0.27106
BIT2	0.157512	-0.036762	1.13103	-0.76377	0.337862	0.870897	NA	0.545343	0.344814	-0.369421	-0.079297	-0.280219	-0.216639	1.180238	-0.912428	-0.391903	-0.675138
BLM10	-1.917801	-0.027596	-0.119333	-0.641325	0.281714	1.844986	NA	-0.628612	0.755392	-0.035232	-0.62961	0.40904	-1.458594	0.675239	1.234117	0.771677	-0.577976
BMH1	NA	0.545259	NA	-0.092793	NA	-1.820889	NA	1.003131	0.184857	0.0279	-1.018826	-0.38518	NA	-2.105374	0.508136	0.104477	0.137303
BMH2	-0.732841	0.66683	0.274553	-1.468125	NA	-0.740194	NA	0.057923	-0.979283	0.311562	1.325684	0.615327	-0.010882	0.283363	NA	NA	NA
BNI5	-0.300116	0.49407	0.448057	NA	-0.464525	-0.51676	0.941718	0.15601	0.688172	0.358034	-0.146233	0.055875	-1.159171	-0.236349	NA	-0.207959	0.813652
BOI1	0.01963	0.153221	NA	-0.414357	-0.47931	1.029349	-7.379364	0.057585	0.08336	-0.79005	-0.52627	0.247142	0.363203	1.085309	0.144601	-0.094438	0.612155
BOI2	NA	0.789596	NA	0.656521	-1.572317	0.181624	-2.671573	-0.284367	-1.235477	1.771136	-0.532014	0.48182	NA	0.355235	0.039143	0.358856	-0.472922
BOP2	0.223907	-0.567908	-0.943085	0.491404	NA	-1.327813	NA	0.230444	0.187599	0.322992	0.167832	1.292355	0.131131	-1.267679	-0.292057	-0.147851	-0.325331
BRE1	NA	NA	NA	NA	-0.799702	-3.053212	NA	NA	NA	NA	-0.057204	0.605082	NA	NA	NA	0.125153	NA
BRE2	0.322797	NA	-3.015563	0.181246	-1.3816	-0.025024	-6.709217	0.431305	NA	0.439945	-1.118694	0.693073	-2.471083	-7.903344	-0.341666	-0.498983	-0.299926
BRE5	0.310143	0.363785	-0.428533	0.188124	0.868736	NA	1.199185	0.656927	0.225872	-0.954333	-1.211861	0.250328	NA	-5.02461	0.445642	-1.359862	-0.151004
BRR1	0.300627	0.252662	-1.347952	-0.060343	-0.039503	0.946633	NA	0.091961	1.143313	-0.265842	NA	-0.017913	0.14998	-3.118572	0.945679	-0.398952	0.962461
BSD2	0.195564	-0.338196	-0.169534	-0.06944	0.250203	1.417038	NA	-0.020087	-0.290285	-0.391799	-0.584811	-0.209798	NA	0.38965	-0.402065	0.470414	0.742659



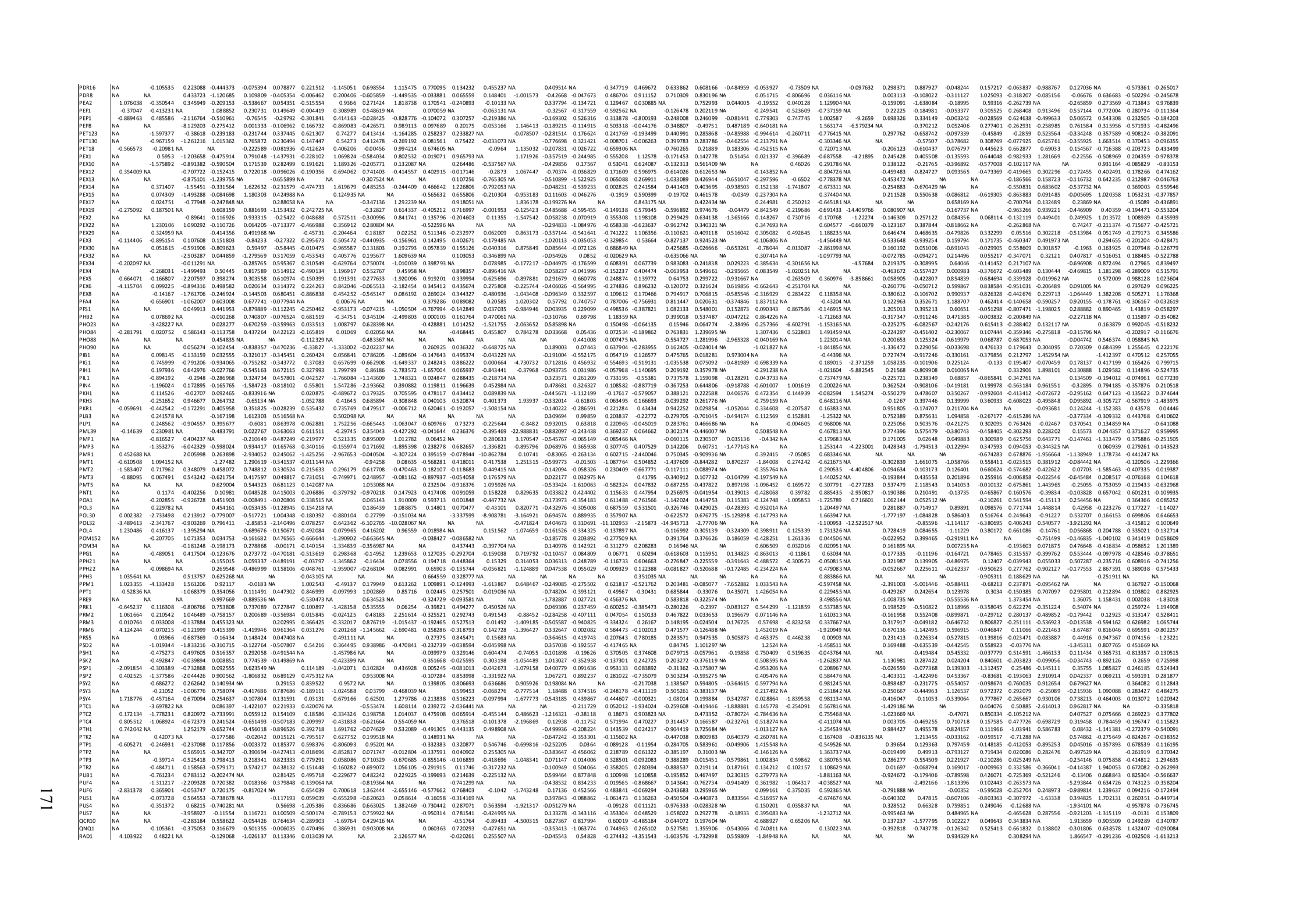
CTK3	NA	-2.515732	NA	-2.280274	-0.520871	0.221684	NA	NA	-0.074213	NA	NA	-3.557039	-0.383186	1.733469	-0.515027	0.618646	-0.645115	NA	-0.305615	0.421685	NA	-0.637184	NA	-0.149365	2.155048	0.225322	-4.336451	-0.215308	-0.80074	2.3319	NA	NA	NA	-0.671948	-0.394553
CTP1	0.225446	-0.233187	-0.338694	-0.898541	-0.06809	-0.774381	-0.369478	0.588753	0.556981	-0.097339	0.631626	0.354997	-0.211505	3.020058	-0.457739	-0.372783	0.432821	0.468585	-0.164016	0.328279	NA	0.141994	NA	-1.122602	NA	-0.201102	-0.127582	0.347512	0.598232	-0.178311	0.999475	0.005394	0.455635	0.334349	-1.004246
CUE1	NA	-0.450322	-2.39654	0.367956	-0.537028	0.644281	0.160599	-1.501591	-1.551271	1.321412	0.090494	-0.051553	NA	0.396735	0.369411	0.294128	0.15097	0.30032	0.642496	-0.012964	-0.454848	0.013282	0.356758	-0.185487	NA	-0.464674	0.210321	0.183045	NA	NA	-1.029093	0.174464	NA	0.255543	NA
CUE2	NA	NA	-0.929596	0.403353	-0.005657	0.425336	-0.270267	0.181773	0.38132	-0.99894	-0.168873	0.407887	NA	-0.040073	0.165162	0.359914	0.104074	0.258023	0.49287	0.241445	-0.243088	-0.274155	-0.5579	-0.328436	NA	-0.376764	0.690817	1.583414	0.089769	0.072261	-0.104702	-0.078553	-1.095135	0.380838	1.146389
CUE3	-1.887867	0.491764	-0.330957	0.553148	0.450083	0.151363	-0.254826	NA	-0.041836	-1.242362	0.054481	-0.154804	0.572888	NA	0.301849	-0.570959	0.182167	0.022193	0.699683	0.699444	0.620788	0.533475	NA	0.545915	-1.608697	0.249627	0.226674	NA	0.221854	0.067922	-0.936803	0.816754	NA	-0.488463	0.472809
CUE4	NA	0.403507	NA	-0.653391	-0.533368	-0.186713	0.315846	-0.091752	0.746602	-0.444404	0.070551	0.574814	-0.321769	-0.686187	-0.073676	0.636378	0.415526	0.506415	1.225495	0.43493	NA	0.707661	0.150394	-0.002158	NA	0.148026	-0.203289	-0.009527	0.445502	-0.308217	0.917346	-0.579947	-0.318127	0.316139	-0.740004
CUE5	NA	-0.062845	-0.244544	0.327755	-0.147095	0.285835	NA	-0.518718	NA	NA	0.371746	0.486071	0.039171	NA	0.393506	0.125503	-0.451954	-0.611385	-0.066912	0.395846	0.324461	0.721948	NA	-0.484184	-6.171317	0.318769	-0.097018	0.298529	1.142994	0.355429	-0.363638	-0.169345	0.475525	0.151095	0.423516
CUL3	NA	NA	0.709313	-0.415828	NA	-0.258504	0.846551	NA	-1.089314	-0.509089	-0.369069	-0.340293	NA	NA	-0.023152	-0.232625	-0.187482	0.907207	-0.250656	0.051168	NA	-0.535975	NA	0.811229	NA	0.189748	NA	-0.38793	NA	-0.185092	-1.393566	0.323791	-1.213621	0.302743	0.860057
CUP9	NA	0.145799	-1.538083	0.823828	NA	-0.22304	0.303434	1.529274	0.492592	NA	-0.728141	0.521594	-0.273769	NA	0.046414	0.51543	-2.18399	0.621146	1.817073	0.025274	NA	0.87536	-1.068021	0.964789	NA	0.563183	-0.197207	-0.293356	0.554205	-0.302488	0.069827	-1.341782	-1.485035	0.110211	-0.050426
CWC15	-0.655792	-0.242933	0.255358	0.325157	NA	-0.580596	0.696081	-2.487925	-0.634853	0.825557	-0.212176	-0.101891	0.148553	-0.753062	NA	0.044037	0.367278	-0.108162	1.08333	0.09536	-0.070993	NA	NA	-0.503264	NA	-0.441266	-0.447703	-0.599782	-0.322652	0.468639	-0.25001	-0.718392	1.134272	NA	0.379294
CWC21	-2.13096	0.045856	-1.01443	0.26853	0.878272	NA	-0.280344	0.013646	0.214956	-2.882183	0.438632	-0.231377	0.702034	NA	-0.09784	-0.676833	-0.162654	0.875798	0.220023	0.005517	1.184346	0.79142	NA	-0.806626	NA	0.232339	-0.03437	-1.277306	0.185252	-0.098257	0.021729	-1.083219	-0.442419	-0.537813	1.330739
CWH41	NA	-0.092871	-0.498165	0.267743	0.892103	0.177347	-0.917149	-1.066723	-0.079536	NA	0.850065	-0.015902	-0.014347	-1.755707	0.466031	0.222452	0.310925	0.184297	0.700046	0.989981	-0.797174	-0.175173	NA	1.764532	NA	0.314754	0.218663	0.591526	0.573392	0.079855	-1.799385	0.073741	-0.64292	-0.076495	1.749014
CWH43	NA	0.198987	-0.116925	NA	0.117757	-1.072308	-0.860643	0.448801	-0.892771	-0.428291	-0.893929	NA	0.74872	NA	-0.462282	0.001621	-0.154315	NA	-0.55269	-0.740828	1.081015	0.319138	NA	0.621842	-1.467348	0.002749	0.589919	-0.569182	0.721345	0.288466	0.676534	0.164586	-2.215405	-0.737359	0.166367
CYK3	NA	-0.795552	NA	0.162175	-2.430288	0.923955	-0.173326	NA	0.537305	1.152139	0.0305	-0.14537	-1.104177	NA	0.86489	0.554278	0.390311	-0.586611	0.025802	0.513405	-1.000899	0.621928	-0.289198	-0.444577	NA	-1.569918	-1.141601	0.41609	-0.523871	-0.306788	1.564425	1.168189	NA	0.110596	0.794694
CYT1	NA	-0.095524	0.137969	0.152518	0.30418	-0.116923	NA	0.135445	NA	NA	-0.397003	0.206638	0.03021	-0.292577	-0.207828	0.149752	-0.028769	-0.472063	0.468155	0.389136	0.291168	-0.186076	NA	-0.670816	NA	0.465843	-0.398027	0.26188	1.100342	-0.407366	0.009661	-0.228922	NA	-0.160716	-0.199743
DAL81	NA	0.66205	NA	-1.388188	0.707901	0.312542	0.24669	0.724431	-0.025395	0.71772	-1.211816	NA	-0.921391	0.292148	0.27178	0.054386	-1.161556	0.162982	-0.548354	-0.02081	-0.813565	-0.993465	NA	1.494811	NA	0.365634	1.486431	-0.657211	0.447165	-0.530843	0.740059	0.491164	1.414949	-0.048131	-0.29275
DAS1	NA	NA	-0.275399	0.234929	0.409476	-0.057944	-0.228155	0.749261	-0.72052	0.306946	0.632509	-0.958572	-0.823995	NA	-0.580005	-7.70E-05	-0.195827	-0.477283	0.179767	0.316217	-0.392135	0.541923	-0.139212	-1.35039	NA	-0.123136	-0.698717	0.346678	-0.12689	0.75609	1.390116	0.689558	NA	0.240826	-0.027649
DBF2	NA	NA	-3.881257	-0.73294	NA	-0.068433	-0.186725	-0.442971	-0.300591	-0.515829	0.327347	0.477794	0.187925	1.175535	0.369384	0.15129	0.106432	-0.411475	-0.006185	0.181814	NA	-0.634428	0.659929	0.187285	NA	0.553007	-0.163275	0.059275	0.292343	0.151852	0.22932	0.228696	-0.436821	-0.555238	-0.574535
DBP1	NA	0.059795	NA	-0.035287	NA	0.308018	0.238666	0.212054	1.092261	NA	-0.466804	-0.095953	NA	-2.030444	-0.275734	0.075331	-0.202056	0.703706	0.398689	-0.115483	-0.602157	-0.271596	NA	1.444052	NA	0.868711	-0.478979	-0.096337	-0.72556	0.4756	-0.532026	-0.38371	0.40492	-0.347687	0.668555
DBP3	NA	0.574644	NA	0.28297	-0.416095	0.091537	-0.365107	1.332424	0.828541	NA	-0.533503	0.075426	-0.028677	NA	0.049426	-0.625033	0.46464	-0.313611	-0.249098	0.582557	-1.757267	-0.101281	NA	0.006959	NA	0.355075	0.337142	NA	-0.835718	-0.295687	0.480499	-0.872757	0.908534	-0.011028	0.704937
DBR1	NA	0.105704	-0.671006	-0.27149	-0.590258	0.299117	0.907064	-0.339868	0.735063	-4.234545	-0.761229	0.799768	0.282524	NA	-0.298375	0.205524	0.116208	-0.171565	1.195754	-0.144141	-1.067596	0.523396	NA	-0.017617	NA	0.200838	-1.179547	0.294816	0.467479	-0.029261	0.266114	-1.658647	0.089101	0.80713	0.538202
DCC1	-2.692162	NA	NA	NA	NA	NA	0.513526	NA	NA	NA	-1.396891	NA	NA	NA	NA	NA	NA	NA	-3.017114	NA	NA	NA	NA	1.016966	NA	NA	NA	NA	0.281235	0.627473	NA	NA	NA	-0.173232	NA
DCN1	NA	-1.140852	NA	-0.032974	NA	-0.437612	0.010303	2.019068	-0.414045	-1.627276	NA	0.187716	0.347124	NA	-0.031	-0.661404	-0.900082	0.242293	-1.880302	NA	0.753497	-0.824755	NA	0.484276	NA	0.163791	0.765391	-0.496277	-0.488819	0.428058	3.301864	-0.804756	-0.263158	0.57738	-0.942963
DCR2	-0.225204	0.075128	0.250399	0.762449	-0.0915	0.55092	-0.100051	0.107553	0.622282	0.522337	0.693632	-0.093513	0.400033	NA	-0.136624	-0.510202	-0.683295	1.131871	-0.044197	-0.680439	0.900132	-0.502254	NA	-0.312846	NA	-0.36192	0.196296	0.429491	0.301931	0.007565	0.083982	1.134649	-0.378198	-0.506739	-0.413798
DDC1	-1.032251	-0.1022	0.414566	0.431916	NA	0.914235	0.770065	-1.10188	0.389535	0.797088	NA	NA	-0.92687	1.09737	1.206252	0.674612	NA	0.644095	1.335795	-1.894364	-1.687208	0.308446	NA	0.29727	NA	1.313519	1.2546	0.680213	0.714458	0.232058	-1.216014	0.319175	NA	-0.795305	0.499489
DEG1	-0.879951	-1.490259	-10.388423	-0.101201	-0.287011	0.174492	0.144243	-1.221756	-1.380407	-5.27623	0.615466	0.320896	-0.061786	0.461624	0.415037	-0.087144	0.64247	0.182666	1.386292	-0.177768	-0.931887	0.353612	-0.949956	0.34479	NA	-1.191627	-0.000588	-0.359973	0.948816	-0.000394	-1.736072	-2.782378	0.463315	0.815188	0.264911
DEP1	NA	-3.462314	NA	-0.555112	-0.158545	-0.836742	-0.422559	NA	0.613204	NA	-0.353378	0.657572	-4.533434	0.660192	0.119498	0.490914	-0.3584	-1.240994	-0.008577	-0.472517	-5.919887	-0.093274	NA	0.511837	NA	-0.329813	-6.540009	-0.256489	0.243064	-0.086464	-3.389124	NA	1.42537	0.590613	-0.082786
DGK1	NA	1.031796	-0.66695	NA	0.192944	0.178003	0.216902	0.476847	-0.840646	3.64551	NA	0.198586	0.236207	NA	-0.299612	-0.253018	NA	NA	-1.175553	-0.220336	NA	-0.189867	NA	1.098769	NA	0.299669	-0.270213	0.03338	-0.081785	0.078771	NA	1.868547	0.127231	-0.437774	0.024085
DGR2	NA	-0.246506	-0.255843	-0.095486	-0.547401	0.140473	-0.120003	-0.332198	-1.476331	0.553434	0.072753	0.017997	0.001732	-1.750318	0.265584	0.739455	0.097153	0.264933	0.794696	0.705729	-0.614244	-0.742017	0.185768	-0.375504	NA	0.061846	0.376656	0.795792	0.507963	-0.275442	-0.38104	-0.195299	1.520851	0.830931	0.632452
DIA2	NA	-0.61824	0.855838	0.769762	2.968108	3.590593	NA	NA	NA	NA	3.451058	NA	NA	NA	-1.300473	0.685158	0.742453	NA	1.357234	3.267972	NA	2.847869	0.183796	3.565758	NA	4.131334	3.601333	-0.310989	NA	3.913381	NA	2.699823	NA	3.572712	2.081683
DIE2	NA	0.138352	NA	0.439467	-0.893892	-0.502623	0.016081	0.234163	0.11384	0.82048	0.119226	-0.189286	NA	0.406242	-0.120227	0.241511	1.131081	0.72881	0.875443	0.362874	-0.282402	-0.558864	NA	-0.478602	NA	-0.005554	-0.370037	-0.363015	0.653028	0.35614	0.161163	0.672137	0.050723	0.232004	-1.537559
DJP1	NA	-0.086819	-0.425487	0.170297	-1.63177	0.227961	-0.242005	-2.156187	-0.407192	NA	-0.331649	0.187233	-0.046024	-2.3987	0.434295	0.22099	0.307448	0.324337	0.324878	0.780448	NA	0.395059	0.216797	0.42672	NA	-0.302077	0.050011	-0.080153	0.444713	0.369062	-1.129874	-0.067603	1.088114	0.552852	0.468782
DMA1	NA	-0.142088	0.398915	0.174857	-0.257078	0.297573	0.132487	-0.449826	-0.951539	0.04657	0.119456	0.699028	0.02293	0.826103	0.831513	0.795546	-0.38377	0.625988	-0.324553	0.385508	NA	-0.397563	0.486326	-1.650814	0.230003	-0.795154	-0.104157	0.354901	-1.345623	0.29349	-0.810124	-0.557338	0.444917	0.487083	0.111441
DMA2	-0.672886	0.267627	-0.640741	0.974242	0.882462	0.54825	0.199362	0.885544	0.571286	0.384015	0.012113	-0.167074	NA	-1.687755	0.332028	NA	0.113058	-0.528945	0.579387	0.256233	NA	0.341096	NA	-0.188992	NA	0.31526	-1.284944	0.499	-0.205134	-0.003795	-0.208542	0.398426	-0.932882	0.424479	0.246844
DNF1	NA	NA	1.140046	-1.046231	-0.305016	NA	0.085487	NA	0.357306	NA	0.260935	0.354501	NA	NA	0.724217	-1.078915	-0.31667	NA	NA	0.022809	0.203959	-1.164462	NA	-0.657845	NA	0.14784	-0.091017	-0.287655	0.328835	0.481165	NA	0.412264	0.479203	-0.15753	-0.007739
DNM1	-0.708184	0.619819	0.38977	0.556108	0.264982	0.386666	-0.546175	0.345689	0.499489	-0.478325	-0.322527	0.588833	0.826492	NA	0.508815	0.489104	0.102662	0.058758	0.273213	NA	NA	0.493222	0.013497	-0.761397	NA	0.540437	NA	0.710439	0.523643	-0.148421	0.287636	-0.510933	0.090757	0.103914	0.535496
DOA1	NA	NA	-8.523878	-0.047639	-0.973066	0.369541	0.030378	NA	-0.245311	NA	0.050052	-0.983802	-5.48535	-1.216356	0.593453	0.084504	-0.196248	-1.383457	-0.292844	-0.771118	-2.1617	0.402739	-4.347155	1.348922	NA	-0.503463	NA	-0.133892	0.578322	0.155241	NA	-5.802354	NA	-0.223083	-0.177694
DOC1	NA	NA	NA	0.090613	NA	0.709253	-0.87882	-0.607975	0.426904	-1.929016	0.385429	-3.791886	-8.954008	NA	0.245662	0.410634	0.101897	-2.220495	0.030352	-1.132336	NA	0.772076	-4.926428	0.520892	NA	-0.363744	-3.913843	NA	0.346677	-0.084292	-0.658044	0.486918	NA	-1.146126	-0.490919
DOM34	NA	NA	0.637411	-0.348452	-0.361491	-0.594056	0.068733	0.455879	0.045095	NA	0.779902	0.01809	0.288018	-1.881303	-0.424043	-0.374687	0.204301	0.186412	-0.082919	-0.065882	NA	-0.285031	NA	0.130878	NA	1.224606	0.2109	-0.226484	0.794958	-0.433108	0.055595	0.835343	NA	-0.403373	0.237096
DOT1	-0.291058	NA	NA	1.088116	NA	NA	-0.690479	0.437222	NA	NA	NA	-0.699841	NA	NA	-0.004153	NA	NA	0.533544	NA	NA	NA	0.938318	NA	-1.563968	NA	NA	NA	NA	-0.19795	-0.230359	NA	-0.398703	1.209208	-0.551912	NA
DOT6	-1.024472	-0.676706	-0.364264	0.281233	0.046151	0.430561	-0.258524	0.007298	0.207584	-0.739857	NA	0.373312	-0.050198	0.795096	-0.585351	-0.150189	-0.286623	NA	0.446007	-0.05637	-1.609122	-0.035981	-1.973549	-0.619264	NA	0.911079	-0.639264	-0.178267	-0.149836	-0.932956	NA	0.384171	NA	-0.017241	0.107505
DPB11	NA	NA	0.434835	-0.203706	0.259242	0.102664	-0.234012	0.996401	0.033052	NA	-1.944324	-0.275128	-0.75643	NA	-0.0311	-0.197181	-0.112422	-0.370031	0.367743	0.097276	-1.257565	-1.115982	NA	-0.265625	NA	NA	0.197232	-0.387786	-0.269485	0.139285	0.578347	NA	0.206979	0.245491	0.559006
DPB2	NA	-0.318953	0.383049	-0.118218	-0.648479	-0.075225	-0.916724	2.309002	0.668697	-15.004167	0.253833	0.224023	0.020042	-0.63561	-0.008922	0.145793	0.300945	0.067979	0.221838	0.840712	0.175947	-0.256839	NA	-0.798156	NA	-0.079629	-1.254707	NA	0.040672	0.336906	1.531514	-7.449253	NA	-0.532966	-0.195519
DPB3	-1.848608	0.260295	1.114353	0.398838	-0.634996	0.413487	0.355821	-2.406601	-1.641437	-6.480082	-0.380317	-1.267016	NA	NA	0.011496	0.183787	0.058531	1.574982	-0.216113	0.242007	0.508517	0.076782	NA	0.049345	NA	1.431364	0.199329	0.317513	0.761998	0.364015	-3.285578	-2.348702	-1.7753	0.035808	0.334046
DPB4	NA	NA	-0.282021	-0.683896	-1.146477	0.959042	0.812888	-3.352495	-2.013261	-6.756608	-0.131326	-0.671065	-0.192348	-3.784476	NA	0.050456	-0.104342	-0.124712	0.313045	0.955487	NA	0.090782	-0.088318	0.995564	NA	1.61754	0.008083	0.030084	-0.622807	0.745867	-2.744769	-2.836153	0.184055	NA	1.237337
DPL1	NA	0.337234	0.145002	0.006608	0.132894	-0.60631	-0.161222	-0.624831	0.067065	-0.796842	-0.210973	0.8298	0.206631	-1.873742	-0.147522	0.358117	-0.033456	0.875385	1.126506	0.214499	NA	NA	0.25759	-0.255006	NA	-0.010161	0.365148	-0.27417	-0.852418	-0.203141	-0.870142	NA	-1.921877	-0.122977	0.387745
DRS2	-0.770313	NA	-2.691523	-0.427762	-0.081665	-0.155072	0.004828	-0.483366	0.316999	-0.455312	0.456916	0.77757	0.380331	-0.399334	-0.11478	0.015195	-0.487577	-0.346039	0.123864	-0.036354	-0.222459	-0.304773	NA	0.047652	NA	-0.173231	-0.75701	-0.348571	-0.044233	0.360935	0.226799	0.263203	0.634669	-0.485797	0.037425
DSD1	0.307618	0.949798	-0.153604	-0.094838	-0.132739	0.316013	0.042376	-0.531309	0.342358	1.206798	0.483457	-0.788875	0.133682	NA	-0.163191	0.129327	0.027303	0.309666	0.277694	0.286034	0.113422	0.067867	NA	-0.274751	NA	-0.525081	0.571502	NA	1.047701	-0.38375	-0.385242	0.405732	-0.409644	-0.12388	-0.340906
DSE3	2.982731	0.989804	-0.377458	0.021978	-0.203693	0.164013	0.261636	0.541666	-0.327098	0.825911	-0.177908	-0.06076	0.378939	NA	-0.578347	-0.010211	-0.254986	0.145353	-0.263486	-0.575726	0.553067	-0.773144	-1.401462	0.293198	1.834292	0.172945	1.120893	-0.087245	-0.237747	-0.245697	0.517422	0.635554	-0.999545	0.435107	-0.137267
DSS4	0.095632	-0.137422	NA	0.541742	0.015217	0.759961	0.305694	-0.655619	-0.254064	0.255492	-0.867067	0.525795	-0.764376	NA	0.513546	-0.270457	0.354085	0.144805	0.937248	0.067205	-1.088101	0.279187	NA	0.029364	NA	-0.251278	-0.947785	0.801533	-0.06813	-0.019343	0.404539	-0.119423	-0.999764	-0.170781	0.556034
DST1	NA	-4.526396	-4.466387	0.54511	-2.248877	-0.386253	0.110912	NA	-0.386389	2.955605	NA	-1.181663	NA	NA	-0.098216	0.770417	-0.055498	-1.143525	0.280823	0.408303	NA	0.72631	NA	3.537329	NA	-2.935435	NA	-0.279073	-0.847092	0.840806	NA	NA	-1.93073	0.235212	-1.196964
DUG2	-2.507827	-0.364193	0.242329	0.311026	0.157533	-0.32508	-0.137894	0.548856	-0.616117	NA	NA	-0.282815	0.361155	3.390356	-0.734891	-0.288311	-0.488801	-0.487009	-1.253794	-0.102709	0.65591	-0.77682	-0.057299	0.633274	-0.034387	0.315276	0.022859	0.315163	0.999796	-0.259183	0.352187	-0.31385	-0.30429	-0.3467	0.434138
DUS3	NA	-0.50836	-0.37655	0.381151	0.031634	0.089718	0.064468	-0.354744	0.707607	0.275368	-0.499427	-0.020778	0.444905	NA	-0.086893	0.482025	0.22427	0.408188	0.526523	0.541945	NA	0.434315	NA	-0.69965	NA	0.484244	-0.179631	1.262691	0.394461	0.773273	-0.694696	0.905433	-0.174673	-0.456311	-1.36477
DYN1	NA	-1.490223	0.358435	0.27704	0.756117	0.172123	0.582081	0.812613	0.623353	NA	NA	0.561486	-1.596175	NA	0.082349	0.85699	0.12457	-2.023472	-1.048289	-1.565622	NA	0.511013	NA	0.374482	NA	-0.165011	-2.067258	-0.422707	-0.455949	0.53385	-0.831373	-0.915558	0.727337	-0.023836	-0.307104
DYN2	NA	NA	-0.242391	1.023631	0.073181	NA	1.102363	0.4366	0.830623	-0.349228	0.538576	0.948455	-0.709759	-1.375666	0.344386	0.636365	0.534836	-0.995346	-0.387613	-0.714123	-0.319922	1.260356	NA	-0.329065	NA	0.407218	-1.499253	0.386233	0.210551	0.6339	0.35576	NA	-4.50E-05	0.456522	0.19985
DYN3	NA	-2.627369	1.176124	-0.445191	0.697514	-0.408803	0.089818	-0.441697	-0.1141	NA	-0.240243	0.830738	NA	NA	1.179723	0.541714	0.0658	0.010684	0.190924	-0.827228	-1.442632	-1.201374	0.099685	0.633416	NA	-0.639101	-1.52695	0.10087	-0.154191	0.476293	NA	-0.814606	0.857706	0.011978	NA
EAF3	NA	-5.6559	NA	0.989757	-1.534012	0.200568	-0.159156	NA	-0.780326	-4.233312	0.000421	-0.417208	0.107825	-5.180709	0.921049	0.761076	0.510245	-0.950484	-0.141481	-0.154055	-0.037075	0.966838	0.969743	-0.003555	NA	0.256885	-1.49228	1.240009	-0.128362	-0.04003	NA	-4.106781	0.985201	-0.673631	0.569276
EAF6	NA	-2.563565	-1.730154	-0.651986	-0.986736	0.629313	-0.69187	-6.712535	-2.053476	NA	-0.996886	0.296154	0.156605	-1.599007	0.27268	0.534389	0.63144	-0.148409	0.735972	0.758167	NA	0.420655	0.294789	0.634888	NA	-0.460276	-0.9891	0.328941	-1.056735	-0.37679	NA	-4.281059	0.835741	-0.152782	-0.021832
EAF7	NA	NA	-1.135312	0.386605	-1.027318	-0.491353	0.235524	NA	0.060903	2.757047	NA	0.794491	NA	NA	-0.19808	NA	-0.338741	0.412677	-0.084291	0.220277	-0.562019	0.375705	NA	NA	NA	0.100628	NA	-0.121653	NA	-0.249532	0.282815	-8.355546	1.022597	-0.430827	-0.264208
EAP1	NA	NA	NA	-0.203696	NA	0.492915	-1.076941	NA	-0.324157	2.786285	NA	0.078149	-5.292923	NA	1.090438	2.119238	-0.088997	0.144905	-0.251229	-0.176448	NA	-0.519577	NA	NA	NA	-2.101713	NA	-0.253026	-0.959824	1.089418	-0.742768	NA	NA	0.555699	-1.846668
ECM18	-1.031117	0.378455	-0.155139	0.784355	NA	0.986072	-0.232775	-0.391865	1.571118	0.796414	0.603083	0.700109	-0.497618	NA	NA	-0.189359	-0.1325	0.220652	0.145288	0.511274	-0.733498	NA	NA	-0.765435	NA	0.410714	-0.141997	-0.624775	-0.283662	-0.743291	-0.666803	-0.011517	0.535552	NA	0.271535
ECM2	NA	0.524044	-1.053093	0.35066	0.410486	-0.082503	-0.824765	0.410885	0.876445	0.960887	NA	0.438747	NA	NA	0.303856	0.064253	0.114014	-0.596571	-0.158299	0.036474	NA	0.820114	NA	1.764663	0.885314	-0.694641	-0.520096	-2.415883	-0.496304	0.081465	-0.276138	-0.0697	-0.453802	-0.159947	-0.701441
ECM21	NA	0.078657	0.788236	-0.528608	0.045911	-0.052998	-0.290373	-0.935148	0.199077	1.225943	0.286554	-0.699645	0.564944	1.026729	0.147599	0.340899	0.264925	0.461375	0.177733	-0.067619	-0.070461	-0.125839	-0.295798	-1.253316	NA	-0.085068	0.890737	0.527396	NA	-0.099373	-0.523295	-0.714506	-1.541442	0.139795	-0.258871
ECM22	0.378288	NA	-0.488734	0.595959	0.555821	0.780051	0.639035	-0.581779	0.194295	0.72032	-0.201868	1.135061	0.255257	-1.825461	0.134223	0.606204	-0.046028	-0.108877	1.106989	0.054869	0.070866	0.248778	NA	0.366236	NA	0.83974	-0.153775	-0.462201	1.453263	-0.066621	-0.757349	-0.631744	1.012902	0.690235	0.477696
ECM30	NA	0.39318	-1.744732	0.431027	-0.530293	0.326237	0.159083	-0.156271	0.652012	0.28644	0.355072	-0.46427	-0.021344	-0.15491	0.127181	0.150515	-0.36249	0.333324	-0.321062	-0.223203	0.262458	1.359644	-0.80342	0.309279	NA	-0.424431	-0.123346	0.147476	-0.799187	0.683721	-0.303746	0.405783	NA	0.971712	-0.566215
ECM33	NA	0.382751	0.356847	-1.093264	0.115809	-0.94365	-0.728547	0.535407	-0.657342	0.468104	NA	-0.344685	-0.742935	1.089984	-0.617802	-0.090941	-0.117793	0.506343	-0.965515	-0.439488	-0.2527	-1.361687	NA	0.89287	NA	-0.141388	0.180252	-1.294305	-0.516213	0.328432	0.972732	-0.295457	-2.686424	-0.455067	-1.552569
ECM5	NA	-0.286345	NA	0.075686	0.225083	0.601036	0.066049	-0.865563	-0.493893	-0.393115	-0.630867	-0.063832	NA	-0.675722	0.182908	0.164016	-0.21553	0.093953	0.398518	-0.145376	-0.622322	0.76051	1.070957	-1.003891	NA	0.586887	0.006529	0.138237	NA	NA	0.416417	0.714005	0.014383	-0.30885	-0.514635
ECM8	NA	0.145138	0.22815	-0.089966	0.515926	-0.569705	-0.347849	NA	0.251802	0.194352	NA	-0.150691	0.08007	NA	0.142759	-0.262378	-0.244727	-0.263107	-0.174936	0.179461	NA	-0.03031	-0.041338	0.985426	1.556247	0.099005	1.153321	0.013977	NA	0.007221	NA	0.179641	-1.307178	-0.268173	-0.564037
EDC3	0.01179	0.034955	-0.972418	0.313922	-0.752593	0.301854	0.923718	-1.124939	1.511692	-1.403068	-0.440546	0.006601	0.165104	-1.45847	0.298467	0.275193	0.28511	-0.54029	1.130515	-0.247719	-1.404995	-0.766964	-0.886084	2.192726	NA	0.139498	-0.060879	0.116006	-0.487642	0.222394	-0.53518	-0.163436	-0.761788	0.584994	0.448095
EDE1	0.106351	-0.466085	1.041875	0.017502	0.979514	0.131236	0.166598	-1.117732	1.286144	-0.522486	0.236569	-0.137892	-0.644984	-0.903962	0.21457	0.062843	0.74136	-0.015057	1.762556	0.57997	-2.318714	0.199222	-0.062109	1.042007	-4.379032	-0.866989	-0.330889	-0.052007	-0.991852	0.129306	-1.190758	-0.231308	1.429896	-0.333133	0.689814
EGD1	-1.242551	-0.412344	0.437557	1.515853	-0.172672	-0.004305	-0.148657	-0.918416	0.086441	1.308572	-0.253911	0.090664	0.438008	-0.925357	-0.140038	-0.109971	0.52101	0.460703	0.015526	0.499811	0.076679	0.711514	NA	-1.164587	-2.362783	0.327314	0.118612	0.557721	0.359277	0.205784	-2.067272	-0.348666	-0.156381	-0.394148	-0.178381
ELA1	-1.908472	-0.478476	NA	-0.315332	-0.293443	1.018445	0.428564	-1.348089	0.80519	-1.458541	NA	0.815496	-0.638419	NA	0.142698	NA	0.071794	0.13722	0.874566	-0.069676	-1.382054	0.743661	-0.449699	NA	-4.193326	-0.169701	-1.030409	-0.142072	0.429531	0.567533	0.259718	0.55465	NA	0.20243	0.087378
ELC1	NA	0.565429	0.461665	-0.744059	-0.481625	-0.0887	-0.244377	-1.082369	-0.015597	1.878881	-0.428734	0.31431	-0.26528	NA	0.994479	0.439811	-0.441312	-0.219168	-0.855476	-0.368574	-0.209717	0.542641	NA	1.490647	1.227079	0.23779	0.399483	-0.562445	0.273698	-0.232393	-0.54085	-0.051744	0.403242	0.441652	-0.304457
ELF1	NA	-1.309717	0.357284	0.565248	-1.876606	0.02119	0.154058	-0.820544	-1.122628	-2.008365	-0.238498	0.035519	0.462615	-0.636778	-0.031768	0.667766	-0.471587	0.45602	-0.274192	0.4653	NA	-0.310881	NA	-0.070806	NA	0.097037	1.278047	-0.092304	0.218955	-0.52768	-0.688901	-1.023308	0.680409	-0.349264	0.661354
ELG1	NA	-4.031484	0.012921	-1.631618	-0.047657	0.087981	0.170292	-9.111097	-1.927467	-1.270922	-0.878112	-5.423875	-13.293569	-7.177702	0.416889	0.752978	-1.026886	0.693706	-0.942109	0.818573	-5.111833	-2.07052	NA	-0.654002	-0.952857	1.230358	-0.270901	0.797918	-3.809102	0.29663	-4.17747	-0.352862	0.435038	0.6132	0.815648
ELP2	NA	-1.02736	NA	0.759913	-2.198925	0.720086	0.37817	-0.491006	-0.279613	-6.599818	0.285609	0.023779	0.20281	-6.905883	0.645385	0.341345	1.050787	-0.972176	0.514921	-0.13363	-1.623986	0.458717	-1.053332	-1.731402	-6.432439	-0.927682	-0.485942	0.163717	0.229965	0.285909	-0.354086	-2.464047	0.451242	0.533124	0.598332
ELP3	NA	-0.779092	NA	0.046684	-1.095511	-0.05385	0.223842	0.344875	0.175292	-2.640397	0.224498	0.722025	0.256087	-4.637054	0.294105	-0.095028	0.411753	-0.201602	0.260317	0.096175	-0.880015	0.123722	-0.327686	-0.547506	-15.179507	0.533046	-0.525999	-0.128091	-0.173116	-0.296777	0.076064	-1.120263	0.024332	0.368684	0.670846
ELP4	NA	-1.327094	NA	0.05811	NA	-0.206451	0.769904	0.742654	-1.108225	-3.856501	0.785421	0.529112	-0.070349	-4.67891	0.422336	0.486419	-0.216749	-1.093415	0.006587	0.317103	-3.366748	0.444126	-1.361364	0.437444	NA	-0.544111	-0.829733	0.556505	-0.406593	-0.105123	-0.800389	-3.346067	1.209623	-0.108917	0.312364
ELP6	-7.310588	-0.740516	NA	0.19998	-2.178932	0.770424	0.013381	0.254665	-0.328876	-4.446724	0.438249	0.498305	NA	-6.749547	1.128646	1.344362	0.420595	-0.049851	0.339383	0.052432	-0.507314	0.405596	0.159882	-2.458012	-3.96416	0.301003	-0.397157	-0.312032	-0.531882	0.145077	NA	-1.935654	1.037898	1.146692	NA
EMC1	NA	-0.179673	-0.985473	NA	0.254543	-0.266165	0.55384	-0.319525	0.400433	NA	-0.51219	NA	0.741134	NA	0.035333	0.536449	0.659035	NA	0.296426	0.837643	0.340989	0.017829	0.660238	1.221187	NA	0.001056	0.004847	0.393588	0.592404	-0.431734	-1.184833	-0.590649	NA	-0.644326	-0.422982
EMC2	NA	-0.12446	NA	0.667625	-0.712045	-0.266636	-0.862893	NA	-1.311033	3.143059	-0.144542	0.134592	NA	2.796473	0.783971	0.036298	-0.694793	NA	0.984687	-0.489396	NA	-1.160067	0.443431	2.17995	NA	0.003063	-0.335779	-0.460949	0.80284	-0.443497	NA	0.958348	0.827414	-0.002651	-1.670783
EMI1	NA	0.151608	0.816319	-1.080976	0.36385	NA	-0.602428	-0.35961	0.306281	NA	NA	0.869772	0.248806	NA	-0.382128	0.208104	-0.658406	-0.110769	-0.869342	-0.333776	1.037221	-1.890161	NA	0.773896	NA	0.10828	-0.172481	-0.415076	-0.125909	0.366658	NA	0.137549	0.879499	-0.803536	-0.051566
EMP70	-0.786206	-0.140509	-0.626243	0.291591	0.202717	0.532544	-0.083985	-0.910251	0.086677	0.152678	0.369975	0.414428	-0.349695	-0.880004	-0.081319	-0.082579	0.463775	-0.256477	-0.146315	NA	0.440827	1.157219	0.106838	-1.023903	NA	0.452013	NA	0.146982	0.483493	0.048189	NA	0.597601	NA	-0.314514	0.29839
ENT2	NA	0.002872	-0.118862	0.160327	0.8622	0.429509	0.759294	0.607042	1.503746	-0.989632	-0.634328	-0.268924	0.051098	-0.115234	-0.046889	-0.314763	0.750597	-0.407454	0.435843	0.198339	NA	0.199421	NA	0.118139	NA	0.044359	-0.248957	1.050976	0.056299	0.047988	NA	-1.102198	-0.367681	-0.020247	-0.246605
ENT3	NA	0.403916	1.157059	-0.424718	0.072918	-1.190802	-0.451397	0.598104	0.47026	-0.664546	-0.250067	-0.067301	0.657436	-0.299885	-0.715041	-0.774108	-0.08448	0.214792	-0.187923	0.018939	0.770863	-1.016461	NA	0.836474	-4.016772	0.16246	0.317023	-0.921998	-0.010019	-0.718622	0.147483	0.863463	-0.984426	-0.234158	0.43107
ENT4	NA	NA	-0.291111	0.539262	0.324079	-0.092752	0.105715	0.159306	0.099103	-0.397205	0.356823	-0.194117	0.799411	NA	0.265393	0.400431	-0.015614	-0.687962	-0.048511	NA	0.5936	0.521645	NA	-1.020763	-1.735307	0.144328	NA	0.146481	-0.570215	-0.181494	-2.647135	-0.214695	0.429933	0.492066	0.251954
ENT5	NA	0.370111	0.589089	-0.497478	0.892133	-0.950434	0.038414	0.402119	-1.75286	NA	-0.361364	0.163878	-0.17794	NA	NA	-0.244885	-0.588762	1.139371	-0.018492	0.3043	0.794507	NA	NA	0.61863	NA	0.578378	0.358618	-0.562135	0.784747	-0.217872	-0.147486	0.276718	-2.148779	NA	-1.352039
ENV11	NA	1.038859	1.140364	0.565469	0.862404	-0.305314	0.023493	-1.255547	0.119816	-5.016208	0.829215	0.771962	0.157135	-1.081105	-0.006645	0.264836	-0.432467	0.302647	-0.218478	-0.247423	0.295212	-0.117014	NA	-1.654215	NA	-0.085145	0.071684	0.233776	-0.613592	0.005016	-1.497488	-1.691306	-0.520306	-0.174814	1.091983
EPL1	NA	-0.443651	0.194152	0.062118	NA	0.001025	-0.076781	0.710966	-0.854318	0.635401	NA	-0.034143	-0.516584	NA	0.244681	-0.074331	0.028088	-0.577449	-0.223037	-0.780788	NA	-0.345345	-0.708419	1.27705	NA	-0.347093	0.103879	0.156453	-0.088172	0.327091	0.22994	0.649327	0.688128	0.30687	-0.095423
ERD1	NA	0.127108	0.240869	-0.185991	1.38714	NA	0.02848	0.952573	-0.072681	1.328754	0.637956	0.571599	0.326098	NA	-0.009406	-0.446046	0.603633	0.897475	0.003573	0.305948	-0.309676	0.07478	0.95809	-1.569976	NA	0.336872	-0.859122	0.523845	-0.534964	0.245396	-0.35288	NA	NA	-0.844571	-0.049633
ERG3	-3.926249	-0.22943	-0.567588	0.827101	-0.474585	0.906676	-0.020788	-0.224496	-0.709921	-1.430166	0.505611	0.388957	-0.614121	-0.958555	0.92692	0.840128	0.590686	0.164938	0.056693	NA	-1.829912	0.704886	0.23662	-1.149653	NA	0.372636	NA	NA	-0.16697	0.263424	-0.512923	-0.096983	NA	0.826043	1.279137
ERG5	NA	0.460142	-0.742633	-0.926896	-0.275264	-0.707282	-0.207463	-0.492973	-0.007875	0.500935	0.37205	0.090999	0.18685	0.609383	-0.111142	-0.003692	0.137958	0.578358	-0.524748	-0.039838	NA	-0.962484	NA	1.198537	NA	0.07034	0.213635	-0.464614	0.249119	-0.268099	0.223738	0.673514	0.432575	0.744048	-0.818486
ERJ5	0.064766	-0.33814	-0.17837	-0.220139	-0.280673	0.020128	-0.472573	0.454262	-0.270043	NA	0.357006	0.108234	-0.001996	0.04539	-0.621436	-0.15057	0.493945	0.672343	0.518532	-0.586176	-0.081011	NA	-0.110146	-0.099226	NA	-0.097653	-0.307165	-0.472053	1.116824	-0.000368	0.187621	0.055507	NA	-0.449001	-0.213916
ERM6	NA	0.538132	0.172693	0.13208	-0.102842	0.295362	0.160655	-1.785793	0.404463	NA	-0.19504	-0.412874	-1.064102	0.994465	-0.398571	-0.168188	0.161496	NA	-0.69088	0.619829	0.608569	0.446171	NA	-0.413791	NA	NA	-0.078473	-0.083212	-0.882542	0.743161	-0.392688	-0.229147	0.631249	-0.719	-0.593393
ERP1	NA	0.541724	-0.652242	-0.102331	NA	0.194949	0.427288	-0.016073	0.056252	1.495639	-0.140462	0.054632	0.365601	-1.137132	0.067811	0.066622	-0.52115	0.123276	0.640156	-0.022072	0.005717	-0.15156	NA	0.618144	NA	0.307911	-0.030948	0.437495	0.274324	0.278706	NA	-0.431647	NA	-0.32781	-1.142962
ERP2	-0.577268	0.254687	0.679076	0.038507	0.332398	-0.765933	-0.435027	0.296935	0.586868	0.425124	-0.271073	-0.194045	0.255311	1.396805	-0.221263	0.711534	-0.266057	0.282331	-0.540186	0.076956	NA	-0.060377	NA	0.151615	NA	0.902494	-0.303624	0.132556	-0.717481	-0.18176	NA	0.628988	-0.11294	-0.506144	0.134823
ERP4	NA	-0.181898	-0.405699	-0.073597	0.120792	0.297689	NA	-0.092669	NA	NA	0.24895	0.417752	-0.312505	NA	0.156765	0.654294	0.582835	0.463792	-0.046086	0.652836	NA	0.601235	NA	1.450423	NA	0.340605	-0.396451	0.629386	-0.023108	0.799549	NA	-0.813396	NA	-0.152587	-0.120558
ERV14	NA	0.350397	-4.392994	-0.554822	-0.273741	-0.912788	-0.330787	2.736815	-0.246941	NA	-0.143076	0.421374	1.225196	3.89847	-0.520939	-0.941777	0.139505	0.12044	-0.675869	-0.271671	1.313438	-0.458603	1.505144	NA	0.231449	0.486455	1.035585	-0.306376	0.126795	-0.00079	2.6467	-2.402686	NA	-0.067384	-1.338445
ERV25	NA	-0.464825	0.702102	0.383261	0.317088	-1.185054	-0.011349	0.012264	0.168574	-0.031938	0.101445	-0.264696	0.134578	NA	-0.392439	-0.704618	-0.356801	0.766169	0.498052	-0.162519	NA	0.044154	0.102355	-0.950784	NA	0.606955	0.001458	-0.406131	0.358185	0.289189	0.307176	0.553373	-0.31152	-0.180337	0.120891



HIR3	-11.932769	-0.051842	-1.05104	-0.339317	-1.304764	0.365771	-0.775226	-2.422329	0.887233	-1.023194	1.021155	0.127522	-0.140309	-0.944282	0.197481	0.059505	0.482247	-0.075432	0.04009	-0.056555	-1.180162	1.049636	NA	0.612311	NA	-0.40943	-0.366323	-0.258355	-0.599444	0.263503	-2.241451	0.032568	1.235806	0.475043	0.297728
HKR1	0.268657	0.113863	-0.568612	0.248056	0.866245	NA	1.04521	-0.270687	0.032891	-0.537982	0.024626	0.752975	0.031558	NA	-0.26842	-0.396005	0.885812	-0.124885	0.343889	-0.772188	-0.454076	-0.899234	NA	2.164098	NA	0.7533	0.496471	0.329164	-0.057797	0.189597	-0.567131	NA	-0.73534	1.227306	0.835676
HLJ1	-1.096371	0.096458	-1.062837	-0.381676	0.855461	-1.005332	0.726761	-0.06008	0.706638	0.796027	0.666024	0.12305	NA	-1.205002	-0.526464	0.454076	0.360374	0.278324	-0.254517	-0.028484	0.221632	-0.103798	NA	1.467906	-4.702146	-0.402666	1.111624	-0.217576	NA	NA	0.114352	0.230006	-1.15962	-0.189766	-0.093855
HMG1	NA	NA	0.200843	0.817067	-0.868446	NA	-0.130775	NA	-0.107769	NA	-0.554619	0.482114	-1.04359	NA	0.012294	-0.050351	-0.375245	NA	-0.451881	0.04325	NA	-0.967302	0.393534	-2.390467	-0.998591	0.300164	0.412225	-0.98321	-0.979031	-0.11919	NA	0.079158	0.39318	NA	0.478218
HMG2	NA	-0.018549	-0.928281	-0.503747	-0.67091	0.059156	0.074357	-0.021655	-0.473934	0.270531	0.452776	-0.141057	-0.150932	-0.789409	-0.257466	0.639343	0.406687	0.102303	0.325199	0.857948	-0.172905	-0.571539	0.581619	0.785582	NA	0.229358	-0.016677	0.47995	-0.039808	0.025712	-0.092531	0.248193	0.243946	0.194979	0.342579
HMO1	NA	-0.765574	NA	-0.29719	NA	-0.065179	-0.028531	NA	0.391879	NA	0.005182	-0.660833	-2.12136	NA	-0.440776	0.262754	-0.284698	-0.261827	0.115769	NA	-3.619107	NA	NA	1.661979	NA	-0.434017	NA	-0.024418	NA	0.321557	NA	-1.075496	NA	NA	-0.348757
HMT1	NA	-0.953266	1.175851	-0.594595	-0.697156	1.126535	-0.883042	NA	0.465632	0.725424	NA	-0.390665	-0.654837	NA	0.183682	0.276818	0.066766	0.190901	-0.008056	0.166893	-0.675186	2.02545	NA	0.671631	NA	0.748737	-0.451123	0.640837	0.765479	-0.250601	NA	-0.48819	0.520422	-0.493077	-0.007851
HNT1	-0.305112	-0.778791	NA	-0.653764	-0.294471	0.19322	-0.124814	NA	0.820146	0.05937	-0.064887	0.745153	NA	-0.061295	-0.185761	-0.009253	-0.028795	-0.452189	0.503783	0.536762	NA	0.460687	-1.204891	1.744716	NA	-0.859656	-1.539466	0.273481	0.813886	0.550726	0.496326	0.754441	-0.779839	-0.164196	-0.583319
HOC1	NA	-1.675485	-2.781939	-0.207197	-0.917901	-0.642297	0.635242	1.803031	-0.054433	NA	NA	0.469457	-1.024819	0.8267	0.746368	0.694636	0.75005	-0.270117	0.806259	-0.202376	-1.511962	1.180746	0.137958	2.431173	NA	-0.51644	-1.35592	-0.336366	1.027796	-0.049638	NA	-0.17501	-0.181384	0.546568	0.093494
HOG1	0.749325	0.380772	-0.618918	0.456679	-0.230806	0.633884	-0.045533	-0.524341	0.590891	-1.892617	0.700872	0.019298	-0.68878	-1.809424	0.219372	0.433636	0.651083	-0.467782	0.144765	NA	NA	0.33021	0.298747	-1.939457	NA	-0.539562	-0.727979	0.698393	1.494717	0.410057	-0.165023	-0.290853	-0.426308	0.447724	0.684224
HOM3	0.774386	0.325543	0.873297	0.224836	-0.123519	-0.612605	-0.743688	0.227714	0.573498	-1.845401	NA	0.060024	0.292565	0.343703	-0.913652	-0.410517	0.18326	0.695911	-0.84835	-0.291652	0.639473	-0.492471	NA	0.210009	NA	-0.224512	0.342112	-0.199678	-0.076603	0.064943	NA	0.243081	0.352417	0.155966	-0.513835
HOM6	NA	0.264458	NA	-1.029973	NA	-0.975081	-0.140479	-0.097212	0.234816	-0.925042	0.290512	1.009844	0.402093	1.112071	-0.262482	-0.484876	-0.096172	0.789265	-0.406781	0.227776	0.85957	-0.354622	0.105035	-0.311446	NA	-0.042403	NA	-0.744197	NA	-0.470114	-1.075665	0.311434	0.579621	-0.232854	-0.510606
HOS1	NA	-0.100573	1.298769	-0.453474	-1.394475	0.914867	-0.418852	0.224367	0.045017	0.340555	0.523457	-0.108807	-0.192111	-2.063393	0.388364	0.568478	0.147697	-0.412111	-0.40538	-0.029699	NA	0.285979	-0.163171	0.666548	NA	0.017965	-0.288952	0.147088	0.966782	-0.38994	-0.315782	0.457127	-0.577534	0.545649	0.743033
HOS2	NA	0.175887	0.166794	-0.829064	1.448029	0.674526	0.941669	-0.137599	1.417967	-10.750017	0.792012	0.326795	-0.090567	-1.048771	0.139793	-0.046948	-0.181127	0.160741	0.113895	0.096606	0.63812	-0.249821	-1.642964	-0.176018	-0.063117	0.473417	-0.680748	NA	0.238242	-0.380519	-0.572972	-0.53411	-0.080448	-0.23855	1.337801
HOS3	NA	-0.415818	-0.414058	-0.30873	NA	0.486715	-0.065321	-0.295496	1.315987	-0.828688	-0.41981	0.437272	-0.170177	NA	-0.245093	0.349718	-0.280195	-0.036692	0.449878	-0.026397	-0.251738	-0.242188	-0.34216	-0.958046	NA	0.394716	-0.201135	0.346772	0.187862	0.484578	-0.380943	0.153982	0.613788	0.17451	0.096858
HOS4	-0.849782	-0.045482	-1.315541	-0.038256	0.787654	-0.026595	-0.260156	0.300898	0.893536	-2.851841	0.558468	0.026192	0.04521	-1.050835	0.231407	-0.114103	0.366769	0.018183	0.046862	0.301354	0.046188	0.309105	-0.214165	-1.997124	-3.273671	-0.109685	-0.371469	0.098539	0.314956	0.277514	0.043005	-0.951918	1.013343	-0.246803	0.532837
HOT1	0.525151	0.158996	-0.504091	0.699726	-0.424517	0.547467	0.42685	-1.352882	-0.517821	-0.380834	-0.168487	-0.422252	NA	0.348657	-0.38213	-0.083653	-0.093137	0.665523	-0.733652	-0.183891	-0.027274	0.194369	NA	0.92003	NA	-0.265548	0.714737	0.087765	NA	NA	-0.462853	-0.423157	0.745218	0.557505	0.008603
HPC2	NA	0.513457	-1.440274	0.189656	-0.015194	0.543469	0.89068	-3.025674	1.08879	-1.290314	NA	-0.153635	-0.418776	-3.657934	-0.39531	-0.084825	0.684959	0.303595	0.434723	0.00309	NA	1.046552	-0.601155	1.023317	-2.860304	-0.237326	0.169351	0.225677	0.309907	0.263667	-1.111156	-0.528682	0.356244	-0.229078	-0.92322
HPR5	NA	NA	-1.039225	1.327984	NA	0.372819	0.90068	-2.318333	0.156291	-2.351805	-4.722355	NA	-8.955721	-15.551135	-0.603044	0.043772	0.571749	2.052914	0.823147	NA	0.060588	-1.452421	2.278481	0.647536	NA	NA	-6.935541	0.382974	NA	-0.7581	-3.388337	-0.64824	NA	0.136864	0.165452
HRD1	-0.847416	0.159562	-0.081941	-0.74053	-0.260152	0.611796	NA	-1.50003	NA	NA	-0.23416	-0.386303	0.266417	0.529261	-0.010773	0.28778	-0.227212	0.977075	0.285234	0.371793	0.570999	0.725714	0.408475	0.477177	NA	-0.5017	0.448045	0.517894	0.790282	0.080775	-1.652646	0.361726	-0.121535	-0.035342	-0.443472
HRD3	NA	0.318298	-1.386534	0.837369	-0.047281	0.161321	-0.214298	0.320197	-0.089485	1.543557	0.424502	0.155978	-0.144137	-1.47708	-0.84299	-0.274921	0.461416	-0.656503	0.453562	-0.13611	NA	0.995257	0.420088	NA	-3.788388	0.470797	0.686915	1.22781	0.167451	-0.137079	-0.544895	0.009332	-0.91255	-0.444711	0.338343
HRT1	-5.935662	-2.327373	-1.618205	-0.50597	-1.229771	0.506994	0.520207	1.519095	0.370892	-2.579824	-0.104479	-0.01441	-4.311582	0.617905	0.108183	0.442351	0.274827	NA	-0.389793	-0.324276	-4.746951	-0.049911	NA	0.43773	NA	-0.780234	-3.115406	0.165467	0.479056	0.13356	1.590326	-2.720704	0.209991	-0.156833	0.52438
HRT3	NA	-0.097395	-0.141224	0.714019	-0.983974	0.53494	-0.320855	-1.193666	-0.677969	0.338917	NA	0.607667	-0.239641	-1.978151	0.000765	0.143282	0.724392	-0.413222	0.446681	NA	-0.043129	0.690729	0.747173	0.394306	NA	-0.505114	NA	-0.027168	0.025707	-0.023977	NA	0.313907	1.136697	0.124823	0.603292
HSC82	NA	-2.096094	-0.469409	0.628072	NA	0.143036	-0.172172	-3.894081	0.035377	0.697801	-1.690033	-1.194244	NA	NA	0.121867	0.485224	-0.649518	0.128898	-0.96749	-0.255345	-1.060235	0.408347	NA	-1.338424	NA	NA	-1.357479	-0.4707	NA	NA	NA	0.256931	0.563327	0.012653	-0.931518
HSE1	NA	NA	NA	0.134332	-0.423794	0.714888	-0.137732	-0.378072	1.108488	-1.119727	0.343169	-0.068224	-0.036855	NA	0.60332	0.271446	0.069132	1.012254	0.129161	-0.400175	NA	-0.027275	0.123544	0.167523	NA	0.810813	-0.588829	0.080633	-0.117916	-0.554598	-0.927587	-0.772108	0.218526	-0.699531	-0.31842
HSL1	NA	-2.181129	0.457353	0.040574	-4.391317	-0.074491	0.191001	0.96548	-2.600248	0.527999	0.1531	-1.611784	-1.738034	-0.372705	0.182229	0.085129	0.39914	-1.951326	0.903578	-2.332239	NA	0.496993	0.101229	2.321409	NA	-2.310916	NA	-0.064949	1.217665	0.220039	0.710995	0.075592	0.672971	-0.116015	-0.232222
HSM3	-0.658724	0.733171	-0.307205	0.537527	0.209258	-0.945499	0.572081	0.944834	0.507024	-1.58634	0.558984	1.000637	-0.607611	NA	0.602969	-0.152554	0.319425	-0.658066	0.186099	-0.207623	NA	0.737079	NA	-0.096364	NA	0.120085	-0.329827	0.563383	0.997715	-0.229043	0.812462	0.554517	-1.019704	-0.110962	-0.190114
HSP42	NA	1.055993	-0.113992	-0.692068	0.275553	-0.034342	-0.278585	-0.265393	0.156376	1.718535	-0.483257	-0.370867	0.157554	-0.232163	-0.159434	-0.27144	-0.029084	0.499342	0.339545	-1.06197	0.554888	NA	-0.29412	1.128869	NA	0.801122	0.86026	-0.071818	1.19161	0.31725	-0.638837	0.128167	0.794927	NA	0.776705
HST1	-4.415195	-0.384429	1.078709	0.291862	-0.367275	-0.159808	NA	0.299153	NA	NA	-0.281693	0.077883	-0.286897	NA	-0.29917	0.069558	-0.41363	0.635917	-0.61274	0.151298	-1.296688	-0.147095	-0.438837	1.258428	NA	-0.595608	-0.630804	-0.075213	0.440274	0.216422	0.28698	-0.210892	-0.113223	0.141374	0.589326
HST3	0.358053	2.026194	1.005769	0.010726	NA	-0.1452	NA	0.382007	NA	NA	NA	NA	0.11018	-0.035294	-2.424847	-1.101511	NA	0.576464	-0.992867	0.98681	-0.522077	-2.536504	2.247662	1.270415	-5.650652	2.602133	1.761741	-2.138559	-8.044507	0.845862	-0.128438	-0.787154	-6.375177	0.237761	0.349481
HST4	0.365853	0.719195	NA	0.421974	1.071285	0.096607	-0.044432	0.49928	NA	-1.887052	0.238201	-1.73416	0.03791	NA	0.228626	-0.406321	-0.195801	0.244608	0.07025	0.659622	NA	NA	NA	0.742668	NA	0.763403	-0.314838	-0.001677	0.08771	-0.51328	-0.510118	0.405086	-1.491225	1.057035	-0.825619
HSV2	NA	NA	NA	0.818594	-0.436283	0.663926	1.017398	-0.845299	-0.09945	-0.285164	-0.307646	0.48942	0.430696	-0.899526	0.299438	0.39923	-0.203335	-0.697439	0.566139	-0.408614	0.002092	-0.647482	-0.459639	0.011721	NA	0.871695	-0.580518	1.041534	-0.143814	0.581051	NA	0.104787	0.800261	0.763802	0.712938
HTA1	NA	NA	0.884229	0.192819	-6.437207	0.867994	0.756896	-2.37943	0.696752	-4.821429	0.010133	-0.783681	-0.196986	-1.786934	-0.134094	0.387004	0.114501	NA	0.057321	0.022388	NA	NA	NA	0.191302	NA	0.479947	-0.13288	0.808566	-0.921647	0.090733	-0.729415	-1.153763	-0.260251	-0.099732	0.341797
HTD2	0.329111	0.785211	-0.519449	-1.434993	-0.002528	-0.172903	-0.393341	0.059684	0.222858	-0.082445	-0.228255	0.636506	0.455271	1.660866	0.639992	0.162486	-0.084672	0.187792	-0.821144	-0.589295	NA	-0.372619	NA	-0.594175	NA	-0.094108	-0.976015	-0.754631	1.009604	-0.448148	0.726404	-0.203875	1.153144	-0.525804	-0.675377
HTZ1	NA	-4.66127	NA	-0.345403	NA	0.618375	NA	-1.747942	NA	NA	0.172186	-5.120145	0.306123	NA	0.761173	2.463596	NA	-0.062977	0.022019	0.025917	0.178264	0.952482	-5.213974	NA	NA	1.061679	-4.799821	0.538363	0.530793	0.187806	-2.267855	2.156616	0.732853	-0.13678	1.546518
HUA2	-0.992238	-0.254565	0.437901	0.03258	-0.561391	-0.768849	-0.230772	0.403007	1.539798	NA	-0.214667	-0.241398	0.107748	NA	0.072176	0.463245	NA	-0.203164	0.319005	1.023925	0.01638	0.199796	NA	0.07057	NA	-0.271001	0.033347	0.740938	1.046163	-0.13216	-0.643808	0.249495	-0.657187	0.176399	0.641637
HUL4	NA	-0.062756	-0.039268	0.325539	-0.022665	-0.284827	-0.131606	-0.018166	0.40737	-0.112688	0.30865	0.574092	0.524911	NA	-0.976136	-0.043969	-0.328853	0.224921	0.383382	0.296569	-0.307767	0.632411	0.150881	-0.279735	NA	NA	-0.110124	-0.252563	-0.164665	0.431691	-0.407638	0.448585	0.300384	-0.30147	-0.349485
HUL5	NA	0.566497	-0.768733	0.535896	-0.123617	-0.328987	0.052564	-0.131383	0.172294	-0.169076	0.154692	-0.033192	0.257061	NA	-0.307258	-0.058632	0.401459	-0.188409	0.171323	0.37868	-0.246391	0.081552	0.194456	1.0787	NA	-0.112873	-0.545485	NA	-0.502085	0.532406	-0.920246	0.356348	0.572643	-0.196273	-0.072407
HUR1	-2.023602	NA	2.110813	0.345784	-2.361132	1.071173	0.162219	-3.380501	1.119774	-6.17592	0.440362	0.453583	-12.072711	NA	-0.22064	-0.927091	0.465984	-2.949607	0.823629	-1.397199	-11.301489	1.676335	-3.296579	0.182163	-4.716587	-7.036808	NA	NA	-1.165675	-0.149259	-1.745244	-2.436005	0.123312	-0.764119	NA
HUT1	NA	0.339449	0.366465	-0.372766	NA	-0.497346	0.152549	-0.277142	-0.330439	-0.539557	-0.043555	0.159481	0.482665	-1.576284	0.494357	-0.1147	0.022995	0.213393	0.308761	0.298645	0.950083	0.692646	NA	1.22093	-7.830143	0.787179	0.683825	-0.041802	0.680964	0.856107	0.164565	0.633972	0.533492	-0.242125	0.077981
HXK1	NA	0.172595	-0.580242	-0.24014	-0.393823	0.237549	0.527745	-0.981627	0.036469	0.314441	-1.724249	0.627955	-0.422808	NA	0.271745	-0.287618	0.505705	0.002899	0.787959	0.154599	NA	-0.375489	0.169093	1.176787	NA	0.176648	-0.740241	0.242326	NA	0.41373	-0.540426	0.545642	1.704177	0.380036	0.166581
HXK2	-6.326602	-0.343113	-3.752035	-0.079453	0.399098	0.157411	0.56597	-0.060952	-0.952122	-3.16326	-0.226454	-0.107752	NA	NA	0.766362	0.79153	0.345708	0.590849	-0.285488	-0.985181	NA	0.213323	0.056547	1.266906	-8.704197	0.598555	0.166643	NA	0.54542	-0.34188	0.736196	-0.897869	-0.417841	-0.462888	-1.244603
HXT10	-0.190414	0.044826	0.279148	0.006228	0.145453	0.589446	0.229103	0.68579	-0.528099	1.531032	-0.366671	-0.320127	0.361331	1.762313	-0.276242	-0.243559	0.093383	-0.789011	0.013338	-0.091405	NA	1.042168	0.587441	0.97114	NA	-0.634936	0.437536	NA	1.216845	-0.550226	-0.077495	0.986956	-0.701815	-0.383518	0.247849
HXT17	NA	0.198847	0.86626	0.075928	-0.954214	0.073393	-0.385929	-0.323521	-1.054437	0.082598	-0.114214	-3.650255	NA	1.037511	-0.185295	-0.244093	-3.655251	0.143135	-0.576505	-0.248992	-0.803036	0.426239	NA	-0.050834	NA	0.786089	0.187468	0.611495	0.399143	-0.536255	-0.518384	-0.377287	-1.174199	0.49139	0.610028
IDH1	NA	-0.192758	-0.263822	-0.315628	0.640475	-0.123147	0.652292	0.780939	0.415348	NA	0.16909	0.214945	0.401645	-1.526355	0.543713	0.384953	-0.252486	-0.606774	0.673737	-0.351141	0.103693	0.352658	-0.370661	-1.234715	NA	0.098708	0.330452	0.30974	0.92991	-0.297213	0.445125	-0.018458	-0.337547	-0.167725	0.989088
IES1	NA	NA	-8.965442	0.393963	NA	0.595269	0.261733	-0.130743	0.423887	-3.801867	0.317138	-0.198812	-0.553367	NA	0.086739	0.350255	1.208208	0.019989	-0.075886	0.045019	-0.735033	0.037779	-0.490021	1.143695	NA	0.643592	-1.496399	0.839801	-0.453223	0.939882	-2.026819	-1.265503	-0.795558	0.250473	0.356838
IES2	NA	NA	-5.004766	-0.223055	-0.751794	0.069219	0.412348	-2.025545	0.775786	NA	0.183307	0.019817	-1.743098	-2.40924	0.566888	NA	-0.096416	-0.933823	-0.236218	-0.145377	-1.297344	-0.275414	-0.770335	NA	NA	-0.52323	-5.255372	-0.256016	-0.236493	0.323222	-6.711174	-0.055965	NA	0.203627	0.085792
IES4	NA	-0.015293	NA	0.044301	0.769007	0.781331	0.386902	0.383898	0.620217	-1.844806	-1.151159	-0.234177	0.567374	NA	-0.181496	0.072194	0.271214	-0.15172	0.421058	0.215366	-0.248405	0.371446	-0.057685	-0.542773	NA	0.525298	-0.312244	0.068439	0.301656	-0.216023	0.112325	-1.04458	-0.436446	-0.531403	-0.655946
IES5	NA	-3.523562	-3.847998	0.15025	0.590491	0.197604	0.162959	-0.82079	-0.025248	NA	0.749336	0.223391	NA	NA	-0.887853	-1.2757	0.10606	0.515296	NA	0.46292	0.62935	1.25346	NA	1.396648	NA	1.077722	-2.004206	-0.316026	0.261172	0.615685	NA	NA	-2.279648	-0.192833	0.683623
IKI3	NA	-0.725644	-13.852396	0.411776	-2.045423	0.68177	-0.210249	0.626477	-0.364983	NA	0.029343	0.754571	0.517855	-5.695673	-0.450857	0.374582	0.351525	0.147841	-0.097074	-0.000874	-0.136875	0.603737	-0.022583	-0.296713	1.990358	-0.201775	0.313581	-0.879637	0.441355	-0.238255	0.094898	-1.161185	2.083991	0.405418	-0.04208
ILM1	NA	0.372181	-2.105378	-0.452515	-2.423157	-0.029234	0.116445	-1.463353	0.340674	-4.351145	0.402755	0.994882	-2.806036	NA	0.602077	-0.019941	0.807139	-2.871179	-0.403265	-1.023733	-3.16139	-0.776192	NA	-0.806443	NA	-1.491707	-2.318243	-0.348454	-1.434373	0.09707	-2.4185	0.373343	1.430599	-0.154539	-0.413304
IME1	0.936326	NA	-0.057786	-0.466567	-0.258353	-0.066593	0.71499	-0.617062	-0.514778	0.214389	-1.926077	0.982622	0.092175	-1.93507	0.240956	0.406138	-0.319356	0.318655	-0.462994	-0.434924	0.546514	0.681474	NA	-0.321723	NA	0.590291	0.593576	-0.357799	-0.322408	0.176021	-0.176709	0.204873	-1.426739	-0.923551	0.587574
IMG2	NA	-0.761311	0.394506	NA	NA	-0.126634	-0.121841	0.538952	0.499134	-3.007237	-0.02601	0.777847	-0.003978	1.391904	-1.136676	-0.20512	-0.309767	NA	0.093224	0.190478	-1.685029	-0.042328	-0.475389	-1.298293	-4.650695	0.301214	-0.269059	-0.810102	0.178305	-0.219785	0.85579	-1.413382	0.49128	0.336012	-0.334059
IML2	NA	NA	0.095811	-0.110001	0.04871	-0.268754	-0.078679	0.971422	-0.397909	-0.590908	0.293072	0.524421	-0.270488	-1.398249	0.397186	0.429625	0.081227	-0.296152	0.232309	0.172333	-1.469783	-0.156747	0.281747	-0.033075	NA	NA	-2.544223	0.445036	0.390616	-0.176211	-0.432676	-0.021274	0.79993	-0.148682	0.466478
IML3	NA	-0.238799	-0.077991	0.843849	-0.580987	0.695931	0.069756	-2.408242	-0.591751	-0.881555	NA	0.444465	0.304606	-3.459065	0.399663	0.521471	0.073215	-0.431761	-0.368472	-0.149283	-1.343392	0.392212	NA	0.682905	NA	0.278493	-0.326112	0.514894	0.41154	-0.330232	NA	-0.753528	0.805442	0.378443	-0.017211
IMP2	NA	-1.288989	-0.110856	0.346808	-0.559246	-0.225311	0.376978	-1.576737	-0.005489	NA	0.704426	0.30399	0.268183	-1.132158	0.180265	0.309381	0.110439	-0.373863	0.030884	0.517665	NA	-0.599361	NA	1.72993	NA	-0.675207	-0.962412	0.117202	0.190754	-0.101161	NA	0.284982	1.44842	0.292815	0.300653
INO4	3.854242	0.809213	-0.188377	-1.530561	-1.995156	-0.541787	0.076845	-1.309672	-0.627982	NA	NA	1.190187	-0.254499	0.081257	0.637613	0.841247	-0.856494	-0.049694	-1.780155	-1.283605	-0.253768	-0.215743	0.854937	1.44026	NA	0.515038	-0.416857	-0.380265	0.140474	0.174603	NA	NA	2.343052	-0.323122	0.60956
INP51	0.600932	-0.180453	-0.728029	-0.100513	-0.658154	0.209384	0.008706	0.215199	-0.68043	0.159732	0.29356	-0.627911	-0.492929	-1.022023	-0.214147	0.486358	0.572415	-0.31382	0.610933	0.773843	-0.853848	-0.098473	NA	1.649595	NA	0.434257	0.03421	0.257953	-0.055445	0.172442	0.991424	-0.228233	-0.381863	-0.065915	0.556769
INP52	NA	-0.047193	-0.347625	0.222715	0.40133	0.409484	0.504792	-0.365458	-0.242928	0.798696	0.671348	0.280642	-0.303705	-0.849007	0.103661	NA	0.450625	0.222814	0.793338	0.730754	-0.328985	-0.060969	0.816202	0.526207	NA	-0.391603	0.119054	-0.56867	0.179377	-0.644254	-2.196595	0.147038	0.744085	-1.33134	0.085176
INP53	NA	-0.618121	-0.674913	0.350745	-0.261453	0.365313	NA	0.063373	NA	-2.426093	0.852535	0.514931	0.238847	-1.268409	-0.052743	0.498809	-0.006804	-0.364608	0.295592	0.244083	-0.1436	-0.033357	0.109628	-0.328875	NA	0.103286	-0.291659	0.64532	0.798477	-0.268258	-0.174631	-0.077864	0.066018	-0.223685	-0.059446
INP54	NA	0.110751	0.609088	0.516854	0.926765	0.144939	NA	-0.055846	NA	NA	-0.046309	-0.137445	0.004525	NA	-0.096755	-0.170846	0.063681	0.459341	-0.494966	0.339407	0.538451	0.34006	0.838826	-0.258916	NA	0.206879	-0.019711	-0.256432	0.210607	-0.971812	NA	0.185687	-0.783044	-0.311513	-0.398227
IOC2	3.498297	-0.119099	-0.937789	0.337386	-0.028573	0.073626	0.067005	0.685553	-0.273944	0.147904	0.333349	-0.043089	0.522717	-1.702557	-0.001604	-0.454373	-0.109056	0.165552	-0.049241	NA	0.499049	1.026455	NA	0.791252	-7.295076	0.836879	NA	-0.385379	0.083463	0.315587	-0.954916	-0.696449	-1.436591	0.695595	-0.138135
IOC3	NA	NA	NA	0.767132	0.571	0.638707	-0.490392	-11.673023	0.582489	NA	-0.096168	1.05765	-0.349236	NA	-0.486989	0.235329	-0.718487	0.545148	-0.088103	-0.648088	NA	-1.372113	NA	1.036545	NA	-0.154508	-0.338995	-0.987895	-0.597376	-0.141296	NA	0.827359	0.385113	0.132754	0.513869
IPT1	NA	0.211849	1.427876	0.20315	-1.133879	0.482675	-0.077929	NA	0.02502	-0.075474	-0.095519	0.705887	-0.214668	NA	NA	0.637746	-0.211943	-0.101357	-0.061278	0.561844	-1.357141	-0.206763	0.036502	-0.020281	NA	-0.090311	-0.345216	0.203885	0.190891	-0.020033	-0.542683	-0.116523	1.303731	NA	0.50172
IRA2	NA	-1.383885	-4.44708	-0.254477	0.118931	0.251434	0.534621	1.24203	NA	NA	0.112833	0.682927	-0.577226	-5.539973	-0.511995	-0.429132	-0.682838	-1.473751	0.573321	0.449073	-1.816799	0.54495	-1.483927	0.050149	-12.861698	0.353207	-0.525398	-0.160842	-0.057974	0.23232	0.67173	-4.200235	-0.502478	0.089505	0.226471
IRC15	-1.762297	-0.26288	0.081667	-0.041869	-0.462657	0.100899	0.505596	-1.583692	0.426557	-3.341868	0.229401	0.334612	0.101657	-3.458772	0.027075	0.349355	0.225061	0.116397	0.444028	0.241317	0.158238	-0.390186	NA	0.442495	-1.104873	0.357762	NA	0.288528	-0.138103	0.830312	-1.039247	-1.006137	-0.29138	-0.183722	-0.023621
IRC21	0.180451	NA	0.23613	0.388238	-0.281405	-0.857956	-0.412799	0.840918	-0.788613	0.442131	0.335684	-0.343423	NA	NA	-0.211864	-0.068316	0.224345	0.953022	0.483311	0.793801	NA	-0.214512	NA	1.309898	-5.427288	-0.832076	-1.364647	-0.194981	0.116071	0.769349	0.212967	0.263492	-0.848138	-0.242491	NA
IRC25	NA	-2.356847	-1.125302	-0.572949	0.160454	0.025857	0.382065	1.720035	0.081543	NA	-1.307747	0.813284	-0.838603	0.703697	-0.543784	0.214851	-0.307587	0.051416	-0.845359	NA	-3.598839	0.048547	-1.046756	0.60348	NA	-0.989146	NA	0.21444	0.268613	0.8242	NA	0.330594	0.757161	0.581562	-0.259678
IRE1	-0.312355	0.232149	-0.646735	0.139224	-0.519026	0.027507	0.164965	-0.317529	-0.113988	NA	0.222875	-0.166711	0.196844	-0.396293	0.425909	1.05588	-0.03574	-1.298307	0.932468	0.283211	-0.027528	1.009615	NA	-1.002915	NA	0.215474	-0.311882	0.573179	-0.644925	0.773269	0.216386	-0.15414	0.286558	0.77057	0.195351
IRS4	NA	0.802043	-3.528546	0.183229	-0.089215	-0.103458	-0.479059	-0.554303	-1.462067	-0.148467	0.833551	0.585705	-0.059428	NA	-0.039829	0.77054	0.238555	-0.069844	0.52038	0.048879	NA	0.835757	NA	1.007388	NA	0.21257	-0.844586	0.897955	0.697799	-0.33533	0.458357	-0.680945	NA	-0.340181	-0.059479
ISC1	3.848572	0.376834	NA	-0.41017	-1.429735	-0.352964	0.419818	-0.76718	-1.223183	-1.302847	-0.052782	0.154922	0.788044	1.150107	0.138663	0.277465	-0.109769	-0.489329	-0.872911	-0.072928	0.233597	-0.572098	NA	-0.06179	NA	NA	0.188568	0.691957	-0.874062	-0.371218	0.234289	0.904167	-0.368539	-0.390799	-0.380064
ISR1	NA	-0.040771	-0.347235	0.590242	-0.512695	0.551021	1.101073	0.088184	-1.346506	-0.214716	-0.003291	0.41916	0.222353	NA	0.026946	-0.063714	0.055729	-0.391397	0.085027	0.027711	-0.57994	0.055831	0.030294	1.487229	NA	-0.182698	0.139982	-0.03214	-0.403161	0.452243	-0.373818	-0.971378	0.819456	0.3814	0.905014
IST3	NA	1.112088	-3.829302	-0.990893	0.435031	0.035826	-0.159608	1.852623	0.53981	3.574386	NA	0.626181	0.810958	NA	0.026627	0.120088	0.097404	0.275088	-0.761421	0.148021	NA	-0.071213	NA	0.182093	NA	0.272023	0.092577	-1.056411	1.698284	0.189182	2.361102	-21.158277	0.692497	0.267879	-0.976587
ISW1	1.86625	0.216962	-0.333664	0.696051	0.369039	0.062734	0.049216	-3.049568	-0.020611	0.003733	NA	-0.424485	-0.11285	NA	-0.078386	-0.305028	-0.017325	-0.328997	-0.175402	-0.319994	0.506789	0.082845	0.057238	-0.84207	NA	1.068469	0.589703	-0.121581	0.312855	0.478342	-4.936539	-0.580287	-0.588125	0.023863	0.168423
ISW2	NA	-0.153575	-1.075763	0.746294	-1.74559	-0.021013	-0.781607	0.246537	-1.558819	-1.907345	1.071528	-0.277955	0.119765	-0.980797	0.331502	1.037287	NA	-0.835048	0.023127	0.736013	NA	0.407968	NA	0.526589	NA	-0.310114	-0.118165	0.139998	-0.151405	1.261483	-0.098474	-0.249228	0.850092	0.85415	0.605251
ITC1	NA	-0.020083	-1.406268	0.625452	-1.396327	0.24361	0.559146	-0.223664	-0.115711	-1.084996	0.321988	0.059947	-0.822363	NA	0.225888	0.650585	0.121584	-0.994162	-0.030712	0.255039	-0.897848	0.80515	0.258001	0.920419	NA	0.169965	0.035856	NA	-0.123191	0.420786	-0.098585	-0.334752	0.665392	-0.111264	0.160942
ITR1	NA	NA	1.234692	-0.058689	-0.363944	NA	-0.275064	1.70687	-0.041343	1.01615	0.089488	0.028013	0.565388	NA	-0.365623	-0.133277	-0.315601	0.625298	-0.497442	0.162718	NA	-0.671768	NA	1.723804	NA	-0.29365	-0.18435	0.315333	-0.922849	0.21543	-0.308352	0.151378	-1.254576	-0.09755	-0.756825
IWR1	NA	-1.223449	NA	0.386118	-1.551056	0.361005	0.469333	NA	0.456873	NA	0.480485	0.28668	-3.35234	NA	0.052392	-0.345767	-0.406731	-2.092553	-0.290797	-1.222509	-2.66351	-0.195354	-2.888374	1.21646	-4.432194	-0.670059	-1.583957	0.244062	-0.513179	0.498679	0.316774	-6.418443	0.450513	-0.110461	0.420242
IXR1	NA	-0.560616	NA	-0.22609	0.451701	0.779732	0.191407	-0.085551	0.075715	NA	-0.911784	0.283018	-2.269287	-0.946174	1.340142	0.546782	0.593067	-0.925284	0.620148	-0.245032	-2.918285	0.58279	-0.930181	NA	2.23462	0.322901	-0.784306	0.870508	0.053091	NA	1.725275	-0.809627	NA	0.445831	0.364829
JEM1	NA	NA	-0.415763	-0.384611	-0.021123	0.195377	0.452664	-0.431757	1.024181	0.349574	0.053526	0.446647	0.138423	NA	-0.188699	0.198734	0.052718	0.264761	0.432078	-0.220154	0.247335	0.300977	-0.418513	-0.724781	NA	NA	0.494199	0.877225	0.138639	0.165398	0.172893	-0.076914	0.171348	-0.509837	-0.154489
JHD1	NA	-0.554408	-1.77593	0.187623	0.120691	0.721851	0.296684	-0.66129	0.753836	NA	0.068784	0.616844	0.017513	NA	-0.389853	-0.280127	0.503717	-1.408904	0.849282	0.103661	-1.25599	0.351186	NA	0.100433	NA	0.234264	-0.012516	1.060365	0.170483	0.202124	NA	-0.555114	-0.230726	0.970916	0.916225
JHD2	-1.63005	0.337731	0.536807	-0.592568	-0.271781	-0.255607	-0.139735	NA	-0.019643	0.019182	-0.81412	-0.15007	0.238142	-0.713312	0.469263	0.523795	0.033164	0.159171	0.233889	0.321222	NA	0.548694	NA	-0.521388	NA	0.820473	0.375315	0.322286	1.10518	0.316765	-1.085943	1.270262	-1.432329	-0.135017	-0.355619
JJJ1	NA	NA	0.351721	0.027129	1.141795	-0.129283	0.114827	0.092547	-0.806349	NA	0.021759	0.257935	0.543603	-0.028309	-1.174718	NA	0.276141	0.023133	-0.309084	-0.432748	-0.819218	NA	NA	-0.031534	NA	0.44082	-0.117757	0.574109	0.46441	-0.138118	-0.391837	-0.471419	NA	-0.891791	-0.457611
JNM1	NA	NA	2.334268	-1.243905	1.422623	0.552553	-0.038745	0.16357	-0.826815	NA	NA	1.252905	NA	-0.094594	1.267544	1.338337	-0.582053	-0.77809	-0.575198	-0.676322	-0.36348	-0.015408	NA	0.06354	NA	-0.296407	-0.056723	0.328382	0.269741	0.106502	NA	-0.453308	1.188802	0.248882	NA
KAP120	NA	-0.751875	-0.385519	0.630709	NA	-0.301699	-0.226999	-0.454006	-1.126172	NA	1.009289	0.402887	-0.005899	-2.775391	-0.391361	0.902725	-0.439815	0.062416	0.099318	0.373281	-1.195439	0.097775	-0.303663	0.004554	NA	-0.691101	0.166805	0.270972	-0.185279	0.836063	-1.523662	0.624984	0.788232	-0.182716	-1.346303
KAP122	NA	-2.491955	-3.623034	0.48293	-2.487851	0.322435	-0.537536	-0.886152	-1.14156	NA	1.452005	-0.901939	-0.539185	NA	1.026301	1.147454	0.213248	0.151095	0.056439	-0.604875	NA	0.029132	0.804795	NA	NA	-1.136131	-0.976333	0.551793	0.804462	0.524536	NA	NA	0.895421	0.448561	0.134689
KAR5	NA	-0.165124	-0.396034	0.237105	0.383675	0.100353	-0.074096	-1.343906	0.32076	1.822745	NA	-0.042551	-0.065035	NA	0.117882	0.513479	-0.589853	NA	-0.337819	0.60917	NA	0.954636	0.334032	0.953968	NA	0.38678	0.873687	0.086319	-0.523839	0.593534	NA	-0.259974	0.150367	-0.384121	0.753687
KAR9	4.695026	-0.05092	0.128796	1.409568	NA	0.467373	0.132215	-0.323486	-0.61124	-0.767602	-0.032821	-0.256613	-0.358632	-2.265378	0.107622	0.519947	0.795464	0.113094	0.701765	0.56656	-0.973681	0.765271	0.468763	0.999103	NA	-0.372174	NA	0.7461	0.067663	0.510541	-0.72979	-0.534872	-0.855922	0.612909	1.177956
KEL1	3.320345	-2.341448	NA	0.2114	NA	0.144651	0.794034	-2.289517	0.950124	-0.937954	NA	0.661014	-1.469138	-4.850112	0.634533	0.579985	-0.462271	-2.068108	-0.142968	0.396948	-2.017299	0.974941	NA	-0.878732	NA	-0.692909	-0.719434	0.907257	-0.106523	0.860187	-4.026344	-0.609243	-1.037465	0.750579	1.110818
KEM1	NA	-2.989081	NA	-0.255788	-6.527991	0.116246	-0.24852	-4.729687	1.06345	NA	-1.215903	1.054366	-1.698728	NA	0.461788	0.633087	-0.050907	-1.100692	-0.389203	-0.653317	-4.456413	-0.312852	NA	1.341981	NA	-0.898901	-7.602998	NA	-1.655638	-0.004889	NA	NA	0.423028	0.320232	-0.210366
KEX1	NA	-0.170408	-0.651573	-0.042925	-0.750845	-0.412587	-0.227864	-2.1045	-0.645107	1.413597	0.276824	-0.224614	0.338544	0.070206	0.075231	0.795088	0.792901	-0.52524	-0.544452	-0.508939	-0.01697	-0.171185	1.123482	0.591277	NA	-0.791867	0.436847	NA	-0.656221	0.649361	-0.549938	-0.851104	-0.449075	0.124412	-0.079634
KEX2	-1.190267	0.005702	-0.299604	0.262484	0.898427	0.286113	0.390889	-1.496428	1.406319	-0.742213	0.505675	-0.148017	-0.127934	-0.274727	-0.207742	NA	0.280609	-0.33146	0.567252	0.39137	NA	0.563543	NA	NA	NA	0.174272	-0.070843	-0.43692	-0.295698	0.755751	-0.919645	0.644963	NA	0.370723	0.848464
KIN1	-0.485575	0.069993	0.893765	0.113952	-0.010342	-0.078316	0.058642	-0.960556	-0.298715	0.686487	0.251007	0.91952	-0.165832	NA	NA	0.17611	0.275072	0.352718	0.98221	-0.020166	0.034288	0.236172	NA	-0.535175	NA	0.150336	-0.271842	-0.056004	0.641191	0.042093	-0.776273	-0.337154	-0.451292	NA	0.323067
KIN2	NA	0.118912	0.348725	-0.329349	-0.240935	0.113824	0.22685	-0.055131	0.385876	-1.422506	-0.067604	0.136406	-0.146365	-0.655757	-0.282055	-0.080051	0.058182	0.042472	0.942254	NA	-0.722741	-0.141475	-0.099975	0.618364	NA	0.801184	NA	0.161582	0.174888	0.266453	-0.275415	0.047486	-0.352205	0.1927	0.396716
KIN4	NA	-0.966434	-1.516954	-0.241248	-0.913623	0.187864	0.655077	0.688741	0.463011	NA	0.187269	0.450601	-0.026943	NA	0.014087	-0.056029	-0.202541	0.031949	-0.033677	-0.108174	NA	0.710968	-1.115804	1.086936	NA	0.675081	-0.888201	0.318202	0.147819	0.633054	0.321823	-0.484948	-0.676797	0.611433	0.047947
KIP2	NA	0.331147	-0.191984	0.137769	NA	0.410558	-0.165441	-0.873715	0.592509	-0.978841	-0.936214	1.175072	0.069829	-2.12731	-0.440496	-0.17114	-0.456838	-1.241805	-0.022246	0.066164	0.265539	-0.258249	-0.543924	0.490964	NA	0.213641	0.383266	0.263039	0.156528	-0.004588	-0.044706	-0.095889	-0.509585	0.383205	-0.620277
KIP3	NA	-2.103208	-2.793468	-0.372368	-1.060508	-0.14055	0.54021	-0.747983	-0.527698	NA	0.505828	-0.171643	-0.35876	NA	0.753535	0.05879	0.756241	0.076022	0.11167	0.116546	NA	-0.026994	1.067787	-0.757529	NA	0.325836	-0.630145	NA	-0.206464	0.326233	0.003791	0.022141	1.144819	0.357682	1.488782
KNS1	NA	-1.128535	-1.495599	0.342829	-0.195821	0.677554	1.069546	-0.40796	0.718969	-0.092759	0.508396	0.98193	-0.627627	-0.844065	0.002053	0.264179	1.147521	-0.878857	0.804601	NA	-1.224582	1.278121	-1.299263	0.696966	NA	-0.029706	NA	0.967821	0.742733	0.000451	-0.564907	0.806761	0.543821	0.632826	1.020816
KRE1	NA	-1.143851	-2.58142	2.142986	0.217319	0.955759	0.01953	-1.393296	0.636215	NA	-0.164697	0.114291	-0.813781	NA	0.199725	0.404181	0.880287	NA	0.756305	-0.030503	NA	1.302813	NA	NA	NA	-1.34298	-1.22233	0.51933	-0.718026	0.985604	-4.021849	-0.251986	NA	0.406401	-0.67429



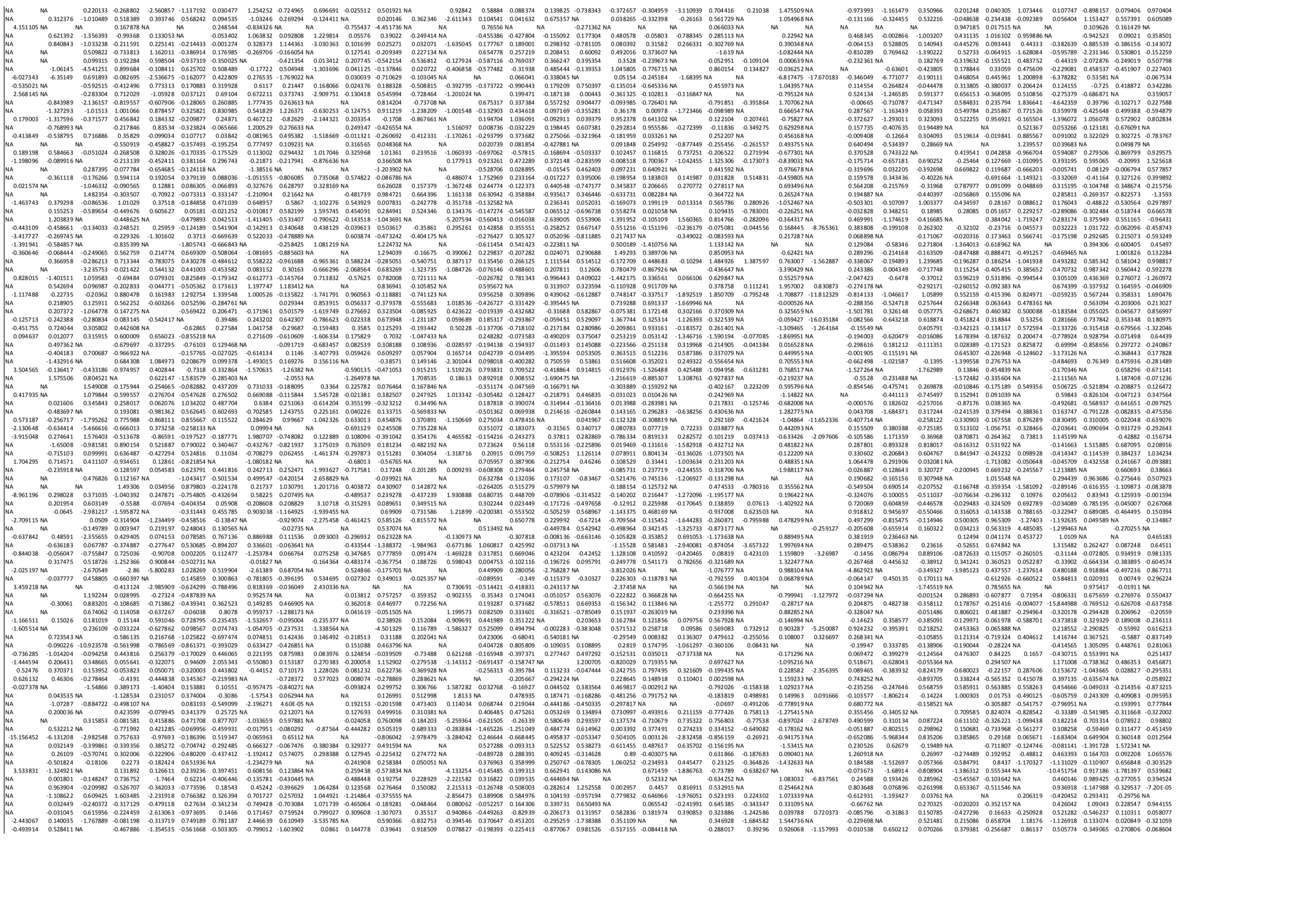
MSC7	-0.565945	0.109838	-0.65094	0.350697	0.339233	0.020729	-0.110135	-0.163581	1.406806	-0.624392	0.033004	1.132143	-0.164583	-1.210898	-0.241151	-0.126918	0.153306	0.887021	1.080704	0.378237	0.310073	0.562446	NA	0.775308	NA	1.314025	-0.325337	-0.58305	0.384672	-0.489489	0.040899	-0.341832	-0.170265	0.787067	-0.373659
MSG5	NA	-0.07857	0.633103	-0.29348	0.048747	1.057642	0.407733	NA	-0.20242	-0.973443	0.349541	-0.220045	-0.032494	-1.695479	-0.209397	0.149922	-0.213383	NA	0.132732	0.437822	0.047112	0.51847	1.055114	-1.248159	NA	-0.496037	0.152089	NA	-0.676006	-0.509268	-2.015983	0.109862	-1.206767	-0.125622	1.224909
MSH2	NA	NA	0.137127	0.711439	0.369652	NA	NA	NA	-0.037602	NA	NA	-0.632907	-1.012284	NA	-0.729395	-0.236217	0.145557	-0.28008	-0.966364	-0.503133	-1.033042	0.349737	-0.177862	NA	NA	-0.538324	NA	-0.11839	0.092033	1.225453	NA	NA	0.990749	0.909942	NA
MSH4	NA	-0.996203	-3.764461	0.015128	NA	-0.901472	0.318843	NA	0.196592	-0.39288	-0.004833	0.172883	0.940151	NA	-0.370105	0.405274	0.699998	1.066709	0.074232	-0.334038	-0.405666	-0.328155	-1.317428	1.108146	NA	0.766969	1.033125	-0.0856	NA	0.969387	0.915611	-0.921414	-0.291691	0.342926	-1.074228
MSH6	0.895845	-1.477635	0.816818	0.378885	-0.380976	0.359687	0.900518	NA	-0.085493	0.543633	-0.043309	-0.570532	-0.42128	NA	NA	0.323333	0.201797	NA	-0.527397	0.277855	NA	-0.513495	-0.176647	-0.705094	NA	0.162446	-0.504055	0.287603	-0.639776	0.298687	-0.502694	-0.607995	-1.377712	NA	-0.151377
MSI1	1.114707	NA	0.562628	-0.163529	0.115382	-0.139788	-0.057562	-1.750992	0.535232	0.1249	NA	0.609522	-1.750561	NA	-0.362662	-0.016078	-0.353364	0.870268	0.032612	-0.436123	0.507356	0.01199	-1.578607	1.955809	-2.899308	0.243356	0.252668	-0.084262	-0.680427	0.063059	NA	0.499876	0.50756	-0.277889	1.233416
MSN1	NA	0.691519	-0.650587	0.133653	0.002695	-0.541836	0.264678	0.766358	-1.16783	-0.075874	0.586389	-0.107624	0.419865	NA	0.956998	0.101685	-0.257971	0.69466	-0.59539	-0.918911	NA	-0.299144	0.36588	-0.018607	NA	-0.173585	0.771072	-0.869825	0.356044	0.256689	-0.272191	-0.629279	-0.414911	0.312197	-0.189236
MSN5	NA	-1.214059	NA	0.02535	0.414207	NA	0.304486	2.247814	0.049693	-1.046732	-0.240159	0.730166	0.353931	1.218906	0.269716	0.053684	0.520092	0.607846	0.318025	-0.285183	NA	0.666887	NA	2.501124	NA	-1.12599	-1.926432	-0.550765	-0.408181	0.509185	1.432196	NA	NA	0.169242	0.10715
MSS18	NA	-0.203034	0.026888	0.154407	-0.075276	-0.493969	-0.12584	0.296517	0.522859	-1.706872	-0.245459	0.43485	0.040193	0.477322	0.099074	-0.241236	-0.082418	0.078712	0.45908	0.309731	NA	0.229296	-0.029742	-1.799627	NA	0.27963	-0.4359	0.162883	-0.379203	-0.825823	0.145794	-0.719535	1.579779	-0.533633	-0.689169
MTC1	NA	NA	-0.278308	-0.1861	-0.37545	-0.898568	-0.50419	NA	-0.708538	-2.607406	-0.708997	0.438761	NA	0.444737	-0.412238	0.221867	0.798959	0.281176	-1.293104	0.184494	0.061358	-0.239557	NA	-0.254895	NA	NA	NA	-1.235818	0.69374	0.118883	0.261715	0.316595	-0.029493	-0.094107	-0.740277
MTC4	0.07036	0.389823	-0.868239	0.226796	0.423149	-0.350629	-0.298549	-0.357925	-1.310389	0.127539	-0.064963	0.44853	0.339317	-0.564005	-0.110497	0.218314	0.261458	0.25646	-0.303985	-0.21288	-0.250789	0.055826	0.186867	1.002705	NA	-0.669992	0.391825	-0.085486	0.131651	-0.179756	0.057735	-0.112682	-0.302155	-0.012531	-0.45014
MTC5	NA	-0.456869	-1.553701	0.264722	-0.548448	0.399649	0.224348	1.413382	0.704186	-0.850799	0.116673	1.06527	-0.758647	0.051514	NA	0.603831	0.272691	-0.191091	0.642166	0.333055	-2.273231	NA	-0.938854	0.470994	NA	-1.617714	-1.304473	-1.186021	-0.918276	0.046929	1.375574	0.191391	0.677987	NA	0.236752
MTC6	NA	NA	-0.600553	-0.035885	-0.407934	-0.444252	0.426149	-0.084345	-0.953058	-0.444194	-0.59952	-0.385807	0.083021	0.199942	0.587111	0.364846	0.091539	0.286454	-0.400264	0.241112	-0.704899	-0.663677	1.568614	0.451899	NA	0.274394	1.077781	-1.346615	0.379575	-0.352071	-0.893582	-0.728537	1.075257	0.612952	-0.145028
MTC7	NA	NA	-0.07573	-0.453906	0.122277	0.043974	0.541451	0.885038	-0.399957	-1.147356	-0.343005	0.228312	0.841239	NA	0.846243	0.258483	-0.416755	0.643937	0.17989	0.220879	-0.28055	-0.914189	NA	NA	NA	0.842079	0.004043	-1.26329	-0.800372	-0.935635	0.394887	1.162107	-2.096878	-0.001564	-1.651629
MUB1	NA	-0.549854	-0.387879	0.306124	-0.291761	0.511403	1.085134	2.293858	0.85242	-1.189509	-0.511539	0.324339	-0.618663	-0.30598	0.179414	0.193912	0.541915	-0.979947	1.390632	0.106226	-2.008007	0.62503	-0.507267	-1.716242	NA	0.202276	-0.266832	0.644885	NA	NA	1.865361	0.02925	0.055879	0.044722	0.091859
MUD1	NA	0.0947	0.340241	-0.072503	0.784424	-0.059145	-0.489299	NA	-0.076916	NA	NA	-0.268601	NA	NA	0.1869	0.206129	-0.289845	NA	-1.194353	-0.321895	0.44821	0.604918	-0.387513	0.467747	NA	0.601217	0.035723	-0.056989	-0.829693	-0.774039	NA	0.183974	-0.837626	0.077818	0.551956
MUD2	NA	NA	0.244259	-0.613772	-1.229563	-0.943758	NA	NA	-1.101068	2.851985	NA	0.593104	0.011485	1.085982	0.259384	-0.130194	0.173686	1.224339	-0.026858	0.050507	NA	-0.801251	0.78947	1.003627	NA	0.947308	NA	-0.779198	NA	-0.29269	NA	-1.942464	0.636298	0.035964	0.472021
MUM2	NA	-0.875256	-1.181613	-0.279917	-0.082584	-0.040496	-0.025351	-1.769194	-1.341933	NA	NA	0.768673	0.098944	NA	0.385934	0.869162	0.205672	-1.089147	-0.158409	1.467661	-0.365876	-0.391131	0.352678	-0.399704	NA	-1.029487	NA	0.099841	0.094886	0.180923	-2.066892	NA	0.586914	0.574242	0.136289
MUS81	0.100435	0.169308	-2.4778	0.312442	0.44633	NA	0.528699	-2.127597	-1.143261	-1.285305	-0.005645	-0.695609	-0.146306	-2.955735	-0.278694	0.120474	0.663999	-0.289866	0.880036	-0.022363	1.042138	0.13896	0.336883	-0.500698	NA	0.534748	-0.170782	-0.085375	NA	-3.094417	-2.766027	NA	NA	0.265199	0.692827
MVP1	NA	-0.280526	NA	-0.193694	0.342169	0.10986	1.144407	-0.215393	0.485646	0.571766	-0.206416	-0.144025	0.094812	NA	-0.589509	-0.074836	0.209691	-0.720319	0.504912	0.260206	NA	-0.316378	-0.783815	0.942288	NA	0.194116	-0.007033	-0.045185	0.8052	-0.24011	-0.581614	0.432876	0.443298	0.628246	-0.388199
MXR2	NA	0.721785	NA	NA	-0.09621	-0.63029	0.307875	-0.171765	-0.096957	-0.430127	-0.015672	NA	0.314728	-1.023441	-0.485606	-0.165569	0.41638	NA	0.078034	-0.402172	-0.200597	0.067532	-0.464146	0.291948	NA	0.474656	-0.106183	0.684003	0.731862	0.316098	0.258013	0.485838	0.144214	0.513767	-0.749623
MYO5	NA	0.029083	NA	0.371379	-1.14811	-0.13326	0.067749	-0.085731	-0.095722	0.5309	0.003918	0.508465	0.13091	NA	-0.162812	0.258226	-0.172525	-0.697709	0.912491	-0.241261	NA	0.078188	-1.73939	0.972943	NA	-0.277573	-0.496779	0.680729	NA	NA	-0.179378	0.405223	-1.444856	-0.190407	0.339589
NAB6	NA	NA	-0.164694	0.466651	-1.352209	0.171465	0.671371	0.078501	0.846666	0.878518	-1.05614	-0.014505	0.116439	NA	-0.186342	0.605546	-0.091417	-0.28683	1.488789	0.786563	NA	-0.486617	-0.203412	-0.451596	NA	0.058532	-0.924433	-0.426009	-0.145631	0.187885	0.374608	0.220797	-0.497536	0.486672	0.44007
NAM7	0.305723	-0.294105	0.033837	-0.524289	0.051823	-0.04859	0.317356	-0.411379	1.198628	-1.896056	NA	0.614813	NA	NA	-0.543722	-0.245006	0.855018	0.289867	0.240837	1.268149	NA	0.585301	0.315027	0.466651	NA	-0.124835	-0.831225	0.341459	-1.603885	0.036219	-0.118144	0.987364	NA	0.196837	-0.845299
NAM8	NA	0.006231	0.417869	-1.20321	-0.398198	-0.95308	0.182504	0.802383	0.450885	-0.44638	-0.829473	0.298123	-0.236132	-1.172311	0.021336	0.395826	-0.465144	0.752275	0.444203	0.817425	NA	0.989751	NA	-0.236602	NA	0.410151	0.068546	-0.418847	0.897611	-0.317351	0.43153	-0.883383	0.940737	0.380953	0.012998
NAP1	NA	0.117286	-0.159114	0.808346	0.070927	0.618228	-0.523017	-0.341933	0.207986	-0.154998	0.433273	-1.039016	-0.399666	NA	0.299278	0.484666	0.201539	-0.046939	0.895906	0.134716	-0.498352	0.913223	NA	-0.458088	NA	0.279702	-1.478376	0.468855	-0.511427	0.05453	-1.049088	0.200874	0.754395	0.672813	-0.416223
NBP2	NA	-2.698509	NA	0.285948	0.085333	0.542158	0.634094	-1.517278	0.347503	0.546577	-0.155033	-0.439868	0.010664	-1.168537	NA	-0.098943	0.102955	0.150768	0.415361	0.116537	0.007508	NA	NA	0.539409	NA	0.570146	-0.851812	0.608224	-1.24127	0.172697	-0.021591	-0.052137	1.0663	NA	0.206714
NCL1	NA	-1.986515	-0.195358	-0.028261	0.162768	0.001666	-0.009211	NA	-1.146153	NA	NA	0.388775	NA	NA	-0.407545	-0.164324	-0.215767	0.067881	0.273385	0.572025	NA	-0.615011	0.918912	1.825549	NA	NA	0.694598	NA	-0.498624	-0.258776	NA	0.068984	NA	0.66049	0.738145
NCS2	-5.934995	0.14678	-12.733831	-0.922762	-1.097015	-0.713345	0.280554	0.611942	-0.345671	-2.319223	-0.140761	1.060565	0.79096	-10.4807	-0.049437	NA	0.325951	-0.026529	-0.208667	0.329618	-0.036124	-0.268091	0.587941	-0.410755	-4.41749	0.19946	-0.279489	-0.730212	0.301021	0.09996	0.684543	-0.515259	1.589987	0.645297	-0.428145
NEJ1	-0.284104	0.341954	-0.084207	-0.170842	-0.013058	0.39509	0.566184	-1.136171	0.576264	-0.912126	-0.057226	0.437036	-0.262823	NA	0.161693	-0.247899	-0.165649	-0.139631	0.38281	0.821085	NA	0.703252	NA	-0.326335	NA	-0.445959	-0.260615	0.013718	0.51999	-0.212675	-0.692704	0.326503	-0.512541	0.191085	-0.862012
NEM1	-1.003015	-1.268021	1.350906	0.534571	-1.374231	-0.668011	0.627913	-1.043492	-0.572816	NA	NA	0.714558	0.444753	NA	0.510469	0.011229	0.430468	0.433796	-0.4763	0.365494	-2.051425	0.711089	0.958599	0.04256	NA	-0.966961	-0.795758	0.391461	-0.213898	0.329729	-1.032064	0.191661	0.946544	-0.184315	0.255294
NFI1	NA	-2.649544	0.108465	-0.94382	-0.990232	0.059448	0.521873	-5.132795	1.243532	NA	-0.327462	0.609693	-1.821403	NA	0.509906	0.391503	0.562361	0.946773	0.292797	0.741996	NA	0.362029	NA	-0.581182	NA	-0.176448	-2.327234	-0.606584	-0.992418	0.602173	NA	0.684566	0.118771	0.059405	0.206284
NFT1	NA	-0.200329	-1.094053	-0.283839	-0.707761	0.168478	0.293503	1.550289	-0.279073	-0.576481	-1.053129	0.495713	0.162812	NA	0.584549	0.313864	0.741853	-0.299874	1.233374	0.370694	NA	-0.226729	-0.381578	-0.321902	NA	0.243767	-0.7073	1.094127	-0.243964	0.000483	0.457635	0.433466	-0.17392	0.062361	0.470279
NGL2	-2.705013	0.690257	0.999839	1.010127	0.06354	-0.256564	-0.524188	0.720346	0.261841	-0.098672	0.150927	0.633296	NA	NA	0.072447	-0.001305	-0.182251	-0.585038	-0.481466	-0.121509	0.647429	-0.113224	NA	-1.448455	-1.162384	-0.147079	0.453836	0.474375	NA	NA	-1.031594	0.778057	-0.464461	-0.345839	NA
NGR1	NA	-0.194558	0.196704	-0.366309	0.202345	0.921368	0.350348	1.121662	-0.11802	-0.064314	NA	0.824132	0.162418	NA	-0.259525	-0.516791	0.154435	1.172136	-0.042803	-0.295776	NA	-0.518421	NA	0.472805	NA	0.461597	0.598778	0.381652	0.839043	-0.091163	0.115773	-0.226689	-0.619863	-0.488538	-0.020139
NHP10	NA	-3.626582	NA	0.203306	-0.540951	1.072239	0.423431	NA	0.430242	-2.112479	0.734216	-0.669877	-1.218517	-0.90975	NA	0.465216	0.733292	-1.427167	-0.353696	-0.529805	-1.375274	0.350883	NA	1.485825	NA	-0.990943	-2.005544	0.716519	-0.205497	1.335753	-1.175239	-1.402872	1.194668	NA	0.562156
NHP6A	NA	-0.88629	NA	0.962443	-0.266618	0.587531	0.421401	NA	0.845893	NA	NA	0.724578	-0.367758	NA	-0.112058	-0.131699	-0.253183	0.753089	0.075113	-0.129684	NA	-0.42332	NA	1.222952	NA	-0.604066	-0.983469	0.658833	-0.24914	-0.439496	1.657292	0.128901	-0.565526	-0.286701	0.021149
NIP100	3.401255	-1.305945	NA	-0.942606	NA	0.392303	0.377515	0.503403	0.013284	NA	NA	1.245477	-1.178242	NA	0.486104	0.792694	-2.872346	-0.512385	-0.256789	-0.105519	0.200972	-0.153719	NA	2.268782	NA	0.02632	-0.250046	-0.344437	-0.020411	0.178981	NA	-0.827237	1.199911	0.030829	-1.070353
NKP1	0.368275	-0.623578	0.436554	-0.095456	-0.669344	NA	0.13395	-0.246549	0.190665	-1.229013	-0.285606	0.170162	0.17871	NA	0.261921	-0.00191	-0.147012	-0.660851	-0.189712	0.92414	0.565672	0.154558	NA	0.494153	-7.486817	0.378155	-1.388672	0.010819	0.093587	-0.100836	-1.003384	NA	-0.92914	-0.179835	0.652941
NKP2	NA	-0.246092	-4.674576	-0.973928	0.3087	0.314263	0.086097	-0.833611	0.164361	0.360216	1.442982	0.308399	-0.538093	-0.623893	0.035801	0.169321	0.104299	0.467829	0.011019	-0.102266	NA	0.121455	NA	-0.399713	-3.860253	0.944781	NA	0.281302	0.317201	0.150676	-0.117446	0.622329	-1.40956	-0.251357	-0.160618
NMD2	NA	-1.255075	-0.640922	-0.563256	0.21368	0.292989	-0.139196	NA	0.447717	NA	0.093678	1.128377	0.21428	NA	-0.831778	-0.200572	-0.100428	NA	-0.322354	1.286733	-0.692587	0.372577	-0.712954	1.112057	NA	-0.034834	NA	0.460527	-1.126139	0.185249	0.44274	0.331006	-0.879354	0.506777	0.758495
NMD4	NA	NA	-0.417337	1.008085	-0.036867	0.389106	-0.203631	-0.089913	-0.443919	-0.419165	-0.416323	0.286583	0.007638	NA	0.620092	0.141864	-0.054138	0.453986	0.253936	0.452602	-0.336301	-0.114134	NA	0.412157	NA	0.30969	0.649822	0.179607	-1.111584	-0.258547	-0.475082	-0.013195	-0.751771	0.26542	0.655914
NNF2	4.284871	NA	-1.482668	-0.207979	-0.856782	0.559756	0.203535	-0.786083	-0.144423	0.952109	0.372525	-0.005586	-0.246942	NA	0.370987	0.422191	0.322365	0.0901	0.438181	-0.459867	-1.176581	-0.135478	NA	1.779826	NA	0.147172	-0.577002	0.79881	0.67802	0.676454	-0.66508	-0.881294	1.371753	-0.252785	0.290627
NOP12	NA	NA	2.133548	-0.612821	-1.176547	-0.919673	NA	1.256737	NA	NA	-0.753354	0.430124	0.120381	-0.001313	0.105597	0.100892	-0.03257	0.871054	-0.60265	-0.078263	-1.35402	-0.13603	NA	1.280368	NA	-0.709861	0.410491	-0.159383	-0.327177	-0.660336	NA	0.043561	NA	0.375881	-0.310296
NOP16	NA	NA	0.428488	-0.306587	0.50819	-0.601096	0.216211	1.076028	-0.735935	-0.731181	-0.433766	-0.187395	NA	-0.131219	-0.042022	-0.129037	-0.475555	0.256452	-0.982268	-0.519979	0.45063	0.361386	0.823737	0.497585	NA	-0.335689	-0.861822	-0.429599	-0.414356	0.369038	1.608307	-0.513969	0.16604	-0.213974	0.136977
NOP6	NA	-0.882431	0.53155	-0.258557	0.035277	-0.438211	-0.52118	0.833997	0.767819	NA	-0.313066	0.143949	0.285112	0.800177	-0.357709	-0.218095	0.267567	0.272625	0.162328	-0.262328	-0.768027	0.393987	0.447241	0.337512	-2.272502	-0.25006	0.362229	-0.423086	-0.497199	-0.162385	0.279609	-1.458809	0.75565	-0.327366	-0.840177
NPL4	4.074334	-0.114457	0.541123	0.054374	0.633154	-0.169793	-0.021654	-1.383009	-0.586759	NA	NA	0.236433	0.220674	-0.902026	-0.298259	-0.671335	0.098649	0.198821	0.815799	0.411543	0.475035	-0.984736	NA	-0.045425	NA	0.076632	-0.553337	0.72175	0.081954	-0.139395	-2.549823	0.209384	0.258933	0.075665	0.244594
NPP1	0.362987	0.172612	-0.448312	NA	-0.861175	-0.269566	-0.139542	0.998995	-0.709497	-0.369175	-0.169562	NA	-0.162974	3.458329	0.015449	0.000745	-0.116039	NA	-0.008383	-0.058874	0.099015	0.430278	NA	1.436145	-3.208963	0.007666	0.146031	-0.040123	-0.449224	-0.464048	0.963008	-0.156147	-0.423281	0.237918	0.276141
NPR1	-1.053706	-0.02	-0.337151	-0.371729	0.113352	0.643988	-0.140331	0.199909	-1.218981	-1.003732	0.438378	-0.143642	1.228464	-1.645676	0.314114	NA	0.329277	-0.569657	-0.546594	-0.684396	0.517515	0.215993	0.638208	0.032816	0.6347	0.373229	0.48614	0.256048	-0.282781	-0.280148	0.373841	-0.359319	NA	0.973045	0.534045
NPT1	NA	-0.323945	0.154619	1.133331	-0.445588	0.446329	-0.229829	0.942524	-0.255678	0.284682	1.353219	-0.707087	-3.007328	NA	0.276756	-0.033899	0.775332	-0.231915	0.507829	0.505525	-0.94563	0.037779	0.155286	-1.093736	-5.751688	0.172604	NA	-0.386863	-0.57981	0.340215	-0.129621	-0.340724	-0.034249	0.118409	-0.632243
NPY1	NA	0.681758	-0.201577	0.487181	0.289044	0.916757	0.193075	0.316508	1.785213	0.130441	NA	-0.006199	-0.115479	-1.243166	0.519872	-1.041123	-0.314908	0.09407	-0.145808	-0.210987	-0.429365	0.864683	-0.678461	1.338772	0.150445	0.182232	0.04753	-0.898645	-0.420652	-0.363418	-1.133357	-0.231323	-0.185714	-1.137622	-0.778659
NRP1	NA	-0.233398	NA	0.200481	-0.33578	0.575017	-0.112595	0.208537	1.09341	-0.033911	NA	-0.499506	-0.750747	1.002157	0.530905	0.789191	-0.324387	0.076696	0.83058	0.395115	NA	-0.028806	NA	-0.457933	NA	0.339501	-0.953499	0.033174	0.728808	0.270816	0.622821	-0.052041	1.187271	-0.193329	0.995038
NTE1	NA	-0.255401	0.629053	-0.115205	-0.198289	-0.266652	0.086478	-0.262487	0.376503	0.159649	NA	-0.595357	0.14958	-0.351801	0.221431	0.218604	-0.322912	0.328829	0.580954	0.520853	NA	-0.16392	NA	0.110679	NA	-0.116369	NA	-0.293807	0.372556	-0.022046	-0.760502	0.418282	0.213016	0.00144	-0.184188
NTO1	NA	NA	-0.020014	-0.312278	0.371796	-0.088662	0.234499	-0.535292	0.004229	0.816116	0.154679	0.490534	0.219165	NA	-0.129399	-0.37095	-0.174947	0.704016	-0.387726	0.321474	0.651761	-0.079409	0.351515	1.008316	NA	-0.538879	-1.02772	-0.327729	NA	0.248551	NA	-0.515271	-0.09975	-0.422876	-0.148113
NUC1	NA	NA	-0.799482	0.058196	0.019582	-0.096818	-0.584674	-0.213505	-0.761647	NA	0.1051	0.586555	0.32011	-0.51616	0.435658	0.666675	0.248771	0.065033	0.464679	0.096897	-0.413593	0.384062	0.449956	0.649448	2.057529	0.278683	0.674407	0.79221	-0.592323	0.246712	0.133293	0.942431	0.891187	0.704329	0.133908
NUM1	NA	NA	2.907081	-0.20753	2.022241	-0.707808	0.026748	1.144871	0.254558	-5.273569	-0.645081	1.327664	-0.502821	NA	NA	1.463716	-0.33438	-0.006477	-0.21847	-0.209747	-0.405874	NA	-0.122775	0.297282	NA	-0.844454	-0.741628	-0.462071	NA	0.00916	0.05225	-1.541416	2.025391	NA	-0.014412
NUP100	NA	-0.285563	-0.066191	-0.469621	0.458968	0.568553	-0.401336	-1.518048	0.676839	-2.955337	-0.087974	0.274474	0.567555	NA	0.337394	0.554649	0.135068	0.401175	-0.531366	-0.051938	0.995862	-0.943312	0.44364	-1.122716	NA	-0.182052	0.322073	-0.431972	0.321062	-0.008239	-0.375426	0.152804	0.012006	-0.068205	-0.549251
NUP133	NA	NA	NA	-2.306178	NA	0.808501	-0.472104	-7.048307	NA	NA	-0.630607	0.046463	NA	NA	-0.009946	NA	NA	0.715004	-1.194612	NA	NA	-0.071013	NA	NA	NA	-2.306998	-7.458196	-0.51584	-3.286991	0.355476	1.475156	-5.849264	NA	-0.307967	-0.539082
NUP170	-5.501982	NA	-1.75265	0.142802	0.393129	0.426675	0.392283	-0.930755	1.186608	-2.786266	0.087068	1.727618	0.416369	NA	0.283875	-0.133451	-0.237238	-0.706988	-0.759876	-0.605275	-2.345362	-0.309096	-2.589942	0.738701	-5.968756	-1.153243	NA	0.958765	-0.864844	0.331632	0.927378	-0.986864	0.316126	0.025094	-0.168767
NUP188	NA	-1.036524	-3.838541	0.454178	-1.053464	-0.07751	0.149731	-0.517091	1.188338	-4.836435	0.931101	0.016064	-0.157125	NA	0.648856	-0.478431	0.210409	-0.115517	-0.390753	-0.415587	NA	0.49803	NA	2.135443	-6.157555	-0.807871	-1.143057	0.222733	0.215557	0.61989	-0.690455	-0.729556	0.40482	0.549473	0.968131
NUP2	NA	-0.550335	NA	-0.646923	-0.429905	-0.580755	0.160616	1.215268	1.451744	0.580745	NA	0.012132	0.41729	NA	0.129558	-0.526553	0.474258	-0.081557	-0.071261	0.243319	0.427781	-0.745765	NA	-0.389209	NA	0.518975	0.681538	0.450858	-1.031364	0.225851	0.5965	0.229717	-0.335161	-0.566127	-0.497715
NUP42	NA	0.695708	NA	0.771797	0.542686	-0.74134	-0.675823	-3.235605	-0.240924	-1.475793	-0.482559	0.129674	0.077221	NA	0.744428	0.106307	-0.275214	0.212478	-0.231934	0.053088	-1.222606	NA	0.352751	0.240258	NA	0.691861	0.363773	0.83032	-0.441243	-0.091305	-1.212552	0.160881	-0.167453	-0.034529	0.284335
NUP53	-1.086865	0.396913	-0.382422	0.493073	-0.349214	0.319477	0.685644	-0.596957	0.914534	0.836146	0.683032	0.497751	NA	NA	0.638985	-0.60754	0.224422	-0.12119	-0.19207	-0.117678	0.400343	0.027789	0.49107	0.825863	-2.036136	0.816591	0.654231	0.50346	NA	NA	-0.170628	0.368494	-0.91515	0.089555	0.615386
NUP60	-1.707768	NA	0.310483	-0.565792	-3.656407	0.649306	0.628145	NA	0.687881	NA	-1.562123	-2.536297	NA	NA	1.035995	-0.429021	-1.772772	1.195426	-0.804406	0.490342	NA	-0.296885	NA	-0.998295	NA	-0.393305	-6.367069	0.45689	-2.076184	0.793536	NA	-9.07065	-0.245718	0.245432	0.258854
NUR1	NA	-1.95225	NA	0.591065	NA	0.215209	0.448812	NA	-0.550922	-1.015703	0.211828	0.340793	-0.403131	NA	0.103989	-0.075175	-0.197223	-0.49938	0.760226	0.672487	0.500013	0.299776	NA	1.742964	NA	-0.191085	-1.053861	0.371305	0.482012	0.621647	-0.417289	0.021149	-0.088521	-0.772111	-0.200373
NUT1	-3.145999	-1.891949	-1.480269	0.887679	-0.704657	1.281626	0.404219	-1.776715	0.41059	-4.358161	0.46799	-0.737779	-0.473236	-1.172278	0.643879	0.553814	0.851843	-0.000173	0.630115	0.405111	-1.521313	0.647131	0.887699	-1.155558	NA	0.945039	-3.006815	NA	0.267535	1.294555	-0.520038	-1.570331	0.525157	0.552367	0.945381
NUT2	NA	0.454618	-0.693278	-0.492157	0.063063	-0.672277	0.192178	0.930266	0.533297	1.079051	NA	-0.210953	0.379812	-0.485844	-0.799737	-0.212002	-0.19608	0.697066	0.375225	0.594003	-0.016551	-0.73754	NA	-0.057517	NA	0.005053	0.133402	-0.321375	1.197332	-0.278792	1.348124	0.148765	0.023592	-0.674792	0.151624
OAC1	NA	0.34622	-1.198136	0.235886	-0.074298	-0.002858	0.690124	-0.631574	0.252403	-0.145918	0.239656	0.194954	NA	-0.493365	-0.247333	0.044109	0.502767	-0.434419	0.501279	-0.097237	-0.649963	-0.08304	NA	0.027808	NA	0.871932	-0.04943	0.826639	0.538217	0.159462	-0.29753	0.229169	-0.077253	0.002242	0.274803
OAF1	-0.249009	0.418516	-0.368273	-0.12517	0.339154	0.021856	0.068187	NA	0.196724	-1.042177	-0.300846	-0.421097	NA	NA	-0.027746	-0.363161	-0.037286	-0.905948	-0.025127	-0.074493	-0.330171	0.53669	NA	0.452315	-3.00664	0.530407	0.69831	0.174961	-0.074879	0.408975	-0.079974	-0.222004	-1.061511	-0.160316	-0.316839
OCA1	NA	-0.118401	-3.796549	-0.202574	0.465843	0.108049	-0.336196	-0.658536	-0.172304	0.15607	-0.282181	0.25219	0.29515	NA	-0.193365	NA	-0.030124	0.840035	0.132962	0.827218	0.282768	0.011957	0.055084	-0.48741	NA	-0.291865	-0.100995	-0.413573	-0.090378	-0.100779	0.65944	-0.184556	-2.454428	-0.405289	-0.565907
OLA1	-1.657246	NA	NA	-0.073711	0.175352	-0.519675	-0.055682	-0.283367	0.52158	-1.515479	0.188034	1.433668	NA	1.765853	0.941347	1.558528	0.216214	0.006346	-0.805087	0.842177	NA	0.05507	NA	-0.116517	NA	NA	-0.220062	-0.461988	-0.154865	0.054803	0.016309	-0.207312	NA	-0.429446	0.397637
OPI1	-2.523287	-0.285551	-0.115576	-0.253861	1.081584	-0.272258	-0.390434	-0.653391	0.174433	-4.579597	0.225071	0.668468	-0.082834	NA	0.490727	0.073123	-0.155328	0.506231	0.39086	0.368126	NA	0.089827	0.029792	-2.352494	NA	0.561324	-0.022721	1.382878	0.603449	-0.299201	-1.134441	-6.877755	0.119367	-0.506465	-0.047208
OPI10	NA	0.592174	-0.240919	0.261872	-0.04578	0.068151	NA	1.147727	NA	NA	-0.008673	0.219036	-0.089631	-0.218516	0.178869	-0.592664	-0.03952	0.639373	0.163672	0.014161	0.09017	-0.328664	NA	0.307111	NA	0.734004	NA	NA	0.087573	-0.028373	-0.172509	0.4929	NA	-0.129829	-0.425086
OPI3	NA	0.303592	NA	-0.168629	0.465152	0.352817	0.950206	-0.116105	0.449757	-3.180395	0.120568	0.946559	0.115874	1.422471	0.589454	0.188335	0.064964	-1.078747	0.003284	-0.118782	-0.630772	-0.141476	0.633662	-0.519172	NA	-1.546303	-1.144037	-0.554782	-0.423438	0.527369	-0.700272	-0.862245	0.931569	1.06689	-0.592523
OPY2	NA	-0.052251	-0.901413	-1.478167	1.752837	0.977003	0.72338	-0.519131	-1.581004	0.044656	0.730205	0.701308	-0.021203	NA	0.800973	0.25467	0.367736	-0.071433	0.534092	0.901428	NA	-1.312962	NA	-1.781205	NA	-0.520247	-0.514339	0.50011	-0.246425	0.130857	-1.819717	-1.437809	0.398993	0.404328	0.298732
ORC1	NA	0.104175	-0.679654	-0.301651	0.361056	0.354511	-0.599372	NA	0.921511	0.984309	0.879029	0.043942	-0.18375	NA	-0.003199	-0.36684	NA	0.761014	0.06841	0.109517	NA	-0.15751	-1.121884	1.004213	-6.846475	0.27404	0.273841	-0.242916	NA	0.202796	-0.62596	0.599843	-0.128786	-0.380942	NA
ORM1	NA	NA	0.159478	0.001913	-0.810829	-0.184849	-0.014828	-0.17555	0.325059	0.443992	0.055896	-0.03734	0.349372	-0.097764	-0.041954	-0.589666	0.697219	0.58945	0.306048	-0.122403	0.357682	-0.855589	NA	0.555003	NA	-0.185861	0.266221	0.102782	0.62373	-0.120588	-0.196278	-0.168604	0.665399	-0.609744	-0.315361
ORM2	NA	NA	NA	-1.022248	-0.315339	-0.208435	0.503155	0.339836	-0.456005	0.067505	-0.335157	0.180163	0.31854	NA	0.382074	-0.003292	0.173583	0.329255	-0.250176	-0.513175	0.061595	0.008075	NA	0.922615	NA	0.395068	0.150926	0.956264	0.124497	0.221366	-1.030848	-1.044053	-1.176734	-0.407965	-0.572131
OST3	NA	-0.006786	-1.916865	-1.176026	0.572365	0.2081	NA	1.069233	NA	NA	0.409854	0.451299	1.39146	0.530715	0.643783	0.368632	0.320047	0.603937	0.595497	-0.01715	0.545776	-0.329969	NA	-0.05395	-5.826596	-0.126344	0.13654	0.065901	0.709517	-0.241381	-0.282766	-1.057274	-0.330278	-0.370602	-1.104925
OST5	NA	0.095016	-0.025108	-0.187996	0.094115	-0.73647	-0.311816	-0.058609	-0.031051	0.155599	0.444891	-0.141808	0.514087	-0.223128	1.081339	0.438096	0.39389	0.455264	0.73596	0.913189	0.337425	-0.468788	0.031844	-0.028617	NA	-0.007553	0.511825	NA	0.529666	-0.952746	0.024165	-0.255815	-0.970406	0.6903	0.873938
OST6	NA	0.159679	NA	0.078611	-0.822627	-1.022309	0.391176	0.717404	-0.132607	-0.462705	-0.969327	-0.051622	NA	0.139458	-0.143251	0.781184	0.465683	-0.161751	0.037971	-0.806058	NA	-0.181982	NA	0.601464	-5.812304	0.096119	-0.204905	-0.18915	NA	0.043179	0.084641	0.417186	0.408616	0.018771	0.280709
OXR1	-1.26036	-0.292562	-1.315973	0.466491	NA	-0.083422	0.081935	0.600324	0.745834	-1.082959	-0.465935	0.046019	0.063277	0.123281	0.001994	0.308204	-2.338379	-0.757575	0.274238	-0.874268	-0.693303	-0.166512	-0.160872	0.334504	NA	-0.076606	-0.304253	0.637882	0.307248	0.109379	-0.384424	0.29552	0.883836	0.917459	0.78411
OYE2	-0.578306	0.513862	-0.71543	-0.957622	0.464913	-0.152097	0.228853	-0.175721	0.33042	-6.30E-05	-0.396894	0.121696	0.17633	NA	0.023676	-0.135911	0.400607	-0.096657	1.068313	0.668577	0.374622	0.085902	-0.271711	0.100581	NA	0.613314	0.369611	-0.267	0.55575	0.331086	-1.319083	-0.103305	0.199616	-0.586888	0.326374
PAC1	NA	-1.049874	0.514771	-1.064454	-0.180233	-0.166246	-0.075245	0.852679	-0.077226	0.145137	NA	0.767134	-0.356073	-1.951353	0.588472	0.796715	NA	0.249239	0.322644	-0.214619	NA	-0.384451	-1.638266	0.579779	NA	-0.000586	-0.759244	-0.109195	0.898801	0.850178	0.0308	-0.577934	0.057481	0.166887	-0.173916
PAC10	NA	-0.80658	-2.406751	-0.161782	0.790209	0.356945	0.55201	1.868107	0.232108	NA	-3.446026	-0.088184	0.021363	-1.790662	-0.523771	0.216039	0.61825	NA	0.801181	-0.246779	-0.410177	0.601525	NA	-2.272924	NA	-0.11424	-2.094803	0.198284	0.27876	0.257107	0.656522	-13.114884	0.317347	0.579369	-0.911224
PAC11	NA	-2.485693	0.901133	-0.412513	0.68148	NA	0.300517	NA	1.005222	0.444855	0.084386	0.26742	-0.293611	0.34244	0.675266	0.583533	0.796164	-0.421689	-0.100507	-0.491967	-1.155516	0.470427	-1.240479	-0.397715	NA	-1.076424	-2.140443	0.199573	-0.789893	0.270688	0.493835	-0.837738	-1.02591	0.13169	-1.079631
PAC2	NA	0.458731	-0.696455	0.971081	-1.33923	-0.83986	-1.407071	0.801452	-0.359096	-3.47921	0.952647	0.693193	-0.108999	0.373363	-0.157768	0.416592	0.096835	0.379809	0.229747	1.208591	NA	0.111343	0.027899	-0.461177	NA	-0.020682	-0.385846	0.422174	0.743695	0.292984	0.531395	-4.291487	-0.270407	-0.102652	0.632897
PAN3	NA	0.030668	-0.880217	-0.387519	0.324693	-0.156844	-0.067883	-0.580323	0.342327	-0.672728	0.127399	-0.332897	-0.044745	-1.92435	0.017727	-0.124131	0.312722	-0.248153	0.556205	0.321478	0.008229	0.047653	NA	-0.963178	NA	0.680732	-0.53373	0.535538	0.756731	0.657406	-0.561366	0.243331	-0.590046	0.232965	0.735017
PAP2	-0.056635	-0.424931	0.226826	-0.070811	-0.465629	-0.109982	-0.214799	0.002094	0.248793	1.282237	NA	0.126423	0.468057	0.478935	-0.64612	-0.749984	0.029067	NA	0.249045	0.193248	0.695132	-0.658174	NA	1.431743	NA	0.407883	0.163282	-0.78164	0.611509	-0.38695	-0.132807	0.308869	0.187837	-0.113893	-0.356599
PBP1	NA	-0.097881	NA	-0.086871	0.333412	-0.731058	0.287769	-1.589231	0.121767	-0.543856	0.253196	-0.1538	-0.461389	-8.385464	0.228912	-0.231713	-0.003348	-0.347468	0.875415	-0.356714	-0.561913	0.694992	NA	0.596966	-0.759778	-0.111499	0.175509	1.160091	-0.318006	0.179676	-1.963357	0.364483	-1.198854	0.210999	-0.101752
PBS2	NA	NA	-0.439011	0.319311	0.327508	0.092185	0.547293	0.269366	1.094559	-0.442836	0.292465	-0.804391	-0.723321	-3.546005	0.363826	-0.00429	-0.179882	0.362212	0.858284	0.238493	-0.033931	0.153289	-0.49644	-2.182217	NA	NA	-1.137049	0.106614	0.453507	-0.082725	-0.020653	0.092166	-1.120557	0.935883	0.86494
PCA1	NA	NA	0.442449	-0.743239	-0.144128	-0.098168	-0.659302	0.300157	-0.545408	0.309111	0.362924	-0.241344	NA	2.867022	-0.602162	-0.068626	0.031894	0.320547	-0.353724	0.126382	0.227629	0.351504	NA	0.902042	NA	0.004229	NA	-0.531215	0.348428	-0.17357	0.265359	-0.090187	0.099966	-0.093711	0.008746
PCH2	NA	0.270925	-0.292173	0.675803	0.598494	0.471293	0.33952	-0.437573	-1.837989	NA	NA	0.165123	-0.320918	-0.748228	0.655255	-0.095015	0.612544	-0.175551	-0.361979	-0.322492	0.15469	-0.244545	-0.031587	-2.546744	NA	-0.119092	-0.039119	0.434877	0.037839	-0.477131	0.535672	-0.697783	0.365718	0.159513	-0.21308
PCP1	NA	-0.150228	0.726546	-0.170294	0.935779	-0.116797	-0.479892	-0.543235	0.254257	-1.040229	0.503019	0.383244	0.571308	-0.275797	-0.283789	-0.027467	-0.310804	-0.765334	-0.235164	-0.180008	-1.397711	-0.376588	0.046927	-1.093735	NA	-0.215667	-1.988427	-0.35661	-1.102325	0.188898	-0.219784	-0.019781	2.141702	0.177692	-0.346698
PCT1	NA	0.130218	0.24147	0.36965	0.522989	-0.543694	-0.470745	-0.092899	-0.394556	-1.00409	0.090904	-0.305147	0.38468	1.220352	-0.373037	0.221299	-0.369204	0.021764	0.325239	0.085452	0.385211	-0.128755	NA	0.825658	-1.525476	-0.203092	NA	0.114561	0.176211	-0.038506	-0.227655	-0.267718	-0.051187	-0.24577	0.228226
PDA1	NA	-0.213417	NA	-1.981371	0.049671	-0.136954	-0.396074	-0.367389	0.021476	3.400562	-0.42711	NA	NA	NA	NA	0.955698	-0.034625	-1.371613	NA	NA	NA	-0.363396	NA	NA	NA	0.574741	-0.854929	-0.011723	NA	0.95561	NA	1.040802	NA	NA	-1.289904
PDB1	-1.017782	-0.88869	0.406658	0.017055	0.470714	-1.401663	-0.503158	1.655989	0.061839	-1.380138	NA	-0.235427	0.470981	3.388518	-0.023374	0.255878	0.490862	1.314635	-0.495368	0.152955	-0.85265	-0.71021	-0.698526	-0.117864	NA	-0.032905	-0.64684	-0.725632	0.569774	0.423505	0.998473	0.1829	0.206106	-0.849599	-0.488963
PDC1	-1.466517	-0.158672	0.136872	0.485662	0.370188	-0.165353	-0.42951	NA	0.362433	1.146474	0.197807	0.303431	NA	NA	-0.055392	0.490358	-0.09146	NA	0.097395	NA	-0.152421	-0.590901	NA	-1.009077	-0.949128	-0.283812	NA	-0.197606	0.311469	-0.281822	-1.906918	0.222329	-0.299772	-0.09753	0.27586
PDE2	-1.248047	-0.532605	-1.407669	0.278488	-0.786234	0.531199	0.577377	0.12555	1.363784	-0.86856	NA	0.855696	-0.090556	-1.664585	0.144971	0.733521	NA	-1.685637	-1.160072	-0.251587	-1.025149	1.16883	-1.504049	-0.570292	NA	0.315728	-1.148544	0.57782	0.24717	0.294519	-0.650203	0.08701	-0.844941	0.53853	0.57139



RAD10	0.165998	1.351516	0.294959	-0.022312	0.474284	-0.675458	0.252042	0.573939	-0.208693	-0.160109	-0.047399	0.317577	0.950821	NA	0.168641	0.106405	-0.15543	-5.073501	0.222103	-2.130311	NA	-0.137882	NA	-0.118358	NA	1.546053	0.990144	0.238679	-1.111866	-0.004483	-0.231812	-0.482103	-0.700099	-0.703948	-0.29007
RAD16	NA	NA	NA	0.324926	-0.967699	0.47139	0.404447	-1.782044	-0.897113	NA	NA	-0.320681	-0.136515	NA	0.218589	0.681918	0.183408	-0.819977	0.934184	-1.221376	0.349355	-0.641383	NA	-0.131881	NA	0.59735	NA	0.181979	0.732312	0.738391	NA	1.065996	0.955274	0.129762	-0.046416
RAD17	-0.268146	-0.687351	0.707268	1.480432	-3.264675	-0.045823	0.484963	0.078068	-0.16763	0.153108	NA	NA	0.287269	-1.234361	0.568525	0.888202	NA	-0.915682	NA	-2.422483	-0.951125	0.263344	-11.504716	1.527854	NA	0.200287	-1.083003	0.5591	0.457548	0.430381	-0.249931	0.099257	NA	-0.223551	0.25225
RAD18	-0.445454	NA	NA	NA	NA	NA	-0.278382	NA	NA	NA	0.020145	0.238853	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.541877	-0.837511	-1.846978	NA	NA	NA	1.198669	-0.110449	NA	NA	-0.113984	0.363985	NA
RAD23	NA	-0.281151	-1.426852	-0.19594	-0.10397	-0.081736	0.347881	-2.524842	-0.287722	NA	0.282943	-0.23739	-0.059273	-0.196528	0.964038	0.530867	0.220429	-4.5573	0.447513	-1.179539	0.629647	-0.00489	NA	1.667036	NA	0.738682	-0.202496	-0.205847	-0.706723	-0.094609	-1.993395	-0.894068	0.246596	-0.299214	-0.543447
RAD24	NA	NA	0.680729	NA	NA	0.797267	0.25341	-0.855326	NA	NA	NA	NA	NA	NA	0.864642	NA	0.943639	-0.870151	NA	NA	NA	0.926552	NA	-0.156285	NA	NA	NA	NA	-0.442935	0.588135	NA	-0.111233	NA	-0.262254	NA
RAD26	-0.95462	-0.323739	0.126526	0.042906	0.614965	0.033338	0.148843	0.418044	0.278418	0.667443	-0.090652	0.493753	-0.323957	-1.021581	-0.182023	0.174634	0.410247	-0.976653	0.440107	-0.49526	-0.436145	-0.101852	NA	0.923714	-4.304294	NA	0.180033	0.845156	0.075052	0.268475	0.084551	0.835722	0.038064	0.002841	-0.808418
RAD27	-0.78336	-11.547434	-0.909926	-5.735348	-1.04139	0.968007	-2.737057	1.442276	-6.184296	-2.906116	-3.192139	-9.998488	NA	-3.081558	-3.911877	-0.559968	-4.64931	0.527223	-4.731792	0.008575	NA	-3.931417	NA	-0.127078	NA	1.150267	NA	-10.850998	-12.001102	0.096663	0.971099	-1.407714	-0.30963	0.114878	1.046575
RAD5	-0.742724	0.274577	-0.798493	-0.832835	NA	0.223626	0.433911	0.66061	NA	NA	-0.884075	0.37633	NA	0.233608	0.370973	NA	NA	2.220495	-3.448625	NA	NA	-2.808924	-2.795213	0.853529	NA	0.404427	NA	0.332833	1.60994	0.480795	-0.127668	-0.009814	1.250543	0.539414	NA
RAD51	-0.149992	-0.432251	0.35239	-0.185509	-0.486487	0.934707	-0.379799	-0.437541	-0.538002	-0.236547	0.24691	-0.156135	-0.506006	-2.327935	0.437369	0.20142	-0.153224	0.211439	NA	0.53826	-0.612989	-0.683167	-0.002364	0.467279	-7.14928	0.310054	-0.149243	1.038052	0.388956	0.130914	NA	0.767733	0.799431	0.898251	1.398621
RAD52	-0.58013	0.68044	-2.953335	-0.082071	NA	1.530832	0.231811	-2.091345	NA	NA	NA	-2.675148	NA	NA	-0.524264	NA	NA	-2.76646	-0.657364	-2.013724	NA	-0.165073	-1.448164	0.450852	NA	1.212935	0.499601	0.081437	0.266731	0.497275	-1.142966	0.73007	NA	0.835362	NA
RAD54	-0.549238	-0.448145	-0.188744	0.000731	0.246947	0.165035	-0.3136	-0.674044	-0.518377	-0.829892	-0.529102	0.177479	1.20305	NA	-0.011124	-0.229614	0.190737	0.076593	0.254741	-0.506668	2.36444	-0.254705	1.129612	0.445242	NA	0.490514	0.021521	NA	1.437203	0.253679	-0.784265	-1.057809	NA	0.443702	-0.172344
RAD55	-2.406377	-0.317959	-1.967642	0.015012	-1.453174	0.179814	0.39126	NA	-0.016673	-0.875896	0.152828	0.194493	1.10043	NA	NA	-0.232492	0.403907	-1.169948	-0.192912	-0.570066	2.333302	-0.298152	1.284412	1.381206	NA	-0.084411	NA	0.226474	1.594347	0.474876	-3.270392	0.074264	0.033668	NA	-1.019079
RAD57	-2.258746	0.277846	NA	0.395443	-0.160574	1.077718	0.012582	NA	-0.069712	-0.478911	0.132381	0.290626	1.756058	NA	NA	-0.426286	0.87337	-1.57696	0.954298	-0.734778	NA	-0.476604	1.456777	0.377788	-3.879695	0.437488	-1.047174	0.421115	1.163832	0.554769	-0.81098	-0.067282	NA	NA	-1.023615
RAD59	NA	0.468819	NA	-0.154143	NA	-0.064275	-0.133006	NA	-0.685955	-0.044311	0.484782	0.403853	0.565184	NA	0.242893	0.015034	-0.130267	-0.046509	0.179245	0.497638	1.290609	-0.552296	NA	0.339491	NA	-0.820388	-1.002343	-0.01682	0.118196	-0.113241	0.789864	0.617058	0.597008	0.030348	-0.25841
RAD61	NA	-0.652862	NA	0.098027	-1.590005	0.324544	0.789511	NA	0.672741	NA	-0.337993	-0.649179	NA	-0.033513	NA	0.340223	-0.135284	-0.164863	0.458271	-0.295798	0.890352	-0.535575	-1.89887	-0.994989	-5.95874	0.043216	-0.342377	-0.019481	1.028689	0.268029	0.997157	0.263979	-0.027273	NA	-0.419738
RAD7	NA	0.635785	-0.046758	-0.818282	0.255612	-0.161891	0.823542	-1.645771	-0.317513	-0.394633	-0.702917	-0.03463	0.267495	-2.446505	-0.33348	0.098992	-0.099494	-1.647851	-0.040198	-1.203396	NA	0.746501	NA	0.123597	NA	NA	NA	-0.165762	0.25945	0.278828	0.010624	0.015181	0.777024	0.145785	-0.410087
RAD9	NA	NA	0.144008	0.535391	NA	NA	-0.236103	-0.241098	NA	NA	-2.682238	NA	NA	NA	0.579816	NA	NA	0.835785	NA	NA	NA	NA	NA	1.653686	NA	NA	NA	NA	-1.788638	0.61087	NA	NA	NA	-1.843229	NA
RAS1	NA	NA	-0.893898	-0.203125	0.212218	-0.142049	NA	0.268012	NA	0.387549	-0.382779	-0.025701	-0.228449	NA	0.755372	0.080244	0.374705	NA	0.253255	-0.205587	-0.508999	0.663485	NA	0.095141	NA	0.531251	-0.528564	-0.08654	-0.120221	0.440233	0.549529	-0.253551	NA	0.204929	0.211071
RAS2	-1.002119	0.517602	-0.063711	-0.054162	-0.142554	0.232281	-0.081852	-0.37747	0.358658	0.25148	0.208439	-0.780135	-0.182032	-2.113106	0.331361	NA	0.795568	-0.077316	-0.759676	0.442019	-0.801745	-0.142166	-3.159135	1.272555	NA	-0.393793	-0.136906	0.480917	0.543415	0.406665	NA	0.537415	-0.026217	0.410088	0.597408
RAV1	-1.053451	0.223402	NA	-0.367351	-0.161348	0.107751	-0.112477	-1.029136	-0.198809	1.49021	0.121708	-0.15469	0.543501	-0.093428	-0.066298	1.06155	0.292379	NA	-0.07341	0.066524	0.789242	-0.496103	-0.14884	0.270427	NA	NA	NA	-0.024904	0.32474	-0.267287	-1.37565	0.344153	NA	0.366281	-0.72833
RAV2	NA	0.243362	-1.447143	0.520673	0.707523	0.32565	0.440428	-1.206044	-0.637408	0.24392	0.837619	0.263398	0.006524	-1.321122	0.972827	0.766862	0.457015	-0.081653	0.315828	-0.130843	0.808771	NA	0.857313	-1.091707	NA	0.406319	-0.948282	0.328597	1.035528	-0.091342	-1.86698	0.503279	NA	0.222497	1.174789
RBA50	-0.246505	-0.384103	NA	-0.170288	0.687765	NA	0.303507	0.437871	-1.162726	1.370041	0.159721	0.377162	-0.424025	0.638657	-0.073772	-0.148848	-0.347998	-0.00124	-0.034606	0.246039	-0.789141	0.17054	0.127837	-0.13291	-3.176468	-0.096241	0.248661	-0.397922	0.176312	-0.181267	0.899678	0.384425	0.148327	0.998463	-0.103786
RBL2	-0.90607	0.005095	NA	-0.383484	-0.035956	0.326919	0.67171	0.095976	0.916934	NA	-0.055366	-0.431195	-0.149479	-1.881852	0.083516	0.199346	0.052252	-0.078712	0.096793	0.333591	-0.217765	-0.321063	-0.8382	-0.501895	NA	0.991848	NA	0.155794	0.793734	0.106105	0.694697	-0.599121	-0.596143	0.033628	0.668948
RCE1	NA	NA	-3.723673	0.291158	0.188952	0.851944	-0.533127	NA	-0.193601	NA	0.002099	-0.12721	NA	NA	-0.630029	0.474529	0.696808	-0.841999	0.320729	0.031836	0.4148	-0.253053	-0.668982	-0.383647	0.900819	-0.533856	-0.138344	0.599489	NA	NA	NA	-1.478584	NA	-0.027063	NA
RCO1	NA	-2.995918	NA	0.62129	-1.037006	0.487531	0.25066	-20.035466	0.719459	-3.455391	-0.666471	-0.817466	-0.007922	-13.527786	0.339001	0.394149	-0.044927	-0.530963	0.905229	0.163561	-0.259309	0.496675	NA	-1.59995	NA	0.382721	-1.293815	0.116232	0.847611	0.193945	NA	-3.328329	1.067482	-0.678214	0.196957
RCS1	NA	-0.444674	NA	-0.481599	-1.364152	-0.324176	-0.362421	NA	-0.450591	NA	NA	0.087437	NA	0.772279	NA	0.241305	-1.89221	NA	-1.255806	0.881747	NA	-0.528325	-0.087162	2.698446	NA	-1.389571	NA	NA	0.014603	0.750114	0.936851	-0.489389	1.237887	0.38674	0.692056
RDH54	NA	-0.715253	-0.054299	0.661668	-0.07356	1.007791	0.774758	-0.318502	1.427851	-1.843452	NA	-0.420764	-1.851259	-0.396849	0.674686	0.158911	0.445748	-1.265724	0.844076	-1.75713	NA	1.043681	1.359412	2.104669	NA	0.285851	NA	0.18814	0.856243	0.35887	-0.617695	-0.616942	0.377328	0.078087	0.248783
REC104	NA	0.365404	NA	-0.948783	0.659109	0.202097	-0.092788	0.149485	-0.490013	0.438594	0.148962	0.092997	0.104392	-0.595902	0.891565	0.480429	0.253237	0.070838	0.215082	-0.540665	0.361263	0.880963	NA	-1.379642	0.760492	-0.114918	-0.305699	0.45117	-0.074356	-0.46199	NA	0.222284	NA	-0.373282	0.688083
REC114	-0.453897	NA	NA	0.285715	-0.04587	0.314955	-0.156331	0.167825	-0.022535	0.283631	0.467682	0.072715	NA	NA	0.071993	-0.237267	0.135766	-0.819703	0.575158	-0.102109	-0.194844	-0.247474	NA	0.44451	NA	-0.033602	NA	0.327009	NA	NA	0.900655	0.723622	0.016945	0.674744	-0.286744
RER1	-0.783731	0.127762	-1.956415	NA	-0.565303	0.237667	0.558442	0.281445	0.793149	-0.076647	0.102988	NA	-0.162218	1.308631	-0.075702	0.139297	0.037451	NA	0.17355	0.150707	0.625758	-0.435487	0.247861	1.062198	NA	-0.387911	-0.493864	-0.597701	0.155299	0.559267	0.10858	0.688834	-0.759993	-0.299124	-0.014019
REV1	-0.273801	0.805512	-0.08782	-0.192249	0.438225	0.074072	-0.225159	-0.367102	0.022189	-0.258335	-0.157202	-0.342806	0.207559	0.620958	0.985818	-0.190323	NA	-0.578915	-1.050285	-0.885554	NA	-0.502551	0.168221	0.820978	1.228241	0.206769	0.452052	0.620634	-0.187431	0.160345	-0.322303	0.021191	0.690245	-1.709842	-0.261357
REV3	-0.937196	0.007441	0.88294	0.352583	NA	0.340646	-0.497193	-0.240473	0.028938	NA	0.204699	-0.155509	0.482023	NA	0.55464	0.087204	-1.12943	-1.007542	-0.606156	-1.898959	-7.847981	0.35844	-0.104734	2.116098	NA	0.847665	0.18786	0.117548	0.851953	0.301679	-0.058979	0.020972	0.544557	-2.207315	0.578605
REV7	-0.243419	NA	0.003588	0.510245	1.509279	0.840629	0.274568	NA	1.304837	NA	0.089207	0.035689	0.329083	1.055693	0.156939	0.751147	-0.253359	-0.696884	0.075629	-1.277373	-5.436419	0.730041	NA	-0.941353	-2.962547	0.627881	-0.122718	0.370599	0.574417	-0.309244	-0.458753	-0.387454	0.100461	-1.249782	1.212357
REX4	NA	0.194533	NA	-0.45512	0.020629	-0.870158	-0.246695	NA	NA	NA	-0.579233	-0.012448	-0.287178	NA	0.114951	0.289461	-0.415946	NA	-0.156985	0.676608	0.135724	0.336882	-0.478308	-0.028725	NA	0.014894	1.144425	-0.0883	0.625471	-0.895526	0.999328	0.53164	-0.472095	-0.742054	-0.18024
RGA1	NA	-0.651082	0.11254	1.528033	0.03734	0.87489	NA	-0.587853	NA	-0.491396	0.924983	NA	0.084573	-0.350747	0.291756	-0.697454	0.849529	-0.065978	0.862488	-0.80293	-0.412392	-0.465698	-0.127037	0.180709	NA	-0.917993	-0.375305	0.330507	-0.811562	0.221363	-1.101611	0.919183	NA	1.092538	-0.84998
RGD1	NA	0.239531	-0.43073	0.046283	-0.057366	-0.175891	-0.034216	-1.000823	-0.66715	-0.166487	NA	0.706493	NA	-1.165965	-0.154253	0.138522	0.134416	0.829563	0.0534	0.15653	-0.227827	0.24924	-0.030889	0.749756	NA	-0.432463	0.266668	-0.344734	-0.194033	0.190452	-1.448862	-0.05745	0.459742	0.435528	-0.541699
RGR1	NA	0.536218	0.619339	-0.595557	0.623256	-0.116801	0.257906	0.202782	0.195341	0.619438	-0.060954	-0.441613	0.130766	NA	-0.49137	-0.270471	0.656345	0.672103	0.267621	NA	-0.185167	-0.792561	-0.318067	0.325544	NA	-0.283739	NA	0.1929	-0.076114	0.13827	0.257724	1.130984	-1.068246	-0.37918	-0.351791
RHB1	NA	0.284634	0.669563	NA	0.331536	-1.167142	-0.339489	1.268461	-0.514598	1.252808	-0.680827	NA	0.538366	3.725776	-0.025176	-0.525675	-0.408149	NA	-0.140898	-0.174534	NA	-0.408911	NA	-0.045586	NA	0.556739	0.102883	0.039857	0.523103	-0.530033	1.532742	-0.17244	-1.612625	-0.236589	0.237619
RHO4	NA	NA	-0.975754	0.813472	0.117986	1.084589	0.116506	NA	1.786748	1.606447	NA	-0.205109	-1.07181	NA	0.604402	0.834765	0.152906	-0.672976	1.408243	0.209262	NA	1.290671	NA	1.938413	NA	-0.182571	-0.721545	1.252047	-0.483692	0.657234	0.227347	-0.759877	0.242776	0.137418	1.16004
RIC1	NA	0.295879	-9.438044	0.243646	-1.13579	0.263874	-0.255567	-1.688143	0.357641	-5.4721	0.549755	1.067633	-0.373887	NA	-0.018681	0.727556	0.093863	NA	-0.046237	NA	-0.463471	0.347556	NA	1.781835	NA	-1.315749	NA	0.516657	0.101652	0.086128	-0.962488	-6.040031	1.967597	-1.365024	0.295012
RIF1	-0.294722	-2.620468	0.381359	0.278043	0.555403	0.256466	0.333242	-2.291275	1.173245	-1.614913	0.158258	0.899115	-5.743744	-1.527016	0.031377	0.049143	-0.24959	0.608457	0.491717	0.608443	NA	-0.58157	-0.211247	-0.544971	NA	-0.746107	-1.246566	0.548153	0.18551	-0.47966	-2.857817	1.110204	-0.240222	0.240023	0.562633
RIM1	0.624833	0.210354	0.01889	NA	-0.229978	0.042703	0.011226	0.849778	0.030069	-0.061002	-0.163109	NA	-0.455086	0.084071	-0.798042	0.025418	-0.390991	NA	-0.408735	0.190085	-0.014818	0.150821	0.196958	-0.801497	NA	0.183221	-0.310697	-0.32463	-0.022789	-0.104902	0.198882	-0.449205	1.337817	-0.221865	-0.480928
RIM101	3.246815	NA	NA	-0.459997	-0.155217	0.616737	0.15373	1.361073	-0.117488	NA	0.980328	-1.090683	NA	NA	-0.530902	0.461744	-0.199405	-0.711629	-0.070078	-0.433775	-6.221021	-0.308193	-0.089677	-1.572681	NA	0.180688	NA	-0.218445	0.832406	1.198389	1.444342	-2.919132	NA	0.317519	0.711353
RIM13	NA	-2.154306	NA	-0.726825	-1.92762	0.058838	-0.046962	1.215525	-1.100934	NA	0.84739	-1.530967	NA	NA	0.287271	-0.001455	0.672095	-1.799292	-0.027755	-0.198115	NA	-0.385118	-1.092723	NA	NA	0.631116	-2.826868	0.057432	NA	NA	NA	-1.51199	NA	-1.022838	0.253443
RIM15	-5.740651	0.71095	-2.038779	0.329299	0.550798	-0.297135	-0.757374	NA	-1.670234	-0.342932	0.304984	-0.198529	NA	NA	-0.087141	0.422272	-0.337477	0.815392	-0.14759	0.143815	NA	-0.166632	0.52346	-0.548665	NA	-0.455507	-0.325736	-0.115474	-0.122264	-0.172168	-0.964362	-0.268561	NA	-0.524164	-0.157046
RIM20	NA	-2.626542	NA	-0.460117	-0.166467	0.65819	0.514015	0.638457	-0.72022	NA	0.496128	-0.750491	-7.19528	NA	0.729578	0.316362	NA	-0.413434	0.153779	-0.46129	-5.924745	-0.949318	NA	-0.069466	NA	-0.291234	-1.384212	-0.376204	0.647515	-0.041887	0.558964	-2.443529	-0.238274	0.803923	0.562552
RIM21	NA	-3.568064	NA	-0.912292	-1.595144	0.365345	0.290626	0.626435	-0.732606	-2.676691	0.147268	NA	-4.50396	-5.945876	0.175081	NA	-0.141567	-2.621036	0.005698	-1.351814	-6.476867	-1.211789	-1.803282	NA	NA	-0.416817	-1.157591	-0.115549	0.610168	0.461771	0.498347	-2.88389	NA	-0.220196	0.147483
RIM8	NA	-2.940918	NA	-1.771728	NA	-1.349667	-0.247509	1.440921	-0.736516	NA	0.882782	-1.749086	NA	-3.344995	0.293571	0.642399	0.01876	NA	-0.155866	-3.046945	NA	NA	NA	NA	NA	0.298272	NA	0.335972	0.40866	2.527909	NA	-3.055372	NA	NA	NA
RIT1	-1.057837	0.37933	-5.44057	0.238966	0.024778	-0.129572	-0.023936	0.697714	-0.105431	-1.09592	0.253533	0.652946	NA	-0.746763	0.338819	-0.594002	0.354232	0.35275	0.177563	-0.118559	0.370599	0.207668	-0.184418	-0.85707	-6.559648	0.679303	0.39086	NA	NA	NA	-0.256442	-0.924066	NA	0.165155	NA
RKM4	-0.608071	-0.784819	0.034656	-0.526916	-0.09788	0.572944	-0.166846	-0.072606	-0.215806	-0.537233	-0.013427	0.81688	0.126823	-0.034849	0.187332	-0.188551	-0.515322	0.163697	0.58803	0.547312	0.681726	NA	0.778051	-0.050364	NA	0.48046	-0.547564	-0.339748	1.451575	0.384301	-0.18633	NA	-0.119885	0.007349	-0.691179
RKR1	-1.546348	0.200154	-0.836469	0.16994	-0.43779	0.780607	0.262475	-0.860841	0.249295	-0.827815	0.056001	0.093138	NA	NA	0.384187	0.585982	0.860621	-0.434881	0.064594	-0.30297	-0.588792	0.860895	0.466496	0.607706	NA	-0.524574	-0.340172	1.559299	NA	NA	NA	-0.691744	-0.963813	-0.042629	NA
RLF2	NA	-7.335693	-1.679869	-0.044796	-2.146531	1.184839	0.228953	-3.453381	0.667777	-1.145976	-0.685641	0.219074	-4.81449	-4.941335	0.580648	0.816117	-0.17424	-0.029267	-0.370562	0.068126	-1.947886	0.643649	NA	0.476388	NA	-0.545254	-2.438096	0.801014	-1.15553	0.363576	-3.73633	-0.393875	0.959658	-0.348932	0.558312
RLM1	NA	0.058397	-0.012485	1.638261	NA	0.073974	-0.486254	-0.148169	0.24808	0.107404	-0.317671	-0.583905	-0.171727	-1.507806	-0.73005	0.22495	-0.1917	-0.20092	0.068998	-0.411944	0.03556	0.055655	-0.043336	-0.661595	NA	0.071675	-0.222249	0.827114	0.456863	0.046726	-0.956793	-0.101062	0.339775	0.659782	-0.027942
RMD11	NA	-0.450627	0.805411	0.251908	-0.521273	-0.430729	0.104913	-1.02226	-1.153553	-0.076229	-0.802803	-0.479784	0.859063	-1.080855	0.450565	0.722866	-0.111792	0.104909	-0.193696	-0.938955	NA	0.83537	0.131056	0.899616	NA	0.494571	0.555497	-0.567069	-0.054056	-0.209708	-0.460452	-0.462475	NA	1.486857	-0.678803
RMD5	NA	-0.781872	-0.61873	-0.825412	0.239926	-0.581657	-0.278456	0.131965	-0.771899	1.217193	0.394723	0.477698	0.271531	-0.993498	-0.225634	-0.330644	0.341632	0.477818	0.526824	-0.108185	0.073789	NA	NA	0.003672	NA	-0.325595	-0.640577	-0.299784	0.415086	0.066489	0.169047	NA	-0.508011	-0.020064	0.531898
RMD8	NA	-0.609906	-0.761528	-0.12928	0.181207	0.594646	0.291783	-1.949464	1.012757	-1.324497	0.031788	0.866478	-0.379084	-0.153595	-0.24955	0.318443	-0.119751	-0.287294	0.631578	0.086227	0.291951	0.692423	0.126694	0.394586	NA	0.207159	-1.27265	0.514797	0.660813	0.061366	-1.853891	0.299665	1.330692	-0.053513	-0.045088
RMR1	NA	-1.447566	-0.90453	0.491599	0.371257	0.86836	0.497287	-2.673205	0.31668	-1.599315	1.159635	0.299719	0.313173	-3.090956	0.357166	0.126095	-0.087289	-0.353487	-0.413797	-0.217288	-0.084172	-0.887887	-0.437319	-1.90859	NA	0.154248	-0.855704	NA	-0.835205	0.237132	0.411089	-0.247109	0.047613	0.623826	-0.465039
RNH201	0.234425	-3.95348	0.525084	0.51199	0.130146	0.457213	0.536084	0.665425	0.102806	-0.19038	-0.526836	0.098009	-8.140436	-1.152334	0.283964	0.231083	-0.274496	0.631118	-0.352269	0.49205	-6.46488	-0.396506	NA	-0.106818	NA	-1.053078	-3.237247	0.079596	-7.142867	-0.410511	-0.585631	-0.811595	-0.440937	0.486589	0.428644
RNH202	-0.486843	-1.781881	NA	0.140957	0.45664	1.029576	0.045762	0.334717	0.063711	-0.395177	0.146425	0.311601	-6.710893	-0.325781	-0.467307	-0.490748	0.508404	-0.13161	0.289251	0.542233	-3.522634	NA	-2.383977	-0.686091	-3.397785	-0.579511	-2.930992	0.241178	-9.645966	-0.771134	0.177427	NA	0.408475	0.796795	0.181891
RNH203	NA	-2.049361	-0.939485	-0.202411	0.437645	0.082909	0.955066	0.547853	0.909744	-0.099245	0.149316	0.425577	-7.068111	NA	0.30687	0.645124	0.566346	-0.503168	0.790261	-0.127494	-9.210586	0.789577	NA	-0.290465	NA	-0.240266	NA	-0.111132	-8.06872	-0.149008	-0.606528	1.318507	0.794879	-0.813078	0.592152
ROT2	NA	-0.37354	0.260849	-0.424894	-0.232749	0.322699	0.922953	-0.021557	1.493092	1.459529	NA	0.37989	NA	NA	0.543019	-0.538168	0.082775	-0.040817	0.691696	1.18536	NA	0.439299	NA	-1.907934	NA	-0.19045	-0.068196	-1.00E-05	0.145802	-0.684485	-1.204751	-0.383106	NA	0.166597	0.055348
ROX1	NA	-0.459089	0.320091	-0.03537	0.768412	0.829225	0.751371	-1.33174	1.304403	-1.131119	-0.3062	1.148396	-1.467308	-0.755655	0.733836	0.417708	-0.058265	-0.807893	0.399666	0.620281	-2.446679	0.269455	NA	0.045798	NA	0.07823	-1.020052	0.885488	-0.27146	0.131166	-0.686202	-0.41751	0.851209	-0.289071	1.145491
RPA14	NA	-5.449122	1.157609	-0.557689	-1.526871	0.718051	0.583281	0.482898	0.545527	NA	NA	-0.558644	-0.84836	-2.284769	NA	0.047545	0.030566	-0.241013	-0.219012	-0.208812	NA	NA	-0.713653	NA	NA	-0.962744	-1.878439	-0.176979	-0.706414	0.359327	0.101254	-0.645431	0.872074	NA	-0.312821
RPA34	NA	NA	0.18358	0.194994	-0.32708	-0.173738	-0.017531	0.822805	-0.223856	-0.351105	0.676119	-0.348658	-3.871407	-1.170557	-0.206349	0.107084	0.171273	-0.001431	0.049424	0.114867	-0.922197	-0.104149	-1.818059	-0.590574	NA	-0.144314	-3.11078	0.333259	0.045374	-0.535583	0.680427	-0.413585	0.627013	0.067985	0.061075
RPB11	NA	0.429323	-2.574009	-0.385387	0.11925	0.773322	NA	0.285941	NA	NA	NA	0.570968	-0.582044	-2.748728	0.176848	-0.131354	0.962456	1.20419	-0.024139	0.383949	NA	-0.161727	1.039012	NA	NA	-0.862566	-1.552461	0.969011	-2.244557	0.110727	0.525586	-4.626486	0.932324	0.400061	-0.90347
RPB2	NA	NA	-0.203002	0.24401	0.198399	-0.362211	-0.222262	0.836425	0.76379	NA	-0.276128	0.759872	-0.686637	0.700482	-0.041455	0.029128	0.506458	0.257066	0.315278	-0.506027	NA	1.133835	NA	-0.060251	NA	-0.03233	-0.358219	0.921327	NA	0.274288	-0.281028	-0.726067	0.100257	0.06177	0.819094
RPB3	-6.79233	-0.599594	-9.18612	-1.077513	-0.143409	0.093176	0.038178	2.324696	-0.547427	-9.24546	0.579571	0.665632	-0.033574	0.492456	0.372788	0.189728	0.256834	-0.261353	0.0035	NA	-0.550577	0.170328	-2.634999	-0.997682	-15.191568	-0.163759	-1.281765	0.374116	1.489319	0.750489	1.893294	-2.178633	0.269673	-0.520397	-0.757538
RPB7	NA	-0.37616	1.440854	-0.073362	0.357636	NA	0.410768	0.671746	1.048501	0.204061	-0.416972	0.522481	-0.35362	-0.88145	-0.075541	-0.068847	-0.353639	1.319905	0.187982	0.388207	-0.685798	-1.04283	NA	0.162125	-4.698023	-0.054091	-0.389064	-1.338483	-1.819389	-0.409665	0.098368	NA	NA	0.178549	-1.263478
RPB9	NA	-1.458825	NA	0.031915	-0.126163	0.67163	0.336291	-0.482471	0.12749	3.045179	-0.433496	0.427441	-1.102946	-1.211086	0.551463	1.196227	-0.454387	-0.166288	0.019451	-0.140422	-3.518975	0.012137	NA	-3.27343	NA	-0.495969	-2.100004	0.136595	0.020864	0.21365	0.805435	NA	NA	0.360621	-0.003204
RPI1	NA	-0.838596	-0.04535	0.186513	0.190686	-0.439469	0.139784	-0.45275	-0.172564	0.771904	-0.014785	0.498266	-0.120648	-0.088979	0.073291	0.228023	-0.066069	0.577801	0.520811	0.628358	-0.750841	0.566636	0.168028	1.041822	NA	-0.057909	-0.070223	0.121792	0.571416	-0.221672	-0.254268	-0.014217	NA	0.171749	0.713576
RPL11B	NA	-0.006399	NA	-1.354787	-0.419024	-0.594466	-0.350785	0.39162	0.661775	0.309264	-1.108518	-0.051208	0.258525	0.848915	-0.572526	0.890106	0.234538	-0.230643	-0.960353	-0.298494	-0.250684	0.105074	0.533154	0.65538	NA	0.043834	-0.72627	0.105062	-0.168829	-0.245328	0.190527	0.390388	0.267516	-0.129536	0.076224
RPL16A	NA	NA	NA	-0.615053	0.424275	0.360555	-0.102564	NA	0.378692	NA	-0.127474	0.088595	-0.505168	-0.295525	-0.869411	0.254783	0.001686	NA	-0.063741	-0.51589	-0.444534	0.452177	0.600832	-0.922022	NA	-0.045619	-0.661813	0.350786	-0.121834	-0.532418	-0.713132	-0.920725	0.601143	0.338738	-0.150319
RPL16B	NA	NA	1.447948	-1.204967	NA	-0.403977	-0.438752	-11.911974	0.02101	-4.276441	0.381246	0.681278	0.344206	-13.03053	-0.130344	-0.589335	0.478167	1.418841	0.583439	0.778885	NA	-0.177865	0.23852	1.443019	NA	-0.066533	-0.795972	-1.042908	NA	-0.418995	NA	NA	1.150629	-0.621932	-0.482584
RPL17B	-0.123752	NA	0.743874	-0.104059	-0.860836	-0.437034	0.409784	NA	-0.954881	0.017494	0.604505	-0.079425	-0.203712	3.131404	-0.411312	-0.363012	-0.136336	0.703089	-0.798427	-0.439923	NA	-0.697642	0.464278	-0.451765	NA	-0.70263	-0.571389	-1.109764	0.121579	0.615249	1.324129	0.376908	0.274918	0.013958	-0.726486
RPL19B	-8.029843	-1.828152	-2.637983	-0.014213	-2.576529	0.798978	-0.047957	1.378307	-1.272645	-3.267435	1.209003	-0.040702	-1.146583	NA	0.973728	1.05115	0.513536	-1.303245	0.734235	-0.37879	-2.929402	0.49821	0.837684	0.001331	-9.079894	-1.075265	-2.279029	0.340807	0.347382	-0.475541	NA	-0.965052	-0.141978	0.555209	-0.560937
RPL23A	NA	-0.940372	0.884316	-0.577085	-0.376191	0.053658	-0.611014	1.499013	-0.579781	NA	0.015086	0.47179	NA	0.054491	0.090113	0.088414	0.130866	0.152678	0.175192	-0.018276	NA	-0.055494	-0.03157	1.266715	-12.63798	0.326506	-0.706549	-0.478283	0.087829	-0.081997	1.376211	-0.012531	0.032893	-0.456006	1.017833
RPL24A	-3.494677	-0.750614	-0.47834	-0.463073	-0.900522	0.658381	0.29438	1.914389	1.155559	-1.367265	0.577896	0.826366	-0.942957	-0.040086	0.258713	0.775089	0.543412	-0.342346	0.840028	-0.274295	-3.627053	0.249502	NA	-0.034217	NA	0.208804	0.002706	-0.540521	-0.153744	0.604398	1.990874	0.333398	-0.422491	0.015719	-0.468067
RPL2A	-0.419332	0.276442	-0.760058	-0.89871	0.325755	-0.578866	0.052528	0.743008	-1.011078	0.788408	0.143465	0.13809	0.78184	-2.649207	-0.262381	-0.15862	-0.337718	0.441752	-0.246484	0.264159	-0.044375	0.570242	NA	0.435929	-3.842925	-0.13594	-0.213263	-0.437409	-0.235344	-0.423114	0.688255	-0.334672	0.647196	0.118085	0.224614
RPL33B	NA	0.100804	0.171388	-0.098393	-0.567145	-0.073497	-0.425198	0.610145	0.195831	1.088781	0.022995	0.233866	0.202791	NA	-0.143408	-0.536982	0.042243	0.324077	-0.321716	0.801889	0.310181	-0.429586	0.539511	0.84424	-4.800643	-0.201476	0.595023	-0.449376	-0.050313	-0.436893	0.367717	0.414021	-0.521164	-0.436711	-0.999226
RPL35B	NA	0.421054	NA	0.282284	-0.621908	-0.522872	-0.341362	-0.068553	0.207324	0.313197	0.258364	0.34103	0.056277	-1.513763	0.119692	-0.355984	0.240374	-0.073013	-0.089827	0.48049	-0.751481	1.011986	0.002792	0.928629	NA	0.068399	0.335127	-0.464503	0.072707	-0.654119	-0.36149	0.114092	-0.376854	-0.080948	-1.171771
RPL41B	NA	NA	NA	0.014994	-1.330488	0.119185	-0.290225	-0.161532	-0.662776	NA	0.188719	-0.571379	0.167617	-0.582435	0.855972	0.13981	0.188464	-0.078712	0.606049	0.443511	0.251562	-0.418781	NA	-0.693521	1.431819	0.180433	NA	0.270498	NA	0.321766	-0.867244	-0.116691	1.270673	0.173677	-0.0445
RPL43A	NA	2.920947	NA	-0.404371	0.506558	-0.013852	-0.400982	0.609461	0.080409	NA	0.339948	-0.365269	-0.799534	-3.031244	0.712537	0.316494	-0.165901	-0.288626	-0.458652	-0.440423	NA	0.498738	NA	1.757756	-10.405011	2.18522	-2.739628	-0.311215	NA	0.223294	1.020575	-2.274447	1.241729	-0.543239	-0.68155
RPL4A	NA	-0.161778	0.227306	0.380886	-0.110979	-1.371785	-0.556623	-0.109338	-1.051312	NA	0.106626	0.196798	-0.663224	NA	-0.445652	0.391697	0.025218	-0.40079	-0.595476	0.292236	-1.291571	0.098539	NA	-0.783084	1.155718	-0.678983	0.017081	0.588095	-1.487248	0.116084	-1.059708	1.744273	0.091397	0.399661	0.900387
RPL8B	NA	-0.148506	0.73219	-0.276579	0.234365	0.134072	-0.468808	-0.223714	0.17032	-0.17231	-0.692524	0.322202	NA	-1.181606	-0.682385	-0.98764	-0.406437	1.399149	-0.084111	NA	0.454714	0.11394	1.032363	0.178902	NA	-0.025363	NA	0.771258	-0.781721	-1.09933	-0.236409	0.310803	-0.831471	-0.528722	-0.025072
RPL9A	0.300512	-0.250808	0.475848	-0.082959	0.102978	-0.304107	0.010501	0.318523	-0.592608	NA	0.134425	-0.026323	0.462418	NA	-0.575432	-0.382937	-0.094205	0.7045	0.107774	0.164937	-0.161532	-0.040992	NA	-0.350214	NA	0.346968	NA	NA	0.155935	0.281681	0.074555	-0.299315	-0.29948	-0.067165	-0.173298
RPN10	NA	-1.859897	NA	-0.248584	NA	0.874227	-0.457806	0.100841	0.079873	-1.231493	0.392437	-2.179346	NA	-0.805891	0.347665	-0.21676	0.026121	-2.87979	-0.401252	-0.859896	-9.214578	0.02306	-2.63922	-1.250137	-2.235584	-0.609125	-4.745407	-0.010927	0.667844	0.441823	-0.618347	0.450352	-0.189076	0.187404	0.674235
RPN13	NA	0.53851	-0.453036	0.87851	-0.851517	-0.140567	0.146528	-1.245338	-0.692342	1.175768	0.307383	-0.13945	0.123864	0.356497	1.0873	0.266016	-0.469943	0.437813	-0.288118	0.621281	0.4564	-0.235746	NA	-0.729609	NA	-0.258786	NA	-0.837863	1.225776	-0.272049	-1.416186	-0.21317	0.439213	0.152268	-0.183618
RPN4	NA	-7.45043	NA	0.149877	NA	0.331968	0.482256	NA	-0.004632	-6.936876	0.374842	-0.202774	-0.671545	NA	NA	0.157816	-0.212252	-0.998963	-0.474426	-0.478324	-0.375288	0.06814	-0.331791	-1.326715	NA	-0.355847	-4.078411	0.195562	0.311793	0.486047	NA	-3.826304	1.134377	0.251765	-0.623689
RPO21	NA	-0.740392	NA	0.382446	-0.119504	0.657304	0.329541	0.320001	0.135758	0.068313	0.161872	0.030494	-1.113929	-1.445401	0.527358	0.145334	0.593649	NA	1.484901	0.095042	-1.223392	0.20602	-0.787343	-0.168953	NA	0.414141	-0.241238	0.251108	-0.078062	0.523777	-0.682944	0.707811	-0.349582	0.267619	0.296908
RPO41	0.307352	-0.300799	0.161594	0.484914	-0.941607	0.100069	-0.27828	0.586654	-0.199859	NA	0.252819	0.593698	-2.593939	-0.589259	-1.172495	-0.072316	-1.076091	-0.092863	0.516156	0.242528	NA	-0.126545	-0.61772	-1.83684	NA	0.290905	-2.255617	-1.260754	-0.021871	-0.281849	0.566336	-1.465715	1.719373	-0.196593	-0.716156
RPP1B	0.318729	0.73012	NA	-0.495339	-0.47801	0.12516	-0.435716	NA	0.940956	-0.977066	-0.157985	0.691761	-0.08873	0.085435	-0.608822	-0.756139	-0.492463	-0.489931	-0.164188	-0.053142	-0.441587	-0.223554	-0.03443	0.710293	NA	0.061792	NA	-0.395727	-0.342628	-0.117935	0.88183	1.319051	1.044721	-0.028715	-1.455688
RPP2B	3.868646	-1.026712	-1.156593	-0.937163	-2.772812	NA	-0.23	NA	-0.193833	NA	-0.369708	0.430128	NA	NA	0.038845	0.369263	0.061899	0.05516	-0.805927	-0.396113	-2.150083	-0.606878	0.215379	0.212556	NA	-0.278183	-1.844624	-0.357065	NA	0.020871	NA	NA	1.008537	-0.088761	-0.872862
RPS0A	NA	NA	2.413454	-0.083932	-0.465915	0.305532	NA	NA	0.026169	0.772855	-0.052141	NA	NA	-1.148556	-0.11578	0.244069	0.172261	0.21162	-0.372164	-0.054543	-0.586359	-0.56746	-0.488407	0.159444	1.869199	-0.112342	0.464669	-0.109258	NA	0.032504	NA	-0.234972	1.828556	NA	0.579437
RPS10B	0.055602	0.217297	0.765986	-0.637949	-0.593336	-0.519257	-0.01852	0.958306	-0.883412	0.946556	0.395855	0.158941	NA	-1.705816	-0.558102	-0.082733	0.060346	0.190254	-0.155658	-0.252157	-1.527562	-0.691454	NA	0.305486	NA	-0.946562	-0.372629	-0.365817	NA	NA	0.702237	0.466957	0.498218	0.124739	NA
RPS11A	NA	NA	NA	0.057262	NA	-0.131459	0.445336	NA	-0.115849	NA	NA	0.817216	-0.214165	NA	NA	0.488186	0.527127	-1.793463	-0.240148	-1.378536	NA	-0.883619	0.780838	-2.41005	NA	-1.387071	-2.275357	0.544204	0.163802	-0.30044	0.194073	-1.759707	-0.096219	NA	-1.332296
RPS14A	NA	NA	NA	NA	0.20167	-1.10864	-0.498155	1.561657	0.045708	-0.99098	-0.334956	NA	0.160603	0.382161	0.076757	-0.472171	-0.163467	NA	-0.695657	-0.13784	-0.183629	-0.625004	0.734668	-0.363691	NA	0.238848	0.423873	0.551339	0.140269	-0.441964	0.790116	-1.830831	-0.471982	-0.068503	0.139296
RPS16A	-0.894665	-0.290309	NA	-0.344968	NA	-0.888322	0.182258	1.414483	-0.053502	NA	-0.506593	0.938879	NA	-8.661578	0.263139	0.646935	0.188582	0.545632	-0.315508	0.486305	NA	0.042914	0.312669	-0.043135	-4.104191	0.485814	-0.061136	-0.845349	NA	NA	NA	-0.460115	0.254318	-0.749297	-1.566575
RPS19B	NA	NA	NA	-1.054403	NA	-0.704126	-0.425646	NA	-0.264837	NA	-0.545272	0.326219	-2.076316	NA	-0.559297	NA	-0.380184	NA	-0.571965	NA	NA	0.16691	NA	NA	NA	-0.518562	-2.910811	-0.245854	-0.954928	-0.144524	NA	-0.777193	NA	-0.56561	-0.626233

RPS21B	-2.321586	NA	NA	0.013005	-1.646489	-0.019061	-0.01727	2.417382	-0.752074	-2.146321	-0.013161	-0.82322	-0.845275	2.571782	0.173439	0.559421	-0.586935	0.574963	-0.062677	0.570455	0.987771	0.353816	NA	0.329575	NA	NA	-0.10989	-0.639235	0.658765	0.418182	2.536967	-1.180358	-0.583847	-0.879518	-1.206408
RPS23A	NA	0.537719	-0.192751	0.052698	0.866509	-0.154156	-0.25621	0.190259	-0.512032	0.024737	-0.389257	1.356138	0.477162	NA	0.083432	-0.233494	-0.849707	-0.283044	0.037026	0.45903	0.634356	-0.64566	NA	-1.264356	NA	-0.914532	-0.193314	0.084795	-0.544212	-0.110524	0.503794	-0.472168	0.35655	-0.428852	-0.572758
RPS28B	NA	-0.438953	NA	-0.850097	-0.189241	-0.887825	-0.320874	0.346404	-1.075433	1.090827	-0.392876	0.696084	NA	-0.581076	-0.738015	-0.078316	0.111396	-0.722423	-0.367749	-0.03719	NA	-0.284012	-0.154811	0.293272	NA	0.642403	NA	0.395745	1.114547	0.06069	-0.222735	1.702587	1.585035	0.391118	-0.698555
RPS29A	NA	0.127091	1.198587	-0.29657	-1.240092	-0.381624	0.337725	1.831639	0.623739	-1.455961	-0.470474	0.106755	-0.065785	NA	-0.055062	0.063111	-0.681626	0.268608	-0.88407	0.812438	-1.8389	-0.399029	NA	-0.046882	NA	-0.341279	NA	-0.553147	0.241484	-0.412472	NA	-0.120585	1.559177	0.201625	0.351513
RPS29B	NA	-0.019788	NA	-0.57728	-0.809432	-0.181088	0.166	NA	-0.220342	NA	-0.09072	0.558761	0.272519	NA	-0.381249	0.111404	-0.069425	-0.34632	-1.034309	-0.276241	-1.434261	-0.304616	NA	NA	NA	0.129916	NA	-0.488073	-0.928676	0.285127	1.156249	0.217205	1.302882	0.032664	-1.820531
RPS30A	NA	0.377296	1.228451	-1.013911	0.055062	0.049633	-0.198716	1.705603	-0.011448	NA	-0.244992	0.801998	0.047032	-1.347664	-0.710374	-0.02104	-0.819657	NA	-0.383663	0.070964	-0.633575	-1.090583	0.452541	-0.578664	NA	-0.736579	-0.172298	-0.135842	-0.873881	0.178057	1.27479	0.562935	1.139902	-0.068209	-0.506956
RPS4A	NA	-0.265123	-2.496754	-0.572405	-5.142485	-0.003719	-0.223861	0.183592	-1.127983	-2.054551	-0.091829	-0.854851	NA	1.26016	0.057708	0.157599	0.007173	-0.209219	-0.058852	-0.37017	-2.711539	0.366711	-0.228398	0.702103	-0.987377	0.447412	0.275277	-0.03166	-0.320777	0.620606	0.561498	-0.519186	0.573792	-0.001563	0.022006
RPS4B	NA	-0.129579	0.195633	-0.929541	-1.634588	-0.551343	0.225765	NA	-0.046084	-0.744044	0.05378	0.323115	-0.672714	NA	-0.353974	-0.455517	-0.409784	-0.061391	-1.231389	-0.013746	-0.363107	-0.531909	0.612964	0.70743	NA	-0.636326	-0.083439	-0.420764	0.326134	-0.109592	0.97817	0.142475	1.131811	-0.060555	-0.777975
RPS6A	NA	-2.598258	-2.598893	0.359338	NA	0.712324	-2.092567	0.398459	-1.128412	NA	NA	0.050199	-0.67982	-0.938212	0.054505	0.29923	0.305378	-1.464094	0.339838	-0.230581	-1.259368	0.036581	-1.076421	-1.210624	-2.703206	-1.672814	-3.299122	0.066455	-0.30542	0.419148	NA	-2.358888	0.559692	0.703174	0.282593
RPS6B	NA	NA	NA	-0.75179	-1.054134	-0.056065	0.448326	NA	-0.121753	NA	NA	0.637435	NA	-5.347375	NA	0.486057	-0.24154	-0.351245	-0.625502	-0.074405	NA	NA	0.2967	0.03279	NA	0.185079	-2.865707	-0.487444	NA	0.808018	NA	-0.233244	0.098408	0.046225	NA
RPS8A	-2.047751	0.208346	NA	0.680349	-2.689343	0.996168	-0.831637	-0.395116	-0.552451	NA	-0.182782	0.022909	-0.415238	-1.778258	1.085851	0.63583	-0.687625	NA	-0.497877	-0.764205	NA	0.866148	0.835898	0.476212	NA	-0.111886	-1.484692	-0.774435	0.467849	-0.53757	NA	-0.292787	0.739101	NA	1.387853
RRD1	NA	-0.164973	-0.664804	0.258618	0.39336	0.448722	0.416816	1.008526	-0.35517	0.264155	0.008278	-0.103391	-0.954502	1.450346	0.318994	0.30832	0.083401	0.710775	0.816025	0.649913	-2.710861	-0.014119	0.124106	0.388701	NA	-1.032241	-0.85119	-0.752908	-0.918113	-0.054039	0.447547	-0.219676	1.294933	0.587853	0.616847
RRD2	NA	-1.198373	1.423211	0.964719	NA	0.270063	0.0031	0.115633	1.392529	-1.786265	0.493099	1.524443	-0.940565	NA	-0.745078	-0.100865	0.203677	-0.414811	0.635271	0.055872	NA	0.750846	NA	-0.530652	NA	-0.303188	-1.401261	0.267746	0.153711	-0.790392	-0.096009	-0.418928	NA	0.151365	0.256576
RRM3	NA	-4.420839	0.37899	0.298969	NA	0.482751	0.23524	-0.96575	0.469263	0.133882	-0.153583	NA	NA	NA	-1.453746	-0.327348	0.258006	1.393394	0.301436	0.326384	-0.77262	-0.383293	NA	1.66268	-3.102512	-19.852541	NA	-1.029616	NA	0.273216	-0.392449	1.019492	0.38931	0.760259	0.152211
RRP6	NA	-2.658579	-2.546253	-0.540962	-0.319514	-0.322024	NA	NA	NA	NA	0.134852	-0.96547	0.097182	NA	0.045515	0.130664	-0.320364	-1.203938	-0.856014	-0.086189	-2.490517	0.751852	NA	0.179306	NA	-2.099101	NA	0.331836	-1.862329	0.458798	0.915628	-7.290427	1.168407	0.165835	-0.979978
RRP8	NA	-0.541955	1.516845	-0.503817	NA	-0.321486	0.426396	NA	0.068464	-0.388994	NA	-0.082451	0.070225	-0.422827	NA	-0.025283	-0.311787	0.637498	-0.113741	-0.280567	-1.340844	0.393699	NA	1.699365	NA	-0.223594	-1.228009	-0.302413	-0.259666	0.815115	NA	-0.198756	1.738888	NA	-0.185535
RSA3	NA	-0.438436	NA	0.142451	0.189587	-0.600993	0.331663	1.828065	-0.648362	NA	NA	0.001531	NA	NA	-1.199967	0.607772	-0.227558	0.189743	0.299705	0.294495	-1.04029	-0.499929	NA	0.516451	NA	-0.050156	-0.614447	-0.632923	-1.029706	-0.346019	0.676469	NA	0.486825	-0.882474	-0.61351
RSC3	NA	NA	1.172038	0.347977	0.639187	0.035591	-0.81804	0.415027	-0.929468	0.259255	0.264897	-0.59114	-0.473515	NA	-0.361031	-1.133843	-0.786055	NA	0.217524	0.67217	-0.80144	NA	NA	-0.685854	NA	-0.132339	-0.424131	-0.241627	0.889149	0.134915	-0.04864	NA	-1.951	0.14434	-1.124842
RSC4	-1.427477	0.223905	0.884361	0.046167	0.194585	-0.267477	0.037604	0.115913	-0.880146	-1.115783	-0.019197	-0.279368	-1.541259	NA	0.189445	-0.297189	-0.519642	0.194955	0.199184	-0.928973	-1.717871	-0.827758	NA	-0.3701	-1.67803	-0.23652	0.420318	-0.416671	-0.057806	0.250234	0.897076	0.498128	0.580029	-0.572171	0.209918
RSC58	0.486639	-0.114089	NA	-0.638293	0.280124	-0.013694	-0.563948	0.993998	-0.951183	0.7623	0.052943	0.25008	-0.489024	0.161296	-0.267398	0.013629	0.076632	0.359604	0.207754	NA	-1.333458	0.552297	-0.428938	-2.119677	NA	-0.140461	NA	-0.671707	-0.186753	0.705033	0.516788	0.339577	0.654686	-0.510999	NA
RSP5	-0.766003	-2.091696	-0.163342	-0.456502	0.081925	0.068947	-0.083667	0.87861	-0.681374	NA	0.26979	-0.039107	-0.574215	0.694598	-0.69379	0.24248	0.548712	-0.243716	NA	0.639331	NA	0.206048	NA	-0.487006	NA	-0.229194	-0.08746	0.287514	0.524173	0.133598	NA	0.273245	-0.118403	0.06206	0.270387
RTF1	NA	-1.429367	2.467868	0.244714	-1.035651	0.476052	0.558194	NA	0.787049	NA	0.340989	-1.482076	-0.824387	NA	0.339478	0.542432	0.564212	-1.029543	0.419486	-0.256207	-1.531874	0.454358	0.056394	-8.195646	NA	1.422869	-4.375709	NA	0.045251	0.698701	-1.195399	NA	NA	-0.19106	-3.626489
RTG2	NA	-0.620306	NA	-0.008312	NA	-0.204571	0.252139	NA	0.714986	-1.07709	-0.011779	0.032771	-0.623577	NA	-0.115218	-0.007145	0.087991	-0.005736	0.74517	0.64032	-0.256242	-0.421922	NA	-1.489576	NA	0.10772	0.361023	NA	0.269445	0.002123	-1.234706	-0.165126	0.275657	0.224085	-0.257977
RTG3	NA	-0.438073	-0.8779	0.258924	-0.295593	1.169184	0.180342	-0.332256	0.243824	-0.954687	-0.005381	-0.274062	0.299608	-2.097832	0.3561	0.12302	0.1751	-0.138282	0.181633	0.081387	-0.029006	0.846667	-0.09234	-0.615005	NA	0.495472	0.102062	0.586243	1.02325	0.304507	-0.162236	-0.335769	0.124463	0.37953	0.596327
RTK1	NA	-0.350913	NA	1.009173	-1.457157	-0.217984	-0.138937	NA	-0.312117	-0.959856	0.399767	0.276725	0.149959	-1.461139	NA	0.241562	-0.209059	0.847503	0.179806	0.964747	0.262153	0.61163	NA	-0.778772	-0.329219	0.262635	0.284388	-0.216443	-0.367009	0.130413	-0.271927	0.229068	0.232083	0.417592	-0.233376
RTN1	-0.191435	-0.095076	-0.382202	-0.243427	-0.215054	-0.251256	-0.541791	-0.813664	0.532698	0.098952	0.085061	0.226164	0.158372	-1.239147	0.020395	-0.528154	0.198123	1.046058	0.304499	-0.052659	0.687341	NA	NA	0.245285	-6.820214	0.177278	0.062427	-0.73024	-0.187918	-0.16152	-1.115096	-0.09068	0.177996	0.165749	-0.928343
RTN2	NA	0.104915	0.0972	-0.195414	-0.078708	0.054134	-0.339553	-0.334958	0.3265	1.598215	-0.025702	0.543801	0.074086	-0.822294	-0.527384	-0.137433	0.151133	0.10906	0.698916	-0.264464	-0.169463	0.589395	NA	0.041552	NA	0.638097	-0.027949	0.086667	0.080691	0.000187	-0.694971	-0.617993	-1.226239	-0.224536	1.201941
RTR1	NA	-0.906467	-7.536711	0.396908	0.049506	-0.341253	0.201368	1.962744	0.077598	-8.820986	0.285076	0.16503	-0.184991	-2.092751	0.126834	-0.162483	-0.28852	0.058778	NA	-0.443172	-1.370854	0.651318	-1.75604	0.888514	NA	-0.443181	-0.900636	-0.085682	0.649793	0.318533	NA	-4.690572	0.748659	-0.140323	-0.228663
RTS1	NA	-2.616225	-2.973322	0.688726	NA	0.572472	NA	2.402142	NA	NA	0.400858	-0.002835	-0.536224	0.381342	0.29459	0.67597	-0.206414	0.496479	0.316752	0.101013	-2.059753	0.293837	0.103561	-0.633865	NA	-1.655741	-3.164052	0.091466	0.688147	0.142855	2.185705	-0.614937	0.645275	0.346247	-0.410481
RTT10	NA	NA	NA	0.370879	NA	1.100824	0.551909	1.514027	0.689613	0.497981	-0.377267	0.751032	0.108947	NA	-0.003861	-0.042144	-3.444246	-0.723145	-0.289459	0.382475	NA	0.563751	-0.47552	0.604081	NA	0.288235	-0.452619	0.690235	-0.794398	-0.504974	1.063819	-0.393519	0.09212	-0.755153	0.183467
RTT101	NA	NA	1.598439	1.123683	NA	0.819456	-0.327494	0.520924	NA	NA	0.656434	1.909288	NA	NA	-0.930425	NA	NA	0.808284	0.513341	NA	NA	0.041085	NA	0.830725	-2.673399	NA	NA	0.515326	-0.795465	-0.571983	-0.108347	0.909724	0.79227	0.338544	NA
RTT102	0.258866	0.244785	-0.64109	-0.353988	0.138637	0.017482	0.095876	0.178142	0.170715	-0.16548	0.381687	-0.195378	0.44882	-0.770323	-0.267672	0.311304	-0.018029	-0.113348	-0.052074	-0.264876	-0.123526	-0.968582	NA	1.185279	NA	0.333439	-0.450503	0.180156	0.142018	0.59765	-0.062609	-0.004322	0.236133	0.147958	-0.418712
RTT103	NA	-0.737599	-10.657348	-0.507875	0.493932	-0.071003	0.257569	-0.737815	0.436809	-7.18187	-0.051515	-0.647868	0.200627	0.127974	-0.06287	-0.607424	0.736569	0.395399	0.440872	-0.000373	0.909105	NA	0.701789	-1.038782	NA	0.40118	-0.209498	0.645752	-0.983584	0.000739	NA	NA	0.595719	0.507592	0.474226
RTT106	NA	0.061179	NA	-0.744729	0.065331	-0.090771	0.36952	-3.47241	0.591192	-0.992164	-0.120043	0.146587	-1.667433	NA	-0.359222	NA	0.08617	0.568328	-0.136884	0.056627	0.052544	0.622297	NA	0.170567	NA	-0.07622	0.857139	-0.670742	-0.374527	-0.028083	-3.078604	-0.480838	NA	-0.631985	-0.19051
RTT107	-0.392346	-0.759618	0.593584	-1.292272	-1.222681	0.215783	-0.043534	-1.641601	0.556287	-0.079162	0.405801	1.270448	-4.196907	-5.123468	0.473971	0.780323	-1.032148	-0.663837	-1.971147	-0.414884	0.419443	0.318343	NA	0.64685	NA	-2.728828	-0.78263	0.352296	-3.166156	-0.55995	-1.844855	0.543265	1.576849	0.184021	0.813544
RTT109	NA	2.520689	-1.283254	1.168624	NA	1.010029	0.350086	-10.466854	NA	NA	0.419834	2.209616	NA	NA	-0.035387	NA	NA	0.376905	-1.616301	NA	NA	-0.29449	-4.204058	0.010173	-3.446751	1.190107	NA	-0.197358	-0.273562	0.293722	-4.007789	-0.630244	1.774987	0.68371	NA
RUD3	NA	-0.02799	-7.136971	-0.705745	0.475258	-0.624646	0.261294	0.612363	-0.065258	0.258208	-0.124141	0.549261	0.625473	-1.094691	-0.142927	0.143182	-0.385585	0.4397	-0.177882	0.345582	-0.954008	-0.432959	NA	-0.474763	-1.510453	-0.092116	-2.447824	-0.703512	0.107772	0.133411	1.767091	-0.841306	-0.196973	0.412069	-1.319279
RVS161	-0.259555	-1.731263	-3.173911	NA	-3.243371	-0.211346	0.224611	0.506806	1.249359	-0.978387	-0.150403	NA	-0.365357	-0.660566	-0.294185	0.609076	0.372191	NA	0.081271	-0.138044	-0.463789	-0.2586	0.42821	1.126161	-5.687911	-0.06363	-1.5332	-0.975567	-0.690278	0.023927	0.256916	-0.890144	-0.029015	0.391043	0.734078
RVS167	NA	-1.605003	-0.581222	-0.844202	0.256073	NA	0.488855	0.264874	0.11915	0.384253	NA	0.360156	NA	NA	-0.746403	-0.024611	0.366225	NA	-0.307845	0.566373	NA	-0.547413	0.266673	0.075938	NA	-0.712283	-1.093161	-0.498061	-0.591306	0.273379	0.595489	NA	NA	-0.179398	-0.840622
RXT2	NA	-3.572407	-7.182685	-0.322323	-0.22956	-0.248023	0.111949	1.259826	-0.128873	NA	NA	0.52809	-1.07012	-2.625165	0.761909	0.080338	0.673518	-0.186862	0.055859	-0.142498	-3.086719	0.021459	NA	-0.897304	NA	-0.204678	-5.21977	0.09283	0.276022	-0.199121	1.127763	NA	0.291804	0.480326	-0.046948
RXT3	NA	0.211397	NA	-0.743882	0.436661	-0.473085	0.040341	NA	-0.321399	0.803677	-0.13839	0.178245	0.150301	-0.851431	-0.075552	0.018686	0.285061	0.045012	-0.108789	0.457159	-1.07442	-0.641973	0.25554	0.9105	NA	0.161803	-0.221532	-0.462293	0.471133	-0.202168	1.040339	0.187546	0.033664	0.181959	-0.206519
SAC1	NA	-1.257967	0.908677	-0.743368	-0.389533	0.010419	0.409754	NA	-0.04381	0.049089	0.467727	0.235493	0.154396	NA	-0.11477	-0.090998	-0.030732	-0.045583	0.11316	NA	-0.847912	-0.19083	0.042609	-1.039505	NA	-1.213408	-0.960077	-0.124607	NA	0.353771	2.08017	0.188483	NA	0.129167	-0.06474
SAC3	4.17117	-3.160259	-0.102015	0.233831	-3.591878	0.243745	0.66264	NA	0.553108	NA	0.234067	-0.161899	-3.830838	NA	NA	0.239088	-0.325858	-0.678077	0.52339	0.158182	NA	NA	NA	1.344564	NA	-0.87963	-4.730796	-0.330467	-1.065128	0.439243	-5.31998	-6.70139	0.43572	NA	-0.717033
SAC7	-2.301033	-0.9836	-2.441061	0.259811	-0.335938	NA	0.384888	-3.69692	0.017498	-0.40405	0.730977	-0.115148	0.067013	-4.329826	0.680922	0.283728	0.679045	0.278949	0.332765	0.181826	0.052226	0.850161	0.804153	0.686788	NA	0.462619	-0.713244	0.418325	0.253216	0.581347	-1.59302	NA	-0.332972	-0.421292	0.51642
SAE2	0.516692	NA	0.550644	-0.069445	NA	-0.198368	-0.254393	0.640376	NA	NA	0.110601	-0.441645	NA	NA	-0.983099	NA	NA	0.747616	0.330469	NA	NA	0.399497	NA	0.249721	-3.682728	NA	NA	NA	NA	-0.197404	1.044454	0.326088	NA	0.143992	NA
SAF1	0.227026	-0.128632	NA	0.353155	0.704895	-0.911547	-0.498602	-0.82665	0.226997	0.319513	0.130466	-0.053552	0.509557	0.902788	-0.601861	-0.765679	-0.132157	NA	-0.178093	-0.371177	NA	-0.654119	NA	0.034273	NA	0.186083	0.286081	-0.345727	0.201502	-0.246808	-0.195566	0.805223	0.276946	0.062593	-0.745258
SAK1	-0.340643	0.790899	0.07994	-1.120159	-0.311019	0.043776	0.585242	-0.313955	0.315353	0.254841	-0.412801	0.261034	-0.435589	1.350396	0.315435	-0.008861	-0.531509	NA	NA	0.627736	NA	0.119778	NA	0.604688	NA	1.004403	-0.199524	0.223023	1.330194	-0.25979	NA	-0.308793	-0.20642	0.882965	-0.313831
SAM1	NA	0.223412	-0.028241	-0.444904	0.436167	-0.354156	-0.506266	-0.328384	0.2125	NA	-0.627581	0.700842	0.195041	NA	-0.209671	0.387188	0.07681	0.970578	-0.155344	-0.497239	NA	-0.070658	NA	0.697754	-1.931939	0.312365	0.17387	0.236518	0.310049	-0.045667	0.047754	0.346549	-0.568544	-0.092805	0.622776
SAM37	NA	-5.392783	-4.034112	0.289711	-6.365705	0.183933	0.426268	-0.980892	0.412935	NA	0.26225	-0.111214	-2.856578	-2.045577	-0.363505	-0.411156	-0.749202	-1.550343	-0.105188	-0.757142	NA	0.745006	NA	NA	NA	-0.788479	-3.651586	-0.519026	0.189527	1.227722	NA	-4.136517	1.099484	0.049706	1.050499
SAP155	NA	-1.194742	-0.872161	-1.031443	-1.380716	0.319137	-0.547626	0.716196	0.1427	0.289127	-0.103559	-0.09456	0.563956	-2.361621	0.069701	-0.170926	-0.295866	-0.137344	-0.135884	0.224452	0.165133	-0.391103	0.146588	-0.114916	NA	-0.127427	0.269515	0.419381	-0.573894	-0.080385	0.76983	0.135893	0.170744	0.269228	-0.482152
SAP185	-0.725555	NA	0.423781	0.445366	0.700082	-0.006228	0.542176	1.56926	0.419406	1.275581	-0.023862	0.119625	-0.511467	0.762213	-0.725841	0.074691	-0.139961	0.17441	-0.274984	-0.244423	0.023159	-0.079609	-0.277588	0.399404	NA	NA	0.106385	0.192081	-0.703514	0.37129	0.533644	-0.295136	0.849285	0.288942	-0.136565
SAP190	5.131547	0.004681	-0.60235	0.149904	1.10755	-0.103835	-0.283718	-1.21251	0.595874	-0.186769	-0.085298	0.904077	0.288714	NA	0.28957	0.004943	-0.055178	0.462571	0.250047	-0.140915	0.231085	0.263365	-0.232535	-0.647421	0.883832	0.433855	-0.396701	-0.275847	-0.801042	0.026975	-0.591673	0.193235	NA	-0.094944	1.128907
SAP30	NA	-4.649847	NA	-0.393124	-0.180024	-0.423215	-0.169257	1.119066	0.101975	NA	0.176882	0.227622	NA	NA	0.453515	-0.194713	0.012009	-0.674699	0.043757	-0.70805	-2.205982	0.348581	NA	0.687071	NA	-0.110309	-5.493132	-0.505185	NA	NA	-0.321046	NA	0.991227	0.745218	NA
SAS2	-0.182153	-5.053267	-9.884834	-0.089895	0.864569	0.283501	0.187596	0.316785	0.894416	-2.283567	0.497029	-0.40374	NA	1.181214	-0.155783	-0.239552	-0.217115	-0.082554	0.200393	-0.173278	0.015561	0.8848	0.054919	0.928432	NA	0.823816	-0.948224	-0.444334	NA	NA	0.39234	-0.056821	NA	0.235952	0.138993
SAS3	-4.79422	-2.253978	-0.845388	0.613662	0.176334	0.247459	0.096872	1.752365	0.447583	-0.239798	0.343615	0.191499	-0.290203	NA	1.042696	0.397415	0.209116	0.493897	-0.100941	-0.793395	0.047501	0.656388	-0.054875	-1.107562	-12.708398	0.252926	NA	NA	0.146954	0.569864	0.233682	-1.220422	NA	-0.283427	-0.363324
SAS4	NA	-4.767736	-12.249568	-0.169901	NA	-0.295229	0.143536	0.25419	0.188626	NA	-1.45434	0.044063	NA	NA	0.13598	0.383345	0.082676	0.06057	0.87607	0.476059	NA	NA	0.060425	1.544656	NA	0.101977	-1.128648	0.38202	-0.195494	-0.753451	NA	-1.155374	-1.385509	NA	-0.943007
SAS5	NA	-2.780765	-11.879326	0.67878	0.230736	0.9475	0.639797	0.359813	0.18176	-2.340876	0.59405	-0.827789	NA	NA	-0.190949	-0.600399	0.327595	0.29953	0.16614	-0.717378	0.656695	-0.02176	NA	0.6756	NA	0.330514	-0.071674	-0.158802	-0.647736	-0.169463	0.061786	-0.363473	0.058072	-0.512758	-0.031132
SAT4	3.504624	-0.620461	-1.752048	NA	NA	-0.700923	0.50349	-0.72915	-0.459703	2.173876	-0.309167	NA	-0.082331	-1.107391	0.275654	1.203827	-0.132693	NA	-0.189913	0.725565	0.258265	-0.143985	NA	NA	NA	-0.255738	0.469433	-0.152287	-1.258763	0.199622	NA	-0.672252	0.080135	-0.091422	-0.516077
SAW1	-3.358175	0.175889	0.664107	0.723946	-0.118652	0.409375	-0.272297	-0.644166	-0.830113	-0.187143	-0.098075	-0.798294	0.691867	-0.84825	-0.359674	0.877077	0.419977	-0.510826	0.21047	-0.470597	0.588744	0.151432	NA	-0.05124	0.518585	0.514996	0.564904	0.008926	-0.629236	0.32653	-0.295054	-0.294029	-0.228876	-0.233292	0.868557
SCD6	0.066598	NA	-0.308611	-0.150918	-0.157288	-0.027412	-0.32833	-0.044858	-0.294266	0.419752	-0.234211	0.554708	0.42075	NA	0.128562	-0.028174	0.061218	1.221387	0.386066	0.146089	0.007117	-0.432023	NA	0.160302	NA	0.547015	0.907773	-0.224023	0.066877	-0.494632	0.133107	0.440889	-1.356318	-0.462599	0.433921
SCJ1	NA	0.102956	-0.000544	0.127072	-0.02056	0.484023	-0.105418	0.064558	-0.447174	NA	-0.00732	0.31555	NA	1.13407	-0.182023	-0.044377	0.300806	-0.814543	0.194613	0.549158	0.457164	0.361652	0.676879	-0.55708	NA	-0.312335	-0.482746	0.176541	NA	NA	-1.300349	0.418874	-1.35528	-0.278441	NA
SCS2	4.606228	-1.709677	NA	0.539138	-2.284113	1.525403	0.213425	-0.682651	-0.684967	NA	NA	0.304094	0.270789	NA	1.156955	1.637617	0.51183	-0.064708	NA	0.262783	NA	0.972888	NA	1.21005	NA	-0.460958	-1.032016	NA	NA	1.432247	NA	0.921409	NA	0.555017	0.922216
SCS3	-1.526778	0.257018	NA	0.955164	-0.232939	0.027074	-0.49553	-0.965967	-1.346751	0.856616	NA	-0.368453	-0.181891	NA	0.457882	0.530383	-0.035468	0.206879	0.021701	0.049673	-0.005447	0.128474	NA	0.487781	-2.245032	0.3585	0.008321	NA	-0.123236	0.200939	-0.960615	-0.379697	0.097217	0.433726	0.712808
SCS7	-7.020482	-3.23833	-8.176182	-0.176754	-1.561944	-0.015167	0.873797	-2.933665	0.686755	-3.316042	0.087085	0.45923	NA	NA	0.125001	0.521086	0.661189	-1.111434	0.628763	-0.432091	-1.491207	0.458455	NA	-0.542597	NA	0.250746	-2.318883	-0.153573	NA	NA	-6.046393	-1.437365	0.013884	-0.095624	NA
SCT1	0.553889	0.197948	0.52166	-0.716969	-0.310154	-0.544077	-0.366128	0.15506	-0.035147	0.582622	-0.502004	0.210174	-0.200481	0.87821	0.010935	-0.078877	0.060073	0.545109	0.68703	0.332894	0.020162	-0.537134	-0.819186	-0.793842	NA	0.593227	-0.316437	-0.551765	1.145353	0.06553	0.113106	0.404051	0.038529	0.27626	0.286489
SDC1	-2.003146	-3.659772	2.023942	0.401404	-0.619793	NA	-0.091106	-6.867658	0.399751	NA	0.692574	0.145566	-3.247516	NA	0.219197	0.616402	0.165664	0.213299	0.440661	-0.216271	-3.201759	0.106724	-1.271905	-0.395374	NA	0.208007	-2.910983	-0.744443	0.834877	0.144026	-3.530031	-5.872883	-0.135424	-0.13828	-0.073624
SDS3	-1.802148	0.477841	0.870996	0.378759	NA	-0.376301	-0.079612	0.726213	0.967343	1.683729	-0.406094	0.202536	0.216614	-0.015679	0.492981	-0.807851	-0.412873	0.156663	0.78671	0.543578	0.220134	0.299647	NA	-0.23225	-5.181541	0.445945	NA	-0.589847	-1.123435	-0.882228	0.810907	0.334552	-2.218397	-0.47653	-0.558827
SEC22	NA	NA	NA	1.118911	-0.025052	0.75468	-0.535818	-0.766883	0.85675	-5.550411	-0.095533	-1.326457	-1.264855	NA	-0.152387	-0.026027	1.045127	0.039508	1.466234	-0.906394	-0.7201	-0.448094	-1.394829	NA	NA	0.093902	-5.492012	0.405117	0.435298	0.300898	-0.527228	NA	NA	0.057708	-0.023975
SEC28	NA	NA	NA	-0.437129	1.707661	0.699754	-0.33178	-1.379366	-0.200641	NA	-0.243179	0.345911	0.542714	-5.160983	-1.048809	-0.60681	0.440917	NA	-0.5531	-0.014581	-0.668014	0.109118	0.234669	-2.489649	NA	0.429736	0.251155	0.311906	0.903107	-0.419771	-2.403195	-3.101718	0.6238	-0.191646	-0.242449
SEC66	NA	0.252873	1.157598	-1.149532	0.777928	-0.027244	0.111382	1.93273	-0.716702	-0.195248	NA	0.24932	0.435324	-0.507172	-0.624037	-0.034844	0.118876	0.169832	-0.587628	-0.504885	0.553168	0.208204	0.581187	0.88767	NA	-1.262701	0.111085	-0.69952	-0.265875	-0.077894	1.721773	-0.008793	-1.999167	-0.346955	-1.290196
SEC72	0.53686	0.249575	-0.461485	-0.400526	0.77003	-0.977027	0.253062	-0.294911	-0.693335	0.98893	0.144979	-0.161609	-0.376084	-0.068832	0.238608	0.101689	0.568838	-0.901111	-0.070149	0.165968	0.262071	0.045504	1.052371	0.07817	NA	-0.696856	0.320827	-0.265541	0.471213	-0.049199	0.547066	0.496139	0.079558	-0.219931	-0.804097
SED4	NA	0.807838	-0.975585	NA	-0.066232	-0.04828	-0.791179	-0.410448	0.311549	1.275621	0.199605	0.121213	0.227732	-0.471336	0.187295	0.213541	0.349911	NA	0.408395	-0.427494	0.25525	-0.128669	0.542327	-0.127312	NA	-0.700544	0.001554	-0.140976	1.15394	-0.320434	0.014356	-0.125157	0.505361	-0.075699	0.245531
SEF1	NA	0.325007	-0.921273	0.057088	0.110318	-0.545707	0.900849	-0.306068	0.317417	1.789008	-0.177533	0.748857	-0.157863	-1.673378	-0.252557	-0.003021	0.496522	-0.542734	-0.098804	-0.149098	-0.995731	0.404595	NA	0.15989	NA	-0.283787	-0.95604	0.167998	0.317133	0.845889	-0.382327	0.239549	-0.23799	0.032219	0.16132
SEM1	NA	-2.65313	-3.461176	0.150769	-1.566499	NA	0.161127	0.27564	0.73589	NA	0.135769	-0.031147	-1.412093	NA	-0.093543	-0.940627	0.333787	-0.070854	0.544797	0.350071	-7.217322	0.717637	-1.542834	1.83658	NA	-0.788781	-2.480638	0.138267	0.585617	0.402024	-0.373989	NA	0.755143	0.172801	-0.881479
SER1	NA	0.737867	0.392366	-0.549465	0.394906	-0.742603	-0.336629	0.280386	-0.682844	0.183724	-0.352276	0.432109	0.152492	-2.585756	-0.68963	-0.715342	-0.45673	0.147431	-0.134227	-0.0724	0.677511	-0.075465	NA	-0.18105	NA	0.234417	0.788433	-0.34282	0.73873	-0.001962	0.307791	-0.440074	0.712322	1.021171	-0.179741
SER2	NA	0.185008	-1.008258	-0.21224	0.871497	0.527587	0.104137	0.673108	1.236395	-2.691863	-0.65689	0.613309	-0.118284	-0.245152	0.025329	0.803601	0.081055	-0.524396	0.390497	0.315674	0.030978	-0.102858	NA	0.800721	NA	0.653298	-0.170975	0.74844	0.77933	0.279389	0.352174	-0.034867	-0.642081	-0.020825	0.72334
SET2	NA	NA	-6.930672	0.292889	-0.689941	-0.201969	0.618404	NA	-1.103468	NA	-0.769537	-0.962481	NA	NA	0.461852	0.151077	0.53208	0.466817	0.116988	NA	-1.12172	0.228195	0.546812	NA	NA	0.081837	-1.847074	0.025818	0.295045	0.361526	NA	-5.011612	-0.352759	-0.052355	-0.269637
SET3	NA	-0.98578	0.089022	-0.927593	0.327889	-0.150182	0.5886	-0.206124	-0.632942	NA	NA	-0.478225	0.529496	NA	0.063213	-0.022264	0.574123	NA	-0.70807	-0.375708	0.686873	0.889536	NA	NA	NA	0.551101	0.01567	0.264355	-0.302814	0.103685	NA	-7.44738	1.047216	-0.022991	1.023508
SET4	0.05852	NA	0.169185	-0.447607	-0.521466	-0.446807	0.115931	0.313915	0.334548	0.9547	0.111008	-0.157464	-0.174359	-0.518595	0.57207	0.188173	-0.363921	0.27966	0.356754	0.317168	0.40214	-0.547479	NA	-1.233019	NA	NA	0.162625	0.092853	0.37028	-0.367154	-0.183886	0.061158	-0.112281	-0.282642	0.241035
SET5	NA	0.143445	NA	-0.614408	0.439701	-0.793446	0.421318	-0.201656	0.104687	1.659684	-0.363582	-0.501395	0.495101	-0.455999	-0.395596	-0.189009	0.00702	1.095296	-0.216067	-0.093127	1.066381	-0.709082	NA	0.35884	NA	0.387778	0.345546	-0.293132	0.589352	-0.526913	0.803262	-0.083714	-1.279378	0.011655	0.510612
SET6	0.522287	0.32216	0.317303	-0.27002	NA	0.189503	-0.129902	1.252529	0.116687	0.065357	0.220144	-0.208829	0.044076	-0.470666	-0.295458	-0.683221	-0.605649	0.89654	0.300395	0.1315	0.818433	-0.106126	NA	0.341955	NA	0.001247	-0.055333	0.118313	0.080254	-0.014974	1.318019	0.095381	-1.129989	0.022048	-1.398413
SEY1	NA	0.249283	-0.083728	-0.143496	0.138458	-0.013588	-0.278212	-0.926802	-1.015576	0.982996	-0.046827	0.211189	-1.005434	0.05722	0.188165	0.163859	-0.544077	-1.170597	-1.27716	0.009971	0.062311	1.35656	0.662843	1.19798	NA	0.674295	-0.231351	0.371182	-0.088358	0.216092	-0.477452	-0.641073	0.730078	0.330598	0.214826
SFB2	NA	-0.272446	-0.668658	0.100486	-0.060415	-0.442759	0.610628	-0.109376	1.014059	-2.04889	0.073091	0.332512	0.139783	NA	-0.082264	-0.019832	0.646942	-0.215989	0.970873	0.06619	NA	0.773272	NA	-1.228347	NA	-0.143135	-0.345483	-0.026342	0.523838	-0.034914	-0.007971	-0.342887	-0.215655	-0.255673	0.107478
SFL1	NA	-2.663969	NA	0.482282	0.203303	0.270215	NA	-0.960355	1.325622	NA	NA	-0.159071	-0.346645	-0.553865	0.123954	1.112135	-0.649441	NA	-0.223849	-0.715462	-0.402019	0.002631	NA	0.655455	NA	0.313624	-3.80279	0.914425	-0.096837	0.078532	-0.638382	-0.496285	-1.448152	0.058573	1.227001
SGF11	NA	-0.767968	1.046696	0.314421	-2.959895	0.825297	0.36182	0.716842	-2.14582	0.648169	-0.028818	-0.376257	-0.82055	-2.014202	0.810351	0.566027	-0.992438	-0.481325	0.05564	-0.397398	-1.397394	-0.879634	-0.041438	0.630947	NA	-1.002419	0.500015	-0.113248	0.065757	0.018953	1.271641	0.079576	0.203445	0.410864	0.106185
SGF29	NA	NA	1.966016	NA	NA	0.012154	0.534396	-1.37566	-0.586103	0.159452	0.458933	NA	-2.038421	-1.740684	1.301459	0.496421	0.257034	NA	-0.045648	0.256747	-2.352776	0.285457	0.752873	1.638508	NA	0.613673	-1.081084	-0.462436	0.294303	0.389184	-1.328275	-0.343042	1.077559	-0.039409	-0.227786
SGF73	NA	-0.313192	0.135951	0.108874	-3.722791	-0.079283	-0.912084	NA	-2.970799	-1.574687	1.056634	-0.447722	-1.024927	-2.942281	-0.696759	-0.442131	0.504835	-0.770267	0.364909	-0.163105	-2.439632	-0.031385	0.138149	0.627201	NA	-0.042696	-0.518822	-0.336808	0.760894	0.247932	1.424496	0.47279	-1.88529	0.028094	-0.76269
SGM1	0.513973	0.263318	0.46428	0.000948	-0.07273	-0.495074	-0.199352	-0.184981	0.612563	0.214886	-0.33824	-0.490789	NA	-0.268303	-0.288743	-0.402632	-0.034098	0.585442	0.735747	-0.286688	1.011705	0.197368	0.086336	-0.332658	-5.999093	0.288659	0.388117	0.003952	1.244671	0.017826	-0.444126	-0.139779	-0.473337	-0.213318	-0.674635
SGN1	-0.1159	-0.664763	-0.963037	0.249857	-0.355927	0.683894	-0.096189	NA	-0.952647	-0.225188	-0.035189	0.243538	-0.253311	NA	-0.313002	0.38285	0.533017	0.088148	0.36362	0.104593	0.114388	0.30114	0.465876	-0.493828	NA	-0.40508	-0.704571	0.336002	NA	0.593199	-0.328824	0.252092	0.437403	0.221243	1.594662
SGS1	NA	NA	-0.178567	-0.704503	0.823046	-0.842707	0.189418	0.249105	0.373809	1.546064	0.233809	0.101118	NA	-0.750033	0.040494	0.385915	-0.660861	1.469287	0.643234	0.376459	-0.943442	0.053691	NA	-0.802027	NA	0.316656	0.24237	-0.01793	NA	NA	-0.0337	-0.075633	-0.524795	0.081437	NA
SGT1	NA	NA	NA	1.018012	-0.072658	0.768363	NA	0.721059	NA	NA	0.551629	0.181826	-0.914067	-0.633801	-0.358878	0.451368	0.317497	-0.90461	0.337765	-0.853621	-1.938997	1.066334	NA	-0.640885	NA	-0.269402	-1.707272	0.651321	1.024371	0.930217	1.186221	-0.281115	-0.177446	0.486088	0.573249
SHB17	0.032705	-0.234085	-0.119276	-0.386151	0.045085	0.23369	-0.082489	-0.216492	0.130137	1.576037	-0.232771	0.27312	-0.290854	NA	-0.160412	-0.076738	0.436346	0.378107	0.564863	0.051329	-0.433273	-0.361095	-0.523091	0.770416	NA	0.285899	0.186273	-0.680753	NA	-0.022767	-0.178557	0.28481	-1.448177	-0.316747	-0.536926
SHE10	NA	0.341771	0.218294	0.387604	-0.624081	-0.804201	-1.589677	-1.222546	0.071107	0.031905	0.68501	-0.160393	0.010388	-2.434468	0.333761	0.216861	-0.163071	-0.01534	-0.138377	-0.161113	-1.093802	0.166449	0.713592	0.474691	-0.200988	-0.337728	0.133083	NA	-0.107946	0.237907	-0.45258	0.082039	0.242256	0.783105	0.965312
SHE4	NA	-3.704781	-1.156916	0.38718	-0.174241	0.925413	NA	-2.440178	NA	NA	1.237498	1.061898	-1.134222	-1.370778	0.196091	0.782283	-0.29729	-2.218611	0.786326	0.571811	-2.660309	0.342663	NA	3.497336	NA	-1.24115	-2.840233	0.757898	-0.44117	1.6996	NA	0.849619	1.180649	-0.070491	-0.273156
SHE9	NA	-0.123437	0.490636	-0.358119	-0.336146	NA	-0.017261	-0.65919	0.590193	1.110545	0.13076	-0.18292	0.137204	-0.405475	-0.390158	-0.257667	0.299799	0.47739	-0.460989	0.539276	NA	0.197496	-0.808181	0.09182	NA	0.521575	0.586542	-1.672856	-0.078265	-0.232213	0.450723	NA	0.23725	-0.961321	-0.746244
SIC1	NA	-1.010491	-1.248897	-2.218269	NA	-0.349742	-0.305333	-0.074271	NA	NA	0.3533	-2.569826	0.478334	NA	-0.290795	-0.48016	-1.853077	1.051914	-1.741181	NA	-0.828071	-1.018151	-0.231663	0.45544	1.017798	0.526601	NA	-0.207251	0.089653	1.198969	NA	-0.756254	0.936918	0.142175	-0.002834
SIF2	NA	-0.57554	-1.368282	0.130709	0.79882	0.852323	-0.143606	-0.131323	0.59487	NA	NA	-0.150938	0.349767	-2.04976	0.598482	0.851019	0.958009	-0.062936	-0.435552	0.286235	NA	-0.831444	NA	-1.067711	NA	-0.455112	-0.227511	1.1312	-0.679369	0.239529	0.1621	-6.883827	0.100378	0.338089	0.74227
SIL1	NA	0.36574	0.505605	0.984383	0.167014	-0.119962	NA	0.51607	NA	NA	-0.164831	-0.217678	0.843423	-1.337884	-0.046348	-0.574104	0.105592	0.309317	0.089046	0.111419	0.022125	0.75935	NA	-0.309537	NA	0.451712	0.242181	-0.975676	0.628112	0.092699	-0.120467	-0.244829	-0.98343	-0.341555	-0.434197
SIN3	NA	-7.179306	NA	-0.387044	-2.29822	-0.814927	NA	-0.762624	NA	NA	-0.589973	0.7821	-1.552058	0.503674	0.936678	1.137713	0.023167	-0.786	0.208682	0.258304	-5.499738	-0.077496	NA	1.525434	NA	0.333639	-4.702806	0.075483	0.629374	0.090843	-0.399632	NA	0.418668	0.648849	0.106524

SIN4	NA	-0.259855	NA	-0.09404	-0.263156	-0.245847	NA	-1.186994	0.313703	0.354997	0.496397	0.145678	0.370371	NA	-0.532216	NA	0.024878	0.118617	0.214406	0.012506	0.273708	-0.05389	NA	NA	NA	-0.770646	NA	0.149018	0.091917	-0.298034	NA	0.045433	NA	-0.228396	NA
SIP1	NA	1.056897	NA	-0.639587	0.081181	NA	-0.060144	NA	-0.275815	-0.404885	NA	0.187595	0.331015	NA	0.29066	-0.353638	0.598804	0.507303	-0.546491	-0.289654	NA	-0.057968	0.35312	0.081262	NA	1.30477	0.378446	-0.078133	0.845554	-0.371017	-0.459991	NA	NA	-0.246563	-1.070031
SIR1	NA	-8.753394	-12.263143	0.303752	-0.841118	NA	0.269242	-2.729123	-0.977505	-0.416658	-0.508321	-3.985131	NA	NA	0.97401	0.970814	0.04021	0.431695	-0.353162	0.764901	0.084477	0.815114	-0.66146	-0.24248	-3.224096	-0.36688	-0.6088	0.480865	0.633379	-0.136193	NA	-1.014354	-0.291289	0.3691	1.149557
SIS2	0.546909	-0.821073	-2.566428	-0.549177	0.362491	0.562643	-0.018107	-0.198286	0.740252	-0.613495	-0.062415	0.301115	0.229787	NA	0.098746	0.016817	-0.036494	0.571783	0.282212	-0.209014	-0.467789	-0.055167	-0.107567	0.776447	NA	-0.619851	-0.188524	-0.584581	-0.47371	-0.140071	0.177896	-0.077689	-0.360349	0.075938	-0.230845
SIZ1	NA	NA	-0.695633	0.044749	0.277251	NA	0.631371	NA	-1.050851	1.442074	NA	0.15852	-0.868928	NA	0.750236	-0.179439	0.281743	NA	1.103657	2.028264	-0.938522	0.598531	NA	1.023888	NA	0.366952	-1.659799	0.037621	-1.765754	0.171646	NA	NA	0.673472	-0.264284	-1.315024
SKG1	NA	0.095179	-0.12591	-0.328578	0.4991	-0.235547	0.874149	-0.308242	-0.165667	-0.608206	-0.014555	-0.028959	-0.029292	NA	0.063589	0.207331	-0.01102	1.195583	-0.432601	0.458067	NA	-0.005985	NA	0.629794	NA	0.637832	-0.265047	-0.294734	1.250365	0.091212	0.064326	0.42131	0.523138	-0.269712	-0.637112
SKI2	NA	-0.990769	NA	0.221119	NA	-0.130978	0.123511	-0.356987	0.516294	-0.310338	0.31034	-0.251635	NA	-0.238716	-0.909638	-0.340111	0.520326	NA	-0.01051	0.260338	-1.449424	0.383697	NA	0.368606	NA	0.061121	-0.725149	0.213102	0.927511	1.078659	-0.859781	-0.461242	0.701723	0.443592	0.262741
SKI3	NA	NA	NA	-1.634145	-1.835017	0.080997	-0.396794	-0.245847	-0.72363	2.211613	-0.097225	0.548189	-0.039659	-4.910321	-0.128666	0.109453	0.525174	-0.160318	-0.183941	0.161807	NA	-0.278796	0.170337	0.425475	NA	0.969251	NA	-0.213202	-0.007124	-0.092011	-1.120438	-0.257145	1.320873	-0.248547	-0.063581
SKI7	NA	NA	0.442868	-0.182693	0.146087	0.115216	NA	-0.110759	NA	NA	0.365525	-0.118838	0.261597	0.864344	-0.965088	-0.66647	-0.568675	0.614302	0.341376	0.243964	NA	-0.306698	0.081272	0.27888	NA	-0.465252	-0.102946	-0.875061	-1.25507	0.413706	-0.467638	0.819041	0.384045	0.330304	-0.702098
SKN7	-0.716351	NA	-0.836765	0.367163	0.397821	0.607917	0.156723	-1.448831	-0.081253	-0.897062	0.876106	0.10357	-8.644629	0.754307	0.288891	0.109451	0.074196	-4.91037	0.748758	-2.453779	-10.608083	0.52728	NA	-0.72977	NA	-0.507795	-1.428832	0.566428	0.090955	0.771337	-0.837874	-0.191694	1.198544	0.690578	1.169119
SKO1	-1.276672	0.816715	0.445156	-1.63968	-0.15428	-0.04798	0.458718	1.059513	0.512249	-0.772179	-0.71405	-0.089624	0.71601	0.17488	-0.358275	NA	-0.536782	0.347248	-0.248084	-0.144405	NA	-0.516589	0.271189	0.225647	NA	0.664295	0.805692	NA	0.154693	0.536765	0.342238	-1.006868	NA	-1.337237	-1.610226
SKP2	NA	NA	-0.586357	0.608838	0.150065	-0.053387	0.033278	-0.331393	-0.142218	0.352795	0.144739	0.115797	0.214307	0.308064	0.23832	-0.217554	0.163886	0.345617	-0.16912	0.366721	NA	0.323114	NA	NA	NA	0.544278	0.394509	-0.73218	0.406946	-0.426387	0.019141	-0.051778	NA	0.008669	0.035891
SKT5	NA	0.334602	0.613254	0.138422	-0.232745	0.505694	0.577885	-0.307188	0.516586	0.652694	NA	-0.214349	NA	1.193623	0.201731	-0.27565	-0.828317	-0.695875	0.121909	-0.700192	-1.125476	-0.800814	NA	0.358393	-2.38741	0.192248	0.306087	0.100197	-0.480482	-0.143673	0.394263	0.836471	-1.568522	-0.04589	-0.301565
SKY1	NA	0.156763	-0.466536	0.563743	0.164332	0.30349	-0.809072	-2.266712	-1.3164	NA	NA	0.299589	NA	-0.336728	0.820279	1.443127	0.311975	-0.181072	1.35855	-0.171211	NA	0.905082	NA	-0.151502	1.123382	0.183401	0.413977	0.01749	NA	NA	-1.917444	0.049916	0.182099	0.37682	NA
SLA1	NA	-5.147348	NA	0.055866	0.191878	0.404675	0.032887	-0.169226	0.676424	NA	0.61387	-0.394574	-1.230802	0.213966	-0.406927	-0.59641	0.460723	-0.576692	0.357601	0.745806	-2.44017	-0.130002	0.473208	-1.320188	NA	-2.135097	-3.449493	-0.519031	-0.646447	0.44606	NA	-1.381346	0.131996	-1.241339	NA
SLC1	1.269322	-0.380445	NA	-0.045159	0.591078	0.030913	-0.358899	NA	0.435091	0.291742	0.165428	-0.033901	0.83105	1.336057	-0.214457	-0.325074	-0.121968	0.451563	-0.44983	-0.469716	0.9823	-0.63692	NA	0.257346	NA	-0.763245	-0.112536	-0.63551	0.611929	0.233581	0.230773	-0.246999	-0.061339	0.056618	-0.433953
SLG1	NA	NA	-1.111043	0.905479	0.405785	0.093514	NA	-0.446728	NA	NA	0.830464	-0.203418	-2.191938	-0.046829	-0.647432	0.058493	0.647804	0.269649	0.925802	0.100277	-0.615444	0.642232	NA	-1.008853	-3.842205	0.605806	-1.011833	0.244014	0.243216	0.341437	-0.102318	0.463138	-0.712285	0.469377	0.009879
SLI15	0.575529	-0.068081	-0.081488	-0.152889	0.114232	0.048704	0.157784	1.38192	-0.457991	0.763699	NA	NA	-0.024335	NA	0.076318	0.000223	-0.355424	0.418924	0.33658	0.614798	NA	0.092025	0.303099	-0.273916	NA	-0.240029	0.139879	-0.552969	0.798327	0.098887	0.272394	0.546788	-0.66088	-0.775341	-0.237322
SLK19	NA	-0.201899	-0.34749	-0.268044	-2.701838	0.470191	0.224789	1.787939	0.61478	-0.714246	-0.269438	0.061847	0.486721	NA	-0.610743	-0.521844	0.017987	NA	-0.010937	-0.117263	NA	-0.120393	0.681672	-0.003739	NA	0.316244	0.095605	-0.782635	1.437727	-0.478202	0.797758	0.457368	NA	0.034239	-0.851709
SLM1	NA	-0.058027	-0.992871	1.034022	-0.212352	0.357076	-0.526011	0.093397	0.889242	NA	0.200225	NA	-0.052896	NA	-0.251253	0.041494	0.275064	0.048028	0.636746	0.386575	-0.730033	0.514664	-0.032542	-0.66154	NA	-0.408096	-0.465285	-0.112459	1.16125	-0.572794	-1.105266	NA	-0.794381	0.165461	0.407286
SLM6	-0.202636	-1.141586	NA	-0.922264	-0.6009	-0.322759	0.502057	1.492251	-1.141987	-2.783222	NA	1.031045	-0.790201	NA	-0.483303	-0.149611	-0.377188	NA	-1.903755	0.092962	NA	0.148273	NA	0.266579	-4.248669	-5.114643	-1.904097	-1.006626	0.069088	0.763926	0.861509	NA	1.167187	0.415204	-1.931305
SLP1	NA	-0.331576	-0.493343	-0.369874	-0.086543	0.423569	-0.319952	0.626709	0.386421	0.969504	-0.385028	0.487062	0.51187	-4.610422	-0.203251	-0.064365	-0.101144	0.634466	0.094712	-0.706027	0.360193	-0.040732	NA	0.623804	NA	-0.267291	-0.075265	-0.717623	0.011464	0.335514	-0.05941	0.298879	-1.092003	0.110139	0.862843
SLT2	NA	-0.444242	-1.226299	0.389679	0.159221	0.247721	-0.316777	-0.077788	0.765395	-2.399238	-0.917693	0.126124	0.263059	-0.41161	0.264952	1.072653	0.639083	-0.20863	0.32063	0.286686	-1.42194	-0.511932	-0.283986	1.313897	-6.103669	0.499024	-0.097358	-0.085111	0.32163	0.536511	0.712936	0.070532	0.549259	0.170134	-0.638765
SLX1	NA	NA	NA	-0.222415	0.212077	-1.009338	0.2564	-1.716261	0.825359	0.437274	NA	0.171204	NA	NA	0.337388	0.643158	-0.37827	-0.018044	0.989632	0.355459	0.383799	1.191236	NA	-2.795672	NA	0.512604	-0.268928	-0.331345	NA	NA	NA	-1.317167	-1.034026	-0.184873	-0.059443
SLX8	-1.420735	NA	-4.035405	-0.489883	NA	0.682022	0.783395	3.893466	NA	NA	-1.014468	-1.269366	NA	NA	0.493605	NA	NA	0.724443	NA	NA	NA	0.484293	-1.141987	-2.349847	-2.88891	NA	NA	NA	NA	NA	NA	-1.074256	-0.751002	0.610353	NA
SLX9	NA	NA	NA	0.13196	0.763495	-1.933489	-0.278493	-1.054041	-0.167854	NA	NA	0.62223	NA	NA	0.362775	0.757619	-0.429631	NA	0.352317	0.904215	-0.643754	NA	0.667312	NA	NA	0.423668	-1.150224	-0.91435	-0.929068	0.298186	NA	0.811668	-0.573443	-0.699189	-0.163947
SLY41	NA	-0.196574	0.221006	0.186896	-0.178668	-1.003023	0.086104	-1.296291	-1.120036	0.390775	0.236814	-0.675973	0.392815	-0.291444	-1.054172	-0.254666	NA	0.133729	0.28394	0.740883	0.914982	-0.502551	NA	-0.689891	NA	NA	NA	NA	0.677602	-0.154134	NA	0.40504	-1.403896	-0.245924	0.286846
SMA2	NA	NA	NA	0.189432	NA	0.187552	-0.596297	-0.095112	-0.283956	-0.068366	-0.326038	-0.553581	0.181644	NA	0.682661	0.417019	-0.23073	NA	-1.275089	0.064827	NA	0.197698	NA	-0.849211	NA	1.274973	0.163129	-0.213827	0.319925	0.015063	0.523299	-0.306591	-0.42575	-1.172126	-0.343916
SMI1	-3.445348	-1.127702	-2.910005	0.306512	NA	0.995548	0.202753	-2.284247	0.366486	NA	0.913695	-0.015281	-2.325074	-1.244339	0.108683	0.652792	-0.0078	-2.077913	-0.034671	-2.058612	NA	0.603978	-0.31919	-1.860028	NA	-1.313543	NA	-0.422631	0.043636	0.620093	-0.867916	0.409443	0.571696	-0.088875	-0.318148
SMK1	NA	-0.943454	-0.448234	1.033136	-1.505642	0.595497	0.183042	-1.40119	-1.816617	NA	0.324474	-0.378683	0.12525	-2.650414	-0.138857	1.089288	0.74507	NA	-0.020195	-0.388729	NA	0.13977	NA	0.532603	NA	0.564236	-0.478134	0.728674	-0.168799	0.414299	-1.170282	-0.250675	0.859983	0.254892	1.236049
SMT3	NA	-6.5067	-0.231746	0.031445	-1.113222	NA	0.248761	NA	-0.017797	-0.629718	-0.830075	0.040765	NA	0.89854	-0.172411	0.341668	0.362848	1.003407	0.578966	0.814676	-3.574378	-0.332713	0.306958	-2.074905	-1.726913	-0.388598	-3.352343	-0.533314	-1.442362	0.68936	NA	0.328089	0.246247	0.066695	-0.805066
SMY1	NA	NA	0.048221	-0.298519	0.628131	-0.767468	0.23314	0.380919	0.067072	-0.474309	0.084784	-0.361917	0.402117	NA	0.370256	-0.013391	0.513642	0.438394	-0.012982	-0.199277	0.328676	-0.306925	-0.460609	1.029092	NA	-0.155675	0.046345	-0.472223	NA	0.111788	0.094379	-0.122199	-0.949849	0.086212	-0.151662
SNC2	NA	-0.444891	0.45477	-0.538054	-0.033074	0.514122	-0.346909	-0.347183	-0.195555	NA	0.56447	0.246445	-0.25267	NA	1.241354	0.246852	NA	-0.745831	0.365719	0.11522	-0.04941	-0.66908	NA	0.200232	NA	-0.932942	-0.479954	0.348017	0.167854	0.120686	-0.19402	-0.197792	0.114306	-0.593884	NA
SNF1	NA	NA	-0.171183	0.443656	NA	NA	-0.290819	0.409323	-1.020226	0.033166	0.188445	-0.181678	0.515638	NA	-1.016404	0.493873	-0.093917	-0.368478	-0.444792	0.073926	0.865195	-0.585362	0.663989	1.089219	NA	0.431098	0.044975	-0.20398	0.118881	-0.080332	0.303324	-0.072199	-0.228004	-0.115797	0.031903
SNF11	-0.041169	-0.218614	0.675693	-0.177601	-0.654567	0.308832	0.715708	NA	-0.379631	0.771086	0.013262	0.173281	NA	NA	NA	0.045872	0.019381	-0.691934	0.74235	0.73118	-0.419903	-0.333617	NA	0.61674	NA	0.34871	-0.310739	1.126202	1.18161	-0.082114	-0.319683	0.358823	0.248051	NA	1.39537
SNF3	NA	NA	0.191464	0.377243	-0.057151	0.478469	0.44026	0.028021	0.333736	0.179854	0.11988	0.431241	-0.061832	-2.306328	-0.310793	-0.083099	0.136558	0.061774	0.05542	0.064549	-0.199965	0.176094	0.233679	0.662024	NA	NA	-0.615195	0.108564	NA	-0.220946	NA	0.092982	NA	-0.218838	0.008448
SNF4	-0.248685	1.000273	-0.844607	-0.27907	0.780928	-1.374557	-0.823316	-0.363577	-0.004422	0.74147	-0.009553	0.614087	NA	NA	-0.423939	-0.54471	-0.204668	0.109058	-0.734349	-0.636586	0.919418	-0.782076	0.754591	-0.415928	-1.739329	0.455359	0.664172	NA	0.312808	0.074624	0.630296	0.120847	0.723803	0.395576	-0.971785
SNF5	NA	NA	NA	0.947778	-0.752869	0.774722	0.998611	NA	1.249126	NA	0.988368	1.015376	-0.208611	0.968441	0.551703	0.93808	0.303564	NA	0.938646	0.019923	NA	1.076414	NA	-0.037776	NA	-1.148122	NA	NA	NA	1.173859	NA	-0.279114	NA	1.28557	-0.736773
SNF6	NA	-1.23411	NA	0.519667	NA	0.211356	0.206511	1.209918	0.445743	NA	-0.039057	-0.741028	-0.959683	NA	0.22889	0.318943	-0.304671	-1.477923	-0.361903	-2.633034	NA	0.190551	NA	0.476937	NA	NA	-0.867988	0.30711	0.142066	-0.128953	NA	-0.383024	2.112897	1.053731	-0.538213
SNG1	NA	-0.705818	-1.265883	-0.504132	0.688676	-0.057043	0.070671	-0.382586	0.251505	NA	-0.046622	0.292979	-0.018316	NA	0.205742	0.443167	0.563351	0.168342	0.153791	0.446166	0.303434	-0.006626	NA	1.229152	NA	-0.020477	-0.800723	-0.585143	-0.181577	0.250819	-1.964743	-0.551023	-0.050204	0.113643	0.133224
SNN1	-0.739692	NA	-0.409889	0.115928	-0.748967	-0.132379	0.072801	-0.219632	0.47507	0.115284	0.531842	0.456944	-0.560495	NA	0.184387	-0.256323	-0.457699	0.364778	1.027756	0.072403	-0.647197	-0.202815	NA	0.36591	-4.332964	-0.056012	0.322015	-0.307155	-0.788858	0.091535	-0.091619	0.692788	NA	-0.245607	0.559673
SNT2	-2.57641	0.178382	NA	0.03003	-0.148351	0.028129	0.44658	0.602919	1.353638	-2.231268	-0.707051	0.696254	-0.250198	0.632316	-0.496352	-0.741073	0.062365	NA	0.688029	0.659991	-0.659541	0.900582	-0.294152	-0.130704	NA	0.392744	-1.094536	NA	-0.712868	-0.579054	0.339128	0.372767	0.181487	-0.276331	-0.425848
SNU66	NA	-0.048038	-1.580567	0.520735	0.383793	0.267758	0.385278	0.694035	-0.344193	-14.31134	0.783059	0.498394	-0.002364	1.802874	-0.307003	-0.554668	NA	0.532507	-1.023924	0.623283	-0.422306	-0.435252	-0.17639	-1.078962	-1.319894	-0.860367	-0.229232	-2.278883	NA	0.271543	0.916515	-11.989903	NA	-0.304688	0.257829
SNX4	NA	NA	-0.3809	0.083159	0.613829	0.006933	0.147422	-0.443489	-1.647359	-0.477087	-0.128136	0.499655	0.156486	0.591417	0.251359	-0.417793	0.023813	1.007383	-0.155673	-0.304423	-0.518653	-0.964622	NA	0.737628	-4.274988	NA	0.607495	-0.076942	0.868661	-0.324302	0.295125	-0.289365	0.607277	-0.602537	-0.525945
SOK2	NA	-2.304963	NA	0.625577	-0.685159	0.582476	-0.429533	0.308772	-0.48078	NA	0.46105	-0.579485	NA	NA	0.809851	0.189925	0.424496	-0.350894	-0.270646	-0.385851	NA	-0.382619	0.621224	0.329885	NA	NA	-1.355584	0.410453	0.341548	0.96474	1.300995	0.295485	1.08494	-0.066209	0.3329
SPA2	NA	NA	-0.282036	1.088468	0.847221	1.240806	0.567623	-0.265871	-0.261054	NA	-0.800827	0.610755	NA	-1.871359	1.627195	0.089989	0.295542	-0.352477	0.332553	NA	-0.929366	1.635133	NA	0.573574	NA	-0.166189	NA	0.878509	-0.092696	0.266653	0.230518	-0.908861	-0.143711	0.610311	1.093764
SPC1	NA	0.084091	0.348912	0.276138	-0.706337	-0.066502	-0.061135	-0.033161	0.169163	0.417855	-0.210773	0.20089	-0.117729	NA	0.613837	-0.065977	0.104781	0.36296	0.581647	0.529386	-0.271416	0.304264	NA	-1.137792	NA	NA	-0.04938	-0.10742	-0.114967	-0.859372	-1.001847	0.554751	0.497407	0.500165	0.32164
SPC2	NA	0.518223	-0.398603	-0.952318	-0.069261	0.069467	0.141269	-0.34601	0.29819	-1.137412	0.29485	0.996158	-0.206575	0.677737	-0.290791	-0.119007	0.799819	-0.069993	-0.398464	0.556343	NA	0.244727	0.097695	-0.17673	-2.012376	1.292614	0.543727	-0.050566	0.342729	0.253551	-0.702183	0.129627	-0.070822	-0.647591	0.200364
SPE3	NA	0.394633	-1.145808	0.067907	-0.186889	-0.193916	0.238223	1.328983	0.024391	-0.885759	0.310919	0.31752	-0.835978	0.447125	0.4594	0.170419	-0.204171	-0.165127	-0.21221	-0.425	-2.255934	-0.072559	-0.471711	-0.496903	NA	0.545025	0.038109	-0.260791	0.576128	0.704952	1.156327	-0.768361	NA	0.638197	-0.522509
SPE4	NA	-1.031049	-0.474074	-0.285404	0.727621	1.343746	-0.571014	-0.258104	-0.299562	0.342369	0.525545	-0.452731	-0.440182	NA	-0.063319	0.353523	0.557255	0.299338	0.079995	0.771265	-1.601715	0.612925	0.449856	0.005179	NA	0.601862	-1.029849	0.342436	-0.123291	-0.095144	-0.225116	-0.370421	0.579431	0.331556	0.494964
SPP1	NA	-0.311192	0.920877	-0.161275	NA	-0.248961	0.370237	-0.429792	0.46855	-1.062741	0.14164	0.340313	0.326451	-2.248115	0.877883	0.312002	-0.41153	0.230968	0.381303	-0.065144	-0.036482	0.297217	NA	0.970557	NA	-0.037718	0.127924	0.318956	0.66153	0.199946	-0.309885	-0.640111	0.593784	-0.319444	0.38632
SPT2	NA	-8.902988	-0.69378	-1.105014	-1.265151	-0.119744	-0.428694	-1.20711	-1.116039	-0.295613	0.11834	-1.661608	0.020447	-1.628373	0.146026	0.16115	0.296347	NA	NA	0.46271	NA	0.239541	1.075686	1.390529	NA	0.770353	0.48343	0.028328	-2.164196	-0.003402	NA	-0.060852	1.023278	0.184513	-0.036554
SPT21	NA	-2.726864	0.877649	-0.301799	-4.008067	-0.229154	0.01135	-5.812705	-1.187807	-3.809837	0.233216	-0.162515	NA	-1.821168	0.299413	0.475798	-0.950633	0.749612	-1.078716	0.517397	NA	0.14252	-0.673799	-2.026881	NA	0.136128	-3.519917	0.272696	NA	NA	NA	-1.54778	-0.810196	0.196941	-0.723721
SPT23	NA	-0.258623	0.328284	0.428056	0.051648	-0.136312	-0.629693	-0.143714	0.216043	0.393541	NA	-0.94978	0.420221	NA	-0.191254	0.079854	0.248219	0.09572	0.218921	0.288614	-0.945595	0.771567	-0.055989	0.071343	0.925509	0.391317	0.079515	0.080202	0.403919	0.44004	-0.548774	0.194016	-0.643528	-0.565506	-0.051751
SPT8	NA	-3.083113	-3.358154	0.945089	-0.302089	0.266123	0.418388	NA	0.224201	2.938215	NA	-0.978892	-1.413205	NA	0.127277	-0.170981	NA	-0.498806	-0.069865	NA	-1.948651	0.596842	NA	2.98712	1.484825	-0.407739	NA	0.095601	0.652688	0.036426	NA	NA	NA	-0.683196	NA
SQS1	NA	0.545928	NA	1.152271	NA	1.879178	0.477478	-2.328876	0.813985	-0.992091	0.564162	0.431512	NA	NA	0.43132	NA	-0.327627	NA	0.429793	-0.603106	NA	0.284021	-0.208938	-2.380664	NA	-0.242027	0.129941	-1.614142	NA	0.279738	-1.0618	0.600442	NA	-0.297822	0.120513
SRB2	NA	NA	NA	-1.445158	-0.418676	-0.692228	0.013024	1.507841	0.04948	3.258125	NA	-0.393926	-2.909247	NA	NA	0.893693	0.354568	-2.006164	0.156455	NA	-4.338656	-0.236445	NA	NA	NA	-0.644769	NA	0.057091	-0.005617	NA	NA	NA	NA	0.139285	-0.364345
SRB4	NA	-0.7484	0.644071	-0.086558	1.28448	-0.355	0.088971	0.808149	0.259134	0.838757	-0.164627	0.21473	-0.620061	0.155171	-0.315321	-0.36305	0.038875	0.171162	0.036035	-0.06899	-0.969216	-0.367493	NA	0.24345	NA	-0.225218	-0.803456	0.706589	1.103172	-0.212301	NA	1.068119	0.357922	0.200545	-0.328848
SRB7	NA	-4.854489	NA	0.127844	-1.793841	0.067302	-0.253898	1.325027	-0.019361	NA	1.066683	-0.939448	NA	-2.963799	0.017959	0.083937	-0.069004	-1.065084	0.612928	-0.110128	-6.187302	NA	-4.117199	-3.786288	NA	0.028308	-6.984114	0.477489	-0.454042	0.372357	1.438491	NA	1.296509	0.28304	-0.291736
SRC1	NA	-1.635403	-0.180925	-0.153978	-0.255426	-0.203168	-0.163858	-1.002624	0.507554	NA	0.954638	-0.089984	-0.119313	-3.10914	0.730439	0.018984	-0.104849	0.301222	0.289369	0.623985	NA	0.022121	NA	-0.916436	NA	0.014374	-1.065263	0.156483	-0.891321	0.902338	-1.17449	-10.266344	0.631736	0.009423	0.887069
SRL2	NA	0.075197	-1.924801	0.677757	0.250274	0.638463	0.400732	-0.319414	-0.068473	-1.647467	0.038393	0.598826	-0.573988	NA	0.06542	0.310252	0.737525	-0.381446	-1.627859	NA	-0.252932	0.33692	NA	0.096853	NA	0.175468	NA	0.162478	0.152976	0.521598	-0.221061	0.027728	0.292993	0.330154	0.10334
SRN2	-5.348902	-1.62076	NA	0.106605	NA	0.006455	0.198942	NA	-0.077958	-0.202968	0.468841	-0.793223	-1.693694	1.547348	0.604667	0.250158	0.120818	-0.189674	0.420652	NA	NA	-0.090587	NA	-0.816389	-6.086498	-0.684726	-2.793144	-0.086705	0.646251	0.624618	-0.501411	-0.033869	0.085095	0.018254	0.406148
SRP40	-1.597768	0.020233	0.794618	-0.014156	-1.072202	-0.223596	0.027885	0.552667	0.740093	-2.439919	NA	0.549806	-0.891934	NA	0.080273	0.283252	-0.176674	0.280547	-0.577977	-0.193447	-0.790775	0.256589	0.143341	0.906118	-4.019893	0.653641	0.021475	0.362121	0.106778	-0.505877	0.7433	-0.887693	0.53806	0.09528	-0.448135
SSA2	0.337654	0.497421	-0.895744	0.42811	-0.327847	-0.139698	0.199324	-0.360013	1.161229	-0.84239	0.282718	0.146271	0.110413	-0.633598	-1.025503	-0.438788	0.082937	0.161329	0.608889	NA	0.521562	0.039868	NA	0.475512	NA	0.211823	NA	-0.313918	-0.64957	-0.010495	-1.001177	0.118192	-0.419876	0.421573	0.764114
SSA3	NA	0.14034	-0.060708	-0.836391	-0.185188	-0.281603	-0.320634	-0.426475	0.1424	1.255044	0.134753	0.062221	0.180282	1.60774	-0.272061	0.167465	0.412317	0.531143	0.998521	-0.107934	0.086132	-0.268726	NA	-0.264384	NA	0.677257	0.60577	-0.162423	0.290821	0.426969	1.137359	0.358838	NA	-0.593191	-0.512529
SSD1	NA	-1.378759	NA	0.410362	1.162906	-0.671917	1.202958	NA	-0.196286	-0.933047	-1.21904	0.089434	NA	NA	-0.517749	-0.678108	-0.287848	NA	0.025615	-0.513518	-0.451895	NA	-0.260165	NA	NA	1.106327	NA	-0.822966	NA	1.905283	3.144904	NA	0.585748	2.391921	-0.389032
SSE1	NA	-2.949715	-3.616144	-1.111445	NA	0.376845	0.198439	-5.58472	0.351299	NA	NA	0.92052	0.069028	-2.750882	-0.07679	0.465955	-0.797151	-0.399616	0.256743	0.791708	NA	-0.566415	NA	0.311555	NA	0.569857	-1.916996	-0.523204	-0.241472	-0.199583	NA	-0.354705	1.633864	0.115767	0.153014
SSF2	0.676598	0.486529	-0.034194	-0.094325	0.377883	-0.982381	-0.19314	0.20661	-0.007669	-0.284793	0.01354	-0.047318	-0.017344	-2.675958	-0.510823	-0.553532	-0.510806	0.450364	0.288393	-0.433712	0.894143	NA	0.091097	0.524466	-3.724201	0.434816	1.071772	0.598741	-2.90E-05	0.463011	-0.641523	NA	0.032882	0.400046	0.241904
SSH1	NA	0.277108	NA	-0.773391	-0.134681	-0.454702	-0.255727	0.948459	0.370521	0.539533	-0.835204	0.217722	NA	NA	0.230477	-0.769344	-0.611528	0.521752	0.080159	-0.502032	-0.80916	-0.103402	NA	0.561357	0.166861	-0.614384	-0.079173	-0.338024	0.317349	-0.06715	-0.413337	1.024668	-0.159112	0.279972	-0.768578
SSK1	0.698278	NA	0.230847	-0.299819	0.148385	0.273141	-0.29699	-0.280074	-0.393977	0.441901	0.066275	-0.087888	-0.401859	-4.645278	-0.279716	0.087363	0.305166	0.465915	0.45128	NA	-0.087762	-0.408114	-0.202755	0.056105	-1.47367	-0.046185	NA	-0.500026	0.479865	0.369793	-0.115206	0.322699	0.599606	-0.021167	1.064481
SSK2	NA	0.182041	0.340358	0.696562	-0.427236	0.519848	0.133011	-0.650459	0.611867	-0.000545	0.368757	-0.548676	-0.120306	NA	0.18988	0.116604	0.45503	-0.239367	0.31073	0.088143	-0.297525	0.432791	-0.626553	0.830542	NA	0.748481	-0.546102	-0.13419	-0.280828	-0.268714	-0.568429	-1.1608	-0.095385	-0.039907	-0.657209
SSM4	NA	-0.219602	-1.634499	0.405298	-0.175872	0.159083	0.838195	0.442449	-0.464217	0.834465	-0.522373	0.832964	-0.574949	NA	-0.574181	-0.390989	0.357071	-0.495519	0.936969	0.313942	0.072613	-0.584049	-0.43499	1.344384	NA	0.080181	-0.412362	0.542609	-0.139033	-0.125877	-0.280327	-0.156209	-0.071647	-0.389848	0.550624
SST2	NA	0.201324	0.489612	-0.054022	-2.161682	0.904163	-1.353838	-1.386485	-1.694491	-0.053493	0.709163	0.204794	NA	-5.291797	-0.036114	0.97588	0.938638	-1.117876	0.442363	0.235375	-0.531971	0.126366	0.112561	-0.607183	NA	0.556029	-0.893851	1.351802	-1.256998	0.088936	-1.992432	-0.516544	2.567418	1.099329	0.883624
STB1	NA	NA	0.080901	0.033504	0.726559	0.296854	0.584931	-0.435068	0.31662	NA	-0.906543	0.165174	-0.017511	1.525066	0.356546	-0.172811	0.362889	-0.500463	-0.680107	0.504163	0.023471	-0.067286	-1.917908	NA	NA	-0.017977	-0.065148	-0.063536	0.74288	-0.268059	0.442658	-0.240084	NA	-0.161827	0.152454
STB5	2.740368	0.863992	2.022547	0.234177	-1.622923	-0.006552	-0.049488	-0.379739	0.899109	-2.065541	0.818546	0.779276	-0.874319	1.181403	0.091837	0.753618	-0.270881	-1.298211	0.300909	-0.225419	-1.425353	0.030397	-2.453748	2.181785	NA	-0.718759	-1.137439	-0.289772	-1.03586	0.009028	-0.869177	0.023823	1.518956	0.734747	-0.196466
STD1	NA	0.346345	-0.416228	-0.271393	0.052347	-0.894577	NA	-1.275928	NA	NA	-0.20697	0.829047	0.015272	-1.306311	0.609821	-0.060393	-0.117105	0.656516	0.656169	0.234974	NA	0.336981	0.431182	-0.719179	NA	0.885866	-0.195318	0.574567	1.20237	0.129002	-0.326646	0.786001	-0.630084	0.206481	0.999997
STE24	NA	0.131667	-1.770645	-0.191379	-0.305307	-0.014006	0.353287	-0.00665	-0.153219	-0.256415	-0.36828	-0.10621	-0.012421	0.647154	0.213695	0.071006	0.650631	-0.192022	1.094236	-0.749806	NA	1.401332	NA	-0.864532	NA	-0.568281	-0.533557	0.377598	-0.733132	0.13024	-0.020762	0.024735	-0.88568	0.60585	0.306537
STE50	NA	-0.031814	NA	NA	-1.294902	-0.540785	-0.089888	NA	0.58794	-0.400484	-0.080704	NA	0.228764	NA	0.408377	-0.179027	0.105206	NA	0.167721	-0.055913	0.15522	-0.315739	-0.119868	0.571841	NA	-0.285711	-3.425895	0.171346	0.344567	-0.601541	-0.888169	-0.866222	-0.209483	-0.160312	-1.818355
STH1	-0.69564	NA	0.753021	0.532134	0.575047	0.299231	0.126594	0.471843	-0.08373	0.251935	0.003974	0.068899	-0.407179	NA	0.355191	0.5843	0.117027	-0.373806	0.139529	0.975153	NA	0.337784	-0.065636	-0.604532	NA	0.280499	-0.6561	NA	0.033585	0.126449	-0.28909	0.486322	NA	-0.005634	-0.136875
STI1	NA	-0.057762	-1.644127	0.274894	0.845765	-0.04264	NA	NA	NA	NA	NA	0.177054	NA	NA	-0.196795	0.140755	-0.398169	1.650829	0.055384	0.194267	-0.026997	0.454608	-0.028568	-0.948606	NA	-0.291802	-0.111089	0.026902	-0.454391	-0.189798	NA	0.372668	0.623555	0.772323	-1.938288
STM1	-6.481329	-1.855318	-3.896238	0.919524	-0.77369	0.680262	0.506566	0.392292	1.264918	-3.804577	0.486211	-0.368363	-1.324475	0.789407	0.327426	0.135211	-0.543733	-1.071166	0.247746	-1.242287	-1.684452	0.516716	NA	-0.032978	-13.62324	-0.118402	NA	0.89416	0.881576	0.708129	-0.631656	-0.854884	-0.135844	0.597211	-0.125661
STP1	-0.396034	0.936298	2.082509	-1.381801	-0.225441	NA	-0.861781	0.258199	-0.636345	0.697038	-0.036208	0.588508	0.208731	-0.414457	-2.069096	0.191301	-0.83674	0.495847	-1.450061	-0.175785	0.759832	-1.583119	-1.902039	-0.374284	-1.155959	-0.139756	0.832483	-0.483414	0.917422	-0.205705	0.127618	1.178027	0.127416	-0.170536	0.477207
STP2	NA	0.186271	-0.052552	-0.285117	NA	NA	-0.02648	NA	0.003659	NA	0.391499	0.355761	0.461416	NA	-0.863862	-0.139975	-0.27801	0.922537	-0.415565	0.156789	NA	-0.06949	-0.385841	-0.243554	2.016303	-0.082987	NA	-0.074166	0.021156	0.419564	NA	0.272027	0.290402	-0.056155	NA
STP4	-0.415894	0.133148	NA	-0.376294	0.190985	0.00834	-0.178017	NA	-0.332186	0.821721	0.851169	-0.226484	0.21812	-0.072246	0.30981	-1.112334	0.345817	-0.07784	-0.279597	0.428073	0.117291	0.6444	-0.313408	0.19174	NA	0.263008	0.261279	-0.210568	0.379262	-0.11767	NA	0.563808	0.179766	0.355901	-0.042736
STV1	NA	-0.161339	-0.933012	0.600891	0.033287	0.39076	1.131226	0.967598	0.799883	-0.598485	0.382707	0.555603	-0.382063	NA	0.278179	0.407284	0.045743	0.099174	-1.410083	-0.279395	NA	0.141349	NA	0.606427	NA	-0.550644	-0.344309	0.410694	-0.310507	0.6654	0.534874	0.286255	0.625293	0.563989	0.014341
SUA7	-1.173197	-0.683673	-0.135224	-0.381957	0.174319	-0.081354	-0.355177	0.542051	-1.059977	-2.5323	0.273419	0.018229	-0.865192	1.131442	0.487653	0.079083	0.008294	-0.284167	-0.089107	-0.27155	-0.544797	0.671854	NA	1.099691	-3.340577	-0.09531	-0.264261	0.488724	NA	0.668504	0.511789	-0.965181	1.068319	0.209332	0.508852
SUB1	NA	-1.288596	NA	0.196213	1.260267	-0.013799	0.295267	0.282004	1.131777	NA	0.240173	-0.130525	-0.277428	-3.487901	0.322075	0.177296	0.084753	-0.540957	-0.604806	-0.289318	NA	-0.9925	NA	2.36867	NA	-0.302372	-1.451804	0.093564	-0.202351	0.531019	0.630418	-0.762363	0.494989	-0.122056	0.480595
SUM1	-8.211762	0.266283	1.680232	-0.40331	-0.647295	0.212363	0.141436	1.726823	-0.211016	NA	0.492219	-0.548198	-0.035096	0.852735	0.3435	0.319204	-0.591104	0.201914	0.124276	0.220081	1.193058	NA	NA	-0.445119	-10.193562	0.136363	-0.465542	-0.584856	NA	-0.331431	1.71846	NA	-0.736955	-0.439585	-0.178862
SUR1	NA	0.405124	-0.475885	-0.135003	0.087992	0.075705	0.77597	0.477065	-0.916676	-0.610313	-0.299545	0.237349	0.444281	NA	0.267107	0.465172	0.506363	0.357055	0.874178	0.211721	0.26278	-0.13976	-1.136119	-0.601667	NA	0.838812	0.28484	0.309643	0.533483	0.540533	0.4677	-0.267803	-1.171971	-0.170451	-0.960429
SUR2	1.147849	-0.008102	NA	0.674766	-0.943502	-0.088443	0.39458	-1.107821	0.834972	-0.174109	0.235898	1.119108	0.424663	NA	0.427798	-0.292507	1.05846	-0.126532	0.842282	0.502938	-1.060411	NA	NA	0.380549	NA	0.956011	-0.207402	0.806627	0.827513	0.33986	-0.962172	NA	NA	-0.352126	0.072841
SUR4	NA	-0.915863	NA	0.889091	NA	-0.22725	-0.209526	NA	0.461132	1.738703	0.449686	0.926007	-0.133512	2.924419	-0.963599	0.126204	0.256285	-0.763191	-0.018764	-0.043454	NA	0.060097	0.576276	0.128388	NA	0.426009	NA	0.202637	0.434868	0.41691	-1.480215	1.910798	-1.488975	-0.160604	0.333949
SUT2	NA	0.005792	NA	0.267104	0.264796	0.048408	-0.508301	-0.074695	0.860862	-0.894541	0.05257	0.615455	0.011282	-1.396817	0.435528	0.195216	-0.044098	0.465817	1.423539	0.233652	0.339693	1.251113	-0.305254	-1.331739	NA	0.76494	-0.075941	0.177747	0.549495	-0.00541	0.158661	-0.357086	-0.825421	0.332635	1.381542
SVP26	NA	0.14776	-0.870412	1.062711	0.583627	0.826385	-0.517756	0.453075	0.909141	NA	0.300538	0.185146	-0.280723	NA	0.164431	0.045143	0.517936	NA	0.628538	0.567188	NA	0.068485	-0.361795	1.972544	NA	-0.178425	-0.249665	0.823411	NA	0.554988	0.013938	-0.008063	-0.72515	0.136294	-0.147417
SWD1	-3.229946	-4.435675	0.420269	0.649465	-2.307923	-0.039631	-0.222763	-4.242099	-0.456532	-7.740136	0.244203	0.204476	-3.259012	NA	0.119299	0.157616	-0.106892	-1.200177	0.064487	-0.238584	-3.184472	0.232074	NA	1.500855	NA	-0.471947	-2.251378	-0.115697	-0.418043	0.203999	-5.25633	-6.143789	-0.169107	-0.175395	0.114857
SWD3	-3.320479	-2.445958	NA	0.406852	-0.815875	-0.162881	0.061303	-2.03673	0.381866	-9.551815	NA	0.978961	-2.502174	NA	0.063014	-0.06358	-0.06137	0.241378	0.217962	0.07824	-2.683591	0.873251	-0.895765	1.441868	-4.337482	-0.487892	-3.003625	0.168854	0.221095	-0.102816	-3.069133	-7.40359	-0.116647	0.219191	-0.740599
SWE1	NA	NA	-1.949551	0.24416	0.479756	-0.15603	0.061014	NA	-1.001565	2.084477	NA	0.616047	NA	-0.014733	-0.388362	0.347448	-0.238872	0.293202	0.156897	0.328591	-0.292494	0.095769	NA	-2.228668	NA	-0.162773	-0.353352	-0.916201	-0.725416	-0.183954	NA	-0.725482	-0.578686	-0.793086	0.467602
SWF1	-0.374238	NA	NA	-1.028227	NA	0.153596	-0.15682	-0.558494	-0.612129	0.985169	-0.307998	0.201216	NA	NA	NA	0.58853	-0.536348	NA	-0.63581	0.502672	0.929951	NA	NA	-1.089844	NA	0.245544	NA	-0.235594	NA	-0.136257	0.643465	0.102481	0.986201	NA	-0.149686
SWI4	-3.430725	-3.713436	NA	-0.12161	0.096057	-0.300115	0.051028	1.92939	1.607932	-1.139926	0.209148	0.49976	0.672676	NA	-0.201012	-0.071258	0.234354	0.264272	NA	-0.661127	-3.495593	0.125728	-2.357725	2.279769	-5.447304	-1.412008	-3.587638	0.528204	-0.608414	0.178786	NA	0.020002	-1.024135	0.086066	-0.292658
SWM1	NA	-3.923083	-1.007993	0.839472	-2.682823	0.351025	0.142586	-4.217743	0.800188	0.046306	0.184495	-1.112387	-4.305082	-4.552379	0.713443	0.322434	0.915379	-1.304746	0.216773	-0.935803	-2.582548	NA	-0.247852	0.595485	NA	-0.041908	-3.000523	0.057462	1.271385	-0.017671	NA	NA	-0.41364	0.143791	-0.337308



UBX3	NA	-1.58289	NA	-0.151549	-0.054395	-0.121109	0.10087	NA	0.372275	0.524518	0.850583	0.391362	0.0213	0.956576	0.623598	0.130173	1.290801	0.131296	0.413614	0.775342	-0.130567	-0.944516	-0.089426	-1.441385	NA	0.362848	0.215888	0.600816	-0.366052	0.014126	0.44576	-0.704098	-0.526462	-0.158752	-0.702489
UBX4	NA	NA	-10.90927	-0.312143	-0.201824	0.532908	-0.231364	0.153567	0.501165	0.43098	-0.276625	0.172185	-0.274516	-0.3495	0.578099	-0.443023	0.027458	0.050196	0.077013	0.930729	NA	-0.002569	NA	1.371075	NA	0.391253	-1.264569	-0.439966	-0.501345	0.483656	0.37921	0.226471	-1.306601	0.994222	-0.604072
UBX6	-1.244768	NA	-0.285732	-0.486504	0.152707	0.383139	0.096522	0.259793	0.589491	0.455267	-0.228022	-0.217694	0.315907	0.83976	-0.397324	0.011015	0.282705	NA	-0.338944	0.339126	0.434408	0.151886	-0.256681	0.134724	NA	NA	0.621416	0.174741	0.21671	-0.173344	-0.551036	0.37914	-0.07327	-0.094248	-0.307015
UBX7	NA	0.571223	1.001001	-0.413799	-0.008522	0.464583	0.334694	-0.038098	-0.783932	0.408821	-1.389803	-0.538048	0.289299	NA	0.005437	-0.473729	0.409084	0.264964	0.107584	0.150363	NA	0.546982	-1.384403	-0.994279	NA	-0.94635	0.445503	0.423737	0.772082	0.63018	0.507545	-0.673025	-0.479994	-0.5044	-0.056347
UFD2	NA	NA	-1.800534	0.291909	NA	-0.623033	-0.10633	-0.878779	NA	NA	NA	-0.191062	NA	NA	NA	0.318759	-0.129002	-1.860646	-0.286915	-0.136578	NA	-1.104376	NA	NA	1.674335	0.115432	NA	-0.576038	NA	1.327333	NA	NA	0.789092	0.068464	NA
UGA1	3.90157	-0.065986	NA	0.666708	-0.695142	-0.523641	0.098116	-1.522672	-0.0767	0.709541	NA	0.245885	-0.654457	NA	0.083431	0.362865	0.141267	NA	0.461866	-0.461292	-0.140007	0.267946	NA	1.630968	NA	-0.646192	-0.382448	-0.363658	NA	0.082207	NA	0.596118	0.321198	0.010173	NA
UGA3	NA	-0.490797	NA	0.385066	-1.067875	-0.364968	-0.013889	-0.112912	-0.203869	0.777031	0.135444	0.091086	-0.323717	-2.45815	0.241665	0.710342	-0.209731	-0.1854	0.304634	0.08243	0.279485	0.22498	0.565691	0.469003	NA	-0.168788	0.130689	0.412266	0.47971	0.714266	-0.607735	-0.083071	0.806173	0.100834	0.222216
ULS1	NA	-0.574236	1.226287	-0.501511	0.525143	-0.170886	-0.336794	-6.777457	0.380069	-2.789737	0.948092	0.396425	-1.670235	0.74213	-0.31356	-0.009728	-0.06413	0.314814	-0.279857	0.519299	-2.623916	-0.05221	NA	1.394532	0.859368	-0.164861	-1.05656	-0.774659	0.409446	0.712355	NA	-0.503826	-0.596188	0.628509	-0.376944
UME1	NA	-0.364858	-1.496192	-0.264767	NA	0.002085	-0.180664	0.301667	-0.08852	-2.947798	0.1548	0.769876	0.511585	-0.429014	-0.372861	-0.127073	0.159128	0.843944	-0.003385	0.83728	0.272783	0.48932	NA	0.339499	NA	-0.411064	-1.159515	-0.058307	1.335866	-0.163169	0.679076	-2.842907	0.022376	0.090955	0.100589
UME6	-7.053091	-0.8223	NA	-0.17868	-0.476316	0.2891	NA	-6.8964	0.926462	NA	-0.074192	0.937355	-1.166401	NA	1.093822	1.223924	0.094296	-1.151247	0.19092	0.169995	-2.865081	NA	-2.965799	2.553865	NA	-1.083693	0.317549	-0.198189	-0.389834	0.087908	NA	NA	2.08779	0.918576	-1.23553
UPF3	0.239611	0.480141	0.483839	-0.190394	0.949873	-0.961578	-0.203641	0.073641	-0.195059	-1.517404	0.138955	0.238235	0.157654	-1.837182	0.519573	-0.474721	-0.091733	1.553175	-0.18166	0.728964	0.018381	0.147359	NA	1.257008	NA	-0.231898	-0.426697	-0.651946	-1.698463	-0.185505	-0.43761	-0.235153	1.069157	0.613904	-1.292269
URE2	NA	-0.071248	-0.940089	-0.305572	0.003226	-0.612666	-0.091925	-0.247847	-0.427668	-1.395586	-0.036319	0.223318	NA	NA	0.104683	NA	0.121492	-1.080156	0.239262	-0.256712	0.306331	0.121427	1.012413	NA	NA	0.220095	0.655092	-0.772053	-0.785366	-0.080255	0.282087	0.13388	NA	0.099328	-0.649406
URM1	NA	-0.287822	-8.565493	-0.188856	0.310983	-0.711201	0.631692	1.311835	0.471917	-2.015074	-0.19945	0.412383	0.299579	-13.155359	-0.327797	-0.277948	0.266306	-0.626244	-0.317332	0.198483	-0.151791	0.833026	NA	-1.74177	NA	0.10268	-0.160053	-0.1912	-0.339989	-0.207382	0.874266	-0.729168	1.686386	0.093102	-1.027884
URN1	NA	-0.090419	0.319147	0.219752	-0.01915	-0.520802	0.290007	-0.207738	0.700522	-2.607036	0.101848	-0.060351	0.659216	-1.422169	-0.318624	-0.837371	0.493424	0.511346	-0.240427	0.682506	-0.003393	0.256904	NA	0.69162	NA	1.218951	-0.51174	-1.629062	0.725153	0.71743	0.332697	-0.026286	-1.551606	-0.735583	0.04872
USA1	NA	-0.316082	-0.890893	0.416165	-0.969511	0.38427	0.286514	-0.631227	0.771126	0.56033	0.608922	0.170059	-0.262513	-2.056675	0.03074	0.345031	0.423612	-0.009177	0.450852	0.386266	NA	0.075228	0.332113	-0.240743	NA	-0.251341	-0.998583	1.197227	0.207391	0.119648	-0.825366	-0.425675	-0.305802	0.043987	0.383518
UTH1	NA	NA	NA	-0.093418	NA	-0.586362	NA	0.462899	NA	2.485838	NA	-1.870996	NA	NA	NA	-0.173126	-1.722709	-0.243117	NA	-0.451345	NA	-0.537938	NA	3.212789	NA	-0.183885	NA	NA	-1.997831	2.48954	NA	2.34118	NA	NA	-0.423356
VAC14	NA	NA	0.91276	-0.294385	0.842402	-0.093329	-0.087066	-0.109104	-0.842284	1.276434	-0.014909	-0.458819	0.112095	0.176112	-0.273635	0.579232	0.061687	0.992109	-0.870933	0.010523	1.029051	0.140606	NA	-0.816826	NA	-0.01743	NA	-0.650669	0.980126	0.089652	NA	-0.787997	NA	-0.624304	-0.492187
VAC7	-0.276203	-0.686844	-0.039529	0.011803	-0.580229	-0.043529	-0.005829	-0.81789	-0.493042	0.753466	0.120288	-0.256244	0.133553	NA	-0.197328	-0.212754	-0.258988	-0.078821	0.223094	0.263686	0.270753	0.336683	NA	1.064279	NA	-0.060441	-0.178317	-0.554229	NA	-0.126835	-0.14061	0.38877	-0.25945	0.130228	NA
VAC8	NA	0.501937	-2.156266	-0.210697	0.032824	0.208903	-0.122601	-1.336067	-0.996577	NA	-5.055128	0.500517	-1.017187	-1.575621	-0.488223	0.367924	1.42051	-0.646354	-0.090717	-0.316447	-1.592541	0.449127	-0.460029	-2.124818	NA	0.496003	-1.094595	0.099252	-0.436126	0.696255	NA	-0.226545	1.643909	-0.081023	-0.596367
VAM10	NA	-0.273166	-10.754603	0.250205	-0.683586	0.002076	NA	-1.047446	NA	NA	0.451519	0.442728	-0.646862	1.233666	0.495129	0.707907	0.186969	-1.12398	0.016904	-0.458862	NA	0.417943	NA	0.894775	NA	0.226601	0.033063	-0.240734	-0.754613	0.459398	-1.09377	0.140881	0.185934	-0.766207	-0.115805
VAM3	NA	-0.410839	-1.012385	-0.331677	-0.316447	-0.364609	NA	-1.162651	NA	NA	NA	-0.006661	-0.422208	1.658636	0.179858	0.392393	-0.169743	0.704787	0.026504	0.114239	-0.465725	-0.319462	NA	0.860426	1.38718	0.535918	-1.780865	-0.289896	0.728712	-0.000608	NA	0.102351	1.251786	-0.526644	0.234546
VAM7	NA	-2.973083	-1.250369	-0.149236	0.151296	0.117533	-0.16703	-2.697175	-0.099052	-0.321612	0.817332	-0.462386	-0.072024	NA	0.646537	0.840138	0.177217	0.335887	-0.33764	0.396204	NA	-0.316285	NA	0.095485	NA	-0.563027	-1.0902	NA	-0.128535	0.326564	-4.143109	-0.322522	0.236814	0.119536	-0.844146
VHR2	NA	-0.827359	-1.062609	-0.518929	-0.159793	1.41911	0.651314	-0.058245	0.539092	-1.976079	0.307857	1.252475	-0.014688	NA	0.432271	0.349741	0.218455	0.092121	1.243726	-0.416125	NA	-0.022821	NA	-0.479181	NA	0.402808	0.244562	0.402173	0.561665	-0.349548	NA	0.035713	-0.301841	0.985295	0.155639
VID22	NA	-0.46122	-0.217401	-1.036787	NA	0.009197	-0.013463	-1.913676	0.140448	-3.590352	0.551897	NA	-3.084669	-3.231659	-0.104349	0.249147	0.508199	NA	0.274763	-0.29525	-4.884288	0.111894	0.559427	0.511657	0.163019	-0.881442	NA	-0.189945	-2.325046	0.425492	-2.015092	-0.041662	1.888043	0.271455	-0.078511
VIK1	NA	NA	NA	0.533405	NA	0.131546	-0.046703	-1.020494	0.631129	-4.151071	0.482881	0.60833	0.124086	-1.679342	0.155311	0.620493	-0.147203	0.893384	0.091435	0.075338	NA	1.410663	NA	-1.065171	NA	0.2041	-0.691563	-0.106052	0.547107	-0.045931	-0.499238	-1.655038	0.91132	0.175987	-0.126327
VIP1	NA	-1.288429	-0.256224	0.076675	-0.242185	0.66613	0.633164	1.135664	-0.274603	NA	-0.095276	-4.669736	-1.177822	-0.144237	0.052648	-0.392102	0.252786	0.374926	-0.391857	0.214092	-1.265788	0.412037	NA	0.681483	-4.110376	0.164086	NA	-0.911808	-0.16971	0.216783	0.9211	-1.021798	NA	0.133823	-0.07246
VMS1	-5.044322	-1.141702	-0.581489	0.372321	-0.10878	-0.016884	0.266162	NA	-0.031078	0.08846	0.309338	-0.078939	0.191137	-0.198741	NA	0.995006	0.050598	-0.06028	0.55872	0.24031	-0.116997	0.216426	-0.445583	-0.12349	NA	-0.6791	-0.017846	0.523518	-1.119884	-0.126878	0.375613	0.970672	0.055271	NA	0.143809
VPS1	0.095721	0.395927	NA	-0.099996	-0.584211	-0.623601	0.122824	0.981792	-0.017827	-2.832959	0.145582	0.167807	0.2622	NA	0.411087	-0.186034	-0.410517	-0.855375	0.363003	0.695062	0.205194	-0.378299	NA	-1.275527	-11.989234	1.080256	-0.058235	-0.575551	0.251105	-0.334449	NA	-4.001108	NA	-0.415908	-1.184713
VPS13	NA	0.126206	-2.031139	-0.474458	0.193133	-0.131548	-0.034873	-0.593132	-0.008882	NA	-0.277524	0.32589	0.613804	1.203689	-0.213061	-0.727765	-0.449229	0.676407	0.2086	NA	-0.066575	0.621715	NA	0.019769	NA	-0.561455	NA	0.262268	0.161613	-0.194864	-0.005444	0.047806	0.188699	0.159948	0.721392
VPS17	NA	NA	NA	0.486827	NA	0.216103	NA	NA	NA	NA	NA	-0.46855	-0.831857	NA	-0.122873	0.054856	-0.259086	NA	0.024487	-0.371058	NA	0.115048	1.073727	0.777638	-0.217965	-0.064889	-1.526986	0.192199	-0.445167	0.084143	NA	0.016083	0.314945	-1.181139	0.10605
VPS21	NA	-0.629814	NA	0.535306	-0.469462	0.044196	NA	2.384694	NA	NA	0.49308	-0.532831	-0.726814	NA	0.331446	0.348653	0.18064	-0.031139	-0.464899	0.337419	-1.015039	-0.741458	0.566	0.685281	NA	-0.514942	NA	-1.141675	0.049865	0.030838	2.314746	-1.985273	0.555128	-0.114038	0.479764
VPS24	0.08492	NA	-0.403661	-0.153956	0.323502	0.00531	NA	NA	0.302451	-4.370235	-0.167391	0.391038	-1.572469	-5.270473	-0.181123	-0.318335	0.587219	0.043352	0.071144	-0.050435	-1.63982	0.530017	NA	0.455954	-1.843391	-0.53398	NA	-0.50793	0.264814	0.086574	NA	-0.696268	1.30807	0.600828	-0.798686
VPS27	NA	-2.670474	NA	0.523582	-0.054522	-1.242798	-0.314854	0.275033	0.446565	NA	0.325712	-0.601789	-0.299034	0.625671	-0.035865	0.962042	0.302234	0.073594	-0.105131	0.047608	NA	0.480176	NA	0.401695	NA	NA	-2.894219	0.679093	1.150056	0.837745	-1.638835	0.002634	0.939637	0.60044	-0.21589
VPS29	-4.492486	-0.633577	-3.860953	0.157267	-0.262957	0.306404	0.308162	0.286232	-0.829953	-0.838007	-0.288655	-0.453331	0.077405	2.300199	0.017439	0.802152	-0.380914	0.136732	-0.925553	-0.316653	NA	-0.353439	NA	-0.132818	-3.362708	-0.190576	0.005779	0.221501	0.701989	-0.020353	NA	0.520719	0.847359	-0.760241	0.029267
VPS30	NA	NA	-2.222907	-0.374806	NA	-0.631273	0.207721	0.132955	0.282375	0.185296	0.043644	-0.236662	0.867533	0.75555	-0.222877	-0.619404	-0.096937	-0.426968	-0.151866	0.087888	-0.836067	-0.061557	0.410496	0.09543	NA	-0.449234	0.181693	-0.664704	0.359582	0.330545	0.942991	-0.161771	NA	-0.220675	-0.328827
VPS35	-3.016143	NA	-4.918706	0.185835	0.289657	0.024818	0.040956	0.136367	-0.61892	0.290484	NA	-0.419121	-0.247554	NA	-0.269553	-0.079858	0.275686	0.168427	0.106837	0.026497	0.545196	0.44505	0.408224	-0.067442	-4.823793	-0.636442	-0.178987	-0.437293	-0.375905	-0.147684	0.222171	0.144898	-0.093871	-0.710535	-0.130957
VPS38	NA	0.34979	-0.239003	-0.701661	0.473261	0.314948	-0.466871	0.615787	-0.527759	NA	-0.117153	0.420062	0.023076	NA	-0.090272	-0.639696	-0.625685	0.240828	-1.084796	0.039188	1.145212	-1.087402	0.363451	0.807578	NA	0.094001	NA	-0.457628	0.852445	0.742079	NA	-0.153722	-0.327894	-0.631589	0.406013
VPS41	NA	NA	-2.463172	-0.184066	-0.360953	-0.145283	-1.576623	NA	0.160897	2.981801	NA	0.305748	0.202658	NA	NA	0.792414	-0.044789	-0.063465	0.085685	-0.410696	NA	-0.719482	0.420952	NA	NA	-0.152511	-1.038226	-0.408084	0.235273	1.138529	NA	NA	0.676237	NA	-0.205496
VPS5	NA	0.357654	NA	0.133113	0.038405	1.136006	NA	1.224719	NA	NA	-0.765987	1.254382	-0.680642	-0.864001	0.129822	0.385811	-0.761204	-2.717155	-0.243808	0.161658	NA	0.456239	NA	-0.256334	NA	-0.835517	-1.706004	-0.759562	0.343111	-0.123837	0.016399	-1.585514	0.946605	-0.699719	-0.261777
VPS51	NA	-0.519499	-2.797153	-0.096477	NA	-0.330722	0.330012	NA	0.529601	NA	-0.102358	0.4729	NA	NA	-0.495647	0.104125	0.567141	NA	0.044163	0.416872	0.122495	-1.291595	-0.012717	-0.760332	NA	-0.405037	NA	0.048328	0.105772	0.254396	0.243643	-1.939467	0.910698	-0.137625	-0.010517
VPS53	NA	NA	NA	-0.136065	NA	0.072054	-0.028356	NA	-0.110042	-1.680965	-0.33682	0.0499	NA	-1.592108	0.288622	0.263229	0.356271	-0.057366	-0.231762	-0.117336	NA	-0.806969	0.70425	0.758605	2.331645	NA	-1.441295	-0.795472	-0.093592	0.410796	0.600643	-0.045704	1.417795	-1.56575	-0.159989
VPS70	0.074973	-0.515547	NA	-0.391937	-1.356978	0.156755	-0.506154	-0.397413	-0.747394	-1.43625	0.003532	-0.340719	-0.006492	-0.683292	-0.003395	0.218564	0.451981	0.860848	0.533968	0.347321	-0.337921	0.262157	0.534287	0.245795	NA	0.691527	-0.071382	0.20533	-0.336039	0.234312	-0.103605	-0.233048	1.090861	0.077775	0.167759
VPS71	NA	-1.663616	NA	0.381144	-0.697782	0.05752	0.546988	-3.128792	NA	2.888329	NA	-3.799518	NA	NA	-0.065004	0.868795	-0.031199	-0.614924	-0.684456	-1.585581	NA	-1.468783	-5.568417	NA	NA	0.25576	-1.897975	-0.247907	0.760669	0.792013	NA	0.88946	NA	NA	0.876313
VPS74	-0.738294	0.211762	0.672243	-0.397916	0.264531	NA	0.358897	0.319469	0.008119	0.766612	-0.259179	0.809542	0.546077	-1.267991	-0.644924	0.13308	-0.567393	-0.260495	-0.457084	0.983621	0.397598	0.496544	NA	0.36905	NA	-0.198661	-0.050188	-0.209018	0.225033	0.096633	-0.009476	NA	NA	-0.52813	-1.579022
VPS75	NA	NA	0.570861	-1.602136	-1.887445	-0.580188	0.483923	0.953863	0.3799	-1.844419	0.601866	0.676063	-1.063208	NA	0.378377	NA	0.471471	-0.408297	-0.064668	-1.410249	NA	0.135618	-1.288998	NA	-8.659134	1.358132	NA	-0.081622	0.012736	0.425457	1.631344	-1.133746	NA	-0.278799	-0.117771
VPS8	NA	-3.860006	NA	0.109992	-0.372284	0.025299	0.72351	-0.841822	-0.083556	-2.011523	0.251416	-0.589579	-0.159257	NA	0.376824	0.228849	0.031268	-0.80919	0.6871	0.051155	NA	0.313995	NA	1.823808	NA	-0.808486	NA	-0.251205	0.455095	0.302532	1.485223	-0.680299	-0.021333	-1.771442	-0.345157
VPS9	-0.418616	-3.457262	NA	0.446597	0.340163	0.580302	0.494601	-1.229577	-0.580807	-0.605736	1.2293	-0.820119	-1.1001	0.659441	0.789371	0.482209	0.242093	-0.711533	0.7288	0.210519	NA	0.283933	-1.687373	1.33465	NA	-1.03107	-2.29169	0.334815	0.595611	1.15426	-2.514327	0.711403	1.058326	-1.910722	-0.021142
VRP1	NA	-4.122308	NA	0.590254	-1.893347	0.020074	-0.596816	-2.773498	0.299494	1.579169	0.828648	-1.095941	-2.175483	NA	-4.013063	-0.037842	0.728028	-1.27384	0.721386	-0.224353	-1.808645	NA	-0.748561	-2.316458	NA	-1.678329	NA	-0.233578	-0.822306	0.453007	-1.05066	0.44335	-2.694997	-1.325589	NA
VTA1	0.448804	0.503498	0.037901	-0.825602	0.50909	-1.10008	-0.091226	0.384725	-0.207299	NA	NA	0.556056	-0.364751	0.038423	-0.785997	-0.448781	-0.135269	0.36527	0.257543	0.329074	0.426927	-0.280974	NA	0.4273	NA	-0.325222	-0.052414	-0.56622	-0.09327	0.042313	0.756904	0.371323	-0.681737	-0.32778	-0.541184
VTC1	-0.571112	-0.671154	-0.335788	0.150384	0.411068	0.272807	-0.511206	0.033462	0.437543	-2.434187	0.457936	0.279495	-0.275019	NA	0.628948	0.526332	0.412564	-0.202237	1.370035	0.860876	-0.726551	1.279912	NA	0.008376	NA	-0.090996	0.651118	NA	0.250724	-1.318074	NA	0.401357	NA	0.894239	-0.19954
WHI2	NA	-0.530612	-1.039432	-0.075762	0.141067	-0.422694	NA	-1.721973	NA	NA	-0.052154	0.292949	-0.188076	-2.738204	0.63172	0.678899	0.345191	-0.118506	0.581099	NA	-1.209838	1.284534	1.036357	1.144207	NA	0.310522	0.056641	0.568869	-0.385203	0.184146	NA	-0.228672	0.769573	-0.109897	-0.001732
WHI4	NA	NA	1.296886	0.099539	NA	0.576933	-0.572109	NA	0.744413	0.746032	-0.098481	-0.066714	NA	-1.66103	1.826003	0.281024	-0.478041	0.485487	0.690116	-0.114268	NA	-1.093955	NA	0.361836	1.954661	0.743195	0.60948	0.776132	0.115851	0.082012	-0.428065	-0.791981	-0.436707	0.455961	-0.290431
WHI5	NA	0.711621	-0.695312	-1.95363	0.218169	0.134915	NA	-1.427986	NA	NA	-1.052446	-0.688439	0.360979	-2.330527	0.472865	0.445958	-1.416653	-0.173693	-1.177954	0.560357	0.541456	-1.635613	0.96136	-0.278229	NA	0.727061	-0.209537	0.461057	0.329876	0.921185	NA	-1.028655	-1.166182	0.323064	-0.532583
WSS1	-0.457975	-0.389395	0.09406	0.645323	-0.147092	0.403059	-0.175029	1.500228	0.377379	-0.032701	0.106799	1.157176	-0.693377	0.211631	0.043049	-0.091472	-0.034976	0.098411	-0.64083	-0.029356	-0.66349	-0.183298	-2.429434	0.069052	-1.047136	0.285826	-0.425575	-0.299042	NA	-3.544466	1.7714	0.198897	0.298133	0.456167	0.246038
XRS2	-1.111911	-1.184578	NA	0.158891	-1.141676	NA	-0.392497	NA	0.364225	0.285991	-0.878853	-2.819804	2.803824	NA	-0.075432	0.678164	0.351791	0.381393	0.161885	0.094668	NA	1.705479	-2.205311	0.498297	NA	-1.348611	-1.444008	0.623179	-1.60316	0.491128	NA	NA	NA	1.036139	-0.844613
YAP1	NA	-0.151818	0.512369	-0.104986	0.385073	-0.035402	-0.002337	-1.199887	0.282088	0.06918	0.360196	-0.096111	-3.624507	NA	0.015369	0.52345	0.273122	-1.384897	0.327975	-0.896825	NA	0.4372	-2.182963	0.413011	-3.611197	0.245358	-0.833993	0.07187	0.082281	0.699792	-0.227566	-0.150467	0.591352	-0.29725	0.197432
YAP3	NA	-0.029919	0.192253	0.311169	0.339036	-0.588858	-0.141869	-1.026098	-1.536435	NA	-0.712849	-0.567013	0.284982	-0.079065	-0.579259	-0.219911	0.034935	NA	-0.886835	0.092819	0.328516	0.010648	NA	2.588678	NA	0.271579	0.412643	-0.608978	0.066254	-0.205224	-1.208686	1.059716	0.343098	0.668065	0.517187
YAP5	-0.061119	0.188115	-0.493782	0.287421	NA	0.232601	-0.426004	-1.612711	-0.651728	0.05254	-0.432171	0.286769	-0.626961	0.563494	0.704815	0.109219	0.393332	-0.092675	0.340752	0.367472	-0.215106	0.187314	0.533219	0.363879	NA	-0.238359	-0.097089	0.163862	0.65777	-0.071072	-0.424572	-0.330028	0.020251	0.510316	-0.385344
YAR1	NA	-0.039125	-1.026923	-0.804281	NA	0.621674	-0.303766	1.308416	0.106845	NA	0.446832	0.113555	0.134707	0.205209	0.157007	-0.42283	-0.728783	0.290249	-0.141679	-0.312424	-0.816958	0.494893	0.554365	0.189137	NA	0.204204	-0.436422	0.037198	NA	0.104894	0.326601	-0.779632	0.606496	-0.292142	-0.264123
YBL036C	NA	0.012693	NA	0.249367	0.040508	-0.068094	0.286775	-0.322327	0.028915	-0.141117	-0.148956	0.337751	-0.393081	NA	-0.151303	-0.289103	-0.265696	-0.231186	0.245923	-0.058149	-0.146863	0.545877	-0.289341	1.572998	-2.191595	0.65278	-0.376437	-0.035666	-0.065437	-0.072272	0.127784	0.077825	0.507311	0.343232	-0.242131
YBL081W	NA	NA	NA	0.397547	-1.125504	0.669802	0.707339	NA	1.352839	-1.319989	0.649804	-0.57403	-0.845774	-1.497793	0.655338	0.975034	-0.037294	-0.229094	0.69518	-0.571194	-1.696528	0.177425	NA	0.549297	NA	0.118623	NA	0.721867	0.454495	0.490736	NA	-0.170496	0.061125	0.271634	0.400646
YBL086C	0.42497	0.097689	-0.012361	0.06178	-0.024753	-0.819509	-0.967247	-0.458039	0.548692	1.976237	0.302465	0.394695	-0.380617	0.540599	0.361755	-0.359422	0.296557	-0.256704	0.526859	-0.390262	-0.641202	0.494806	-0.28641	0.744264	NA	0.112328	0.182125	0.010777	-0.966637	-0.077277	-0.653747	0.208098	0.61006	0.434823	-0.308609
YBP2	NA	0.236182	NA	-0.241899	-0.787531	0.369146	0.3068	NA	0.155387	-0.638598	-0.887221	0.155385	0.220185	NA	0.071427	-0.235975	0.433676	-0.055858	-0.252541	0.801335	0.471829	-0.619391	0.3216	1.272979	-3.666489	0.024168	0.664124	-0.071588	0.461796	-0.333915	0.712669	0.445742	-0.55024	-0.305551	0.626287
YBR141C	-0.481714	0.10903	-0.170787	-0.410288	0.100256	0.057717	0.218418	0.172729	0.158327	0.16487	NA	0.368301	0.039145	NA	-0.100902	0.002155	0.561664	-0.19877	0.269431	0.112696	-0.19922	-1.389962	NA	-0.102846	NA	-0.336353	-0.51872	0.348512	0.708753	0.076673	0.047471	0.43218	-2.174782	-0.078487	1.071303
YBR238C	3.845954	-2.600768	0.837395	0.128138	NA	NA	-1.138677	-0.608518	-0.087383	2.225068	NA	-0.434116	NA	NA	-0.494096	-0.352076	-0.147326	-0.457714	NA	0.123405	NA	0.109078	-0.573531	-0.464332	NA	-0.103091	NA	-0.436192	0.013747	0.032324	NA	0.858643	NA	-0.327237	-0.685066
YCH1	0.210662	0.077385	-0.431867	0.133487	-0.249907	-0.207127	0.003632	-0.052302	0.710448	-0.545707	-0.385559	0.112641	-0.163583	-0.217145	0.028077	0.190096	0.066572	0.29328	-0.053043	0.066049	0.529887	0.762498	-0.205274	-0.136702	NA	0.043042	0.662524	0.325918	0.421398	-0.081537	-0.009777	-0.027764	-1.072362	-0.31013	-0.68623
YCK1	NA	-0.221913	-0.736275	0.431958	-0.206509	-0.287874	-0.229583	-0.62736	0.47644	-0.523654	0.860625	0.645437	-0.116481	-1.250131	-0.248464	-0.153421	0.016144	-0.33025	1.106843	0.932305	0.417205	0.292614	0.057386	0.402206	-1.616947	-0.025611	-0.284309	-0.115822	0.572184	0.129748	NA	0.727195	NA	0.05296	-0.628508
YCK2	-0.850492	-0.889625	-0.083222	0.372017	0.362538	0.424892	0.018829	-1.060935	-1.163638	-1.030767	NA	0.353657	0.385018	-0.486441	-0.140994	NA	-0.26269	0.036624	-0.150219	0.29511	0.203687	0.751916	0.554903	0.400402	NA	-0.550496	0.812656	1.227173	-0.192982	-0.079171	-0.680933	0.163904	1.095553	1.130353	-0.402839
YCK3	-0.421356	0.108664	0.287929	-0.314001	-0.608382	0.035921	0.7667	-1.693862	-0.918691	0.338368	-0.574386	0.2179	0.039165	-4.151493	0.104769	-0.152674	-0.538726	0.295307	NA	-0.106834	0.772249	-0.164434	0.262553	-0.480552	NA	0.457235	0.528052	NA	NA	-0.25908	NA	0.467703	NA	0.141947	-0.80153
YCL001W-A	NA	NA	-0.04187	NA	NA	-0.939251	-0.411363	0.965878	-0.921492	2.09231	NA	NA	-0.246422	2.882966	-0.644679	0.082329	-0.148774	NA	0.542821	-0.034336	-0.239197	-0.168268	0.283557	0.592362	NA	-0.08795	-0.603322	0.232138	0.929771	0.36148	0.917745	-0.461142	-0.608993	-0.292921	-0.498592
YCR050C	0.039598	0.686372	-0.173076	NA	0.462236	-0.302871	-0.31166	1.065614	-0.599051	0.657958	-0.549238	NA	0.135638	NA	0.439862	-0.161285	-0.014969	NA	0.329146	-0.690382	0.6632	-0.223964	0.605578	0.832898	NA	0.456182	0.483476	0.126313	0.583153	-0.21324	1.021366	0.06069	0.028099	0.273835	-1.023581
YCR061W	0.315353	0.916694	0.191537	NA	-0.586696	-0.494741	-0.23624	-0.241846	0.035897	-0.097376	0.173525	-0.009153	-0.315998	NA	0.640017	-0.438202	-0.205724	NA	0.800689	-0.284759	NA	-0.476519	-0.197493	0.023828	NA	0.193047	0.580602	0.386085	0.112473	-0.462357	0.910912	-0.265235	-0.45984	0.05083	0.729813
YDJ1	NA	-0.768507	NA	-0.90159	-2.181033	0.609464	0.19992	-2.950039	0.69559	-1.98784	-1.424605	-1.235533	0.479599	-0.503772	0.698736	0.56011	-0.512188	-0.769649	-0.651998	-0.369249	-0.975508	0.096696	-5.862575	2.068335	-4.714107	-0.244205	-1.823529	0.140621	0.576162	0.600223	-1.924685	0.387216	-0.803347	0.447216	NA
YDL176W	NA	NA	NA	-0.361538	0.906547	0.266914	0.497977	0.283389	-0.842225	-0.809237	-0.119298	0.451452	0.38295	0.935896	0.127367	0.025581	-0.304228	-0.475476	0.324195	0.309794	0.550987	-0.377261	NA	0.591858	NA	0.121869	0.067869	-0.368763	-1.530659	-0.025691	-0.61858	-0.66711	0.38048	0.0546	-0.465169
YDR061W	NA	0.104447	-1.297782	-0.064689	-0.066841	0.767485	-0.084325	NA	0.778355	1.209826	-0.657544	-0.444703	-1.052407	-1.291033	NA	0.098996	-0.21661	-0.000486	0.623834	-0.367619	NA	-0.917419	0.228612	-0.706236	-0.789667	0.399798	-1.189119	1.411378	0.62461	-0.089217	0.158659	0.1558	-1.121855	NA	0.940816
YDR131C	NA	NA	-0.109857	-0.257884	-1.626734	0.310795	0.105549	-0.237559	1.168075	2.318053	NA	0.397173	NA	NA	NA	0.151147	0.239711	NA	-0.083401	-0.157842	0.285697	NA	NA	NA	NA	-0.181043	NA	-0.455161	NA	0.079418	NA	1.444487	-0.169296	NA	-0.249116
YDR161W	NA	-1.582827	0.481797	-0.167865	-0.485358	0.440579	-0.435806	-0.960455	0.338344	NA	-0.029253	-0.050523	NA	-2.72673	NA	0.28117	-0.453037	0.266756	0.374802	0.175337	NA	NA	NA	1.395192	NA	-0.328873	0.036894	-0.318066	-1.826152	-0.056368	NA	0.86043	0.283736	NA	-0.42698
YDR306C	NA	NA	0.127416	-0.632858	-0.106165	0.370736	0.013162	-0.651457	-0.697696	0.09956	0.178611	0.003076	0.292344	-1.877787	0.355525	0.151339	0.721895	0.975617	0.498412	0.302746	0.537218	NA	0.674742	-1.038173	NA	-0.016859	0.197791	-0.043559	0.389919	-0.25283	0.077234	NA	NA	0.89933	-0.875893
YEF1	NA	-0.426581	NA	0.053647	0.553862	-0.500005	0.21373	-0.118576	-0.282458	0.59745	0.061082	0.261517	0.377934	NA	-0.855338	0.116183	0.47689	-0.236375	0.317439	-0.105448	-0.320797	-0.57701	-0.346225	-0.409825	NA	0.295879	0.11914	-0.955257	-0.897283	-0.542854	NA	0.647186	-0.200502	0.128805	-1.728089
YEL043W	NA	-1.488429	-0.918601	0.027639	-1.358385	0.462087	0.124167	-0.697107	0.34365	-0.503212	0.636821	-0.645719	-0.012096	1.33906	0.243343	0.148665	0.644052	0.689214	0.361082	0.92131	NA	0.442672	-0.193406	-0.450282	NA	-0.425207	-1.553003	-0.470004	-0.271038	0.362764	0.123373	-1.250739	1.27563	-0.369159	0.799328
YER156C	NA	NA	0.798254	NA	NA	NA	0.280909	NA	NA	NA	NA	0.775822	NA	NA	-0.114409	-0.330299	0.471291	-0.101458	NA	0.463535	NA	-0.181051	NA	-1.404904	NA	0.975674	NA	NA	NA	0.848163	NA	0.615575	-0.523203	-0.713563	NA
YGL081W	-1.062746	0.437379	NA	-0.368086	-0.788167	0.56433	-0.289598	-0.268736	0.233288	-1.63896	-0.040369	0.263285	0.191281	NA	-0.059785	0.396218	-0.729364	0.704143	-0.184277	1.538468	NA	-1.038271	NA	0.580099	NA	0.118585	-0.137782	NA	1.534652	-0.221484	-2.537503	-0.649805	0.181845	0.758153	-0.724078
YGL242C	-0.003612	-0.027949	-0.073083	-0.482287	NA	0.960684	-0.286305	NA	-0.399589	-0.428389	0.359684	-0.154326	0.101248	-0.795074	0.276377	-0.075509	0.318342	1.215714	0.752444	0.413925	0.181414	-0.081982	0.676866	0.251403	-8.41114	0.263935	0.416295	NA	1.045642	-0.564412	-0.200655	0.826808	NA	0.433081	0.532763
YGR054W	NA	NA	NA	0.465584	0.310931	1.236487	0.598925	-0.20334	1.373357	-1.585969	-0.259186	0.529728	NA	-1.807586	0.446232	0.771818	-0.618134	0.166295	0.382155	-0.232184	-0.509591	NA	NA	1.720562	NA	-0.408523	-0.191344	-0.15219	-0.562441	0.092964	-0.1612	-1.050448	-0.810082	-0.242468	0.37825
YGR122W	NA	NA	NA	0.207613	-0.106865	-0.81676	0.245909	0.753183	-2.296221	3.434284	0.850446	-1.712833	NA	NA	0.083067	0.530783	-0.342959	-2.585077	-0.135214	-1.589373	NA	0.480606	NA	-2.753281	NA	-0.137742	-2.471948	0.083407	0.517885	-0.38267	NA	-2.53595	1.598111	0.061147	0.032061
YGR237C	NA	-0.100557	-2.636438	0.912845	0.285486	0.036658	-0.336662	0.44521	0.392596	0.90919	-0.004758	0.661525	-0.611262	-0.740694	0.10987	0.024318	0.769767	-0.391166	-0.458917	-0.522857	-0.484318	0.241069	NA	1.112996	NA	0.806183	-0.481256	-0.202921	0.368253	-0.164848	NA	0.284968	0.327511	0.061905	0.013703
YHP1	NA	-0.638342	-0.174381	0.066137	-0.569097	NA	-0.41236	-0.991459	-0.17762	1.672564	0.502666	0.813354	0.205672	-1.971929	1.441042	0.500618	0.131913	0.484154	0.298475	-0.404387	-0.020167	0.510915	NA	-0.697843	-2.09881	0.411701	0.404867	0.405734	0.427444	-0.094409	-0.898748	-0.480156	0.918124	-0.418346	0.810611
YHR078W	NA	0.400633	0.448599	-0.880869	0.245051	-0.364255	-0.113375	-0.061371	-0.126583	2.806108	0.467344	0.261948	0.387025	0.445182	-0.366953	-0.006427	-0.327905	-0.297158	-0.662685	0.00685	0.390569	-0.985201	NA	-0.306157	0.813341	-0.039903	NA	NA	0.966309	-0.325761	NA	0.416529	NA	-0.512272	-0.913785
YIL029C	4.258302	-1.379746	0.482053	-0.160071	-0.4284	-0.088732	-0.225245	-1.440017	-0.446673	NA	NA	0.69468	0.023331	-1.67048	0.050376	0.356279	0.609343	0.062469	-0.054228	-0.433764	-0.306229	-1.210182	0.813539	0.472687	NA	0.040535	0.525601	0.265367	-0.889187	-0.003883	2.861436	-0.711716	1.31162	-0.467019	0.783315
YIP3	NA	NA	-0.314688	-0.406137	0.605147	-1.093006	-0.457742	0.514504	-0.230561	1.437809	0.214323	-0.048479	0.501541	NA	-0.91256	-0.560906	-0.533126	0.175933	-0.01825	0.399092	0.528214	0.033568	-0.11306	-0.314088	NA	0.646056	-0.595049	-0.279791	-0.480162	-0.179691	-0.12858	0.962478	-0.773516	-0.506368	-0.038384
YIP5	NA	-1.451164	-0.045375	-0.296123	-0.122972	0.110398	0.052217	-1.07892	0.91791	NA	0.233223	0.074586	NA	-2.481379	0.085785	0.07195	0.130022	-0.204537	0.468434	0.308429	NA	-0.637297	-0.193168	1.247797	NA	-0.001261	-0.114268	NA	0.049694	0.300431	-1.238676	0.333313	0.119828	0.230161	-0.06266
YJL055W	NA	NA	0.397668	NA	NA	0.195373	0.768084	-1.507551	-2.507972	3.495719	NA	-0.345991	NA	NA	0.067316	-0.145152	-0.137807	NA	-0.769493	NA	NA	0.424906	NA	NA	2.262674	NA	-0.341608	0.677677	-0.616411	-0.102147	NA	0.5494	-0.556526	0.368997	NA
YKE2	NA	0.583737	-0.224773	-1.856705	-10.360784	-0.877232	-0.839216	0.924878	0.335773	NA	-0.42565	0.731136	0.423137	-3.282012	-0.216778	-0.376963	-0.701115	-0.445347	-1.195876	-0.104078	0.628241	-0.521452	0.542224	0.071381	-2.788624	0.031863	NA	-1.930619	-0.212318	-0.230235	1.226997	NA	0.405668	-0.321506	-0.758595
YKL023W	NA	NA	0.25221	-0.087254	NA	-0.125528	0.893377	NA	0.367587	NA	NA	-0.23698	NA	NA	-0.191634	-0.270035	0.022672	NA	-0.363214	0.14993	-1.326048	0.081055	NA	1.04332	NA	-0.191495	NA	-1.024015	-0.122912	0.313343	NA	-0.435172	NA	0.317917	NA
YKU70	NA	NA	-0.507119	0.410021	NA	1.028932	-0.08045	0.735711	NA	NA	0.743683	0.09145	NA	NA	0.356356	NA	NA	0.417374	0.677229	0.053744	-0.754196	0.69623	-0.307755	0.82593	-1.422319	0.134775	0.098051	0.980237	NA	NA	0.808514	0.340643	-2.225073	0.784659	NA
YKU80	0.356559	-0.511956	-0.579379	0.141888	0.080274	1.061742	0.974895	0.07905	-0.082355	0.22273	0.411599	-0.4379	-2.19112	-1.156629	0.281367	0.314752	0.809585	0.245779	-0.659905	0.261016	NA	-0.160998	1.475999	1.146891	NA	0.222717	-0.342252	0.660371	NA	NA	0.150411	-0.384444	NA	0.795595	-0.165351
YLR177W	-0.242185	-0.44064	-0.107047	-0.073062	-1.149771	0.402621	-0.565721	-1.934123	-1.012911	1.11016	0.557097	-0.176261	-0.763004	-1.93788	0.485527	0.442412	0.256783	-0.437549	0.228961	0.337396	-0.158862	0.018742	NA	1.063288	-6.385864	0.892919	0.091979	0.497506	-1.472394	0.499346	NA	0.379279	1.24627	-0.238586	-1.144037
YLR224W	NA	0.076375	-0.521488	0.544285	0.526395	-0.228059	-0.318089	-0.039195	-0.251796	0.042438	-0.004504	-0.410442	0.339109	0.338804	-0.204242	-0.481559	-0.244251	0.097243	0.399263	0.261862	-0.525707	0.590263	NA	0.47768	NA	0.175568	0.549807	0.170624	-0.511616	-0.376383	-0.886766	0.571822	-0.917376	0.090931	-0.526033
YLR278C	3.874654	0.074439	0.168649	-1.027616	0.28744	0.141757	0.172917	-0.127092	0.189818	1.40713	NA	-0.293862	0.328486	0.520032	-0.179612	-1.265029	0.253488	-0.387903	-0.000843	0.142794	0.049729	0.397893	0.07848	0.145929	NA	-0.622948	0.72786	-0.405212	-0.010014	0.10855	NA	-0.118929	0.032237	-0.068647	0.543335

YLR287C	0.10981	-0.203052	-0.142776	0.382654	0.131613	0.943288	-0.009442	-0.928173	-0.295115
YMD8	-0.555519	-0.07932	-1.376972	-0.286763	0.199263	0.358151	-0.232472	0.124695	-0.132908
YME1	NA	-0.468542	-0.088231	0.028367	-0.774814	0.028984	0.16238	-0.550362	0.460256
YML108W	NA	0.036395	0.284882	-1.318937	-0.221076	-0.370633	0.747976	0.088485	0.41016
YML119W	NA	NA	-0.667276	0.593805	0.536639	0.452685	0.502087	-0.50306	1.012785
YMR010W	NA	-0.575342	-0.999227	-0.578655	-0.183282	-0.270589	-0.223971	-1.891606	0.357867
YMR102C	NA	-0.096765	1.55854	-0.606216	-0.643875	-0.900131	-0.66166	0.226838	0.132375
YMR111C	NA	0.25401	-2.501808	-0.574082	-0.211688	0.280508	0.461806	0.88143	0.594064
YMR209C	NA	0.393062	-0.565974	-0.060533	-0.492291	0.605746	-0.829612	-0.642257	-1.026163
YND1	NA	0.19819	NA	-0.918368	NA	-0.505164	-0.958622	0.054199	-0.843923
YNG1	NA	-0.768364	0.032014	-0.1279	0.686011	0.106533	NA	0.21534	NA
YOR342C	0.074294	0.491896	0.129232	0.510446	0.700692	-0.547361	0.450114	-1.263699	0.174073
YOS9	NA	0.338468	-0.13739	-0.11461	-0.037611	-0.451496	-0.211333	NA	-0.024966
YPL041C	NA	-0.323669	-0.410265	-0.313152	0.422245	-0.34537	0.230736	0.364546	-0.463727
YPL068C	NA	-0.487526	0.215003	-0.592602	-0.909495	0.620284	0.474914	1.174918	0.472169
YPL113C	NA	NA	-0.587989	0.397476	NA	0.25521	0.148069	0.779963	1.09228
YPL150W	-1.570363	0.16401	-0.798845	0.274205	NA	0.105036	0.11057	0.807596	-0.018746
YPR022C	NA	-0.330676	0.056873	0.131985	0.090602	0.50049	-0.356371	-0.068453	-0.269752
YPR063C	NA	0.213984	-0.286627	-0.817255	0.506432	-0.717167	-0.124981	0.924116	-0.449128
YPR174C	NA	0.223934	0.161179	0.090041	0.326643	-0.009944	-0.022112	-2.54359	0.080106
YPT31	NA	-1.079446	-1.894573	0.049302	0.030856	-0.028583	0.75531	0.812438	0.572478
YPT6	NA	-2.745333	-14.949139	0.30968	-1.360655	0.97334	-0.164856	0.159239	0.144886
YPT7	-4.047993	-2.037995	-4.570093	-0.073712	-0.027145	0.022601	0.29665	-1.140852	0.368656
YSN1	NA	0.002647	NA	-0.413475	0.444323	-0.221829	0.386218	-0.608774	0.736978
YSY6	0.382451	-0.171691	-0.322934	0.104023	-1.121529	-0.041705	0.051074	-0.287038	-0.508791
YTA7	NA	-0.868892	NA	-1.294093	-2.15615	-0.061243	0.539068	1.429739	-1.224755
YUR1	-1.466841	NA	-0.857751	0.819944	0.55804	0.855987	0.025418	0.415013	2.09142
ZDS1	NA	-0.068953	-1.870043	0.83929	-0.196104	-0.324194	0.142564	0.637211	0.650885

YLR287C	0.391959	0.334541	0.008918	-0.405362	-0.259799	0.916258	0.313816	0.667764	0.008548
YMD8	-0.938672	0.148346	-0.162921	-0.460773	0.045519	0.242948	0.076651	0.463577	-0.058688
YME1	-8.225522	-0.139471	0.345578	0.354925	-0.352525	0.800673	-0.017335	0.133479	0.364053
YML108W	1.311267	0.18635	-0.027503	NA	0.090239	-0.349082	-0.059482	0.583134	0.432262
YML119W	-0.80395	0.586521	0.089415	0.075173	0.100912	0.089966	-0.070154	0.64994	-0.401044
YMR010W	-1.323407	0.812066	0.600991	0.082957	-0.813245	0.10402	0.364657	-0.290785	0.205646
YMR102C	0.530073	-0.102143	-0.959764	0.141845	0.58663	-0.055627	-0.046261	-0.213396	1.324051
YMR111C	-5.217387	-0.420206	-0.099695	-0.204938	NA	-0.288627	0.094061	0.746542	-0.371938
YMR209C	NA	0.670395	0.647944	NA	0.095735	0.685459	0.664141	0.746548	-0.515412
YND1	1.347607	NA	0.215585	NA	NA	0.341064	0.382823	0.323135	0.067568
YNG1	NA	0.912686	0.023821	0.751363	-1.191765	-0.205735	-0.119683	0.363704	0.452514
YOR342C	-0.107207	-0.356855	-0.694235	-0.018706	NA	-0.621458	-0.68757	NA	-0.192147
YOS9	1.390282	0.396352	0.115929	0.217792	0.869935	NA	-0.494955	-0.1124	0.353979
YPL041C	0.121056	-0.050609	0.003252	-0.484543	1.299328	0.63292	-0.258621	-0.253908	0.111673
YPL068C	-1.632593	0.220529	0.02876	0.417051	1.616446	-0.035919	-0.052195	-0.122925	0.277111
YPL113C	-1.067165	0.377423	0.890123	0.22834	NA	0.48357	0.235222	0.659405	0.341111
YPL150W	-5.733261	-0.012943	0.576019	-0.089723	-0.323032	-0.116455	-0.226239	-0.440524	0.499993
YPR022C	0.667961	-0.2895	-0.233987	-0.285995	NA	-0.015069	-0.077892	-0.181636	-0.246742
YPR063C	NA	-0.786765	0.807737	0.044133	-2.159945	-0.183528	0.176567	-0.051811	0.969155
YPR174C	0.697247	0.202871	-0.830421	-0.033608	-0.927708	0.49451	-0.101722	0.38789	-0.704163
YPT31	-5.818734	-0.084144	0.11961	-0.094117	-0.222413	0.594754	-0.025655	0.264341	NA
YPT6	-2.22118	0.572075	0.767952	0.386278	NA	-0.28854	1.699002	-0.14601	0.303653
YPT7	NA	-1.080404	-0.602868	-0.661101	NA	0.378677	0.287288	-0.767637	-1.258381
YSN1	NA	0.312262	0.476528	-0.341145	-2.318131	-0.485036	-0.16286	0.856931	0.347149
YSY6	-0.323283	NA	0.404179	-0.860467	-3.358833	0.369876	0.128826	0.003161	0.0361
YTA7	3.484018	NA	0.246956	0.286661	1.403984	1.226981	0.805388	-1.125515	0.592866
YUR1	-2.123481	0.397217	NA	-0.583192	-1.833873	-0.082204	0.6289	0.328602	-0.667302
ZDS1	-1.519627	-0.159438	0.28134	NA	NA	0.00862	-0.362249	0.399928	-0.673636

YLR287C	0.626182	0.606626	NA	0.477585	0.146284	0.076292	NA	-0.032558
YMD8	-0.161763	-0.311896	NA	0.454439	0.104031	1.501331	NA	0.235
YME1	-0.012799	0.128302	-0.905556	-0.452033	0.491057	-1.778337	NA	-0.152776
YML108W	-0.367865	0.1552	NA	0.293932	NA	0.605404	NA	0.065314
YML119W	0.312682	-0.365659	NA	1.181817	-0.217873	-0.404751	NA	0.005489
YMR010W	0.061542	0.533932	NA	1.003154	0.337583	0.76579	NA	0.228845
YMR102C	0.255131	-0.160219	0.698729	-0.761348	-0.447123	0.729809	NA	1.206731
YMR111C	0.004553	0.352279	NA	1.656356	-0.171865	-1.78474	NA	0.410412
YMR209C	0.297259	0.500363	-0.767477	1.624811	0.66896	0.240739	NA	-0.524443
YND1	0.502989	-0.230869	-1.024583	0.088193	1.130266	1.92173	NA	0.663639
YNG1	0.555655	0.090275	-0.042509	0.260282	NA	0.459215	-7.917282	0.762393
YOR342C	0.065373	-0.08318	0.276214	0.228095	0.52287	-1.004337	-0.147914	-0.022396
YOS9	-0.015243	0.049722	NA	-1.099857	-0.358643	0.843868	NA	0.432833
YPL041C	-0.266303	0.593516	0.402093	-0.593901	-1.488134	-1.010408	NA	-0.308955
YPL068C	-0.046264	0.259244	-0.069213	1.025676	NA	-0.170396	-3.130925	0.411605
YPL113C	1.184289	1.328729	-0.609356	0.187477	NA	1.872192	NA	0.160805
YPL150W	-0.107968	-0.316183	NA	0.37116	NA	0.32587	-8.160198	0.328063
YPR022C	0.185968	0.515994	0.979085	0.056704	-0.064299	0.30423	NA	-0.251348
YPR063C	0.333125	0.211152	0.600329	-0.843718	NA	1.631709	NA	-0.01048
YPR174C	0.287429	-0.521016	NA	0.671396	NA	0.756689	NA	0.913526
YPT31	0.400405	-0.132052	0.131773	-0.200303	NA	-0.256772	NA	0.287381
YPT6	-0.586251	1.015495	0.721973	-1.964608	NA	0.170647	NA	-0.800722
YPT7	-0.058461	-0.891306	NA	0.697535	0.335557	-0.1453	NA	-0.48828
YSN1	0.444782	0.029317	NA	-0.309184	-0.663486	0.274947	NA	1.464149
YSY6	0.133668	1.120024	-0.736141	-0.817056	-2.11194	1.824584	NA	0.042024
YTA7	-1.284732	0.287789	-2.437115	-0.626845	0.777426	NA	NA	0.573274
YUR1	1.105605	0.057143	-0.508293	1.929672	NA	-2.426009	NA	NA
ZDS1	-0.539958	-0.849913	-0.267903	0.500403	0.106778	-1.104498	NA	0.154064

YLR287C	-0.404692	0.629079	-0.565894	0.258468	-0.90991	0.529436	-0.232898	0.236301	0.229167
YMD8	-0.75351	0.324759	-0.374925	-0.052736	-0.620468	0.146779	0.768372	-0.808236	-0.641757
YME1	-1.942493	-0.170708	-0.428723	-1.074425	NA	-5.42542	1.422273	0.776871	-0.269506
YML108W	-0.315381	0.348128	-0.314569	0.064259	0.279044	0.804186	-0.449674	-0.193466	-1.163443
YML119W	-0.470067	-0.228653	0.054329	0.069978	-1.938335	-0.314018	-0.563027	-0.010825	1.398783
YMR010W	0.294562	0.599379	0.29361	0.210878	-1.133476	-0.182395	-1.087108	0.232742	0.482897
YMR102C	0.437346	-0.209687	NA	NA	0.54689	-0.012932	-1.416724	0.406362	-0.025749
YMR111C	-0.044402	0.32644	NA	NA	0.314239	-2.28985	0.26052	0.415398	1.197462
YMR209C	-0.854877	0.577781	NA	NA	NA	-0.296032	0.656399	0.314158	NA
YND1	-0.797188	-0.011745	-0.783918	-0.456879	NA	-0.361434	0.151551	-0.615588	NA
YNG1	-0.208457	-0.664146	0.006269	0.167046	-0.372631	-0.304866	-1.194157	-0.057878	-0.025255
YOR342C	-0.125579	-0.075202	0.03976	-0.347895	-1.820236	0.127556	-0.199581	-0.021783	-0.097718
YOS9	-0.327848	0.091329	-0.120409	-0.68055	0.504466	0.645856	-0.326279	NA	-0.254605
YPL041C	-0.048017	0.305729	1.21729	0.56464	0.367459	-0.698901	-0.574047	0.395396	0.576306
YPL068C	-0.515793	-0.398704	0.111428	0.016336	0.40173	-0.846433	-0.048013	-0.40405	0.52717
YPL113C	-0.190645	1.853338	1.257535	-0.23589	NA	-0.492783	-0.927993	1.000917	1.813639
YPL150W	-0.55562	0.135434	0.240307	-0.051362	0.218063	-1.3845	-0.476947	-0.113393	-0.289207
YPR022C	0.020731	-0.317308	-0.075721	0.320367	0.426379	0.677552	-1.368115	0.097209	0.773628
YPR063C	-0.384698	-0.622094	NA	-1.040962	0.432384	-0.729168	-0.857231	-0.160271	0.896044
YPR174C	NA	-0.255605	0.908534	-0.200161	-1.669704	-0.236002	-0.76809	0.442392	-0.102541
YPT31	-1.082968	0.289874	-0.212411	-0.04144	NA	-2.396912	0.020388	-0.321108	0.436536
YPT6	-1.211618	0.104994	0.654454	-0.150203	NA	-4.4077	1.484988	-1.151016	0.512209
YPT7	-2.556331	0.219226	-0.469428	0.635008	-0.307815	-0.623901	1.235181	0.420325	0.247534
YSN1	-0.246478	0.468056	0.709521	-0.113395	-0.645545	0.540484	-2.000642	-0.274223	0.018844
YSY6	-0.035255	0.031648	NA	0.245875	-0.947987	0.056759	0.045006	0.752147	0.831337
YTA7	-14.360926	-0.489178	-1.303464	-0.393498	NA	NA	NA	-0.277567	-0.271501
YUR1	-0.33625	0.636306	1.116643	0.063511	-1.843778	-0.14027	-0.2965	0.310602	0.711517
ZDS1	0.432372	1.42133	NA	NA	1.417697	0.308412	-1.905961	0.467772	NA

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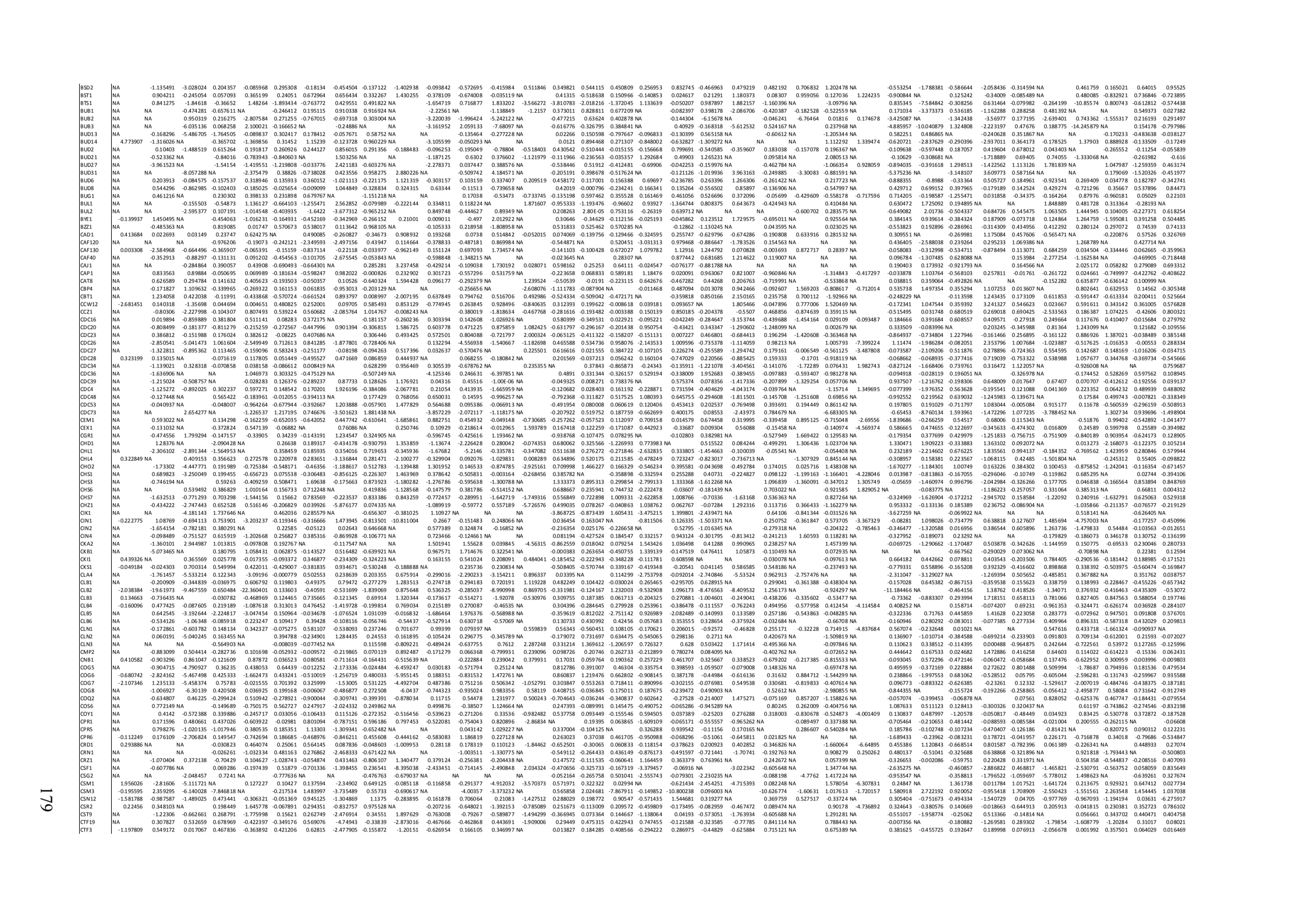
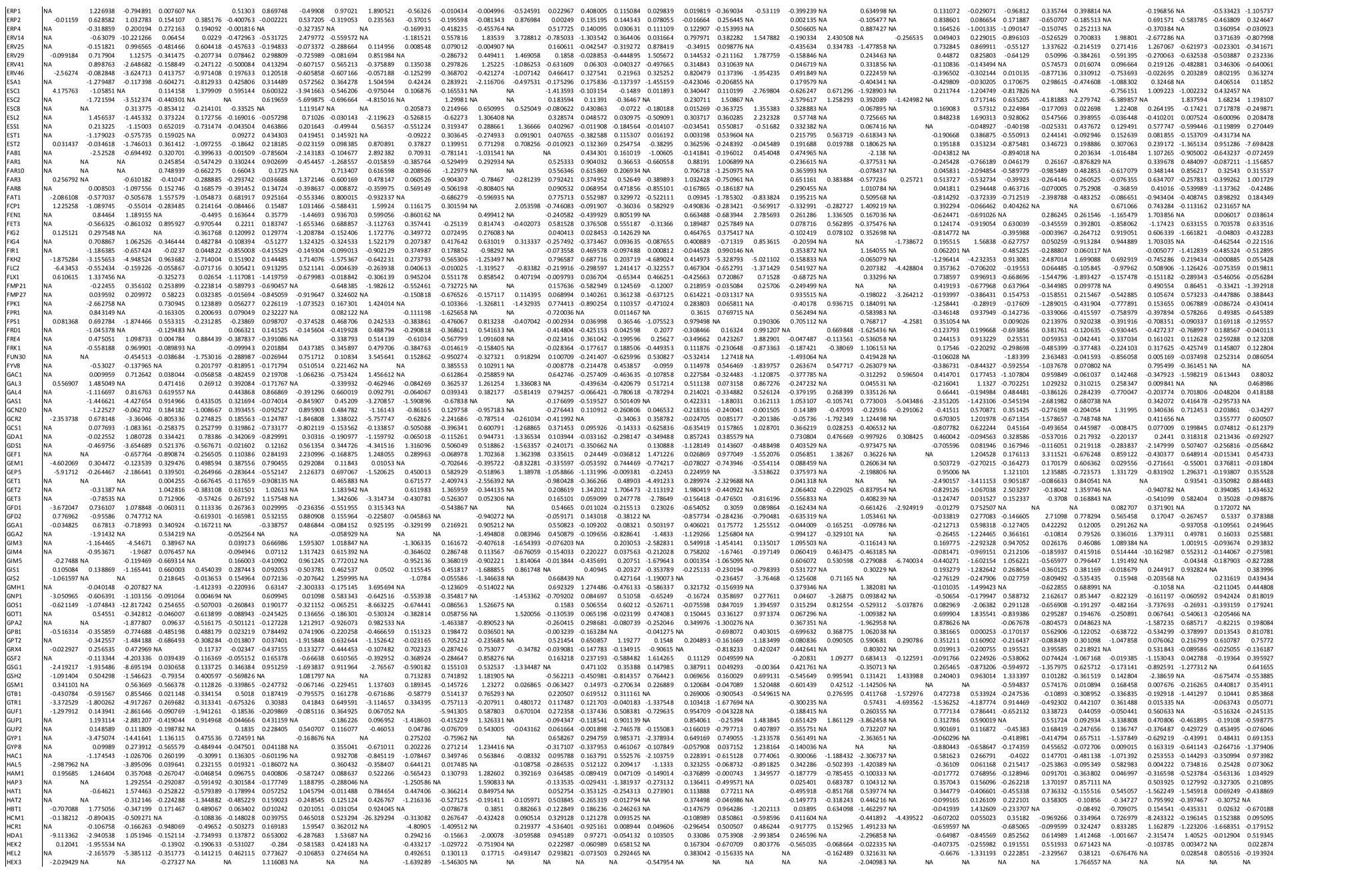
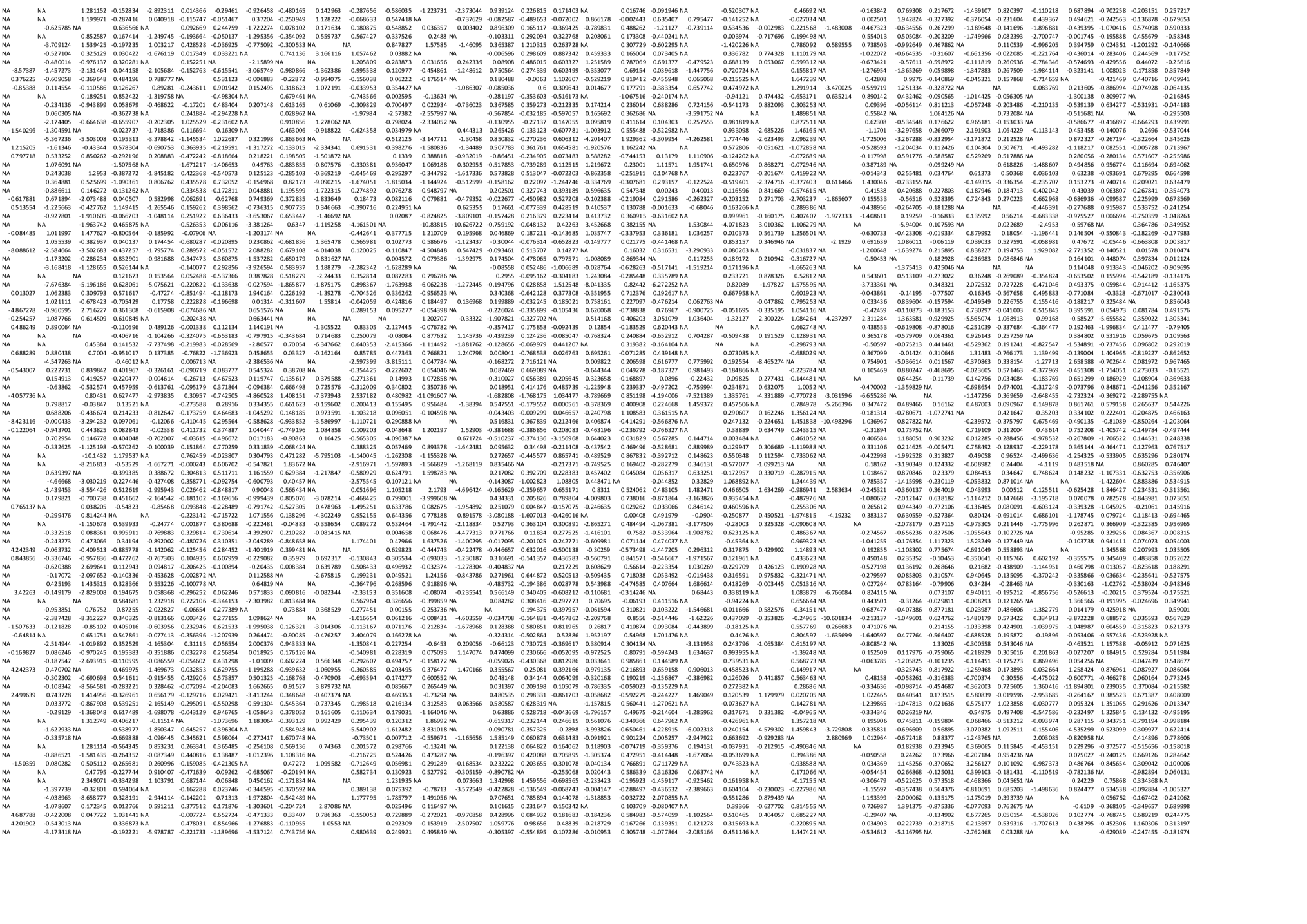
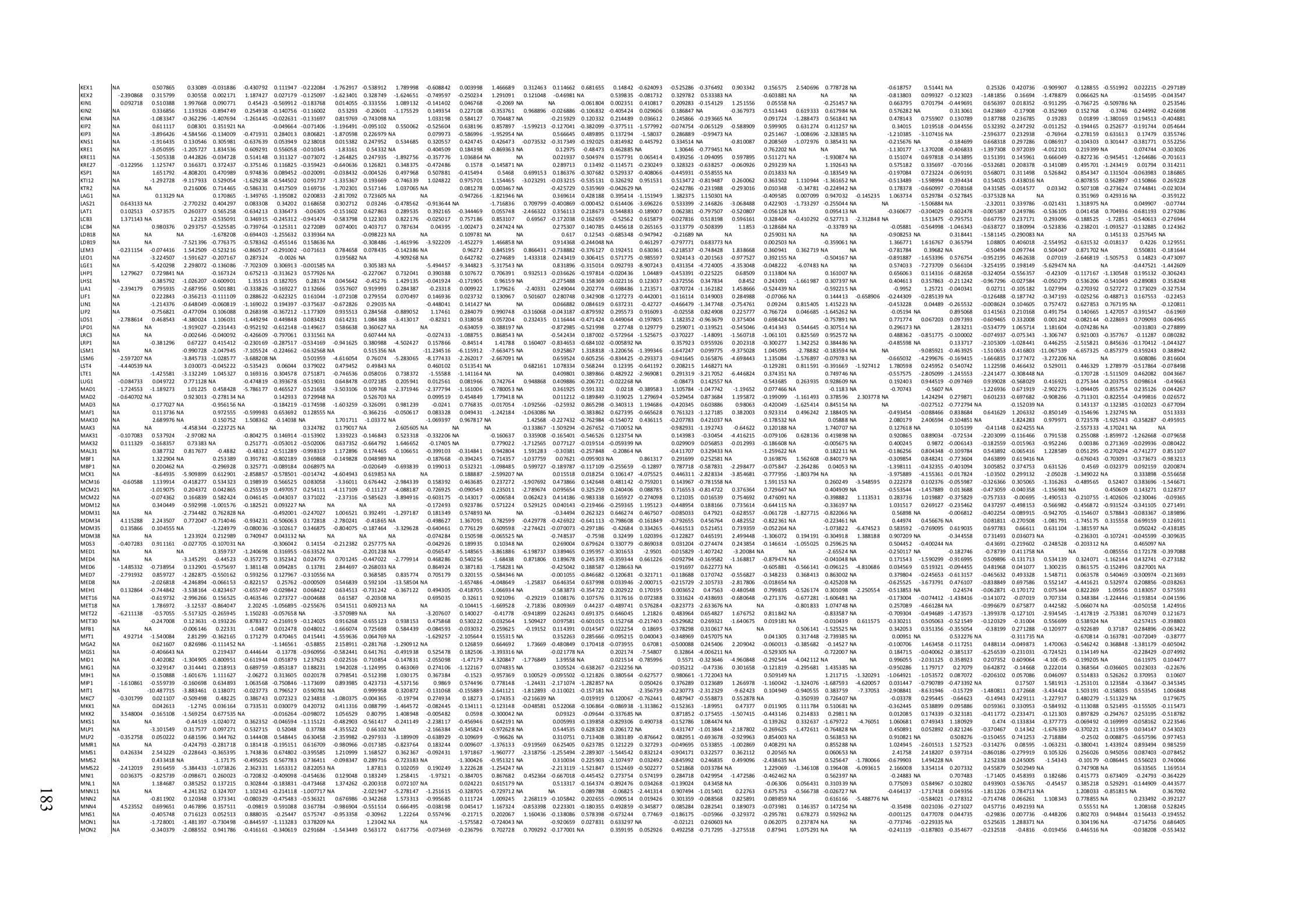
Gene	ARP8	ASF1	BRE1	DCC1	DDC1	DOT1	EXO1	HEX3	HST3	HTZ1	MEC1	MRC1	MRE11	NUP133	PPH3	PSY2	RAD17	RAD18	RAD24	RAD5	RAD52	RAD9	RFA1	RPD3	RSC1	RTT101	RTT109	SAE2	SGS1--NULL	SGS1--PM	SLX8	SWR1	TOF1	UBC13	YKU70
AAD4	NA	-0.511724	-0.721456	-0.448584	0.751041	0.17216	0.092305	0.533411	0.007529	-1.873229	0.124257	-0.362738	0.597568	1.198202	-0.49766	-0.445319	-0.374593	1.014402	-0.210786	1.09269	1.386971	-1.605037	NA	1.252564	-5.699935	-0.051413	1.140709	0.113975	3.428082	0.259496	-0.46897	0.673347	0.108924	0.022668	0.058188
ABP1	NA	NA	1.525668	NA	0.187619	-0.294278	-0.470654	-0.595168	-0.366261	0.323785	0.208993	-0.238042	-0.015355	-1.859061	0.003877	0.11656	-0.018135	NA	0.301491	0.287254	2.377165	-0.565979	NA	0.497905	NA	-0.300063	1.664134	0.247265	-0.232884	0.142199	-0.252251	0.312088	0.04828	0.114764	-0.436496
ACB1	0.975229	0.978489	0.17299	0.264703	0.297093	-0.563716	-0.026206	-0.793722	-0.910225	-0.185568	-0.220883	-0.39905	0.120067	NA	-0.299533	-0.012816	-0.137867	-0.294833	-0.008216	0.326538	NA	0.198828	NA	0.192007	NA	0.53423	-0.39791	0.222144	0.016976	0.682343	-0.68631	0.593219	-0.576715	-0.646572	-0.593643
ACE2	NA	0.192682	2.859871	-0.271546	0.498908	-0.093411	-0.219538	2.089898	-0.253411	NA	NA	0.095194	0.740051	NA	-0.463578	-0.085637	-0.626504	NA	0.080831	NA	2.02389	-0.271813	1.550101	0.556612	NA	0.497791	0.468095	0.012028	-0.342317	-0.147023	0.294797	0.283926	-1.089526	-0.347474	0.270651
ACK1	-0.084519	0.900553	NA	-0.47775	-0.742243	-0.218625	0.091097	-0.529725	-0.53163	0.860328	-0.043718	-0.3258	0.57276	-0.492489	-0.147475	0.056899	0.58598	NA	0.358292	-0.149158	-1.050028	-0.141854	NA	0.600248	-2.11862	0.563235	0.298383	0.254977	-0.419232	0.365499	0.29131	0.182696	-0.525667	-0.008884	-0.469334
ADD66	NA	1.650841	1.051235	-0.249	-1.403354	-0.327372	0.210359	1.427403	0.544828	NA	-0.399975	0.61034	0.62249	NA	-0.944795	-0.405984	-0.818297	0.190263	0.015149	1.151812	NA	0.609778	-0.504602	1.092218	NA	-1.180048	0.869906	-0.528145	-0.484368	-0.017577	0.069344	-1.202973	-0.08805	-0.077515	-0.571689
AGE2	NA	-0.961616	-2.289566	0.353574	-0.395424	0.422532	-0.23244	-1.294597	0.113431	-1.545712	0.055451	-0.920115	0.73724	NA	0.197273	0.405234	0.119764	-0.693357	0.078401	0.847029	0.979265	0.383324	0.265119	-1.325943	NA	-0.069594	-0.897171	0.030071	-0.662899	0.336024	-1.47373	0.112333	0.610259	-0.21396	-0.447008
AGP2	0.277343	0.729287	0.42192	0.185071	0.866511	-0.066512	-0.012516	-1.240373	-0.357259	-0.211423	NA	-0.020713	0.843426	-0.073351	-0.128158	-0.302825	-0.094656	0.295181	-0.36437	0.132782	1.629955	-0.755386	NA	-0.996005	-2.286618	-0.339474	0.443809	0.02899	0.25517	-0.607725	NA	0.368155	0.242005	0.005087	-0.426573
AGX1	NA	-0.182626	-0.158613	0.304484	-0.066961	-0.191011	0.363999	NA	0.393873	1.054517	-0.660803	-0.089104	NA	-2.316183	0.867187	0.108267	-0.330694	-1.068675	0.008717	-0.89154	-0.373093	0.681945	0.345537	-0.127983	NA	0.180899	0.064532	-0.81912	1.282909	0.547127	NA	-0.359979	-2.013163	-0.424131	0.183025
AHC1	NA	NA	-0.171398	-0.655497	0.606036	0.142963	NA	-1.67409	NA	NA	-3.230082	-1.093006	-0.005832	-2.859621	0.262357	0.584176	-0.120924	0.931778	0.475546	0.839248	1.001673	0.130687	NA	-0.404947	NA	0.063612	0.991879	0.141729	-0.004498	0.472338	-0.411681	0.160795	-1.048448	0.175214	0.067122
AHC2	-2.218691	-0.187167	-2.383284	NA	-0.128684	0.1036	0.04374	-3.63594	0.50786	-1.503405	-4.536163	-1.1852	0.260831	-1.481304	0.784163	0.594687	0.209713	NA	-0.274009	0.16136	0.275629	0.339866	-0.795254	0.488256	NA	0.284886	0.449452	0.139255	-1.071748	0.166588	-2.445648	-1.140267	0.192804	0.598056	0.510917
AIM21	0.366645	0.78674	0.600871	0.090494	-0.225903	-0.038286	-0.633837	0.52472	-0.473717	0.568325	-0.227471	0.235035	1.654491	1.407134	-0.481478	-0.316631	0.004089	0.805296	-0.480471	0.38266	1.636527	-0.424434	NA	0.198172	-0.222861	0.066472	0.824523	-0.601199	0.854714	0.098435	NA	0.51479	-1.321342	-0.333774	0.126585
AIM22	NA	NA	0.981796	-0.806567	-0.412343	-0.523967	-0.11165	1.264844	0.293039	-0.54182	0.41265	0.64863	1.355741	-0.75214	0.030767	-0.469286	-0.034045	-0.130484	0.050086	0.287754	0.505443	-0.591471	NA	-0.298446	NA	NA	-0.696378	0.415311	0.547813	-0.865639	0.752268	-0.013726	1.219429	-0.938018	-0.680804
AIM26	0.588386	0.537066	1.234704	-0.035277	1.201278	0.02531	-0.060876	-0.236221	-0.572412	0.374853	-0.264826	-0.637936	0.616133	-0.692108	0.179885	-0.16289	0.410543	0.68188	0.414434	-0.635737	0.294384	-0.050314	1.069298	0.126573	NA	-0.548651	-0.119079	-0.949624	0.319249	0.057779	0.396461	-0.063303	-0.790201	0.250448	-0.110693
AIM29	-2.470841	-0.674	-0.893474	0.037739	-2.846384	0.057747	-0.20958	0.273635	0.378563	-1.823355	0.851144	0.225998	-0.374342	NA	0.410762	0.135631	0.262931	-1.843341	0.257849	-0.958348	-1.561766	0.790165	NA	0.616272	NA	0.686308	-0.136125	0.0442	0.264645	-0.219334	0.622734	0.273575	0.259335	0.112105	0.009325
AIM3	0.334242	NA	0.333042	0.191308	0.373077	-0.596386	0.092062	0.491438	-0.861366	-0.023248	NA	0.332023	NA	1.144177	0.416765	-0.171735	0.057315	-0.292516	1.000923	-0.760891	1.053979	0.319102	-0.56623	-0.939995	NA	0.005638	0.873797	-0.561695	-0.064116	0.100912	0.167652	-0.124286	-0.598483	-0.102408	0.306445
AIM32	NA	-0.489716	-0.99855	-0.003301	-0.573345	0.447531	0.245802	1.170775	-0.115752	0.34498	0.502019	-0.524566	-1.480398	0.095794	0.504287	-0.08943	0.415889	-0.492581	0.485984	-0.541131	NA	-0.090977	-0.172555	0.023072	NA	-0.841643	-0.808967	0.695693	0.453688	-0.188073	-0.945636	-0.889081	0.091119	0.122227	0.142532
AIM34	-0.580877	1.526523	-0.230129	-0.576411	0.452646	-0.509745	0.173867	-0.602522	0.769717	-0.194466	-0.24031	0.320155	-0.96535	NA	-0.370993	0.083659	0.138997	-0.585907	-0.440516	1.338035	NA	-0.807228	-0.791672	-0.003251	-5.416916	-0.177939	0.800023	-0.596439	NA	0.066304	0.602497	0.14044	-0.115862	-0.13006	0.703956
AIM4	NA	NA	1.635703	-0.951065	0.376239	-0.592181	-0.394865	NA	-1.302412	1.846941	NA	-0.162985	0.209667	NA	-1.525515	-0.375747	0.040925	1.795395	-0.690499	0.449445	NA	-0.277968	-0.096005	0.135672	NA	-0.860754	NA	0.16276	NA	-0.401716	NA	0.699096	0.204687	-0.563154	NA
AIM44	NA	-3.361373	NA	-0.078883	NA	0.149087	0.027665	0.090009	0.727347	2.415477	-0.81405	-0.289495	-1.616689	1.453721	0.979922	0.684926	-0.163824	-1.453545	1.137079	-0.594801	-1.226659	0.696477	-0.989439	1.799124	-7.867912	0.490237	-1.873027	0.46369	-0.186667	1.14423	-0.754987	1.93005	1.256016	1.037488	0.700497
AIP1	NA	-0.296194	NA	0.407954	-0.588525	-0.109077	0.563	-3.428257	-0.172975	NA	-0.220127	-0.721218	NA	NA	0.496771	0.290918	-0.41084	NA	0.505646	-0.193979	NA	0.636684	-1.529315	-0.374626	NA	NA	-0.473788	-1.16181	NA	NA	NA	0.648001	NA	-0.250155	0.138525
AIR1	NA	1.33523	0.472032	0.493897	0.164448	-0.293594	-0.199544	0.371255	-0.84088	-0.042479	-1.268872	-0.340473	0.582438	-0.351038	-0.275331	-0.005814	-0.332896	0.392244	-0.620039	0.077971	0.990277	0.126807	NA	0.864399	-2.221496	1.060757	0.099383	0.035974	-0.065682	-0.517479	0.019184	0.103816	-0.7944	0.404099	0.419377
AIR2	-1.409423	0.242942	NA	-0.147267	0.303456	0.178697	0.215714	-1.305926	0.827637	0.448726	0.237136	0.248254	0.962961	NA	0.308113	-0.310231	-0.34297	0.431999	0.23461	0.965875	-0.512026	-0.475343	NA	0.460981	NA	-0.263948	-0.087455	-0.690474	2.630925	0.660016	-0.905746	-0.508417	-0.413609	0.036804	0.285135
AKR2	NA	-1.572917	NA	1.248383	-2.330729	0.071205	NA	-1.164233	NA	NA	0.314475	-1.200233	0.469444	-1.474555	0.818004	0.080631	0.989919	-1.449738	1.171519	-0.816058	-1.801152	0.370594	0.947671	0.4995	NA	0.57062	-0.308991	0.808834	-0.094252	0.982288	-1.237891	-0.932292	0.767129	-0.118865	0.685987
ALB1	-0.982152	NA	NA	-0.234886	-0.884301	-0.581444	-1.079779	-0.431204	0.481641	-0.536787	-1.560752	1.282733	1.887014	NA	0.514771	0.39621	0.141586	0.635218	0.846306	-0.000944	NA	0.498408	NA	-0.214299	NA	NA	0.052852	-0.357046	-0.101206	0.261202	-0.15494	-0.719376	-0.941431	-0.474992	0.755831
ALG12	NA	1.115769	1.357025	0.671995	-0.364044	-0.073561	-0.353071	-0.822435	0.59947	0.712156	-0.958182	0.068188	1.148858	0.756192	0.142892	0.064888	0.111089	-0.483345	-1.065869	0.062521	0.923447	-0.537779	0.076407	-1.294943	0.584404	0.317617	0.464666	-0.499151	0.527788	0.16982	-0.84632	1.31418	-1.107288	-0.522216	-0.203217
ALG3	NA	0.236868	2.088273	-0.719893	0.364753	0.066963	-0.346818	NA	-0.569589	NA	NA	1.169641	NA	NA	-0.099777	0.188151	-0.147672	NA	0.124574	-0.115559	NA	-0.155328	NA	0.838288	0.401752	0.330496	NA	-0.756985	0.349226	-0.687596	3.827794	0.486006	-0.489082	-0.096947	-0.060555
ALG5	-0.463193	0.291495	NA	-0.336521	NA	-0.113486	0.260652	0.003681	-0.057362	0.560166	-0.614563	-0.494147	1.154092	1.897922	0.025127	0.102836	-0.177405	-0.073361	0.302331	0.032948	0.797482	0.167071	1.366848	0.17769	-3.573607	0.060349	0.600362	-1.099977	0.479871	-0.244784	0.330666	0.455537	NA	0.386162	-0.070019
ALG6	NA	NA	-1.476842	-0.220128	1.097192	0.141963	NA	-0.227253	NA	NA	0.028875	-0.296698	NA	1.556025	-0.402627	-0.315597	-0.202545	0.173451	-0.072752	0.299854	1.97355	-0.339766	0.528853	0.017365	NA	0.409445	1.304045	-0.460742	0.47664	-0.558653	-0.585682	-0.108031	NA	0.098178	-0.661477
ALG8	NA	1.14775	-0.134787	-0.439104	0.17662	-0.334511	NA	-0.341886	NA	NA	-0.655071	-0.561207	0.5872	NA	0.185362	-0.132675	-0.649824	0.285934	0.108509	0.754911	0.571935	-0.326457	0.623055	0.735067	NA	0.362781	0.415074	-0.512861	2.970599	0.739209	0.166752	0.547559	-0.478295	-0.095628	-0.491185
ALT1	-3.351544	-1.418025	-2.902511	-0.050868	-0.328397	-0.164255	0.049917	2.138136	-0.471367	-0.077527	-0.290069	-0.147421	-1.687926	NA	-0.248813	-0.292517	0.51516	0.13134	0.311194	NA	-2.513485	0.367564	0.564175	0.311968	NA	-0.387556	NA	-0.58375	-0.657312	0.403433	1.631843	0.425753	-0.228697	0.360493	0.2354
AMD1	NA	0.65198	0.878688	-0.380607	0.212498	-0.215334	0.323409	0.614812	0.20169	NA	-0.454282	-0.206477	0.440023	0.914705	-0.002521	-0.352736	-0.253358	0.298346	0.765452	0.328923	NA	-0.106584	-0.192861	-0.404613	-2.539462	0.748335	1.446141	-1.106072	-0.614489	-0.04961	0.305365	0.364199	-1.75714	-0.207045	-0.92089
APA1	-1.649154	0.990101	0.103488	NA	-0.038021	0.022948	0.213164	0.102087	-0.241378	-0.056515	NA	NA	0.135678	1.229357	0.127419	0.321477	0.320085	NA	0.25899	-0.469042	0.612861	-0.042766	NA	0.920752	-3.338809	-0.1992	1.993982	0.002923	-0.51355	0.176256	0.140205	-0.17299	0.259044	0.024037	-0.198061
APC1	NA	NA	-0.997483	0.157736	0.173636	0.055	0.214933	0.567778	-0.570479	-0.777421	0.547805	-0.315931	-0.417847	NA	0.00049	NA	0.219667	0.51222	-0.562512	0.407458	0.197209	-0.215952	-0.351936	-0.946708	NA	-0.224463	-1.008198	0.267544	0.891095	0.114044	0.857701	0.423875	NA	-0.850372	-0.475519
APC11	NA	0.499955	NA	0.165389	-0.86005	-0.00111	-1.191166	NA	-0.838158	NA	0.811706	-0.730806	-2.157901	0.74641	NA	0.170978	0.360317	-0.374026	0.285348	0.110603	NA	0.167077	NA	0.77931	NA	-0.246134	NA	-0.033899	-0.150582	0.495809	NA	-0.24864	0.632584	NA	-0.300149
APC4	NA	-0.279295	-0.314152	0.094017	0.239892	-0.051493	-0.058452	1.124199	0.266442	0.666532	0.126101	0.539233	-0.07764	-0.39551	NA	-0.638435	-0.138378	-0.130098	0.175887	0.855321	-0.270117	-0.319067	NA	-1.056571	NA	-0.036387	0.255634	-1.156804	0.035713	0.049386	0.313935	-0.000359	-1.578201	NA	0.231395
APC5	0.307028	-0.569821	-0.444029	-0.210648	-0.878489	-0.178223	0.064009	1.687331	0.606854	-1.030893	NA	0.496624	-1.692211	0.307047	-0.615434	-0.47828	-0.360938	0.60541	0.468334	0.448932	NA	-0.148512	NA	-0.590554	NA	-0.080885	0.341079	-0.967502	0.643829	-0.633241	0.744079	0.722668	-1.562837	-0.353218	-0.291455
APC9	NA	-0.744901	-2.112063	0.38104	-1.342514	0.080126	0.373207	0.369306	-0.209541	-0.214144	NA	-0.294177	-0.204312	-2.82602	0.329425	-0.119573	0.949796	-4.019029	0.755608	NA	NA	-0.116235	-0.185314	0.830955	-0.584863	-0.628796	NA	-0.598699	0.910676	0.820468	-0.459043	0.308314	-1.20622	-0.460354	-0.395622
APE3	NA	-0.02962	NA	0.855701	-1.239972	-0.213509	0.027402	-0.049655	0.222931	NA	-0.303911	-0.468845	-0.445889	-0.193279	-0.165814	0.53486	-0.037912	-1.397646	0.41321	-0.29477	-0.158585	-0.272584	0.675985	0.310764	NA	-0.740407	0.212338	0.492174	-0.530941	-0.653121	-1.107712	-0.067224	-0.469601	-0.318949	-0.048382
APL5	NA	NA	0.418131	-0.583315	NA	-0.035237	0.275015	0.550965	-0.373056	NA	-3.776192	-1.101628	1.820168	-0.297024	-0.314322	-0.056445	NA	NA	-0.106287	0.158239	1.973799	-0.107761	0.646785	-0.208359	NA	0.949575	2.186158	-0.181767	0.680747	-0.218005	-1.102174	0.934606	-1.940137	0.201519	-0.866757
APL6	NA	1.061678	NA	-0.966533	-0.46113	0.168213	0.452083	-1.165775	-0.054657	0.131897	-0.656565	-0.452551	1.710318	NA	0.235586	0.066116	-0.065576	NA	-0.572169	0.588562	1.557669	0.084735	-0.904182	-0.515587	NA	0.964026	1.074609	-0.989618	NA	-0.124218	-0.149757	0.678293	NA	-0.119306	-0.727684
APM3	NA	-0.035228	-0.024885	0.505981	-0.807902	-0.049965	0.957441	-0.476682	0.577229	-0.173903	-0.428535	-0.184247	0.629829	-0.129734	0.309727	-0.579063	0.59755	NA	0.045194	-0.393333	-0.584298	0.264723	NA	0.176967	NA	0.489449	-0.237268	-0.532667	-0.970452	-0.548386	-0.225216	0.759368	0.109233	NA	-0.444637
APM4	0.095559	NA	-0.589231	0.056461	-0.00804	0.13361	NA	-0.08763	NA	NA	-0.133779	-0.362576	1.058708	NA	-0.454725	-0.377515	-0.02348	0.965994	0.061036	-0.294762	NA	0.431764	0.520353	0.240879	NA	0.155113	0.633489	0.076054	NA	-0.352261	-0.705198	0.813405	-0.181269	-0.539944	-0.133481
APQ12	2.755357	-1.129948	-5.316918	0.433097	-1.743667	-0.398456	0.601964	-4.630467	0.871815	NA	-1.95604	-1.428577	-1.127406	NA	0.435577	0.246206	0.410472	-1.448709	0.389602	-1.038247	-1.614708	0.396055	-0.574958	1.775608	NA	0.09332	-2.853272	0.276406	-1.564652	0.006341	-0.903158	-8.057301	-1.149745	-0.363675	0.526314
APS3	NA	NA	0.752128	-0.389303	0.011184	0.200987	-0.509563	-0.495689	-0.33773	0.271737	-0.809678	-0.573148	1.328271	NA	-0.626302	-0.067993	-0.390338	0.758026	-0.135502	0.417275	2.232605	0.363144	0.231348	-0.14682	NA	NA	1.24285	-0.298832	0.42664	-0.301396	0.070812	0.660937	-0.83542	0.113927	-0.0952
APT1	NA	NA	NA	-0.756826	-0.944726	0.307761	0.411608	-0.525163	-1.097279	-0.09356	NA	-0.332526	0.085713	0.93694	0.081476	0.547383	-1.107405	0.312966	0.989092	-0.608834	NA	0.725498	0.720758	-0.593251	NA	0.487798	-0.035809	NA	0.551933	-0.264351	-0.531157	-0.428771	NA	-0.837758	-1.267431
ARC1	NA	0.841102	-1.009724	-0.154022	-1.083869	-0.919152	-0.14615	NA	-0.130004	NA	NA	1.137706	NA	1.741939	0.010602	-0.250947	-0.164807	0.840824	0.320953	NA	1.212673	-0.408505	1.311563	NA	NA	0.230191	-0.847458	NA	-1.312021	0.311658	NA	0.463484	0.736247	-0.201068	-1.659348
ARG80	-0.665987	0.275497	NA	-0.023004	0.710367	-0.251551	0.203211	0.6922	0.045303	-0.000407	-0.041315	1.013051	-0.125716	0.187296	0.368144	0.035569	-0.449765	0.732166	0.172818	0.701163	NA	0.589493	NA	-0.510212	-2.783741	0.087148	0.243653	-0.120262	0.41096	-0.44194	0.272907	0.076077	0.241853	-0.239611	0.627106
ARL1	NA	-0.368113	-4.358389	0.197735	-0.638682	0.524367	0.316515	-1.38129	0.146471	NA	NA	-0.246217	0.797127	-3.119548	-0.016648	-0.141142	0.599943	0.407995	0.132986	0.022904	0.744147	0.324818	1.276229	0.130356	NA	-0.298944	1.198716	0.108022	0.256423	0.198475	NA	0.441587	NA	0.651799	-0.153608
ARO1	NA	-2.315116	-1.41421	0.604928	-1.312223	1.016869	-2.789127	0.674226	-4.743139	NA	-0.647021	NA	-2.756193	1.044425	NA	0.504654	0.15061	-3.20251	1.344343	-0.650234	NA	NA	-2.33941	2.176467	NA	0.554667	2.026301	0.935974	-0.185348	0.631623	-2.001119	-2.53925	NA	NA	1.20428
ARP1	NA	-2.391218	2.163535	-0.578969	1.264792	0.2812	0.257078	0.104736	0.17848	NA	-1.230607	0.943569	-1.911499	0.647542	1.071961	0.97759	-0.842105	-0.636193	-0.348426	-0.85842	NA	-0.337524	NA	0.359366	NA	-0.282762	-0.917768	1.105521	0.572806	0.385417	0.386434	-0.887088	1.396256	0.617396	-0.31221
ARP4	NA	NA	-12.374187	-0.273119	-0.781787	0.188323	-0.109964	-3.127482	-0.804544	1.251599	0.331837	-1.41142	1.191499	-3.114599	0.223025	0.525958	-0.075355	0.142471	0.31341	0.49418	1.237283	0.310935	-0.331603	-0.87192	NA	NA	-1.027262	0.907769	0.271217	0.136507	-3.532655	0.572428	1.431888	0.185257	-0.315188
ARP6	NA	NA	NA	NA	NA	-0.526156	0.387421	NA	-1.728181	3.242198	NA	NA	NA	NA	NA	-0.827543	-1.456037	-0.737845	-0.874937	NA	NA	0.294104	-2.376184	0.940334	NA	-0.374214	NA	-1.132891	0.206812	2.306194	NA	2.509848	-0.286944	0.680734	-0.713176
ARP7	-0.612918	1.058682	-2.716764	0.016125	0.110257	-0.307634	0.062858	NA	-0.318994	NA	0.260412	0.586024	1.292416	NA	0.182255	0.077449	-0.257347	0.36062	-0.021335	0.380296	NA	0.051487	-0.559838	-1.010322	0.483062	1.129876	0.7394	0.233826	0.384796	-0.433419	0.133792	-1.309795	-0.856202	0.434614	-0.039412
ARV1	NA	NA	-2.572244	0.947823	NA	0.174531	0.197236	-1.011396	-0.211157	-2.055606	-1.488266	-0.485971	1.210652	NA	0.183611	0.023665	0.832167	-1.168146	0.265816	-0.996693	1.060917	-0.58405	NA	-3.006995	NA	-1.242215	0.078111	-1.240315	-0.436778	0.461742	-1.355282	-0.20276	-1.454803	0.595829	-0.157691
ARX1	4.816781	1.012745	1.427694	-0.448259	-0.165759	-0.741119	-0.594864	1.226181	-0.302093	1.740254	-0.498555	0.253166	0.527531	NA	NA	-0.588917	-0.081907	0.415392	0.317049	0.852628	1.642444	0.341152	NA	1.205706	NA	0.809597	NA	-0.095682	-1.085255	0.378216	NA	0.30819	-0.329975	NA	-0.877285
ASF1	NA	NA	-2.877172	1.258393	NA	1.484392	0.453511	-5.026093	NA	NA	-1.462711	2.281734	NA	NA	-0.202629	NA	NA	-0.749718	-0.637339	NA	NA	0.646421	NA	-0.985733	-1.33643	NA	NA	0.772131	-0.165012	0.878049	-3.703063	-2.017771	1.92091	0.865664	0.063968
ASH1	NA	1.584026	0.330178	0.031601	-0.09927	0.105159	-0.078	-0.099143	0.331245	2.01813	-0.70116	0.455008	0.953258	NA	-0.064099	-0.139372	-0.250123	0.53927	-0.532903	-0.02709	NA	-0.154245	NA	0.146327	NA	0.909364	NA	-0.43953	1.130439	0.093254	0.520202	0.27887	-0.548207	-0.321495	-0.320947
ASI1	NA	-0.564495	-0.644176	0.124351	-0.44229	0.185846	0.387763	-0.584441	0.236092	0.054728	0.809872	-0.540717	-0.118786	-0.440906	0.382306	0.111356	0.717732	-1.163578	0.225819	-0.416837	-2.036084	0.346298	-0.014311	0.137602	NA	-0.138187	-0.233551	0.49878	NA	NA	-1.021626	-0.326039	0.540908	0.614315	0.567054
ASI3	0.59996	0.453499	NA	-0.304513	0.252152	-0.001315	0.151418	-0.694845	-0.235198	1.552356	-0.011181	-0.191266	1.042121	-0.494388	0.081457	0.268239	0.1493	-0.385691	0.221699	-0.193154	-0.240668	-0.487049	-0.017807	-0.168817	NA	0.312467	0.416164	-1.015854	0.402159	-0.191574	-0.328598	0.509817	-0.478982	0.402885	0.41514
ASK10	1.238158	1.459513	1.281305	-0.067931	0.453574	0.509481	-0.123127	-0.436804	-0.348013	-1.32091	-0.306341	-0.924579	1.368712	1.051673	-0.354288	-0.397445	-0.245807	-0.014646	0.406415	0.801923	1.934972	0.199575	0.187839	-0.513293	NA	-0.164027	0.78294	-0.619494	0.677306	0.102733	0.21542	0.303432	-0.621942	-0.312243	-0.38286
ASM4	0.633892	-0.700459	NA	-0.088899	0.453345	0.158887	0.349146	NA	0.355101	-1.84686	-0.785672	-0.25634	-0.198609	-17.070796	NA	-0.129748	-0.078556	NA	0.155114	-0.350977	0.634343	0.41086	0.530898	0.669681	NA	-0.031638	1.595914	-0.211202	NA	-0.394097	-0.28175	0.483719	0.327142	0.062195	0.426552
ASR1	NA	-2.352403	-0.084642	0.703093	-0.746013	0.309769	0.473975	NA	-0.222438	0.033227	0.248883	-0.51723	NA	NA	0.115755	-0.319445	0.457295	-0.249139	-0.108783	-0.562517	-1.099012	0.286127	0.027448	0.021122	NA	-0.507855	NA	-0.122436	-0.42351	0.119133	0.746805	-0.4257	-0.71381	0.518951	-0.560677
ATG21	NA	-0.447892	-1.489502	-0.033414	NA	-0.152917	-0.547502	-0.340803	0.22954	-0.797548	-0.045322	0.152894	0.901253	NA	0.312927	-0.220663	0.680793	0.560811	0.081934	-0.184605	NA	0.289407	NA	0.577163	NA	-0.949128	-0.47585	0.184985	-0.230472	-0.297265	-0.275306	1.016783	0.526893	-0.070667	-0.67231
ATG8	NA	NA	0.273054	0.386057	-0.1843	-0.287149	0.557511	-0.235536	-0.251075	-1.239886	-1.388883	-0.223315	0.418135	1.084454	-0.239892	-0.335688	0.161797	1.188711	0.125814	0.581895	NA	-0.282058	0.070889	-0.27619	NA	0.434108	0.414649	-0.277985	-0.591051	-0.059112	0.873545	0.345592	-0.513656	-0.10796	-0.214749
ATP23	-0.405209	1.939808	0.304237	-1.061993	0.110456	-1.254244	-0.011614	0.303316	-0.344294	-1.6656	-1.326874	1.146933	2.967838	-1.464	0.53774	0.070158	-1.715583	0.954921	-0.729812	0.524168	3.046189	-1.157192	NA	0.024969	NA	0.403297	1.222762	-0.208409	0.471054	0.070058	0.246906	-0.196491	0.977289	-0.536736	-0.38955
ATS1	NA	-0.337204	-2.722234	0.027469	0.080115	-0.121727	-0.63235	-0.272276	0.486538	1.057926	0.669976	0.493267	0.652408	0.324325	-0.074893	-0.136725	0.436088	-0.040183	0.276823	0.260083	-0.673466	0.334017	NA	0.850903	NA	-0.627052	-0.647292	-0.122671	-0.138736	-0.138393	-0.544991	-0.27196	-0.972521	-0.265293	0.928356
AVL9	NA	1.874981	-3.877946	-0.055105	0.388219	-0.501993	-0.316869	-0.496886	-0.834435	-0.516836	-0.252246	0.100314	1.176269	-1.165293	-0.340531	-0.520773	-0.069044	0.141763	0.19637	NA	1.582462	-0.400252	0.909411	0.425209	NA	0.112517	NA	-0.494041	0.035685	0.19107	-0.175034	0.096864	-0.002748	-0.145188	-0.422376
AVO2	NA	0.287643	0.278786	-0.173017	0.936162	0.20312	0.020811	-0.043186	-0.492272	NA	-0.267044	0.250195	NA	-0.558568	-0.170521	0.381347	0.323072	-0.228008	0.34955	0.182866	NA	-0.307697	0.630012	-0.958475	NA	0.855504	0.908069	-0.18909	-0.197984	-0.183006	-0.227372	-0.424049	-0.739485	-0.309927	-0.625576
AZF1	NA	-1.488405	-0.421258	0.735475	-0.497192	0.541702	NA	-0.691256	NA	0.383824	0.901366	-0.466539	-0.339875	-1.699008	0.269717	0.812278	0.126176	0.119114	-0.163976	-0.188856	-1.094372	0.669546	0.441724	0.667548	NA	-0.595292	-0.825673	-0.234326	-0.452024	-0.041712	0.13436	-1.083455	0.448054	0.022838	-0.15467
BAS1	NA	1.040724	-0.007827	-0.575842	-0.043749	-0.27638	-0.660583	0.705412	-0.058471	-0.206514	0.327201	0.322059	1.986659	NA	-1.037381	-1.053031	-0.03078	1.009896	-0.137191	1.124597	2.216029	-1.432211	NA	0.163659	NA	0.915276	1.30687	0.541587	-0.04483	-0.197761	1.138459	-0.041257	1.558906	0.25874	-0.607387
BBC1	NA	0.153618	-0.187747	0.272129	0.532533	0.221253	-0.336189	0.092995	-0.274048	0.428611	-0.158996	-0.236131	0.726089	NA	-0.274334	-0.16102	0.04045	-0.586456	0.680263	-0.230056	0.009065	0.675844	NA	0.208163	NA	NA	0.127423	-0.222773	0.666452	0.274891	0.475182	0.165801	-0.439324	-0.354598	-0.244245
BCK1	0.542306	NA	-3.534483	0.41217	-1.587099	-0.151861	0.377481	-0.134104	-0.158863	0.412367	0.413268	0.206017	-2.408775	0.784941	-0.000217	0.603174	0.467488	-0.928163	0.569313	-0.679089	-4.462299	-0.344559	-2.027088	1.711365	NA	NA	-2.65191	0.016118	-2.290508	0.117409	-0.280986	0.360136	-0.023467	0.205856	-0.427401
BCK2	NA	0.529101	-9.058155	-0.771301	-0.07673	0.194058	-0.172423	0.344328	0.731502	0.695845	0.462572	-0.746786	-0.237957	1.226883	0.425378	0.680588	-0.050368	-0.465295	NA	-1.188477	-0.933347	-0.262917	NA	0.263233	-2.83506	-0.019527	0.030139	-0.250537	-0.94629	0.185007	NA	0.667585	-0.371024	0.108132	0.391962
BDF2	-3.536378	NA	NA	0.138315	0.093635	-0.094893	-0.600354	NA	-0.387182	-4.089704	-0.671964	0.227035	0.874629	NA	0.493276	-0.184623	-0.878635	0.802344	-0.226432	0.159574	1.169791	-0.428231	NA	-1.019792	-2.60495	0.628503	2.158294	0.315678	0.614996	-0.534023	0.461441	-1.815904	-0.151729	-0.546495	-0.14566
BEM2	NA	-2.83182	-0.007934	-0.979319	-0.955586	0.320205	0.257011	0.243725	-0.446737	1.550943	-0.758773	-0.339479	-2.107971	NA	0.334013	0.284788	0.178389	-1.060988	NA	-2.123554	-2.732414	0.53505	NA	1.056708	NA	-1.276356	-0.632828	-0.018458	-3.055606	0.983456	NA	0.660289	0.149542	0.493505	0.009507
BEM3	-0.335815	-0.568494	0.335466	0.011296	NA	0.801121	0.746182	-1.823244	0.252816	0.346979	0.051725	0.474218	-1.230273	-1.320302	0.054431	-0.694914	-0.268166	0.436141	0.746654	0.837637	-0.858491	-0.209083	1.573604	0.496497	NA	-0.716304	-0.281421	0.858165	0.089523	-0.08235	-0.425682	0.00303	0.790482	0.316105	0.115481
BEM4	NA	-0.108935	-4.721664	0.558842	NA	0.540125	0.180495	1.769258	0.599879	-2.106863	-0.871	-0.586312	-0.114689	1.717604	0.143545	-0.580577	0.717134	-0.651754	1.08291	-1.437006	-0.188325	0.382625	0.326437	-1.073745	NA	-1.426647	-0.635049	0.751528	0.362058	0.912315	1.393904	0.092243	0.77499	-0.019998	-0.180303
BFA1	NA	-11.278137	0.775539	-0.225968	-1.224093	0.545297	0.531418	-2.279316	-0.064201	NA	-1.753033	-1.952203	-9.311712	-1.114333	0.656465	0.268041	0.094708	-8.245728	0.211902	-7.65457	-12.089618	-0.333087	-7.076436	-0.152358	NA	NA	-10.83911	-0.039405	-2.330695	0.54308	NA	0.233252	-0.327187	0.21574	-0.131196
BIK1	NA	0.54929	-1.939373	NA	-0.66251	0.088266	-0.382743	0.669407	0.242366	-4.994076	-0.222199	NA	-0.307116	NA	-0.259685	-0.493277	-0.241308	NA	0.330214	0.238271	1.165445	-0.347734	-0.467812	0.349933	NA	0.798032	2.364199	-0.592845	0.374099	-0.647016	1.106434	0.04857	-0.30155	0.270897	-0.000171
BIM1	NA	-3.49065	0.95214	0.605773	NA	-0.058622	0.419861	-0.05552	-0.270528	NA	0.566784	-6.968951	-2.133622	NA	-2.698893	-0.879541	0.449497	-3.186979	0.756749	-2.622489	-3.206936	-0.033064	NA	-0.74392	NA	-0.654983	-2.506034	0.271531	1.299184	0.351921	-0.499187	-3.560768	NA	-0.179104	0.559829
BIT2	NA	0.399079	0.352773	0.418948	1.328893	0.468947	-0.495473	0.411601	0.491619	NA	-0.827651	0.27383	-0.171693	1.55259	0.124792	0.460066	0.262816	-0.538135	0.83108	-0.134977	1.918106	0.247682	-0.171907	1.041177	NA	-0.607948	0.413096	-0.742805	0.08071	-0.561746	-0.251395	0.332504	-1.423462	-0.821464	0.441999
BLM10	NA	0.429151	-0.39744	-0.791752	1.755152	0.080769	-0.990063	0.159971	-0.021643	NA	NA	-0.789454	-0.119426	-1.282549	0.825555	0.494693	-0.412231	0.155689	-0.251837	0.49524	1.254424	-0.176563	0.220853	1.520157	NA	-0.203632	1.179915	-0.168934	-1.540416	0.392278	-2.235326	0.405402	0.28431	0.578055	0.004541
BMH1	NA	NA	-3.207602	-0.72822	-1.480151	-0.17176	0.322044	0.256177	0.325265	-2.958564	-2.12251	-2.211017	2.196312	0.126812	0.286957	0.432413	-0.557163	-0.257741	NA	1.3183	NA	-0.400014	NA	-0.255417	NA	1.269305	1.126565	0.495678	-1.927161	0.270696	NA	-1.727042	-0.625011	0.376913	0.642561
BMH2	NA	-1.232928	0.24575	-1.500665	-0.354884	-0.089493	0.715659	-0.630668	0.397844	NA	-0.672387	-0.351983	0.85201	NA	NA	0.510729	-0.795337	0.182024	-0.419774	1.176566	0.375328	-1.702317	NA	0.117918	NA	0.395306	-0.233806	-0.670596	2.999252	0.663181	-0.368908	0.063492	NA	NA	NA
BNI5	NA	0.803724	0.768804	-0.312068	0.333115	-0.061191	0.070435	-0.252108	-0.492213	0.455572	-0.365851	-0.202781	0.392755	0.279725	0.685493	NA	0.076854	0.24307	0.016327	0.281	1.603859	NA	-0.153608	-0.31311	1.706296	0.209657	0.281389	-0.525073	0.135056	0.163554	-0.648256	0.143459	NA	-0.390519	-0.042338
BOI1	-0.008621	-0.669123	0.67351	-0.201077	-0.384236	0.255246	-0.120772	1.174642	-0.082608	0.610284	NA	-0.074341	-0.047057	-0.198409	0.012301	0.03398	-0.277213	-0.462253	-0.683307	-0.031245	NA	-0.212438	0.098362	0.810233	-4.302013	-0.0983	0.554499	0.237983	-0.657658	0.274001	0.072151	0.799098	-0.087138	-0.560449	0.643383
BOI2	-0.359974	-0.763353	-0.764189	-0.113813	0.687839	0.118893	1.416537	-1.737499	1.300718	NA	0.060281	-0.480646	-0.309488	1.538909	0.197961	0.256414	0.62757	-1.700343	NA	-0.60219	NA	0.016895	-1.977887	-0.039297	-3.241308	-0.266557	-1.41452	0.296778	-0.829114	1.091993	NA	0.269703	0.499837	-0.067252	-0.857973
BOP2	-0.049319	-0.766501	-0.650319	-0.059044	-0.635251	0.197722	-0.466572	NA	-0.17187	-2.144939	0.091069	-0.144397	-0.325512	NA	0.061926	0.600884	0.037746	-0.34279	0.12449	-0.196369	-0.736434	-0.041309	NA	-1.226442	NA	0.689543	0.828996	0.550924	0.180898	0.598959	0.516152	-1.531445	-0.129068	0.306993	-0.30838
BRE1	3.268014	NA	NA	0.371287	NA	0.248622	0.501415	NA	NA	NA	-3.610169	-10.243143	NA	NA	NA	NA	NA	0.364579	NA	NA	NA	NA	-0.303104	-2.941721	NA	NA	NA	NA	-1.723325	1.480902	NA	NA	NA	-0.094373	NA
BRE2	-6.903211	-6.706188	2.413618	0.002325	-2.235118	-0.015592	0.267313	-0.316107	0.640675	NA	-3.075409	-0.091053	NA	-4.690562	0.530315	-0.222441	0.752081	-3.373829	0.454909	NA	-5.557955	0.46547	-2.571725	0.214067	-3.056574	-0.966751	NA	0.990172	-1.992038	0.549818	-2.98863	-6.860336	0.761079	-0.323342	-0.052585
BRE5	NA	0.291342	1.864604	0.162619	-0.753791	-0.993106	-0.783446	1.486401	-0.845525	NA	-1.592814	-3.551307	0.237146	NA	-0.75435	-1.366017	0.497062	0.266415	0.453175	1.038388	1.099971	0.637923	1.119953	NA	0.128147	0.757216	1.007605	-1.385016	-4.337415	-0.002786	NA	-4.734624	-0.470339	-2.446424	0.026957
BRR1	NA	1.4211	NA	-0.858818	0.347907	0.146874	-0.086248	-1.040222	-0.644455	-8.708634	-0.5661	-0.257104	0.090245	0.396499	0.11843	-0.009487	0.005463	0.964216	0.30406	1.311866	-0.787523	0.430804	0.259494	1.402023	NA	0.540815	1.939964	-0.625871	NA	0.031865	-0.229336	-0.76298	0.121291	-0.255353	0.403851



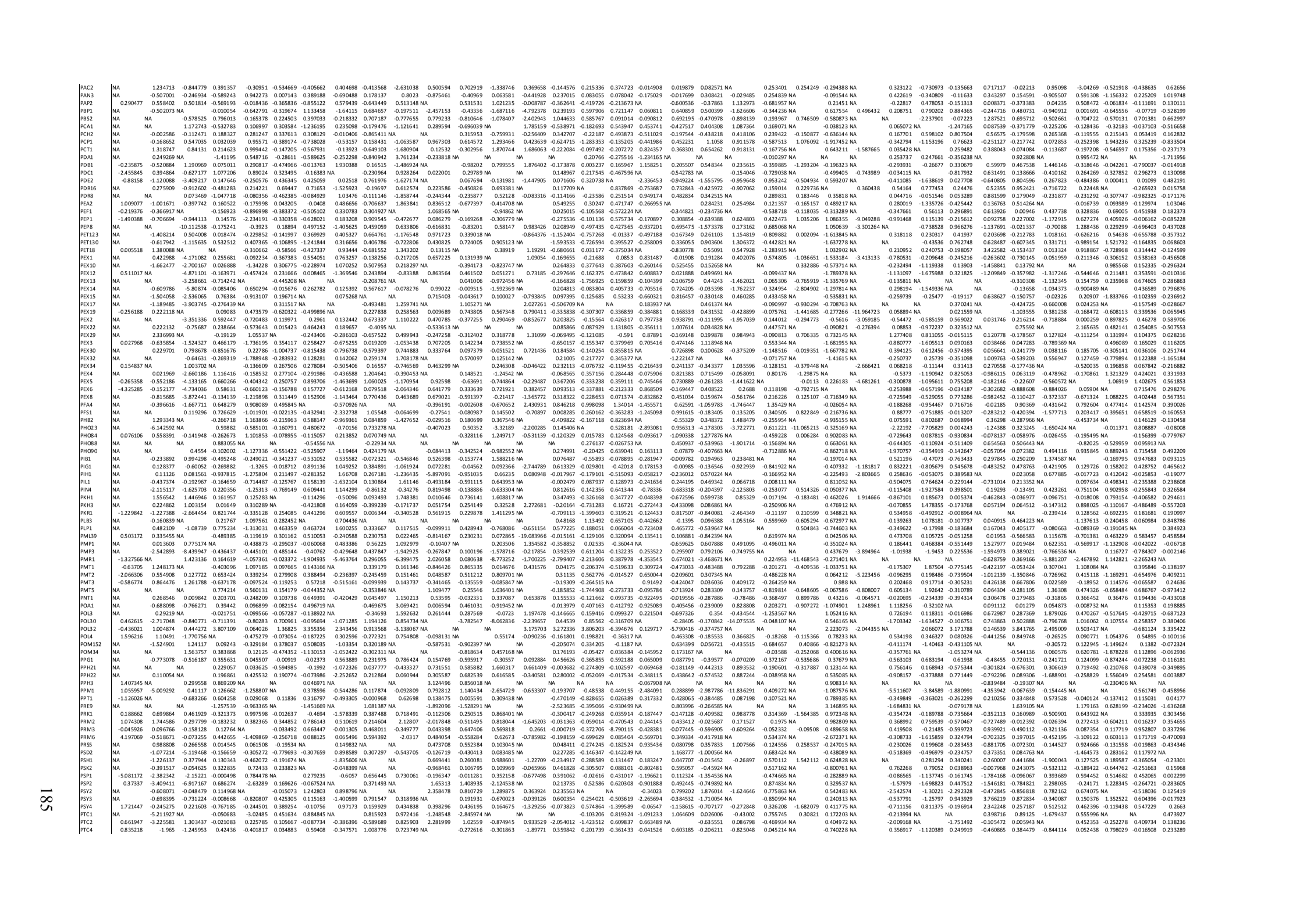
CTF4	-4.33713	2.377806	-3.568319	-0.599278	NA	1.287744	0.84377	NA	2.023616	-1.1019	NA	NA	NA	NA	0.615783	0.683442	0.379836	-0.844938	-0.359476	0.564203	-0.232417	1.157813	NA	1.333082	-2.145038	2.378284	NA	1.218471	0.606735	0.662576	NA	-0.838635	1.117255	0.272166	0.909652
CTI6	-9.274018	-1.78439	-4.652316	0.199168	NA	-0.143606	0.350645	0.725714	-0.278498	NA	-0.240558	-0.040006	0.016355	-1.45215	0.184618	0.046265	-2.32194	-1.644723	1.056527	-1.447934	NA	0.795638	NA	-0.641707	-7.755689	0.390084	-2.16494	0.098829	0.283038	0.525231	0.400368	-14.589341	-0.460188	0.210407	0.778762
CTK1	NA	-9.366093	NA	-0.731405	-1.955399	-0.450652	-0.126853	0.502567	0.292827	NA	-9.261493	NA	-0.604441	-8.141702	0.187687	0.415092	0.551431	0.928997	-0.461238	0.53296	NA	0.08389	0.41898	1.724361	NA	-0.172205	-1.619129	0.706876	-1.56247	0.11443	NA	NA	0.539071	-0.114557	0.004016
CTK3	NA	-3.367616	NA	-3.4304	-2.155101	0.075407	NA	NA	-0.216051	NA	NA	-4.688253	1.202849	1.657302	-0.785245	0.356562	-1.935106	NA	-0.861847	1.096433	NA	-0.492819	NA	-0.202386	2.387682	0.487291	-6.785611	0.6881	-1.148266	2.265432	NA	NA	NA	-1.197565	0.044987
CTP1	0.68359	0.773005	0.404827	-1.412118	0.06631	-1.047036	-0.437779	0.414616	0.512688	0.295207	-0.68954	0.464195	0.319721	2.452134	-0.39368	-0.40379	-0.278249	0.784743	-0.749924	0.982592	NA	0.129001	NA	-1.602171	NA	0.214682	0.945078	0.415979	-0.243041	-0.905283	0.640047	0.253587	0.254772	0.253524	-2.081723
CUE1	NA	-0.257062	-1.568419	0.77988	-1.340467	0.16813	-0.052732	-1.06487	-1.050007	1.628843	0.433342	0.086088	NA	0.468561	0.469614	-0.06057	0.513758	-0.369691	0.102959	0.060472	0.051602	-0.150653	1.197924	0.769817	NA	-0.195473	0.115496	-1.056124	NA	NA	-0.398263	-0.424882	NA	-0.142971	NA
CUE2	NA	NA	-0.884032	0.223603	-0.15036	0.07237	-0.025983	-0.224606	0.227958	-1.042725	0.326914	0.480199	NA	0.945094	0.225357	0.152119	0.522052	-0.400388	0.078239	-0.459818	0.846888	0.314035	-0.099917	0.349081	NA	0.234753	0.624458	0.349895	0.15262	0.251111	0.11929	-0.879332	-0.065803	-0.167169	0.537621
CUE3	-1.845561	2.125655	-0.536993	-0.008432	1.365693	0.165989	-0.17028	NA	-0.721678	-0.666759	-0.072468	0.47178	0.556975	NA	-0.049299	-0.134388	0.26367	0.867483	0.446525	1.891392	1.23532	0.120745	NA	0.086504	-2.641694	0.202049	1.52701	NA	-0.040846	-0.048963	-0.66362	1.197126	NA	-0.181705	0.236509
CUE4	NA	1.186206	NA	0.069677	-1.319157	-0.090508	0.194778	-0.301491	0.51341	-0.340976	-0.161405	-0.271912	-0.260969	0.704209	-0.473517	-0.051594	0.050787	0.379875	0.382218	-0.355617	NA	0.513292	0.630365	-0.208726	NA	0.376575	-0.63965	0.102939	0.248524	-1.029336	0.869895	-0.323026	-0.279146	0.673609	-0.403878
CUE5	NA	-0.50565	0.80868	0.119815	0.306893	0.167565	NA	-0.345564	NA	NA	0.149273	0.31709	0.893266	NA	0.453008	0.378405	-0.094757	0.170079	-0.206595	0.02848	0.41154	-0.033209	NA	-0.120066	-5.027285	-0.523656	0.576629	0.053683	2.206403	0.142442	-0.112695	-0.026912	0.503385	0.02731	0.676292
CUL3	NA	NA	0.351858	-0.667806	NA	-0.027377	0.032648	NA	-0.206539	-0.470485	-1.069924	-0.09614	NA	NA	0.092541	-0.099256	-0.491922	0.993089	0.096212	0.080379	NA	-1.389762	NA	1.146942	NA	0.132674	NA	-1.237365	NA	0.075499	-1.442134	0.402502	-1.903409	-0.051897	0.601968
CUP9	NA	0.650856	-2.018686	-0.130417	NA	-0.538884	0.143979	1.418777	0.073893	NA	0.225499	-0.082353	0.18649	NA	0.320255	0.185843	-2.457793	1.035328	0.777082	-1.391694	NA	-0.332238	-0.046916	0.661152	NA	0.788175	0.948942	-0.220522	0.162518	0.017048	0.684299	-0.783933	-0.829748	0.081711	-0.570151
CWC15	-2.140519	0.520641	0.404594	-0.036061	NA	-0.206692	0.700991	-2.430236	0.009249	0.603164	-0.544043	-0.315467	1.282011	-1.106261	NA	0.468313	-0.299676	0.269786	0.876564	-0.325598	0.684861	NA	NA	-0.281664	NA	0.594047	-0.32217	0.002658	-0.784878	-0.006269	-0.096989	0.158373	-0.071074	NA	0.337747
CWC21	-3.494989	0.21392	-4.381197	0.046699	0.684408	NA	0.212567	0.260563	-0.014582	-3.405648	-0.451192	-0.138377	1.048762	NA	-0.231159	-0.173122	-0.73473	1.062304	-0.394488	0.188088	1.474185	0.271722	NA	-0.668504	NA	0.82949	0.972863	-0.602604	-0.25133	-0.235464	-0.188556	-0.928053	0.010808	-0.145248	0.472613
CWH41	NA	0.078575	1.220466	0.308238	1.041213	0.080345	-0.696833	-1.933432	0.649387	NA	0.167584	-0.340673	0.757557	-0.903346	0.335859	-0.194928	-0.049174	-1.130906	0.36313	-0.569238	-1.114032	0.161191	NA	0.870903	NA	0.937023	-0.29197	0.015764	-0.561893	0.000523	-1.440036	0.12303	0.22315	-0.306903	0.453736
CWH43	NA	0.265521	-0.326436	NA	-0.767594	-0.20136	-0.336391	1.091369	0.087391	-0.314233	-0.012102	NA	1.236767	NA	-0.407382	0.134806	-0.245358	NA	0.340898	-0.428788	1.487447	0.1016	NA	0.938597	-3.331605	-0.54056	1.269642	-1.08435	0.176064	-0.063483	0.547658	0.297162	-0.722601	0.117798	0.075985
CYK3	NA	-1.706972	NA	0.154745	-1.685238	0.012521	0.272578	NA	0.462541	1.035879	-1.056654	0.030118	-1.893935	NA	-0.287459	0.470487	0.574966	-1.48712	0.299652	-0.090706	-1.217944	0.381692	0.081818	-1.31773	NA	-1.507984	-2.199841	-0.655023	-1.921109	-0.045742	0.975136	1.255957	NA	0.343653	-0.526584
CYT1	NA	0.555261	0.393762	-0.316996	0.883472	-0.432754	NA	0.251147	NA	NA	-0.229936	0.194124	1.72477	-0.687553	-0.783877	-0.637073	-0.114815	0.295182	0.576027	0.168982	2.073444	-0.32574	NA	-0.66188	NA	0.188618	1.073779	0.514719	1.650071	-0.442613	-0.200808	-0.019193	NA	0.067462	-0.363802
DAL81	NA	-0.177159	NA	-2.398066	0.973326	0.475987	0.419348	0.759696	0.00423	0.19014	-1.005842	NA	-0.940921	-0.464455	0.633607	-0.002435	-1.367827	-0.051117	-0.273275	0.229215	-0.001078	-2.125627	NA	1.403366	NA	-0.352073	2.096604	0.237407	2.155638	-0.502615	0.255134	-0.247691	1.67084	0.321154	-0.780753
DAS1	NA	NA	-0.97305	0.640505	0.291084	-0.0321	0.61183	0.272114	-0.275822	1.328474	0.502119	-0.898912	-1.127959	NA	0.160648	0.360378	0.401465	-1.325768	0.515615	-0.368083	-1.580245	-0.159971	-0.231215	-0.752075	NA	-0.457695	-0.240271	-0.05657	-0.732658	0.859241	0.938245	0.678778	NA	0.489575	-0.048575
DBF2	NA	NA	-6.999286	0.09584	NA	-0.262508	-0.587294	-1.334777	-0.118342	-0.600629	0.048444	0.508621	1.560731	0.312306	-0.826113	-0.333574	0.074885	1.101074	0.215229	1.205426	NA	-0.121438	2.05435	0.156284	NA	0.925823	1.553777	0.416956	-0.043538	0.510633	-0.333552	0.553596	-0.502425	-0.356133	-0.451595
DBP1	NA	0.110626	NA	-0.329204	NA	0.172425	-0.606796	0.795116	0.437833	NA	0.361095	0.11497	NA	-0.27765	-0.010757	0.091766	0.266634	0.536198	0.543489	0.232537	-0.187912	-0.643742	NA	0.481523	NA	0.962889	-0.345254	0.173605	-0.575338	-0.105788	-1.259505	-0.463733	0.095398	-0.235206	-0.538195
DBP3	NA	0.87627	NA	0.122105	-0.820354	-0.376558	0.203674	1.467433	0.67827	NA	-0.653689	-0.189688	0.883549	NA	-0.466948	-0.967356	0.515191	-0.185317	0.159943	0.193739	-1.213426	0.135285	NA	0.197383	NA	0.17402	1.037047	NA	-0.827083	-0.268155	-0.414328	-0.612392	0.720521	-0.089161	0.516037
DBR1	NA	1.029002	-2.626451	-0.139896	-0.144283	-0.475387	0.531184	-1.692218	0.406565	-2.816517	1.262469	0.77717	1.076757	NA	-0.45494	0.099332	0.56082	0.575393	0.282982	-0.319178	-0.06545	0.431951	NA	-0.423018	NA	0.152291	-1.187486	0.055121	-1.141395	0.018187	-0.031455	-0.815192	-0.113757	-0.237492	0.306717
DCC1	-4.226765	NA	NA	NA	NA	NA	0.604569	NA	NA	NA	-11.049362	NA	NA	NA	NA	NA	NA	NA	-14.523545	NA	NA	NA	NA	0.964561	NA	NA	NA	NA	0.306605	0.838101	NA	NA	NA	0.009345	NA
DCN1	NA	-2.266699	NA	0.39761	NA	-0.699895	-0.743373	1.825411	-0.632911	-1.446106	NA	0.58972	0.411249	NA	-0.367887	-0.914985	-0.484921	-1.627365	-0.243615	NA	0.844739	-0.246814	NA	-0.569648	NA	0.18749	0.865643	-0.411099	-0.331189	-0.387612	2.633138	-0.200924	-0.23246	0.49016	0.273208
DCR2	-0.074032	1.232594	-0.660139	0.479559	0.178138	0.394592	-0.316339	0.666908	-0.552409	0.734526	0.672791	0.319316	1.765026	NA	0.008765	-0.286718	0.108188	1.35587	-0.366673	0.447861	2.657532	-0.453608	NA	0.092636	NA	-0.00907	1.223818	-0.996577	-0.11785	0.575949	0.50601	1.429968	-0.161072	-0.187427	-0.975742
DDC1	-2.246083	-0.22647	-0.265713	1.230931	NA	0.020876	0.239437	-0.506479	-0.090901	0.209839	NA	NA	-3.500629	2.316418	1.109765	0.844222	NA	0.131237	1.792505	-1.268213	-2.118328	0.146745	NA	0.244867	NA	2.112176	0.596637	0.693249	-1.844769	0.180291	-2.256356	-0.99292	NA	-1.298446	0.642695
DEG1	-0.874505	-3.347632	-10.898045	1.18323	-0.8695	0.254875	-0.028014	-2.904615	-1.011843	-6.029531	2.184264	0.081682	0.101585	0.107617	0.392368	0.049064	1.539211	-0.350504	1.806695	-2.490578	-1.898105	1.188239	-1.408021	-0.000378	NA	-2.400649	-1.331918	-0.257069	-0.171358	0.763614	-0.995643	-2.05228	0.387695	0.282714	0.296411
DEP1	NA	-2.849806	NA	0.25417	-0.152285	-0.441493	-0.430923	NA	1.142977	NA	-1.070923	0.204175	-4.664962	2.485992	0.048905	-0.130358	0.404259	-4.122775	0.923548	-3.74083	-5.927774	0.573376	NA	1.54478	NA	-1.415896	-6.972712	0.115425	-1.499946	0.15702	-4.879224	NA	1.586947	0.321566	-0.073839
DGK1	NA	-0.714483	-0.553256	NA	-0.840831	0.053073	-0.761776	0.381933	-0.596738	4.227192	NA	0.45001	0.026618	NA	-0.03595	-0.135893	NA	NA	-0.843978	-0.089999	NA	-0.119841	NA	1.118242	NA	0.698044	-0.172657	0.122123	-0.754456	-0.236968	NA	0.779938	-0.478659	-0.362062	-0.320573
DGR2	NA	-0.222763	-0.202208	-0.184735	-1.296337	0.389556	0.758395	0.190432	0.557292	1.216429	0.162028	-0.275646	-0.169724	-1.019708	0.207233	0.273823	0.371228	-0.656119	1.15503	-0.430767	-0.728723	-0.254618	0.401773	-0.497571	NA	0.309186	-0.647134	0.571342	0.379812	0.192019	-0.540048	-0.024543	0.313901	0.050852	0.44217
DIA2	NA	-3.944566	-5.45063	-3.841719	-0.513405	0.663115	NA	NA	NA	NA	-0.233224	NA	NA	NA	-5.202041	-4.128159	-4.430466	NA	-2.720203	0.60801	NA	-0.14507	-2.62244	0.856834	NA	1.949943	1.712751	-1.135509	NA	1.836997	NA	-0.737727	NA	0.87535	-0.359913
DIE2	NA	1.084371	NA	-0.106404	-0.957898	-0.498974	-0.354244	0.323309	-0.827152	1.454618	-0.431957	-0.261579	NA	0.12445	-0.492507	0.050033	0.472999	1.085301	0.518693	0.240771	1.660679	-0.434158	NA	-0.725484	NA	0.303382	0.778495	-0.750271	0.400305	-0.223812	-0.12056	0.772527	-0.546392	-0.262179	-1.0816
DJP1	NA	-0.582087	0.52075	0.581266	-2.101891	-0.031533	-0.179446	-2.511151	0.299404	NA	-1.489228	-0.002534	0.836653	-1.392196	0.596315	0.131733	-0.454146	0.803528	0.862458	0.760399	NA	0.105828	-0.060148	0.275838	NA	0.090393	0.174216	0.426569	-0.105705	-0.073999	-1.179638	-0.099293	0.35783	0.024686	0.132172
DMA1	NA	-0.449837	0.315129	0.348509	-0.375714	-0.092618	0.329736	-0.352799	0.398225	1.116867	-0.54896	-0.170892	-0.12289	1.568296	0.992655	0.210599	-0.291352	0.636866	-0.227727	0.021289	NA	0.043594	0.663187	-0.203767	0.628626	-0.508924	-0.897953	0.041527	-0.195809	0.850838	-0.564445	0.221234	0.955708	0.538134	0.359072
DMA2	-1.662519	-0.353938	-0.577383	0.563441	0.896897	0.688	0.613397	0.998249	0.370242	0.185775	-0.606665	-1.041787	NA	-1.593786	0.492036	NA	0.339687	-0.419459	1.033578	0.204193	NA	0.065146	NA	-0.215662	NA	0.118826	-1.334635	0.687435	-1.040816	0.032574	0.664106	0.772052	0.125005	0.310126	-0.116847
DNF1	NA	NA	1.999626	-0.864282	0.217699	NA	0.106215	NA	-1.179672	NA	0.382838	-0.566489	NA	NA	0.701037	-0.32675	-0.170352	NA	NA	-0.764029	-0.776696	-1.556525	NA	-0.434135	NA	0.026701	0.257024	-0.201769	0.372256	0.689045	NA	1.270051	0.500259	0.840402	-0.165803
DNM1	-0.361245	2.008245	0.921145	0.047252	0.188382	0.237875	-0.017377	0.071727	-0.093069	-0.425822	0.004247	0.181397	1.395727	NA	0.103591	-0.105939	-0.00207	-0.097508	-0.239506	NA	NA	0.206033	0.273919	-0.441171	NA	0.862914	NA	-0.188602	0.633828	0.274395	-0.278331	-0.613911	-0.4032	-0.066679	0.409606
DOA1	NA	NA	-10.607327	-0.26431	-2.016337	0.540164	-0.326342	NA	0.695509	NA	-3.496756	-3.893366	-11.612318	-0.750557	0.60233	-0.229068	-0.232294	-2.53748	-0.069472	-1.948559	-5.858311	0.218059	-12.417904	1.087071	NA	-0.162719	NA	0.516277	0.078812	-0.090764	NA	-5.59174	NA	-0.507535	0.091139
DOC1	NA	NA	NA	0.20068	NA	0.362404	-0.794784	-2.217304	1.388093	-1.968688	-4.032707	-5.58223	-10.28033	NA	0.012068	0.285572	0.932684	-5.370243	0.718918	-3.67264	NA	1.183083	-7.971358	0.31934	NA	-0.623306	-7.538714	NA	1.724506	-0.028236	-1.067094	0.162448	NA	-1.467682	-0.76223
DOM34	NA	NA	0.148811	-0.013223	0.412195	-0.501631	0.006694	0.518878	-0.22835	NA	0.444445	0.302915	1.065704	-1.330998	-0.755446	-1.068894	0.107796	1.526501	0.530458	0.848502	NA	-0.00511	NA	-0.825905	NA	1.043843	1.926048	-0.800908	0.311963	-0.52488	0.073382	0.485304	NA	-0.211765	0.158757
DOT1	-0.558395	NA	NA	-0.338195	NA	NA	-0.11727	0.544156	NA	NA	NA	-1.755191	NA	NA	-0.094957	NA	NA	0.684635	NA	NA	NA	0.427632	NA	-3.467098	NA	NA	NA	NA	-1.928238	-0.255634	NA	0.07522	-1.36751	-0.529903	NA
DOT6	-0.226131	-0.557386	-0.712388	0.2452	-0.284657	0.537089	0.060353	-0.300016	0.721421	-1.723429	NA	0.357471	0.775563	0.938135	-0.242984	0.262528	0.4324	NA	0.10116	-1.188601	-4.418722	-0.09321	-1.474072	0.084439	NA	0.16314	-1.294408	-1.238391	-0.517311	0.389664	NA	0.51138	NA	1.339538	0.100911
DPB11	NA	NA	0.089586	0.358332	0.097582	0.042181	0.048908	1.409831	-0.230201	NA	-2.334842	-1.315828	-1.328332	NA	-0.025434	-0.002216	-0.098665	-0.960792	0.530375	0.260621	-1.476387	-0.399633	NA	-0.673786	NA	NA	0.054059	0.381733	0.246882	0.169093	0.448728	NA	0.499191	0.124329	0.280361
DPB2	NA	0.021609	0.426485	-0.038702	-0.090636	-0.113256	-0.709226	3.157577	-0.090116	-9.470799	0.382407	0.521522	0.555311	-0.666443	-0.408413	-0.270016	0.313324	0.353651	-0.228939	0.923271	-0.183601	-0.34988	NA	-0.748795	NA	0.097588	-0.740038	NA	0.323621	-0.197865	1.323652	-4.909174	NA	0.042653	-0.194356
DPB3	-2.054294	0.130032	1.406862	-0.507435	-1.650155	0.105167	0.207796	-2.385217	-1.304725	-6.070652	-0.341442	-1.184795	NA	NA	-0.40159	0.112796	0.144118	1.099379	-0.03861	0.166239	0.785509	0.126225	NA	0.104246	NA	1.853571	0.29716	-0.546248	1.371409	0.394051	-2.474595	-2.366815	-1.406935	0.165254	0.523509
DPB4	NA	NA	-0.823055	-1.418665	-1.175104	0.078339	0.216903	-3.115143	-0.762782	-6.927214	0.690726	0.86454	0.703697	-3.370638	NA	0.461568	-0.531146	-0.101365	-0.245355	0.241028	NA	-0.220216	0.042976	0.836807	NA	2.024416	0.246184	0.628062	0.030042	1.014851	-1.60097	-0.968778	0.706622	NA	0.367644
DPL1	NA	0.678557	0.819347	-0.300803	0.693873	-0.072475	0.32049	-0.889677	-0.07797	-0.398578	-0.809166	0.364083	0.230568	-0.684924	0.426931	0.035493	0.069772	0.672676	0.294726	0.289675	NA	NA	0.399919	0.329082	NA	0.75108	0.56536	-0.077635	-0.311294	0.227359	-0.760943	NA	-1.34728	-0.152892	-0.048611
DRS2	-0.763733	NA	-5.90816	-0.16445	0.119107	0.190155	0.237692	-0.679075	0.087382	-0.569315	-0.134182	0.282859	1.770101	-0.710403	-0.926954	-0.26801	-1.103805	-0.221294	0.178685	-0.278611	0.486728	-0.129499	NA	-0.637998	NA	-0.386181	-0.21678	0.250339	0.30047	0.579961	-0.486606	0.278402	-0.231448	-0.285372	0.479899
DSD1	0.896832	0.653665	0.26669	0.188913	-0.100498	0.28146	0.114388	-0.575296	-0.426673	1.879879	-0.106984	-0.416456	0.310657	NA	-0.448204	0.236397	0.105979	0.130608	0.296558	0.551717	0.104473	-0.052548	NA	-0.206287	NA	-0.944088	0.47163	NA	0.549314	-0.256122	-0.312912	0.046102	-0.010085	-0.219974	0.106888
DSE3	3.696431	1.517158	0.855652	0.18832	0.231471	0.244871	-0.148891	0.916571	-0.292126	0.304453	-0.187063	0.698333	0.06266	NA	-0.351293	0.053071	0.096253	0.253011	-0.463309	-0.414275	0.417395	-0.420161	-0.570678	-0.172317	1.498568	0.096993	0.999014	-0.014207	-0.167732	0.022598	0.415944	0.011482	-0.039989	-0.189179	-0.24965
DSS4	0.359479	-0.120167	NA	0.302099	0.292635	-0.049766	-0.069572	-0.295487	0.139653	0.127378	0.058021	0.362499	-0.252533	NA	0.721525	0.348616	0.735722	0.117923	0.138841	-0.479739	-0.445384	0.382932	NA	0.32736	NA	-0.365195	-0.66636	-0.371009	-0.560122	-0.042468	0.312552	-0.23268	-1.378276	-0.71418	-0.064366
DST1	NA	-3.800374	-5.002391	0.626464	-2.547581	-0.430417	0.299924	NA	-0.036752	2.965866	NA	-1.43932	NA	NA	-0.078621	1.002585	0.199074	-1.485868	0.168577	0.452035	NA	0.141556	NA	3.433567	NA	-2.866223	NA	-0.789157	-0.953867	0.856622	NA	NA	-1.603292	-0.004375	-0.239136
DUG2	-3.139746	-0.08542	0.767573	-0.084031	0.894518	0.11786	0.125411	0.813451	-0.944467	NA	NA	-0.055971	0.219932	2.160622	-1.04048	-0.467621	-0.427133	-0.028372	-0.037613	-0.238604	0.821926	-0.368321	-0.456756	0.193877	-0.299539	0.52556	-0.311105	0.470534	0.347044	0.16399	-0.157665	-0.418527	0.6633	-0.563012	-0.206582
DUS3	NA	0.426592	0.458521	-0.169305	0.210097	0.08392	-0.320386	-0.026717	-0.053661	0.24517	-0.968806	-0.185298	0.696006	NA	0.122695	0.101626	-0.540555	-0.19631	-0.230606	-0.182068	NA	0.128882	NA	-0.128675	NA	0.588183	-0.159682	0.108287	0.274138	0.643106	-0.140166	0.745808	-0.209881	-0.583898	-1.038061
DYN1	NA	-1.936107	0.474859	-0.536103	-0.143249	0.084347	-0.294312	0.51401	0.539681	NA	NA	0.631333	-2.19539	NA	-0.215896	0.773972	-0.007688	-3.704765	0.618069	-0.891965	NA	0.115437	NA	0.545561	NA	-0.301669	-1.119768	0.107396	-0.976719	0.65516	-1.410945	-1.231698	0.710766	0.005985	0.342231
DYN2	NA	NA	0.134073	0.339993	-0.540991	NA	0.8517	0.686717	0.271439	0.200196	-0.018612	0.426851	-1.076449	-1.063527	0.03891	-0.390471	0.191648	-0.991408	0.706498	-0.883542	-0.214606	0.552168	NA	-0.093249	NA	-0.086585	-1.179877	-0.234927	-0.027541	0.392802	-0.397583	NA	-0.004496	-0.071458	0.121198
DYN3	NA	-3.174718	0.981834	0.296733	1.088146	0.175258	0.218433	-0.228443	0.247995	NA	-0.638282	0.528846	NA	NA	0.999469	0.664118	0.041999	-0.483391	0.245426	-0.867472	-2.202609	-0.817083	0.07016	0.48238	NA	-0.522933	-1.094687	-0.406165	-1.004277	0.648447	NA	-0.432485	0.229052	-0.112097	NA
EAF3	NA	-4.92667	NA	0.035254	-1.917249	-0.502929	-0.352842	NA	-0.420972	-3.685747	-1.731721	-1.550552	1.180981	-6.219707	0.571362	0.374846	-0.170724	0.17149	-0.930015	0.578132	0.800693	-0.199236	1.418032	0.624225	NA	0.436393	0.070718	0.649572	-0.024518	0.134341	NA	-2.754264	0.370648	-0.902152	0.212336
EAF6	NA	-2.246631	-2.214324	0.345348	-0.07397	0.135909	-0.469226	-6.644373	0.008425	NA	0.859704	0.231831	1.104514	-0.772083	0.557201	0.081945	0.475336	0.066695	0.483336	-0.210046	NA	-0.412209	0.866489	0.074479	NA	-0.938277	-0.948038	-0.642733	-0.744823	-0.711404	NA	-2.772907	0.619292	-1.027116	-0.098254
EAF7	NA	NA	-3.049413	0.617488	-1.185948	-0.713172	-0.856869	NA	-0.705935	2.921633	NA	0.973963	NA	NA	-0.348461	NA	-0.141666	1.033937	0.674721	1.257818	1.541757	0.421834	NA	NA	NA	-0.640781	NA	-0.520627	NA	-0.622303	1.01512	-5.921711	-0.004257	-0.5104	-0.783947
EAP1	NA	NA	NA	0.132881	NA	-0.177912	-0.490642	NA	0.712683	3.475835	NA	-2.375122	-3.592878	NA	1.155396	2.195471	-0.096461	0.223545	0.13178	-0.095219	NA	-0.188823	NA	NA	NA	-2.254492	NA	1.017332	-0.643351	1.194158	-1.311745	NA	NA	0.295788	-0.473423
ECM18	0.00757	0.944312	0.418339	0.714676	NA	0.158092	0.362194	-0.150376	0.672285	0.41242	-0.062807	0.500418	-1.355791	NA	NA	0.084642	-0.351751	0.377183	0.131864	0.449406	-0.366487	NA	NA	-0.549059	NA	0.185951	0.27196	-0.417041	-0.208689	-0.152749	-0.4204	0.094089	-0.423389	NA	0.02947
ECM2	NA	0.120351	-2.10199	1.086892	0.31662	0.043221	-0.67684	0.649632	0.805715	1.54807	NA	0.482611	NA	NA	0.05383	-0.067602	0.249461	-0.861759	0.065126	-0.132773	NA	0.190853	NA	1.134025	2.01694	-0.520028	-1.139121	-1.944806	-0.671575	-0.193842	-0.669026	-0.03794	0.071332	-0.066151	-0.538105
ECM21	NA	1.627093	1.514188	-0.03652	-0.224143	0.02892	0.139199	-0.542183	-0.232139	2.259988	-0.610357	-0.121065	0.718203	1.643249	-0.579264	0.365186	-0.288696	0.660417	0.175956	0.299925	-0.372341	-0.672491	0.035167	-0.677155	NA	-0.097695	1.288017	-0.453637	NA	-0.047878	-0.204691	-0.518862	-0.974306	0.458464	-0.625525
ECM22	1.237054	NA	-0.447062	0.268893	0.739207	0.608921	0.321896	-0.533836	-0.157286	0.477958	-0.611754	0.112108	1.316845	-0.827418	-0.656575	-0.409324	-0.096536	0.203738	-0.142263	-0.048864	0.492685	0.64834	NA	0.469424	NA	0.121248	0.171358	-0.248163	0.697283	0.420487	-0.050038	-0.707804	-0.255142	0.148487	0.213781
ECM30	NA	-0.43121	-3.024987	0.443578	-0.843576	0.090252	0.993679	-1.332637	0.930168	-0.000564	-0.12878	-0.704525	-0.523731	0.801338	0.798992	0.34237	0.525001	-0.594706	0.163629	-0.844292	-0.358198	1.000888	0.115739	-0.252706	NA	-0.155145	-0.034248	-0.831422	-0.86719	0.347113	-0.706908	-0.163814	NA	1.272182	0.080812
ECM33	NA	0.536811	1.192599	0.010016	0.862817	-0.119556	-0.3312	0.186153	1.037862	0.686641	NA	-0.13897	-0.337516	0.581114	0.122116	0.266992	-0.178982	0.899069	0.255253	0.437741	-0.384303	0.03381	NA	1.305157	NA	0.089961	1.345126	-0.542098	-0.845317	0.064084	-0.035807	0.063481	-1.034755	-0.138605	-0.094923
ECM5	NA	0.186471	NA	0.04765	-0.514261	0.165344	-0.087506	-1.488547	0.294886	0.386786	-0.353579	-0.020224	NA	-0.163562	0.12146	0.378599	-0.10476	-1.060187	0.104035	-0.245906	-0.700755	0.160071	0.498225	-1.210208	NA	-0.093016	-0.037092	0.475636	NA	NA	0.599831	0.122521	0.251836	-0.493953	-0.157087
ECM8	NA	0.997031	0.299507	-0.045065	0.932416	-0.266421	-0.006036	NA	0.350468	1.118553	NA	0.323589	-0.138226	NA	-0.292725	-0.5277	-0.544184	0.205544	-0.404726	-0.088216	NA	-0.189724	0.181858	0.458809	1.925366	-0.051215	1.703263	-0.824947	NA	-0.019589	NA	-0.23414	-1.6227	-0.014678	-0.507591
EDC3	0.014235	0.334979	-0.773197	-0.197069	-1.517898	0.289845	0.534279	-0.697159	0.124997	-1.644224	0.536608	0.279978	0.974641	-1.975928	0.367408	0.036667	0.211338	-0.122309	0.524763	-1.084994	-0.918563	-0.48597	-0.112437	1.291508	NA	-0.538931	0.768048	-0.108237	-0.691806	-0.218787	-1.086112	-0.499417	0.03554	0.432792	0.425354
EDE1	-1.715826	-1.770376	3.821522	-0.089263	0.903702	0.016231	0.028084	-1.771057	0.533552	0.28379	0.832476	0.190524	-1.720475	-1.483401	-0.027981	-0.399056	0.919663	-0.562994	1.216171	-0.630881	-3.109711	0.730181	-1.429445	1.17103	-6.020914	-1.206981	-0.477192	-0.111103	-1.628803	-0.058871	-1.587394	0.709546	0.83328	-0.602716	0.184222
EGD1	-0.455076	1.108527	-0.0669	0.837001	0.190407	-0.022467	-0.358055	-1.33992	-0.491296	1.723209	1.432695	0.930653	2.08813	-0.395928	-0.267574	-0.863792	0.322916	1.145526	-0.253156	0.888915	1.576409	0.416221	NA	-1.049392	-1.794101	0.45397	1.324283	-0.700753	0.408741	0.295959	-1.166675	-0.174163	-0.206087	-0.346128	-0.043695
ELA1	-3.413412	-0.490314	NA	-0.198454	-0.244808	0.378563	0.103279	-1.127584	0.512206	-1.949824	NA	0.391478	-0.015432	NA	-0.096437	NA	-0.294612	0.045531	0.677923	-0.619707	-1.455701	-0.049331	-0.087958	NA	-3.139709	-0.656234	-0.866906	-1.304525	-0.253008	0.489014	0.33175	0.157754	NA	-0.230257	-0.143287
ELC1	NA	0.266329	0.781112	-0.489905	-1.799333	-0.220948	-0.431171	-2.191161	0.415425	1.744151	-0.282575	-0.485886	-0.559971	NA	0.696106	0.222446	-0.401347	-1.4426	-0.311773	-1.625419	-0.670717	0.714203	NA	0.807044	1.382657	-0.431295	-0.41566	0.033375	0.448204	0.451575	-0.590496	-0.090615	0.196087	-0.113014	0.424288
ELF1	NA	-1.088591	-1.334766	0.62759	-2.762562	0.349673	0.637397	-1.171793	0.265499	-1.984152	-0.209006	-0.015687	0.634769	-0.502073	0.479823	0.675243	0.056635	-0.330848	1.022691	-0.630576	NA	0.481503	NA	0.033729	NA	-0.3411	0.689286	0.031038	-0.858171	0.062931	-0.30362	-1.236442	0.710966	-0.287297	0.724047
ELG1	NA	-2.960914	-1.080759	-1.339042	-1.373242	0.391605	0.855759	-7.752483	0.336768	-0.209996	-2.550441	-6.818783	-10.974129	-7.759601	0.527939	0.769314	-0.874899	-0.077997	-0.498964	0.997924	-8.308884	-1.835599	NA	-1.465831	-0.119868	1.430979	0.11424	0.807408	-3.007626	0.562278	-2.727694	0.499759	0.654519	0.942989	0.946845
ELP2	NA	-0.361455	NA	0.060709	-3.467811	-0.320013	0.254647	-1.548507	-0.202817	-5.401518	-0.003394	0.102969	2.226746	-7.901698	0.08099	-0.697948	0.641713	0.175456	0.386675	0.559136	0.453674	0.674287	0.31762	-1.834052	-7.471804	-0.764892	-1.708649	0.883937	-1.167071	-0.01455	0.216446	-1.716301	1.120324	0.949538	-0.078045
ELP3	NA	-0.344121	NA	-0.891746	-2.084002	-0.524015	-0.588219	0.08221	-0.705854	-3.634381	0.054763	0.617088	2.056821	-5.765812	-0.13323	-0.928858	0.94428	0.693778	0.422831	0.631418	0.71347	0.041844	0.39976	-1.087414	-10.25008	0.57939	-0.930331	-0.082918	-0.569596	0.251948	-0.115687	-1.056439	0.327318	0.29688	-0.318528
ELP4	NA	0.055411	NA	0.534777	NA	-0.03534	-0.190472	0.577188	-0.256161	-3.710361	1.227638	1.116759	1.949898	-1.868624	0.03491	-0.165428	0.341052	0.718403	0.254537	0.496935	-1.373736	0.021721	0.680839	-0.436012	NA	-0.549929	-1.409294	0.964559	0.215969	-0.045971	-1.353553	-1.759253	1.296507	0.557798	-0.294679
ELP6	-4.042944	-0.424547	NA	0.438719	-2.532773	0.005328	0.629961	0.140438	0.316156	-4.233285	0.022159	0.48706	NA	-5.701086	0.903567	0.030068	0.789479	0.885765	0.943628	0.138777	0.120382	0.228829	1.188722	-2.62806	-2.399748	-0.151003	-1.143576	0.707751	-0.990185	-0.103746	NA	-1.221784	1.658659	0.963669	NA
EMC1	NA	-0.885471	-1.605195	NA	0.019638	0.120885	1.413657	0.041039	0.858257	NA	-0.800816	NA	0.433893	NA	0.282529	0.255283	0.356577	NA	1.23687	-0.106185	0.831606	0.601114	0.807357	0.448194	NA	-0.250566	-0.395086	-0.551747	-0.123912	-0.11713	-0.373381	-0.051152	NA	-0.404088	0.204588
EMC2	NA	-0.190255	NA	1.265273	-1.396105	-0.506012	-0.456723	NA	0.361026	3.549167	-0.209899	-0.149301	NA	3.207774	0.556486	0.050923	-0.822713	NA	1.269518	-1.112285	NA	-0.596456	0.750548	2.034807	NA	0.12582	-0.907833	0.272131	0.627774	-0.042403	NA	1.201264	-0.011965	-0.420917	-1.12408
EMI1	NA	0.88368	0.384868	-1.247791	0.669221	NA	-1.192886	-0.296986	-0.354777	NA	NA	0.499183	1.634562	NA	-0.784442	-0.37484	-1.016266	0.461608	-0.877863	0.413231	3.151606	-1.3868	NA	-0.030744	NA	-0.286934	-0.185461	0.506272	0.149357	0.670841	NA	0.245554	0.805331	-0.410904	0.473246
EMP70	-0.629975	-0.598594	-0.014297	0.003258	-0.092851	0.086694	-0.208931	-0.660646	-0.113673	0.134682	0.037492	-0.479177	0.044554	-0.664852	-0.000994	-0.063747	0.090706	-0.080578	0.117456	NA	1.260346	0.728497	0.164957	0.08901	NA	0.71834	NA	-0.80857	0.133597	0.429948	NA	-0.028372	NA	-0.515977	0.270467
ENT2	NA	0.26305	1.088905	0.035321	0.187502	-0.117735	0.377964	0.790359	0.417731	-0.045842	-0.642553	-0.073547	0.99743	0.273578	0.328925	-0.462503	0.449301	0.02211	0.362735	0.60834	NA	0.018131	NA	-0.058421	NA	-0.171357	0.282503	0.74071	-0.208958	0.065669	NA	-1.310313	-0.287034	-0.570381	-0.604427
ENT3	NA	0.305281	0.477674	-0.165176	-0.349364	-0.321309	0.125465	0.298467	0.600081	-0.623229	-0.304691	-0.144381	0.8379	0.478043	-0.154071	0.063118	0.184816	0.167633	-0.376147	-0.391203	0.719286	-0.44923	NA	0.401832	-4.01669	0.289242	-0.015285	-0.055702	0.278038	0.303133	-0.412067	0.733787	-0.972704	-0.172209	0.636831
ENT4	NA	NA	0.694014	0.408151	0.913616	0.342977	0.543445	0.973249	0.032018	-0.043638	0.683711	-0.357669	0.208808	NA	-0.135683	-0.151509	0.166423	-0.593986	-0.369742	NA	1.116047	0.45269	NA	-0.112556	-0.499837	0.068678	NA	-0.189272	-0.141971	0.105024	-1.118381	0.047427	-0.675638	-0.498956	0.24302
ENT5	NA	1.045123	0.219172	-0.050803	0.572598	-0.310729	0.078924	0.716202	-1.953997	NA	-0.393108	0.483657	-0.137931	NA	NA	-0.217735	-0.224111	0.810483	-0.352053	0.441638	1.726132	NA	NA	0.600717	NA	0.437516	0.666987	-0.011015	0.113107	0.126666	0.064548	0.123661	-0.653154	NA	-0.858274
ENV11	NA	1.309427	0.894731	0.321631	0.539842	-0.453776	-0.230376	-1.427569	0.296434	-3.584617	0.704576	0.281082	-0.251178	-0.738644	0.504101	0.604778	-0.506026	-0.190458	-0.744813	-0.637555	-1.535914	0.361985	NA	0.052438	NA	0.339211	-0.176733	-1.081012	-0.781146	-0.03939	-1.887569	-1.202453	-0.154672	-0.094037	0.353101
EPL1	NA	-0.273695	0.677564	-0.178474	NA	-0.108203	-0.122175	0.901708	-0.432157	0.516249	NA	0.65188	-0.715395	NA	-0.065417	-0.537015	-0.505111	0.106352	-0.810214	0.756653	NA	-0.699269	-1.232425	0.208625	NA	0.085973	0.888936	0.132541	0.289617	0.083904	0.604576	0.535923	0.658226	0.499393	-0.183638
ERD1	NA	0.386218	0.657713	-0.688487	1.237977	NA	0.005269	0.878005	-0.670644	1.362553	-0.950797	0.216393	0.801125	NA	-0.346554	-1.208147	0.547418	0.120333	0.518439	-0.144812	1.204734	0.624828	0.110742	-2.210974	NA	0.193915	-0.535699	-0.178948	-1.71308	0.224765	-0.006114	NA	NA	-0.54373	0.172854
ERG3	-5.218407	-0.834506	0.416383	0.980662	-1.533893	0.377494	1.046764	-1.911089	0.762294	-1.635747	0.059512	-0.520907	0.802673	-2.398614	0.636951	0.360406	0.126051	0.26805	0.372184	NA	-0.050359	0.770313	0.90865	0.344946	NA	0.100634	NA	NA	-0.108623	0.599933	-0.732795	-1.415451	NA	0.594295	0.608953
ERG5	NA	0.417414	-0.606213	0.058595	-0.070908	0.110452	-0.078563	-0.804544	0.277069	-2.28059	-0.478392	-0.196887	1.647425	-0.07092	0.647255	0.260722	0.166665	0.313789	-0.328837	0.620706	NA	-0.052147	NA	0.298813	NA	0.30402	-0.359838	1.09434	0.652621	0.637286	0.067961	-0.849516	1.373377	0.434055	-0.476761
ERJ5	-3.617569	-3.051664	0.104176	0.439063	-1.068818	0.583819	0.200716	-1.092201	0.253342	NA	-1.344121	-2.534128	0.465587	-0.045989	0.090152	0.697732	0.393353	0.153584	0.321444	0.054844	-0.881257	NA	0.553817	-1.034805	NA	0.155869	-2.461432	0.72074	-0.001246	0.193283	-1.128352	-0.758381	NA	0.279485	0.887018
ERM6	NA	1.09696	-0.241446	0.241522	-0.037246	0.216331	-0.173362	-2.43107	0.028001	NA	0.099978	0.170557	-0.99799	1.317454	-0.075853	-0.549978	0.142628	NA	-0.6661	0.911924	0.824935	0.375984	NA	-0.413812	NA	NA	0.400066	-0.364069	-0.504833	0.608151	-0.522606	0.031496	-0.159393	-0.619008	-0.304103







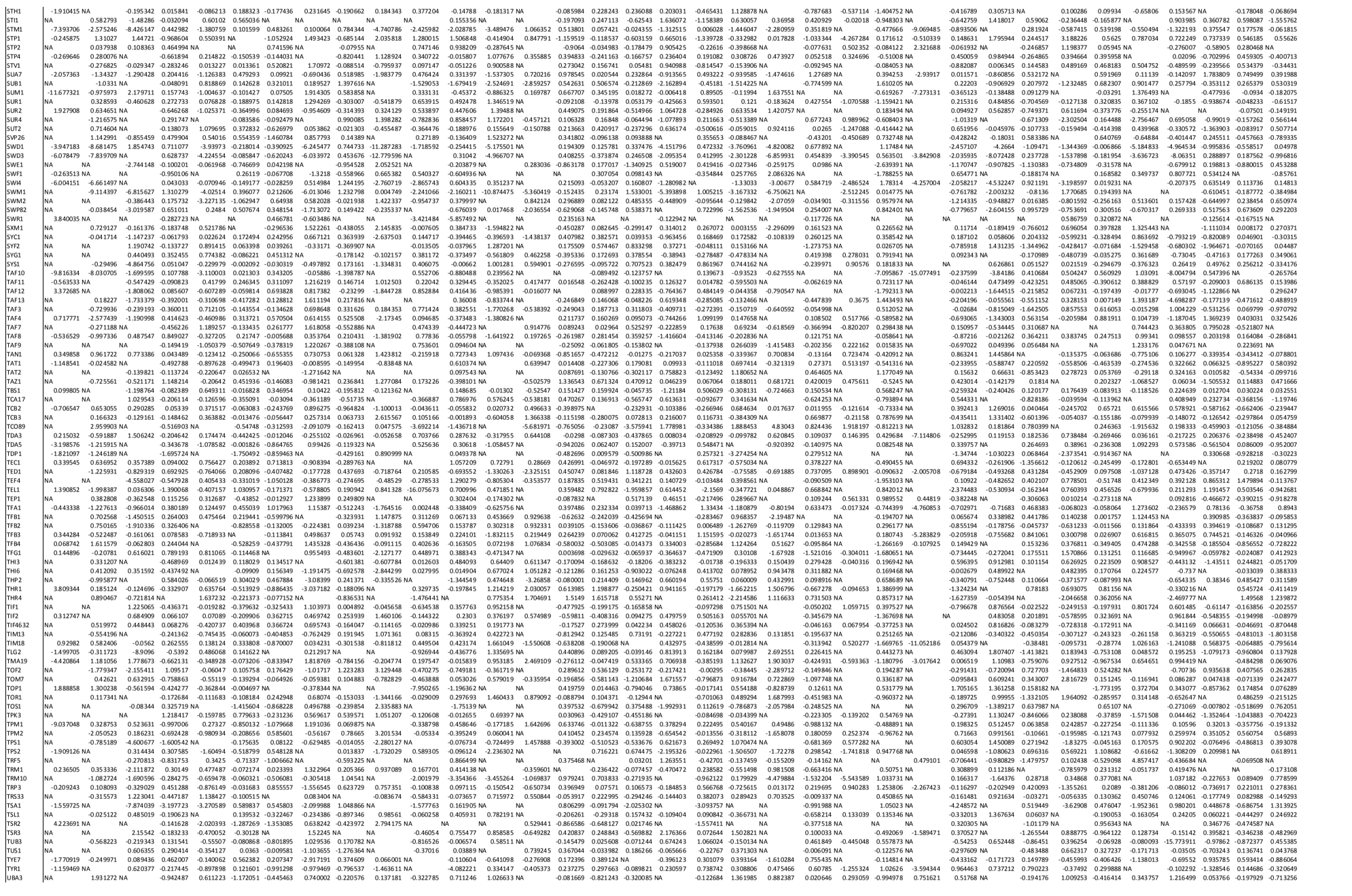
MOT3	-3.888533	-1.231733	NA	-0.124273	NA	-0.277229	NA	NA	0.887351	0.460762	-0.310643	-0.777021	0.06728	NA	0.150199	0.19398	0.478791	-1.643148	NA	-1.067309	NA	-0.279521	-0.892282	-1.731002	NA	0.678361	-0.891627	-0.179625	-0.255426	-0.213707	-1.811717	0.380001	0.624886	-1.118616	-0.65107
MPD1	NA	1.54368	0.604905	-0.001475	0.555234	0.111615	-0.29473	0.346237	-0.496776	0.172506	-0.225075	-0.09107	0.522728	1.004611	-0.36121	-0.63565	NA	-0.155086	-0.033282	0.329782	0.717899	-0.696675	NA	-0.371137	NA	0.297846	1.081657	-0.608366	0.210855	-0.824957	NA	0.929078	-1.901728	0.119045	-0.048768
MPE1	NA	NA	-0.997043	0.155701	1.635241	-0.173458	-0.179488	-0.084835	-0.464561	NA	1.365324	0.428969	-0.111685	NA	-0.311838	-0.114864	0.14811	-0.041567	0.60973	1.419685	NA	-0.056329	NA	0.091028	0.698203	0.022469	-0.072772	0.585606	0.339337	-0.564223	NA	0.528551	0.811939	0.059572	0.095559
MPH1	-0.51024	-0.183055	-1.340758	0.101631	-0.450974	0.217292	0.569556	0.764647	0.357138	0.72129	-2.418357	-0.154807	-1.188311	NA	0.732761	0.288717	-0.446757	-1.88131	-0.141396	-1.836157	-2.360584	-0.53587	NA	-0.162208	NA	-0.816396	-0.756438	1.017964	0.283047	1.273731	0.099419	0.267998	0.942479	0.547421	0.234182
MRC1	NA	NA	NA	NA	NA	NA	0.216213	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.375627	NA	NA	NA	NA	NA	0.479088	NA	NA	NA	0.205653	NA
MRE11	-1.178251	-1.522549	-2.274156	-0.018916	NA	1.061491	-0.105132	-1.055928	NA	NA	-1.669755	-6.149358	NA	NA	1.030666	NA	NA	-0.356782	0.630722	-0.422174	2.166928	1.42009	-0.616737	0.846075	NA	-0.421956	-0.490731	1.377306	NA	NA	-4.035232	0.124056	NA	0.681571	NA
MRN1	-1.944025	-1.986133	-2.234606	0.297877	NA	0.530124	0.562948	-1.436714	0.221161	-3.178561	-1.518203	-1.292772	-0.091955	NA	0.132237	0.421792	-2.114214	0.227706	0.827232	0.648613	-0.83882	0.215463	1.334687	-0.812288	NA	0.488524	-1.033765	1.001212	0.650111	0.5925	-1.942768	-0.356244	0.383491	0.578821	0.223414
MRPL10	NA	-3.622361	0.124534	0.027819	-0.395288	-0.462826	-0.08209	0.073373	1.028741	-2.839329	1.712791	0.696484	-1.004687	-0.342058	-1.262692	NA	0.484735	0.096581	0.530402	0.637645	-2.070445	-0.202988	NA	NA	NA	0.557304	NA	NA	0.572632	-0.201149	0.18038	-2.003814	NA	0.504467	0.515054
MRT4	3.403604	-0.319288	1.517483	-0.948316	-0.545656	-0.42661	-0.402071	0.684046	-0.754197	NA	0.382495	0.437663	-0.590056	NA	-0.177814	-1.455038	0.715224	-0.777193	0.49352	0.106655	NA	-1.239094	0.114722	1.139075	NA	NA	0.703587	-0.150085	-1.725619	0.151961	2.008911	0.027461	1.309499	0.103898	-1.157737
MSA2	NA	0.482901	-1.93701	-0.21691	0.542765	-0.163804	0.068632	-0.760314	0.538088	0.824594	-1.155358	-0.155222	-0.178699	NA	0.250836	-0.33271	-0.127785	-0.476215	0.065646	0.301667	NA	0.382832	-0.835777	0.985957	NA	0.297138	0.298168	0.090412	-0.56159	0.104829	0.443029	0.258674	-0.243151	0.853242	-0.246736
MSC1	3.973633	1.113044	NA	0.030644	-1.595943	-0.38054	-1.03108	NA	-1.651601	1.814182	NA	0.403082	NA	NA	-1.431566	-0.124504	-1.728105	-0.330283	-0.202907	-0.492489	NA	-0.584704	NA	0.009517	NA	NA	NA	NA	NA	0.168241	NA	NA	NA	NA	NA
MSC7	-0.155224	0.122884	-0.561956	0.253469	0.598974	-0.206389	-0.506925	-0.534639	0.418571	-1.045929	0.221827	0.816628	-0.484473	-0.688571	-0.601941	0.234711	0.103921	0.229723	0.019155	-0.151975	-0.78449	0.320579	NA	0.266886	NA	0.510759	-0.389493	0.014644	0.606214	0.247878	-0.066857	0.361348	-0.502336	0.546907	-0.305322
MSG5	NA	0.557648	1.609064	0.050745	0.132109	0.691023	0.419723	NA	-0.57199	-1.602781	-1.268752	0.021787	0.443958	-0.035107	0.202608	0.312229	-0.27146	NA	0.271141	0.815282	0.595754	0.231823	1.183193	-0.982112	NA	0.156218	-0.067338	NA	-0.995426	-0.421278	-0.807921	0.203813	-0.854853	-0.198969	0.94561
MSH2	NA	NA	0.542673	0.830628	-0.714212	NA	NA	NA	0.777905	NA	NA	-1.111127	-1.261019	NA	-0.078843	-0.121203	0.285317	0.467939	-0.156262	0.269188	-1.052889	0.581757	0.982157	NA	NA	-1.240014	NA	0.524457	0.307153	1.055266	NA	NA	0.632502	1.072207	NA
MSH4	NA	-3.125835	-3.778441	0.051377	NA	-0.241301	-0.248518	NA	-0.101406	-1.151504	0.288291	0.339828	0.508701	NA	-0.27527	-0.478059	0.02755	0.070036	0.032557	-0.591039	0.003985	-0.150148	-2.101987	0.358885	NA	-0.016967	0.678861	-0.140849	NA	0.547649	-0.358891	-0.139439	-0.257179	-0.273281	0.092686
MSH6	1.625256	-1.259019	-0.219698	0.294028	-0.67599	0.133182	0.90806	NA	0.078064	0.616097	0.234267	-0.830643	0.022281	NA	NA	0.475847	0.608085	NA	-0.594209	-0.424622	NA	-0.28779	-0.194713	-0.469226	NA	0.474108	-0.306345	-0.174112	-0.562851	0.420104	0.384828	0.280467	0.024127	NA	-0.548273
MSI1	0.322313	NA	-0.092106	-0.205042	0.323908	0.202177	0.015747	-1.434867	0.230505	1.018779	NA	0.459426	-2.161136	NA	-0.409134	0.140139	-0.297249	0.907731	0.440866	-0.985985	1.274269	0.145588	-2.022113	1.338775	-2.183143	0.782435	1.008931	-0.274198	0.352475	0.162419	NA	0.988393	-0.098746	-0.16021	0.719939
MSN1	NA	-0.581299	-2.295286	0.485569	-0.130246	-0.253347	-0.557505	0.910541	-0.666107	-0.564231	1.092212	0.231985	0.176927	NA	0.28623	-0.525783	0.165861	0.255023	0.112126	-0.436789	NA	0.294129	-0.039523	0.123507	NA	-0.233232	1.126375	-0.362952	-0.383389	0.398989	-0.527036	0.248602	0.057045	-0.040648	-0.038938
MSN5	NA	-4.070275	NA	0.779173	0.040825	NA	0.251321	1.474262	-0.105766	-3.707949	-2.223557	-0.080882	0.297687	0.714649	-0.308615	-1.068784	0.458681	-1.180838	-0.182957	-1.287449	NA	0.725017	NA	1.202358	NA	-2.089868	-1.860515	-1.006084	-2.901928	0.090147	0.411921	NA	NA	0.162366	0.290321
MSS18	NA	0.975302	0.092673	0.310483	0.001823	-0.6493	-0.569732	0.614889	0.032833	-1.097993	0.117454	0.046188	1.412917	0.642262	-0.258771	-0.463417	-0.310596	0.762967	0.381095	0.302293	NA	0.25573	0.710739	-1.828506	NA	-0.106606	-0.257503	0.549671	0.565655	0.129292	0.157227	-0.20407	-0.370132	-0.635057	-0.519657
MTC1	NA	NA	-1.177741	0.071529	-0.418669	-0.665882	0.034667	NA	0.146762	-3.037693	-0.371327	0.071066	NA	0.817591	-0.265008	-0.147299	1.104725	-0.192217	-0.373313	-0.10958	0.104591	0.651218	NA	-0.956612	NA	NA	NA	-0.525359	-0.059462	0.297295	-0.07801	0.705574	-0.682125	-0.23744	-0.023309
MTC4	-0.503158	-0.099465	-3.635071	0.732641	0.584952	0.165185	0.284257	-0.609114	-0.116175	0.704394	0.665777	0.223259	-0.218572	-0.026365	0.26224	0.060362	0.742955	-1.028265	0.135058	-1.213064	-1.319016	-0.136851	0.064005	0.977301	NA	-0.972489	0.448081	0.266818	-0.229292	0.651948	0.112333	0.047754	-0.073465	0.234421	0.04424
MTC5	NA	-1.596441	-3.750358	-0.002239	-0.700892	0.148511	0.135665	0.635238	0.613463	-1.624094	0.420891	0.374926	-0.953018	-0.279182	NA	0.180426	0.20925	-1.535685	0.301982	-1.183784	-2.880967	NA	-1.275243	0.761883	NA	-1.700731	-1.48959	0.517043	-1.403579	0.387435	0.439152	-0.629161	1.035109	NA	-0.223361
MTC6	NA	NA	-2.13733	0.184392	-0.967289	-0.242331	1.350125	-0.737316	0.178229	0.311237	-0.190415	-1.136984	-0.245863	0.482439	0.634008	0.083643	0.52064	-1.276023	0.327614	-0.627365	-0.90302	-0.338771	0.658208	0.787714	NA	0.047559	-0.637473	0.134565	-0.153606	0.41762	-0.861037	-1.373032	0.153689	-0.008145	0.081853
MTC7	NA	NA	-1.936194	0.003265	0.185004	-0.4501	-0.361941	0.906825	-0.060093	-1.106328	-2.406976	-0.642197	2.41501	NA	0.022479	0.008905	0.094567	1.96137	0.616167	2.444211	1.588097	0.462413	NA	NA	NA	0.540514	0.142231	-1.039992	-5.600929	-0.760249	-0.350439	0.741293	-2.115054	-0.815313	-1.325033
MUB1	NA	-0.917572	-0.992908	0.864884	-1.63824	0.047721	0.819805	2.120968	0.370958	-2.422864	1.091958	0.056535	0.090209	-0.404964	0.066552	0.167619	0.441143	-1.643974	0.976115	-1.229368	-2.87117	0.190232	0.576333	-0.313555	NA	-0.031348	-0.274653	0.301128	NA	NA	1.371395	-1.032785	1.776513	0.011849	0.304136
MUD1	NA	0.79724	-2.005415	0.600298	0.941537	-0.145994	-0.591898	NA	0.14684	NA	NA	-0.181337	NA	NA	-0.284347	0.202256	-0.363074	NA	-0.942521	-0.486493	0.431827	0.382634	0.906728	0.01616	NA	0.157458	0.539961	-1.209048	-0.288449	-0.379413	NA	-0.135958	-0.329227	-0.038277	-0.462731
MUD2	NA	NA	-3.915997	-0.451799	-1.658336	-0.434382	NA	NA	-0.346941	3.230954	NA	-0.170157	-0.039156	0.109009	0.248716	0.080245	0.660195	0.70787	0.360838	0.053922	NA	-0.253618	0.885374	1.278881	NA	0.43235	NA	-0.368994	NA	0.082356	NA	-1.688382	0.294482	0.241968	0.248896
MUM2	NA	-0.820753	-0.982771	-0.485893	-0.157421	-0.657996	0.51396	-1.730118	-0.110661	NA	NA	-0.689343	0.271373	NA	0.034105	0.028094	-0.087492	-2.450664	0.108359	-0.170285	0.806821	-0.726715	0.065251	0.759022	NA	-2.153155	NA	-0.001757	0.142081	0.016831	-2.326518	NA	0.672885	-0.232091	0.546276
MUS81	-1.539329	-0.722944	-5.876815	0.810746	-2.156286	NA	0.036763	-4.026689	-0.50586	-2.03221	-6.71203	-4.999255	-0.610083	-3.69355	-0.205792	0.199981	0.665248	-1.926778	0.941769	-0.190822	1.49866	0.397291	0.125449	-0.86949	NA	0.352765	-0.162158	1.117747	NA	-5.266623	-2.989579	NA	NA	0.569612	0.718026
MVP1	NA	-0.448599	NA	-0.308344	-0.28288	-0.068028	0.747168	-0.402219	-0.274062	0.043788	0.222321	-0.128301	0.908514	NA	-0.221909	0.507974	0.215907	-0.400876	0.327799	0.362538	NA	-0.570835	-0.888631	0.13438	NA	0.419075	0.466674	0.477864	0.685871	-0.381412	-0.164151	0.406768	-0.066875	-0.035177	0.010979
MXR2	NA	0.605211	NA	NA	0.4195	-0.20805	0.687503	0.057488	0.279488	-0.066247	0.287424	NA	0.831083	-0.169389	-0.197571	0.084804	-0.085566	NA	-0.098286	-0.535528	-0.76641	-0.319145	-0.155147	0.480662	NA	0.132284	-0.169959	0.385533	0.227466	-0.295528	0.096769	0.665637	0.543012	0.106963	-0.349257
MYO5	NA	-0.070196	NA	-0.115494	-1.867867	-0.159087	0.072036	-0.16881	0.014874	1.43535	0.618287	0.229522	0.541889	NA	-0.411393	-0.37399	0.245514	-0.546566	0.260316	0.052439	NA	-0.150619	-1.050889	0.680252	NA	-0.406851	-0.079028	-0.523942	NA	NA	0.013528	-0.12318	-1.611712	-0.172074	0.214194
NAB6	NA	NA	0.629545	-0.591115	-1.645111	-0.302333	1.008198	-0.115906	0.219607	1.408349	0.651834	0.632796	0.800015	NA	-0.150438	0.089748	0.094386	-0.180621	1.238443	0.488466	NA	-0.262523	0.122155	-0.6434	NA	-0.035803	-0.893895	-0.094188	0.045899	0.291137	0.842156	0.84484	-0.221224	0.180077	-0.426574
NAM7	0.074858	0.582325	0.243773	0.056266	0.240632	-0.416962	0.109038	-0.560097	0.77454	-1.648735	NA	-0.084536	NA	NA	-0.118974	-0.044745	0.244474	1.643982	0.126087	1.151496	NA	0.344312	0.886828	0.29389	NA	-0.09886	-0.100494	-0.509645	-5.090137	-0.038454	-0.666009	0.889425	NA	0.029257	-1.481395
NAM8	NA	-0.34666	-0.835541	-0.180123	-1.231829	-0.381389	0.126953	0.745406	1.124727	-0.544782	-0.047764	-0.179673	0.088036	-0.441357	0.052779	-0.026653	-0.284055	1.047795	0.313104	0.706478	NA	0.722585	NA	-0.208825	NA	0.369029	0.128424	0.234037	0.244666	0.159033	-0.050537	-1.272691	0.431788	-0.337614	-0.445107
NAP1	NA	0.634178	-0.337209	0.40844	-0.33562	0.012052	-0.132429	0.063369	0.336498	1.083851	-0.260668	-0.958288	0.98004	NA	0.093563	-0.097724	-0.032732	0.661957	0.811658	0.33801	1.091876	0.009768	NA	-0.973687	NA	0.502368	-0.121514	-0.564129	-0.552834	0.041959	-0.584121	0.825986	-0.399291	-0.059657	-0.564969
NBP2	NA	-3.151444	NA	0.193159	-0.772394	0.219992	0.256025	-1.410128	0.597318	-0.03579	-1.240613	-1.165889	1.714314	-0.577592	NA	0.230545	0.066392	0.075616	0.342109	0.029813	0.915095	NA	NA	0.521412	NA	0.197759	-1.01074	0.269885	-0.336091	-0.138177	0.108853	0.023387	0.742315	NA	0.627847
NCL1	NA	-3.65174	0.322521	0.469086	0.176262	-0.063051	0.270229	NA	-0.736795	NA	NA	0.670607	NA	NA	0.549966	0.076031	-0.097583	-2.542899	0.080797	-1.213267	NA	-0.626117	0.310002	1.384471	NA	NA	0.486144	NA	-1.050554	0.253121	NA	0.127639	NA	1.01674	0.950714
NCS2	-7.561723	0.586802	-16.618456	-0.385488	-1.327485	-0.859387	0.558471	1.076811	0.294401	-1.772599	-3.005516	0.508078	2.260955	-10.350179	-0.114943	NA	-0.071218	0.415669	0.647597	0.830133	1.327939	0.571482	1.311904	-0.579276	-0.986014	-0.144597	-0.326722	0.540964	-0.177457	-0.333468	1.028884	-0.870427	1.489765	0.722051	-0.590123
NEJ1	-0.110045	-0.759187	0.247776	0.273402	-0.027304	0.144489	-0.215244	-0.651596	-0.246723	-0.957784	-0.430346	0.004722	-0.551455	NA	0.337124	0.103868	0.060463	-0.426686	0.579574	-0.27981	NA	0.306822	NA	-0.037166	NA	-0.808641	0.388543	-0.277431	0.479352	0.275821	-1.052513	0.314047	-0.318716	0.041624	-0.497253
NEM1	-0.453297	-1.681473	2.050013	0.481175	-1.357383	-0.266467	0.328184	-1.705181	0.175172	NA	NA	0.459784	1.233995	NA	0.33881	-0.346162	0.222701	0.908395	-0.056201	0.460297	-1.789356	1.136764	0.933089	0.003493	NA	-0.317533	-0.891767	0.786134	-0.194857	-0.042653	-1.532462	0.630336	1.032443	0.164568	-0.159642
NFI1	NA	-2.617589	-0.723992	-0.616995	-1.39098	-0.18027	-0.099052	-4.80483	0.892549	NA	-0.075867	0.279644	-2.04037	NA	0.460215	0.290856	0.054405	1.112437	0.430834	0.701012	NA	-0.23058	NA	-0.518181	NA	-0.559925	-1.741729	-0.705963	-1.741976	0.56358	NA	1.01254	-0.561509	-0.021902	0.274703
NFT1	NA	0.386688	-0.466806	-0.113372	-0.428394	0.103876	0.088266	1.64385	-0.697922	-0.916816	-0.175159	0.321778	1.135623	NA	0.598418	-0.120277	-0.107445	-0.521261	0.871019	0.582867	NA	-0.192689	0.253915	-0.023136	NA	0.079941	-0.699017	-0.153089	-0.390524	0.075328	0.605606	0.093993	0.322103	0.017485	0.176071
NGL2	-2.752638	1.128756	0.200999	0.684481	0.242307	-0.462322	-0.48538	1.127889	-0.329557	0.231649	0.106426	0.560693	NA	NA	0.165008	-0.653366	-0.036853	0.150032	-0.743218	0.616589	0.735505	0.00244	NA	-1.403337	-1.839576	0.439973	1.753061	-0.510133	NA	NA	-0.143702	0.653781	-0.739293	-0.026653	NA
NGR1	NA	0.311639	0.855775	-0.518949	0.352104	0.257848	0.241395	0.611326	-0.342977	0.532895	NA	0.15242	0.507607	NA	-0.339036	-0.439776	-0.063414	0.246035	0.278614	-0.525992	NA	-0.124741	NA	0.887423	NA	0.715715	1.362255	-0.152909	0.583793	0.193353	0.013314	-0.21021	-0.292886	-0.715105	-0.51078
NHP10	NA	-5.153675	NA	0.265049	-1.583903	0.595546	0.306689	NA	0.497255	-1.216169	-2.175504	-1.579987	-1.467439	-0.662856	NA	0.236647	0.628892	-1.768796	0.685558	-0.146501	-1.410888	0.184434	NA	1.1397	NA	-0.968879	-1.304095	0.904527	-0.625715	1.186468	-0.968589	-0.595873	1.314483	NA	0.792968
NHP6A	NA	-0.967557	NA	0.49022	-0.509292	0.685017	-0.021768	NA	0.088966	NA	NA	0.243927	-0.338386	NA	0.097957	0.153222	-0.5548	0.87079	-0.152	-0.257108	NA	-0.182129	NA	0.966466	NA	-1.06524	-0.436217	0.171415	0.474525	0.514487	2.121191	-0.094523	-0.4416	-0.127655	-0.188376
NIP100	3.885956	-1.719412	NA	-0.76	NA	0.302331	0.048827	0.373433	0.606138	NA	NA	1.163938	-2.786861	NA	-0.142351	0.106174	-2.536744	-0.218898	0.404519	-0.216621	0.590702	0.257871	NA	1.769203	NA	-0.266965	-0.587326	-0.145294	-0.449441	-0.438905	NA	-0.783263	1.401283	0.311341	-0.904165
NKP1	1.007337	-0.849162	0.255337	-0.817315	0.347623	NA	-0.626785	-0.86552	-0.003142	-1.290888	0.026058	0.416044	0.768915	NA	0.091237	0.575946	0.12916	-0.834341	-0.037696	1.342567	1.631111	-0.52432	NA	0.34511	-4.959228	-0.256756	-1.553171	-0.28589	-0.189469	0.328262	-0.954881	NA	-1.344099	-0.353563	-0.249111
NKP2	NA	0.50135	-7.476036	-0.733431	1.546949	0.103122	-0.122214	-1.52515	-0.117563	1.024405	0.391075	0.396471	-0.482842	-0.31524	-0.239058	-0.238723	0.029645	0.512005	0.476115	0.35024	NA	0.237213	NA	-0.823583	-2.697797	0.721799	NA	-0.272011	-0.498044	-0.45194	-0.980367	0.540427	-0.390473	0.097724	-0.093844
NMD2	NA	-0.298238	-1.882742	-0.89922	0.528334	-0.301968	-1.361607	NA	0.325977	NA	-0.262892	-0.017719	2.108858	NA	-0.961857	0.357904	0.497854	NA	0.186601	1.719003	0.641392	0.863622	0.675169	1.409377	NA	0.325771	NA	-0.301443	-5.578284	0.750564	0.255385	0.79136	-0.025501	-0.025066	-0.29081
NMD4	NA	NA	-0.926848	0.296519	-0.264977	-0.169259	0.041869	-0.107432	0.480836	0.350404	-0.630135	0.063222	0.637531	NA	0.560027	-0.045097	0.392843	-0.040127	0.012992	0.215441	-0.71307	0.519348	NA	0.025401	NA	0.229283	0.234009	-0.483871	-2.106264	0.027166	-0.790184	-0.053557	-0.106273	-0.176713	0.370619
NNF2	4.315806	NA	-2.664549	0.453474	-1.699196	0.006683	0.383551	-1.594788	0.450624	0.45123	0.254555	-0.132328	0.140333	NA	0.449103	-0.166209	0.616536	0.164124	0.988689	0.63191	0.259575	0.141304	NA	1.351427	NA	-0.416003	-0.178187	0.985427	0.329147	0.472991	-0.735496	-0.760416	0.766967	-0.805999	0.477589
NOP12	NA	NA	2.024021	-0.306179	-0.220614	-0.594921	NA	1.577274	NA	NA	-0.687181	0.603704	0.905194	0.09861	-0.55417	-1.018247	0.216766	1.527141	0.343213	0.539563	0.897618	0.41911	NA	1.103898	NA	0.463199	1.204506	-0.699848	-0.309672	-0.837808	NA	0.361606	NA	-0.148335	0.317383
NOP16	NA	NA	0.548329	-0.400657	-0.435574	-0.372283	-0.406827	0.403677	-0.414267	-1.242901	-0.227258	0.263548	NA	-0.269698	-0.652302	-0.226591	0.160569	0.842021	0.185782	0.913548	0.596136	0.258501	1.247497	0.487611	NA	-1.260828	-0.829797	-0.10506	-0.738013	-0.380123	1.177416	0.029078	0.440317	-0.204217	0.017393
NOP6	NA	-0.714105	1.637379	-0.713787	-0.700095	-0.321449	-0.721845	0.909552	-0.159914	NA	0.509507	0.284343	0.753446	1.017344	-0.574555	-0.35079	0.242696	0.712851	0.120542	0.489794	-0.766104	-0.040472	1.069854	0.492423	-2.379026	-0.380335	0.435738	0.105988	-0.262757	-0.170332	-0.20446	-0.399363	-0.120849	-0.398615	-0.847691
NPL4	4.355245	0.36096	0.038255	-0.327701	0.670335	0.309568	0.430691	-1.016718	-0.689348	NA	NA	0.957855	0.747535	0.000343	0.210105	0.244388	-0.280997	0.031595	0.082158	0.531976	0.158501	-0.370988	NA	-0.060037	NA	0.168265	-0.406551	0.011733	0.832231	-0.302568	-1.556541	0.408059	-0.150195	0.624453	0.180745
NPP1	0.410694	-0.021632	-0.315609	NA	-1.085242	-0.17061	-0.069474	1.666946	0.142615	-0.165175	-0.097471	NA	-0.150517	1.723851	0.4411	-0.102143	0.125064	NA	-0.412668	-0.137162	-0.224162	0.106243	NA	1.079544	-3.656387	0.546762	-0.446432	-0.060112	0.436601	-0.092959	0.833466	-0.861042	-0.469734	0.011336	0.27146
NPR1	-1.931369	-1.26299	-0.20727	-0.170566	-0.186768	-0.031433	0.113509	-1.275927	0.54426	-1.146765	0.656898	-1.796922	1.083001	-2.206913	0.18616	NA	0.273226	-0.655387	0.270138	-0.197322	0.549656	0.513835	0.832701	0.144785	0.168632	-0.128242	0.039199	0.114705	-0.585936	-0.413776	-0.228293	-0.836421	NA	0.185115	0.167045
NPT1	NA	-1.455799	0.614598	1.200186	-0.684235	0.336793	0.351962	1.192677	-0.227053	1.259657	2.085644	-1.09563	-3.98982	NA	0.133371	-0.14128	0.801494	-0.187662	0.373429	0.700187	-1.627731	0.347676	1.106841	-0.567104	-1.119536	0.476288	NA	-0.292499	-0.104121	0.195336	0.266154	-0.244914	-0.063861	0.271692	0.010267
NPY1	NA	0.426254	-0.371142	0.363718	0.081193	-0.254274	0.150132	0.34864	0.539152	0.188294	NA	-0.207674	1.27473	-0.883064	0.083511	-1.203704	-0.154881	0.066362	0.297413	-0.034378	0.337364	0.308846	-0.703695	0.502389	0.594662	0.30427	-0.418946	-0.663576	-0.291319	-0.127228	-2.519207	-0.388621	-0.257102	-0.639213	-0.373509
NRP1	NA	0.238527	NA	-0.347437	-0.187667	0.224013	-0.669681	0.535538	-0.078316	-0.521323	NA	-0.983836	0.629955	1.014396	0.054089	0.212248	-0.21905	0.53108	-0.45892	0.108714	NA	-0.297266	NA	-1.387031	NA	0.575438	-0.082666	0.821946	1.304182	-0.314422	0.728779	-0.255114	1.060653	-0.859192	0.66832
NTE1	NA	-0.289461	1.195885	-0.280594	0.098053	-0.252342	-0.394614	-0.111714	-0.388929	0.007976	NA	-0.050976	0.072739	0.692189	0.259485	0.116962	0.069641	0.4704	0.188181	0.085408	NA	-0.042646	NA	0.13425	NA	-0.066861	NA	-0.757776	0.383789	0.224753	0.293219	0.417719	-1.157428	-0.253192	-0.386122
NTO1	NA	NA	-1.809339	-0.425889	0.31592	0.013389	0.049088	-0.263383	-0.376699	1.402146	-1.802136	-0.303263	0.515116	NA	-0.024549	0.277079	-0.291076	0.556455	-0.315483	0.159756	1.269013	-0.280845	-0.127676	1.328057	NA	-0.608875	-1.141258	0.055469	NA	0.505716	NA	0.250682	-0.079128	0.023861	-0.034397
NUC1	NA	NA	-0.819861	0.58993	0.085982	0.113469	-0.157514	-1.326226	0.564722	NA	0.28552	0.431491	0.478804	-0.158757	-0.019937	0.203882	0.483989	-0.327079	0.342927	-0.536418	-0.875487	0.459311	1.115843	0.716107	1.923604	-0.257894	0.25757	0.445409	-0.568596	0.331977	0.086323	0.988747	0.306758	0.071383	0.662166
NUM1	NA	NA	2.172725	-0.365052	2.005913	0.003586	-0.086633	0.282847	0.347116	-4.89863	-1.964419	0.643695	-3.081814	NA	NA	1.176366	0.135889	-1.06085	0.485422	-0.387354	-1.167081	NA	-1.645315	0.350535	NA	-0.454066	-0.515049	0.546589	NA	-0.016745	-0.055192	-0.956089	0.906747	NA	0.165941
NUP100	NA	0.113527	-1.146079	-0.209441	0.65907	0.22577	-0.280883	-1.865261	-0.098441	-3.724654	-0.891087	-0.017135	0.532653	NA	-0.01375	0.098492	0.393368	0.10369	-0.485651	-0.336611	1.459213	-0.325342	-0.12046	-0.590145	NA	0.359344	1.18658	0.210875	0.291568	0.084652	0.071391	0.406655	-0.408665	0.025025	-0.75208
NUP133	NA	NA	NA	-2.603585	NA	-0.051855	-1.564953	2.427549	NA	NA	-5.084291	1.923102	NA	NA	-0.880463	NA	NA	3.401257	-1.245052	NA	NA	-0.385195	NA	NA	NA	-2.666308	0.265105	-0.539233	-4.609463	-0.399969	0.210642	-6.473565	NA	-0.21742	-0.751693
NUP170	-5.999144	NA	-2.176036	-0.457161	-0.903219	0.07115	0.034749	-1.511282	0.493398	-1.64189	-5.694864	0.243233	0.580758	NA	0.023645	-0.462424	0.306591	-0.407924	-0.152524	0.189999	-1.728537	-0.09527	-4.09748	0.198094	-4.879165	-1.234916	NA	0.302823	-1.672668	0.59897	-0.566182	-0.216233	0.075013	0.33221	0.147147
NUP188	NA	-0.898139	-3.696464	0.592254	-0.954082	0.516103	0.55873	-1.624871	0.752352	-6.509852	-6.785622	-1.701689	-0.618134	NA	0.641185	-0.288564	0.348416	-0.590549	0.046186	-0.369693	NA	0.559963	NA	1.702384	-3.255864	-0.153258	-0.808868	0.153291	-0.763654	0.955294	-0.252287	-0.714269	0.408667	0.53743	1.124421
NUP2	NA	-0.221129	NA	-1.036232	-1.347949	0.055986	0.181337	1.667434	-0.089272	1.396025	NA	-2.187797	0.476712	NA	0.008857	0.110472	0.296384	0.231842	-0.518115	0.364241	1.136606	-0.240113	NA	-0.653645	NA	0.355074	0.758296	0.275731	-1.848983	0.179336	0.657157	0.836809	-1.764157	-0.393278	-0.768699
NUP42	NA	1.124121	NA	0.305187	0.599002	-0.266373	-0.257493	-3.306599	-0.365176	-1.285095	-0.051956	-0.165756	0.560836	NA	0.508908	-0.270364	-0.351162	-0.427169	0.160026	-0.962417	-1.092455	NA	0.759931	0.038935	NA	1.083466	0.221211	0.417246	-0.157168	-0.126484	-0.758017	0.216135	-0.399933	0.022939	0.22978
NUP53	-0.999089	0.116924	0.085658	0.053261	-0.57516	0.540209	0.812472	-0.399695	0.089556	0.631875	-0.138139	0.320563	NA	NA	0.522139	-0.360975	0.022923	-0.151745	-0.066618	-0.291938	0.237004	0.372905	0.775385	0.73818	-1.508729	0.930798	0.409902	0.092543	NA	NA	-0.334739	0.236899	-0.378691	-0.120527	0.374158
NUP60	-1.828428	NA	-0.830954	-0.406707	-4.04999	0.666278	0.281723	NA	1.0979	NA	-3.281341	-2.865957	NA	NA	0.757223	-0.667768	-1.253164	2.244226	-0.277633	2.277392	NA	-0.073392	NA	-0.761552	NA	-1.512762	-5.360794	0.009575	-4.036375	0.525718	NA	-8.751342	-0.514467	0.500283	0.410668
NUR1	NA	-3.371512	NA	-0.179609	NA	0.148064	0.310841	NA	-0.022154	-2.365724	0.240173	-0.285215	-1.636017	NA	0.551967	0.572345	0.139395	-0.812698	0.666768	0.807523	-0.068875	-0.463958	NA	1.366251	NA	-0.342256	-1.847195	0.24837	-1.174229	0.482052	-1.067007	0.239477	1.017569	-0.558159	-0.539744
NUT1	-3.913942	-1.181255	-0.72158	0.522295	-1.544485	0.433482	-0.397175	-1.142537	0.180254	-4.75207	-0.142038	-1.072689	0.589524	-2.130595	0.153806	0.087438	0.434997	-0.053748	0.665771	0.011574	-0.813529	0.064284	1.678382	-0.740127	NA	0.793712	-1.348537	NA	-0.294392	0.611377	-0.193028	-0.717787	0.430401	0.475867	0.64449
NUT2	NA	0.066309	-0.545879	-0.130064	0.480301	-0.410775	-0.060178	1.012338	0.701155	1.757482	NA	0.139892	-0.574228	0.661715	0.075697	0.014729	-0.35856	0.16654	0.592865	0.781101	-0.617375	-0.683442	NA	0.152091	NA	-0.018476	0.319667	-0.161863	0.823443	-0.209737	1.247366	0.304745	-0.373315	-0.08412	-0.008781
OAC1	NA	0.540176	0.189509	0.115074	-0.399927	-0.073531	0.448058	-0.079194	-0.450453	-0.510486	0.046559	0.418879	NA	0.677247	0.006123	0.085853	0.178854	-0.140695	0.06037	-0.288028	-0.183585	0.130939	NA	0.379628	NA	0.494714	-0.122549	-0.720449	0.835912	-0.070523	0.057384	-0.11495	-0.295124	-0.11526	0.404136
OAF1	-0.805785	-0.177927	-0.096495	-0.031635	0.034342	0.008515	0.256551	NA	0.45504	-1.14487	-0.270058	-0.131098	NA	NA	-0.137105	0.210125	0.514445	-0.751508	0.239373	-0.83717	-1.408183	0.567803	NA	0.551336	-2.754376	3.00E-04	0.011639	0.077731	0.1765	0.17218	0.570853	-0.26348	-0.265575	0.010879	0.072242
OCA1	NA	-2.141294	-1.750864	-0.150117	0.860481	-0.328165	-0.604378	-0.742475	0.416144	0.275552	0.837053	0.186446	0.987582	NA	0.186601	NA	-0.074055	0.953383	0.274359	0.362082	0.461175	0.22295	1.194223	-0.717501	NA	-0.903513	-0.787605	-0.679688	-0.511688	0.000399	-0.141687	-0.239974	-0.451851	0.18121	-0.726616
OLA1	-1.716286	NA	NA	-0.126683	0.023581	-0.563232	-0.710562	-0.699001	0.40564	-1.354644	-1.986433	-0.233943	NA	1.396885	0.648493	0.81896	0.354936	0.640731	0.246198	-0.078752	NA	-0.387454	NA	0.354307	NA	NA	0.121349	0.384085	-1.350654	0.388161	0.193692	-0.410789	NA	-0.520977	0.266144
OPI1	-3.160006	-1.087575	0.006075	-0.017587	1.189241	-0.348014	-0.880494	-2.065697	0.257531	-5.781761	0.318723	0.689487	1.151389	NA	0.126364	-0.190094	-0.347036	1.140651	0.450521	-0.175043	NA	0.070981	-0.038904	-2.633925	NA	-0.492498	0.127533	0.600609	0.124743	-0.435092	-1.476884	-5.330346	1.112407	-0.629615	0.529511
OPI10	NA	0.581252	0.165366	0.147197	-0.522603	0.124142	NA	1.009075	NA	NA	0.206979	0.399519	-0.00828	0.238835	0.110908	-0.091996	0.410109	0.327865	0.101881	-0.376693	0.606875	-0.143028	NA	0.397254	NA	0.347916	NA	NA	0.710983	-0.01156	-0.04696	0.370988	NA	-0.149086	-0.531687
OPI3	NA	-0.279026	NA	0.397821	0.614964	0.066528	0.131036	-1.323403	0.901098	-4.129753	-1.064713	0.114489	1.127855	0.411919	0.195602	-0.682034	0.624034	-1.792572	0.779904	-1.013608	0.330444	0.617215	0.87456	-1.343445	NA	-1.649416	-0.707366	0.623028	-2.563826	0.91385	-2.019151	-0.76872	1.092515	0.41913	0.002145
OPY2	NA	0.58894	-1.160361	-0.460638	1.587104	0.051189	0.296608	-1.526324	-0.757657	0.625814	-0.763848	0.281618	-0.010412	NA	0.474673	0.033576	0.512544	-0.502519	0.048753	-0.075243	NA	-0.256312	NA	-1.006451	NA	-0.266689	-0.104757	-0.147118	-0.226661	0.443077	-1.401813	-1.25922	-0.415247	-0.626786	-0.045692
ORC1	NA	0.877134	-1.099898	-0.894218	0.791192	0.093683	-0.208914	NA	-0.212388	1.377891	0.802125	0.185301	-0.102404	NA	-0.157491	-0.332984	NA	0.651118	0.280403	0.371629	NA	-0.972811	-1.126075	-0.453229	-5.340276	0.607031	0.634686	-0.29635	NA	0.540814	-0.601749	0.890015	0.276118	0.017601	NA
ORM1	NA	NA	0.57452	-0.040769	0.03977	0.091454	0.316364	0.130821	-0.138472	0.49393	-0.327737	-0.130154	0.454408	0.303259	0.075387	0.195169	0.217272	-0.137005	-0.386282	-0.542705	0.578169	-0.212206	NA	0.43907	NA	-0.023292	0.822384	0.582763	0.431957	-0.245553	-0.170822	0.193905	1.297533	0.059558	-0.457835
ORM2	NA	NA	NA	-0.522696	0.357943	-0.19943	0.06223	0.277219	-0.035141	-0.0191	0.214558	0.382015	1.469223	NA	0.097284	0.303394	0.199781	0.105196	-0.204414	-0.094992	-0.014547	0.093777	NA	0.139294	NA	0.436861	1.100369	0.240457	-0.128853	0.214846	-0.834587	-1.002636	-0.699407	-0.016834	-0.875526
OST3	NA	0.330438	-1.262304	-0.59892	1.115953	-0.228119	NA	1.093141	NA	NA	-0.975177	0.427849	1.774318	0.197151	0.391469	0.309378	0.426246	0.345343	0.54841	-0.668275	-0.150672	-0.323371	NA	-0.420319	-6.2444	-0.02108	0.693919	-0.180384	-0.094882	0.367122	-0.443384	-0.119809	-1.208462	-0.425692	-0.341412
OST5	NA	1.246183	0.192595	0.079917	1.035792	-0.698833	-0.124794	-0.627393	-0.448232	0.028493	-0.64055	-0.558994	1.837722	0.673046	0.425862	0.287958	-0.047475	-0.268326	0.019193	-0.012684	0.420081	-0.997391	-0.134809	-0.259424	NA	1.139738	0.814341	NA	0.59139	-0.593491	-0.745945	0.788788	-1.160395	0.298407	0.282477
OST6	NA	0.022718	NA	-0.514688	-1.485863	-0.344848	-0.03937	0.776291	0.137924	-0.43062	-0.066919	0.290326	NA	0.504417	-0.484895	0.085653	0.02223	0.092956	0.162591	-0.717487	NA	0.19885	NA	0.861082	-5.29021	0.334998	0.205533	0.352149	NA	0.231847	-0.256321	-0.262889	0.400979	-0.078228	0.094539
OXR1	-0.681071	0.017776	-1.583642	0.460562	NA	-0.288017	0.346718	1.04458	0.090612	-1.459788	0.524831	0.004686	0.635802	0.759312	-0.397751	-0.057596	-4.217619	-0.872637	0.491401	-0.441103	-0.017389	-0.22037	0.170892	0.151784	NA	-0.807915	-0.672135	0.171467	-0.051354	0.228374	-0.367867	-0.346055	0.856417	0.065977	0.340982
OYE2	0.339205	0.538248	-0.769519	-0.54237	0.259748	-0.033319	-0.015141	-0.028029	-0.119332	-0.134606	-0.084672	-0.150353	0.780011	NA	0.129344	-0.15208	0.244261	-0.205229	0.781989	0.442162	0.668523	0.858869	0.38302	0.277653	NA	0.10877	0.706796	-0.389951	0.441896	0.182831	-0.191832	-0.138198	-0.432323	-0.682857	0.024262
PAC1	NA	-1.397788	0.888158	-0.861804	-0.141685	0.272511	0.344396	1.023171	0.357305	0.090511	NA	0.917184	-0.466398	-1.694042	0.381227	0.69642	NA	-0.584396	-0.187843	-0.528185	NA	-0.461511	-2.879796	0.376509	NA	0.541539	-0.005847	-0.039341	2.673504	0.497942	0.078243	-0.507445	0.683032	0.451437	0.244731
PAC10	NA	-1.942584	-5.209484	0.208531	1.503041	-0.095749	0.274383	0.871764	0.207791	NA	-2.471221	1.337279	-0.128445	-0.945056	-0.69567	-0.824072	0.781068	NA	1.137047	-1.450386	-0.420833	0.491255	NA	-1.860833	NA	-0.543426	-2.100598	0.541752	0.216432	0.431216	0.269356	-12.580338	0.616979	0.248055	-0.313992
PAC11	NA	-3.735372	0.786426	-0.559922	-0.220367	NA	-1.001438	NA	0.238218	1.433423	-0.980527	0.475357	-1.013848	1.381591	0.536541	0.543554	0.589185	-0.749744	0.167917	-0.956715	-1.952338	0.471827	-1.963274	-0.16619	NA	-1.904494	-2.825913	-0.11655	-1.442657	-0.019445	0.448079	-0.045708	-1.723408	-0.084734	-0.868938



PTH1	1.34598	NA	1.085449	-0.737686	-0.271708	-0.906604	0.11084	1.628447	0.013528	-0.157097	-0.723565	0.399334	0.979846	NA	-0.745408	-0.470378	0.03779	0.688314	-0.346005	0.863858	NA	-0.887949	NA	-0.842488	NA	0.869339	0.723787	-0.802804	0.86219	-0.448278	0.587179	-0.33583	-0.414736	-0.33805	-0.464234
PTK2	NA	1.199762	NA	0.141961	0.570618	-0.317849	-0.678454	0.213782	-0.55916	NA	-0.065246	NA	NA	NA	-0.692244	-0.253504	0.097854	NA	-0.767272	0.541202	-1.093464	-0.259945	NA	-0.252779	-0.900388	NA	1.067309	-0.107041	0.214008	-0.374502	NA	0.865934	0.112811	0.544346	-0.338064
PTP1	-0.576675	0.604435	-0.352234	-0.082701	-0.001989	0.033489	0.642264	-0.399768	-0.003601	NA	-0.12078	-0.595346	0.806503	0.034083	0.045783	-0.172266	0.155536	-0.083978	0.124324	0.401329	0.139856	0.462975	NA	-0.206793	NA	0.13559	0.227737	-0.075738	0.235291	-0.280432	-0.661508	0.189932	-0.498463	0.518309	-0.042982
PTP2	NA	NA	0.984951	-0.684597	-0.34738	-0.316904	-0.199113	-0.233379	-0.396033	0.032989	-0.135232	0.099742	0.745682	NA	0.027838	-0.172562	-0.06818	0.860222	-0.176066	0.681243	NA	-0.085037	NA	1.285057	NA	-0.361182	1.247648	-0.882534	0.885283	-0.063743	-0.087224	0.872397	NA	-0.343465	-0.606687
PTP3	NA	0.2724	0.739728	-0.072609	0.748966	-0.162201	0.452344	-0.140585	0.553369	0.261549	-0.689379	-0.694842	-0.114191	0.244054	-0.025127	0.21387	0.359414	0.747834	-0.106505	0.49727	1.143345	0.542494	0.690617	1.335841	NA	0.080622	-0.632854	-0.017918	-0.031574	0.53223	NA	0.759596	-0.534276	-0.461556	0.118403
PTR2	NA	-1.04023	0.420611	-0.797451	0.670015	0.20905	0.162644	-0.297957	0.134409	1.157803	-0.152207	-0.083778	-0.269919	NA	0.173541	0.210633	-0.218734	-0.295033	-0.133271	-0.405135	0.031313	-0.042688	1.117853	0.37704	NA	-0.089628	-0.18094	0.72461	0.195596	0.58361	-0.79032	-0.009925	1.717458	0.082541	0.355385
PUB1	NA	-0.219784	0.881286	-0.399623	NA	-0.09149	0.370381	-0.736628	0.767371	0.84569	-0.275107	-0.263627	0.656754	NA	0.276967	0.359253	0.062457	0.597167	-0.551814	0.628964	0.138088	0.096723	NA	-1.527057	NA	-0.759543	0.258513	-0.572239	0.60019	-0.13527	-0.109431	-0.348449	-0.447433	0.54758	-0.086262
PUF4	NA	-1.833657	-2.875412	0.133052	-0.149408	0.461214	0.133347	NA	-1.378972	NA	NA	-1.022053	NA	NA	-0.394089	0.708018	0.397197	-0.92973	0.109876	-0.024364	-0.470506	0.32363	-1.020028	-3.112239	NA	NA	-1.36079	0.07702	-0.591126	0.270569	NA	-2.768613	0.332339	0.099181	-1.073489
PUF6	-2.205969	0.060753	-1.020703	0.758745	-1.769523	NA	0.20601	0.35087	0.294666	-2.855879	1.402972	0.875455	0.796989	-2.08692	-0.242373	-0.075387	0.510434	0.335932	0.167614	-0.188954	NA	-0.002343	1.906844	0.136706	NA	-0.657014	NA	0.920257	-1.047078	-0.031636	-0.831352	-0.544672	1.551593	0.122012	-0.234794
PUS1	NA	-0.83059	0.086888	-0.002932	NA	-0.01069	0.565557	-0.005059	0.222105	1.000752	-0.602002	-0.902241	NA	NA	0.98152	-0.186638	-1.261173	-0.196418	0.580626	-0.710694	1.896441	0.552053	NA	-0.06465	NA	-0.074364	-0.500902	-0.258032	-0.898012	0.509016	-1.30836	0.265591	0.875214	0.223431	-0.118377
PUS4	NA	-0.785655	0.939339	-1.035546	NA	0.299862	-0.649116	0.55605	-0.020082	1.038408	-1.025268	-0.177272	1.178644	-1.04513	-0.247738	NA	-0.17322	-0.236229	-0.684154	-0.865393	NA	-0.202605	0.281132	NA	NA	0.125291	0.577935	0.095165	-0.342226	-0.077492	NA	-1.414716	NA	-0.296524	-0.97736
PUS7	NA	NA	-2.412247	0.200217	0.512641	0.19752	0.148826	0.255849	0.717932	NA	-0.338216	0.168889	-0.523877	NA	0.377707	0.192024	-0.160097	-0.118454	0.253642	0.074375	-1.576052	0.119459	NA	-0.131277	NA	-0.553416	NA	0.26146	NA	0.08845	0.407267	-0.498148	-0.914189	-0.167316	0.170938
QCR10	NA	NA	-0.745731	0.611461	0.143025	0.882726	-0.398592	-3.428471	0.483332	NA	NA	-1.435947	-1.680216	-2.413	0.808619	0.316564	0.359758	-1.613032	-0.115399	0.115411	NA	-0.392759	-0.312428	NA	NA	0.6556	-1.118531	0.663882	-0.791436	0.787574	NA	2.416053	0.580073	0.236523	0.100946
QNQ1	NA	0.161765	-0.545044	-0.097413	-0.666588	-0.081828	0.642457	-0.168835	0.676862	NA	0.131616	0.315443	-0.352277	NA	-0.354998	-0.854558	0.458979	-0.048005	-0.35641	0.125349	-0.291122	-0.204257	NA	0.227071	NA	-0.665635	-0.86054	0.163523	-0.564601	0.422812	-0.31088	-0.053084	0.516531	0.576195	-0.023663
RAD1	4.07121	0.928528	NA	0.278212	0.604174	0.14077	0.182947	NA	NA	2.674346	NA	-0.751795	0.667183	NA	0.335304	-0.340574	-0.531065	-6.78282	-1.890639	-4.412962	-0.576226	-2.473864	NA	NA	NA	NA	NA	0.170163	NA	0.789511	NA	1.976107	-1.052758	-0.897103	-0.416138
RAD10	-0.231833	0.745758	-0.050767	-0.236467	0.881502	0.283702	0.178829	0.157176	-0.009258	-0.005356	-0.795001	0.58936	0.198883	NA	0.15624	0.691001	0.434027	-13.22348	0.646803	-7.357758	NA	-0.538075	NA	0.571594	NA	0.792536	0.159371	-0.106122	-1.521836	0.692273	-0.440799	-0.034461	-0.209585	-0.877742	-0.26638
RAD16	NA	NA	NA	-0.589901	-0.988439	0.286417	0.424953	-1.638817	0.333624	NA	NA	0.03549	0.217942	NA	0.261331	0.281192	0.055306	-4.000156	1.059444	-3.404597	-0.784971	-0.561842	NA	-0.431018	NA	1.043903	NA	0.794697	1.206023	0.714769	NA	0.695411	0.685079	-0.357797	-0.238183
RAD17	-2.627241	-1.289912	0.677657	1.417685	-16.905084	-0.319211	0.387186	0.106257	0.30275	-0.417632	NA	NA	-0.147697	-2.282805	0.992143	1.064093	NA	-1.579474	NA	-0.729322	-0.262349	-0.263945	-13.887188	0.722782	NA	-0.519661	-0.969174	0.577354	-2.172902	0.385091	-0.402747	-0.326783	NA	-0.605074	0.992567
RAD18	-0.198998	NA	NA	NA	NA	NA	-0.536801	NA	NA	NA	0.596109	-0.051887	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.953998	-0.321113	-0.796194	NA	NA	NA	1.919436	0.364499	NA	NA	-0.113335	0.790151	NA
RAD23	NA	-0.249673	-2.148204	0.340427	-0.70051	0.450165	0.478451	-2.514517	0.021484	NA	-0.369365	-0.01295	0.060607	0.322344	0.823515	0.3604	0.332307	-7.580462	1.267779	-2.747966	0.805058	0.321274	NA	0.635149	NA	0.413288	1.022312	-0.009147	-0.392736	0.63683	-1.433039	-0.763336	1.026718	-0.590974	0.340419
RAD24	NA	NA	0.927861	NA	NA	0.070299	0.377946	-0.550123	NA	NA	NA	NA	NA	NA	0.801367	NA	0.904482	-1.028417	NA	NA	NA	0.244534	NA	-1.012407	NA	NA	NA	NA	-2.556082	0.039566	NA	-0.788607	NA	-1.165558	NA
RAD26	-0.185819	0.346537	0.583927	-0.424261	0.375236	-0.013616	0.345175	0.908272	-0.12753	1.313043	0.164803	0.735854	-2.031575	-0.083226	0.112907	0.123989	-0.333203	-2.089055	-0.267204	-1.540393	-0.090085	-0.079236	NA	0.927108	-3.574928	NA	-0.600468	0.550586	0.710641	-0.008626	0.045574	1.076257	-0.324439	0.156146	-0.359689
RAD27	1.347866	-8.782415	-0.047457	-0.84847	2.364719	2.481099	-0.061541	4.019144	-1.311815	-0.738034	-1.312224	-3.553451	NA	-1.518708	-0.877058	2.153094	0.030175	1.931041	0.211225	2.630868	NA	-0.3629	NA	2.344777	NA	3.663086	NA	-1.032313	-4.223138	2.920992	3.154875	1.651168	2.161946	2.446588	3.262969
RAD5	-0.282082	0.128673	-1.08439	-1.00783	NA	1.552282	2.757955	0.386133	NA	NA	0.236507	1.077145	NA	2.351992	1.975006	NA	NA	3.628381	-0.76729	NA	NA	-1.656136	0.146651	2.00109	NA	1.622067	NA	2.789234	3.211814	2.783713	-0.533901	1.487059	2.93415	2.275465	NA
RAD51	-0.005637	-0.567283	0.148624	-0.343008	-0.016808	0.194166	0.738732	-0.214135	0.697482	0.710791	0.167503	-0.855861	-1.41253	-3.100512	0.536488	0.084055	0.156925	-0.144574	NA	-0.133308	-0.203917	-1.241808	0.268139	0.269396	-6.91798	-0.030064	-0.052996	0.325207	2.626732	0.052964	NA	0.6205	0.578512	0.782513	0.056087
RAD52	0.706315	0.469827	-1.673968	0.658277	NA	1.208055	0.289005	-2.561614	NA	NA	NA	-1.489595	NA	NA	-0.552248	NA	NA	-2.430053	0.475987	-0.867021	NA	-0.570565	-0.363644	-0.106739	NA	1.225029	1.082256	-0.569113	1.264837	0.655647	-6.094034	0.8105	NA	0.787218	NA
RAD54	-0.7159	-1.693849	-2.348515	1.139936	-1.088437	0.96212	0.338949	-2.15779	0.91473	-1.214336	-1.054946	0.708002	2.095828	NA	-0.24279	-0.897425	0.910887	-0.553273	1.135965	-0.725382	2.689101	0.552814	1.341443	0.225981	NA	0.453676	-0.246202	NA	2.161286	1.157138	-0.084487	-1.248918	NA	0.552233	0.461956
RAD55	-2.606014	-1.029096	-3.005057	0.996024	-2.676819	0.744343	1.296238	NA	1.650977	-0.597184	-0.536508	0.163209	1.718218	NA	NA	-0.039879	0.732155	-2.26398	1.156074	-1.528094	2.444828	0.725425	1.103175	1.788983	NA	-0.017746	NA	1.206529	2.215333	1.094724	-2.856358	-0.018259	1.293273	NA	-0.500309
RAD57	-2.174571	-1.624273	NA	0.907049	-1.583005	0.410722	0.549275	NA	0.413292	-1.031081	-1.315342	0.615254	2.31939	NA	NA	-0.35263	0.754791	-1.331514	0.97747	-0.961446	NA	-0.100604	1.300927	0.628342	-4.382816	0.470839	-0.703438	1.337756	1.666867	0.551847	-1.90144	-0.349941	NA	NA	-0.241785
RAD59	NA	0.05746	NA	-1.900306	NA	0.44411	0.213715	NA	1.235626	0.076772	-3.699151	-1.367808	0.980287	NA	0.318904	0.040584	-2.291856	-1.478927	-1.690832	-0.666945	2.103375	-1.248118	NA	0.294194	NA	-1.460259	-0.41691	0.719632	1.866568	0.63296	-0.288985	0.431821	0.967516	0.677209	0.520754
RAD61	NA	-1.713605	NA	0.132677	-2.226418	0.157453	0.139161	NA	0.569481	NA	-0.639529	-0.764516	NA	0.661574	NA	0.382834	-0.499927	-0.190284	-0.075078	-0.81246	0.72113	-0.60638	-4.507087	0.157354	-7.21872	-0.541356	-0.249112	-0.005197	1.567272	0.163606	0.242488	0.276285	0.172067	NA	-0.100135
RAD7	NA	1.40942	0.412262	-0.251663	0.306896	0.217298	0.360094	-1.200961	-0.663423	0.595222	-0.413213	0.259338	0.561239	-0.784045	0.239481	0.097004	0.166723	-3.391601	0.014292	-1.514828	NA	0.448645	NA	0.506117	NA	NA	NA	0.221808	0.207226	0.227303	0.140832	0.419882	-0.495079	-0.533369	-0.239549
RAD9	NA	NA	0.887293	0.311028	NA	NA	0.160322	0.129182	NA	NA	-12.330719	NA	NA	NA	0.955079	NA	NA	0.44959	NA	NA	NA	NA	NA	0.565216	NA	NA	NA	NA	-11.128226	0.337773	NA	NA	NA	-1.998881	NA
RAS1	NA	NA	-1.151359	-0.18686	-0.427412	-0.230131	NA	0.234723	NA	0.759223	0.186872	0.019826	0.077085	NA	0.339053	0.044333	0.381894	NA	0.228773	-0.393357	0.222001	0.83781	NA	0.000556	NA	0.04443	0.83918	0.377028	-0.061517	0.724074	0.266987	-0.895534	NA	-0.094893	-0.113969
RAS2	-1.963767	0.223814	-1.091658	-0.554583	-0.586654	0.108461	0.323577	-0.215116	0.263214	0.179558	-0.454328	-1.2303	-1.93518	-0.796566	0.345715	NA	-0.237546	-1.746217	-0.681383	0.056647	-2.360975	-0.707343	-3.436631	1.034301	NA	-1.732398	-0.600575	1.065434	2.041618	0.887199	NA	0.357797	0.242657	0.541762	0.841254
RAV1	-0.751877	0.54546	NA	-0.593526	-0.026938	-0.101231	-0.459167	-0.731761	0.064785	0.93765	0.406368	0.0364	1.530903	0.803363	-0.010954	0.904846	0.594473	NA	-0.405701	-0.23042	2.47683	-0.207871	0.423289	-0.190408	NA	NA	NA	-1.339513	0.9197	-0.745956	-0.235739	0.65388	NA	0.583497	-0.482038
RAV2	NA	0.3575	-0.58496	0.393818	1.459674	-0.058193	-0.424486	-1.634233	-1.525752	0.201535	0.130405	0.17205	1.109593	-0.497261	0.287305	0.25353	-0.270475	0.998613	0.065655	0.391432	2.385458	NA	0.537628	0.026645	NA	0.788249	0.980808	0.22883	0.71368	-0.01694	-1.17541	-0.26668	NA	0.228401	0.272509
RBA50	-1.006457	-0.038778	NA	-0.264425	0.621264	NA	0.531456	0.287323	-0.029765	-0.082125	-0.673853	-0.315974	-0.415412	0.798892	0.248039	0.452027	-0.726352	-0.377338	-0.141286	0.346965	-0.637307	-0.168831	-0.527999	-0.707451	-1.807537	0.023549	-0.208343	-0.626661	0.726737	-0.121814	0.835851	1.243987	0.963381	0.129482	-0.203631
RBL2	0.009882	-0.071418	NA	-0.630075	1.181524	-0.107203	-0.478412	-0.433526	0.28025	NA	0.581501	-0.203385	0.085244	-1.304521	-0.534598	0.253071	0.593308	0.089674	0.335728	0.782235	0.873768	-0.660296	-1.397963	-0.796747	NA	-0.160327	NA	0.023127	-0.759367	0.211606	0.127084	0.050862	-1.153835	-0.90413	-0.57765
RCE1	NA	NA	-7.477861	0.11016	-0.221307	0.078992	-0.454583	NA	0.033862	NA	0.48107	0.290077	NA	NA	0.145156	0.429879	0.788542	-0.488126	-0.212624	0.261672	-0.044673	-0.683703	-0.428173	0.168612	1.740011	0.386019	0.273207	-1.576059	NA	NA	NA	-1.647765	NA	-0.0863	NA
RCO1	NA	-2.320731	NA	-0.510919	-1.724613	-0.036462	-0.393623	-15.986174	0.451755	-2.486657	-2.406265	-1.907361	1.618519	-10.547745	0.44707	0.85769	-0.661557	1.127703	0.341662	1.259907	1.038903	-0.473267	NA	0.010746	NA	0.377241	0.490133	0.8323	0.293045	0.008523	NA	-1.632419	-0.307402	-0.035113	-0.001493
RCS1	NA	-0.593482	NA	-0.190571	-0.810715	-0.123634	-0.912591	NA	0.117995	NA	NA	-1.213604	NA	1.25545	NA	-0.004305	-1.427246	NA	0.157423	1.002385	NA	-0.833781	0.602043	2.621223	NA	-1.581225	NA	NA	0.135867	0.618809	0.582079	-0.112478	0.754035	0.108215	-0.01099
RDH54	NA	-3.644167	0.1569	0.292987	-0.211733	0.255975	0.933384	-0.520127	1.042905	-1.679644	NA	-0.234898	-1.473002	-0.473282	0.755289	0.132323	0.033459	-2.453574	0.517996	-3.628916	NA	1.030718	2.197389	1.426544	NA	-0.197601	NA	0.498001	0.027844	0.68068	-1.254774	-0.180192	0.695979	-0.079915	0.291843
REC104	NA	-0.921824	NA	-0.338514	0.713337	0.027611	-0.164671	-0.450867	0.681733	0.632887	-0.187452	0.056158	0.516499	-0.317968	1.045657	-0.045577	-0.524684	0.004103	0.001937	-0.237134	-0.589875	0.542801	NA	0.016527	0.910788	0.148671	0.29978	-0.957115	0.123346	0.073558	NA	0.214471	NA	0.029641	0.043175
REC114	0.419944	NA	NA	0.175354	-0.752869	-0.258436	-0.535254	0.745738	-0.075736	0.878885	0.905239	0.208269	NA	NA	0.755618	0.312697	-0.366651	-0.934836	0.531086	0.025669	-1.042985	-0.547534	NA	0.170037	NA	0.313772	NA	0.307201	NA	NA	0.656089	0.589863	0.104129	-0.51759	-0.059257
RER1	-2.752936	0.099767	-2.314578	NA	-0.894506	-0.15132	0.051821	0.156823	0.141279	-0.352081	-0.241249	NA	0.771765	0.878371	0.202881	0.299252	0.195545	NA	0.236255	-0.750684	1.808824	0.237429	0.383427	0.960036	NA	-0.204964	-0.419997	-0.30008	-0.250928	0.491008	-0.274906	0.080507	0.165984	0.229309	0.094253
REV1	-1.524517	-0.198514	-0.752293	-0.558015	-0.300771	0.195536	-0.845665	-0.01948	0.873939	0.323243	0.294252	-0.432601	-0.028126	-0.533555	0.870317	0.483308	NA	-3.215341	-1.576051	-4.325644	NA	-0.158308	-0.739683	1.09398	0.585175	-0.008102	0.072535	0.919861	-0.049315	0.095137	-0.395409	0.167752	0.222611	-7.342362	0.537123
REV3	-0.585014	0.257955	0.180312	-0.413776	NA	0.274822	-0.982373	-0.145585	-0.060669	NA	-0.055546	-0.411749	0.782117	NA	0.697099	0.299542	-0.455162	-3.332528	-0.475651	-3.841261	-17.793634	-0.066411	0.058065	1.157548	NA	0.334884	-0.128862	0.242691	0.766553	-0.251629	-0.42906	0.359303	1.152229	-4.739166	0.315264
REV7	0.040901	NA	-0.211598	-0.223619	1.476973	1.071802	0.671406	NA	0.886378	NA	0.41118	-0.40599	-0.42913	1.846672	0.92698	1.478536	-0.533781	-3.268706	-0.981638	-5.174972	-10.356241	0.072704	NA	0.059552	-0.92094	1.280203	0.43878	0.060498	-0.121547	0.889224	-0.372954	0.287561	-0.444758	-5.677579	1.399928
REX4	NA	0.401777	NA	0.534128	0.978512	-0.161622	-0.102635	NA	NA	NA	-0.168403	0.345143	-0.507415	NA	-0.082643	-0.495769	0.023286	NA	-0.211537	-0.380052	-1.20667	0.139074	1.157507	-0.002462	NA	0.387825	1.733249	-0.831528	0.534348	-0.499993	0.671705	0.10347	-0.037557	-0.143605	-0.18404
RGA1	NA	-1.188802	0.651844	0.736426	-0.038735	0.728992	NA	-1.480472	NA	-0.228962	-0.341347	NA	0.423484	-0.025215	-0.076301	-0.328239	0.325362	-0.258359	0.470417	-1.083354	0.157886	-0.595476	-0.442312	0.404013	NA	-0.770045	-0.202503	-0.744894	-2.179658	0.00722	-0.683564	0.287254	NA	0.247946	-0.033878
RGD1	NA	-0.387368	-0.98956	0.004973	0.026137	-0.246133	-0.599306	-0.565898	-0.312056	0.031511	NA	0.59984	NA	-1.268523	-0.087315	0.233013	0.128909	0.125435	0.097758	0.024123	-0.732493	0.348881	-1.90E-05	0.443778	NA	-0.579439	0.657287	-0.374905	0.185145	-0.147593	-0.813794	0.245966	0.370722	0.2342	0.166895
RGR1	NA	0.473161	-0.419573	-0.090191	0.309238	0.083136	0.312271	0.527062	-0.689891	0.604958	0.498035	0.082342	-0.038196	NA	0.002786	-0.420227	0.310705	0.343914	0.008603	NA	0.467326	-0.468608	-0.043585	0.373748	NA	-0.325477	NA	0.124072	-0.255446	-0.243771	0.529938	0.650879	-0.468738	-0.082199	0.113685
RHB1	NA	0.836495	0.581825	NA	0.059393	-0.558276	-0.701528	1.982036	-0.129553	0.959508	0.010962	NA	0.93902	2.327729	0.407661	-0.304865	-0.361	NA	-0.369969	0.477714	NA	-0.599403	NA	-0.491511	NA	-0.029572	0.329706	-0.881757	0.854928	-0.581389	0.942609	-0.540429	-1.535372	-0.267507	0.677182
RHO4	NA	NA	0.76658	-0.687989	-0.889469	-0.07858	-0.082893	NA	0.686221	2.157818	NA	-0.293438	-0.643432	NA	0.105837	-0.063944	-0.174417	-1.00178	0.522291	0.072006	NA	0.381947	NA	1.577468	NA	-0.609513	-1.59018	-0.002955	0.063419	0.371727	-0.244635	-0.241905	-0.014145	-0.50314	-0.065171
RIC1	NA	0.554866	-14.821436	0.616352	-0.300297	0.396591	-0.866364	-1.823854	0.190769	-6.272424	0.334522	0.637181	0.808599	NA	-0.228883	0.08752	0.152256	NA	-0.115338	NA	1.100375	0.551358	NA	0.926406	NA	-1.362539	NA	0.367631	-0.30792	-0.141446	-0.847911	-7.98914	1.348256	-1.391818	-0.656701
RIF1	0.442134	-2.816024	-0.043689	-0.683443	0.321409	-0.168091	0.320957	-3.838121	0.582647	-0.849439	-1.391459	0.269349	-6.135235	-2.47909	0.062936	0.580049	-0.03415	0.397379	0.253119	0.483249	NA	-0.669085	-0.021604	-0.208059	NA	-1.03752	-0.842256	0.336898	0.848478	0.244226	-2.258616	0.724838	-0.616876	0.795488	0.71758
RIM1	-0.039134	0.233872	0.884454	NA	-0.259204	-0.213378	-0.639142	1.127645	-0.073641	-1.706532	0.579065	NA	-0.369274	-0.815319	-1.6081	-1.294769	-0.311151	NA	0.117422	0.870038	0.814516	-0.501015	0.802391	-2.500718	NA	-0.06616	0.31356	0.269208	0.482058	0.035654	0.718197	-0.936107	1.489505	-0.013446	-1.028062
RIM101	3.393138	NA	NA	-0.231471	-1.723198	0.336429	0.280682	1.747703	0.795356	NA	1.103255	-0.85017	NA	NA	0.346001	0.390876	-0.21649	-0.321714	0.307242	-0.086473	-2.848094	-0.555324	0.222426	-0.53739	NA	0.828943	NA	0.683978	0.853874	1.661619	1.336544	-2.015195	NA	0.628325	1.111342
RIM13	NA	-2.462971	NA	-0.410525	-2.380932	-0.26986	-0.065845	0.882832	-0.121454	NA	0.663165	-2.555856	NA	NA	0.293409	-0.304936	0.424386	-1.351751	0.265011	-1.124302	NA	0.122111	-0.412743	NA	NA	0.066845	-2.44808	1.061131	NA	NA	NA	-1.243633	NA	0.049413	0.158553
RIM15	-3.960039	1.287859	-2.144196	0.535862	0.795458	-0.011842	-0.789521	NA	-0.79799	-0.157344	-0.295933	0.216677	NA	NA	0.257084	0.818721	0.096863	0.903214	0.009448	0.520352	NA	0.255743	0.548332	0.070853	NA	-0.298134	0.389573	0.426127	-0.474916	-0.066268	-0.540722	-0.625034	NA	-0.298162	0.336961
RIM20	NA	-2.304335	NA	-0.260664	-1.947653	0.387455	0.15244	0.597977	0.067497	NA	0.504343	-1.252117	-5.048398	NA	0.38009	0.257224	NA	-0.666389	0.262231	-1.000953	-4.694903	-0.612148	NA	0.112131	NA	-0.526946	-1.365037	0.692086	1.422615	0.827459	0.460555	-2.420578	-1.09025	0.912181	0.552521
RIM21	NA	-3.583564	NA	-1.139858	-3.004552	0.542627	-0.045482	0.467417	0.379153	-2.322312	-0.159729	NA	-3.374466	-5.472978	0.349639	NA	0.12899	-2.475901	0.407774	-1.090097	-3.673997	-0.414037	0.085419	NA	NA	0.147111	-0.957461	1.048004	0.483074	0.331447	0.624916	-3.566162	NA	0.009357	1.029604
RIM8	NA	-4.332186	NA	-0.832884	NA	-1.05421	0.334122	2.244801	0.66746	NA	1.215867	-1.898845	NA	-2.23449	1.351024	0.890548	-1.408496	NA	1.155019	-2.133105	NA	NA	NA	NA	NA	-0.085622	NA	1.885345	0.965643	3.459868	NA	-1.733412	NA	NA	NA
RIT1	-0.521727	-0.165087	-3.283821	0.479994	-1.129927	-0.003422	0.808382	1.328929	0.6603	0.169465	0.069208	0.281819	NA	-0.018133	0.774515	-0.933845	0.406601	-0.699466	0.353938	-0.509793	-0.58754	0.518785	0.039892	-1.044645	-3.82811	0.27945	-0.06141	NA	NA	NA	-0.384318	-0.711305	NA	0.500987	NA
RKM4	-0.257218	-0.274786	0.338396	-0.175353	-0.288684	0.070758	-0.38418	0.00245	-0.285335	-0.889583	-0.377102	-0.066673	0.404267	-0.281149	0.711843	-0.214277	-0.527656	0.261012	-0.263865	0.556733	1.209495	NA	4.122633	0.250865	NA	0.208208	0.734791	0.535634	2.743623	0.934075	-0.330797	NA	0.219058	0.345796	-0.467807
RKR1	0.172517	-0.18103	-0.498573	0.235556	-0.07944	0.142487	0.395762	-1.521855	0.289291	-0.480342	-1.024049	-0.124185	NA	NA	0.338954	0.677546	0.719875	-0.339816	0.098986	-0.713655	-1.045132	1.022146	0.074734	0.64942	NA	0.349381	0.389684	1.21247	NA	NA	NA	-0.413042	-0.297246	0.018578	NA
RLF2	NA	-7.695815	-2.873205	-0.238731	-3.013278	0.247752	-0.529623	-3.136455	0.703054	-0.537379	-2.23488	-0.610404	-7.062576	-4.443573	0.699689	0.863029	0.313311	-0.876587	0.357173	-0.268109	-1.379684	0.304914	NA	0.594104	NA	-1.387586	-1.607972	1.129565	-0.311804	0.734388	-3.216324	0.515497	1.192315	-0.580401	0.355517
RLM1	NA	-0.979069	0.559714	1.218224	NA	0.407953	-0.249799	-0.036747	0.665391	0.243235	-0.621223	-0.723986	-1.096909	-1.497855	-0.028833	-0.011061	-0.085795	-0.914153	0.472074	-0.709046	-1.245861	0.476282	-0.395629	-0.838734	NA	-0.229682	-1.036394	0.373086	0.045382	-0.372127	-0.997171	0.306058	0.520503	0.590156	0.566672
RMD11	NA	0.585085	2.977652	-0.235233	-0.135308	-0.5444	-0.319689	-0.718244	0.389175	0.959694	-3.680981	-1.89721	2.443612	-2.351632	-0.255946	0.449292	-0.423821	0.891382	-0.400221	0.122252	NA	0.618685	0.607104	0.396631	NA	0.966718	2.119286	0.00581	1.551353	-0.508436	0.132149	-0.054047	NA	0.220156	0.077406
RMD5	NA	-1.403411	-3.90149	0.008816	-0.335441	-0.033261	0.160162	-1.916139	0.192971	1.262817	0.482345	0.262044	0.551831	-1.094289	-0.121236	0.140362	0.564021	-0.806674	1.34364	-0.16095	-0.554586	NA	NA	-0.082543	NA	-0.048761	-0.874222	0.259973	-1.178234	0.356269	-0.892788	NA	-0.048083	0.677744	0.366251
RMD8	NA	0.153588	-0.191561	-0.057547	0.099724	0.1302	-0.007963	-2.853062	-0.039084	-0.903048	-0.380507	0.145747	0.307078	0.243167	-0.569654	-0.148096	0.137994	0.352695	0.647419	-0.547531	0.985704	0.156919	0.037246	-0.022	NA	-0.009568	-0.595069	0.634168	0.124031	0.445898	-2.131826	0.508975	0.576696	-0.227893	-0.094527
RMR1	NA	-1.204191	0.319555	0.155548	0.434395	0.118218	0.0673	-2.515396	0.009957	-2.137906	1.002977	-0.635569	0.010069	-1.665319	0.150326	-0.110062	0.017914	-0.576314	0.595362	-0.178476	-0.471818	-0.599813	0.160869	-0.964227	NA	0.714349	-0.69218	NA	-2.154075	-0.062318	0.495118	0.305568	-0.073869	-0.542109	-0.6443
RNH201	0.315506	-7.228057	0.841483	0.205994	0.085241	0.399583	0.02545	0.61597	0.206036	-0.537699	-0.099085	0.22615	-8.360786	0.144281	0.542786	0.214162	-0.0495	-0.009837	-0.148875	-0.129802	-8.287485	-1.302417	NA	0.738129	NA	-1.241189	-5.310043	-0.76431	-7.3837	-0.060242	-0.578031	0.050711	-1.555078	-0.086029	0.03403
RNH202	-0.794462	-5.0777	NA	0.158319	0.110436	0.466575	0.456089	0.227228	0.054501	0.38051	0.224789	0.490435	-9.311435	0.49455	0.117721	0.010368	0.10243	-0.857736	0.475083	-0.382259	-6.71935	NA	-3.531481	-0.579965	-3.32002	-1.251864	-5.364985	0.065182	-9.786523	-1.062163	-0.007899	NA	0.420406	0.596809	0.156817
RNH203	NA	-3.529469	-1.191753	-0.395786	0.418834	0.284506	0.79535	0.518424	-0.066621	-0.506659	0.335146	0.724719	-11.453736	NA	0.313921	0.750829	0.069561	-1.951539	-0.215085	-0.990017	-10.914493	0.097944	NA	0.108362	NA	-1.625223	NA	0.00758	-8.006254	0.13687	-0.904472	0.610988	0.139164	-0.318556	0.818883
ROT2	NA	-0.650102	0.857494	0.11923	0.092996	-0.423538	0.615699	-0.925843	0.821367	1.926055	NA	0.448676	NA	NA	0.293071	-0.135605	0.798479	-0.153189	0.855945	0.255328	NA	0.965246	NA	-1.564121	NA	-0.136017	0.542369	-0.864945	-0.306429	-0.42386	-0.654982	0.16121	NA	-0.381532	-0.354848
ROX1	NA	0.523073	1.627563	-0.387634	0.685887	-0.009728	0.273648	-2.656834	0.520764	-1.946086	-1.175364	0.404507	-0.068127	-0.386543	0.331864	0.3282	0.411179	-0.530667	0.360624	0.108809	-0.848678	0.76773	NA	0.792867	NA	-0.120353	0.011132	0.650953	0.484649	0.339693	-0.934067	-0.510293	1.572357	-0.046888	0.322241
RPA14	NA	-6.126854	1.337559	-0.39131	-1.558743	0.636157	0.794673	-0.587298	1.051645	NA	NA	-3.136048	-1.099714	-2.420672	NA	0.37952	-0.389585	-1.012477	0.106513	-0.776955	NA	NA	-1.904158	NA	NA	-1.222126	-0.488463	0.198404	-1.518247	0.78997	-0.132902	0.083284	0.387438	NA	-0.310413
RPA34	NA	NA	-0.958458	0.568612	-1.230956	0.423123	0.184857	0.284038	0.002721	-0.526328	-4.308277	-2.278699	-2.213249	-1.07282	0.071751	0.267916	0.462502	-0.486912	0.523507	-0.098184	1.037102	-0.078326	-2.00248	0.234103	NA	0.12258	-2.651904	1.079394	-0.799628	-0.138178	-0.245097	-0.078849	0.967423	0.50949	0.279831
RPB11	NA	0.65551	-5.256893	0.263557	-0.364001	0.726055	NA	0.22205	NA	NA	NA	-0.95363	0.79239	-2.58354	-0.205077	-0.487031	0.881852	1.76843	1.115464	1.106758	NA	0.363492	1.803792	NA	NA	-0.689105	-0.831745	0.670188	-4.502879	-0.025791	0.335872	-3.580369	0.327682	0.586021	-1.168393
RPB2	NA	NA	-0.018925	0.16435	0.639284	0.002775	-0.031274	0.653526	0.08745	NA	-0.664697	0.766581	-1.519128	1.63824	0.017128	0.207105	0.624318	0.421979	0.890615	-1.004589	NA	0.117055	NA	-1.549212	NA	0.083302	-0.199007	-0.602254	NA	-0.750314	-0.568017	0.405513	0.049477	0.24148	-0.213373
RPB3	-7.631096	-0.250519	-10.983678	-1.2719	0.059265	-0.002088	-0.536347	1.487963	-0.080528	-6.506294	-1.109408	0.627065	0.281384	1.30222	0.062792	0.215978	-0.374139	-1.353941	0.049783	NA	-1.384374	0.236191	-1.245666	-0.925865	-10.534028	-0.66752	-0.147437	1.315695	0.737818	1.085871	1.461603	-2.575931	0.871743	0.213883	-0.879616
RPB7	NA	1.094013	0.662695	-1.049347	-0.121355	NA	0.179396	-0.068434	0.227888	0.257298	-1.739612	-0.442048	0.597778	0.712292	-0.465692	-0.685666	0.127223	1.665913	-0.147672	1.55911	0.726458	-0.169013	NA	-0.961631	-5.027643	1.021389	1.139719	-0.539323	-5.461798	-0.75129	-0.59364	NA	NA	0.591142	-1.087568
RPB9	NA	-0.923698	NA	0.685296	-0.766749	1.052093	1.187339	-0.082116	1.799035	3.941252	-5.199295	-1.183698	-1.408721	-0.059061	0.901169	1.584452	-0.107305	-0.394825	1.117555	-0.714179	-2.804976	1.160831	NA	-1.43075	NA	-0.156942	-0.6992	2.189865	-1.002556	0.987662	1.430071	NA	NA	0.896098	1.459533
RPI1	NA	-1.134685	-0.097324	-0.30323	1.021726	-0.071726	0.055217	-0.390995	-0.460117	1.104205	-0.31957	0.657485	0.259771	-0.278989	-0.179242	-0.174322	0.304707	0.820288	0.29017	0.162772	-0.994788	-0.369178	0.562086	-0.013253	NA	-0.154164	0.941883	-2.082587	0.192069	-0.391091	-0.342285	0.25409	NA	-0.093475	-0.165374
RPL11B	NA	0.579195	NA	-0.6557	-0.404254	-0.655939	-1.004135	-0.037252	1.08665	1.372709	-0.364878	0.264429	1.410781	1.156166	-0.813432	0.311333	0.270567	0.543086	-0.294205	1.735382	1.119622	0.518088	1.90832	0.448527	NA	-0.248748	0.967503	0.130536	-0.399853	-0.525432	-0.314371	0.495444	-0.442231	-0.13207	0.083409
RPL16A	NA	NA	NA	-0.297199	0.062052	0.108737	-0.484825	NA	0.230018	NA	-0.047026	-0.271982	-0.053729	0.019568	-1.06127	-0.24347	0.051316	NA	0.41066	-0.120115	-0.551032	-0.097156	1.254404	-1.370549	NA	-0.283329	-0.875657	0.801996	0.316436	0.087535	-1.60621	-0.464116	-0.558807	0.282933	0.104928
RPL16B	NA	NA	0.272115	-0.683694	NA	-0.51113	-0.169922	-11.491699	-0.270588	-3.338394	0.63255	0.315363	0.777268	-10.145425	-0.245807	-0.497288	0.602944	1.590399	0.879423	1.98025	NA	-0.2484	1.346442	0.66213	NA	0.141812	0.320765	0.013585	NA	-0.89564	NA	NA	1.008334	-0.071356	-1.244656
RPL17B	0.107988	NA	1.572798	-0.600291	-1.118334	-1.044065	0.36057	NA	-0.036639	0.377389	0.34409	-0.041928	0.586698	1.098195	-0.10902	-0.925063	0.138158	1.572385	-0.420756	0.197828	NA	-0.280432	1.080283	-0.886965	NA	-0.582674	0.68804	-1.332174	0.773109	-0.52185	0.889954	-0.065483	-0.607202	0.050021	-0.779619
RPL19B	-5.991737	-0.682806	-1.001779	1.214014	-2.850913	0.60721	0.398284	1.551122	-0.968308	-2.79092	2.313484	-0.13741	-0.787831	NA	0.482305	-0.087287	0.954113	-1.384597	1.493985	-0.421532	-1.814107	0.728914	2.073466	0.137268	-4.611255	-1.634093	-1.326833	0.316766	0.989409	0.084104	NA	-1.432029	0.165052	0.209095	-0.203809
RPL23A	NA	-1.114672	1.036263	-0.436091	-0.323521	0.047205	-1.09191	1.023866	-0.538987	NA	-8.192909	0.288955	NA	-0.009993	-0.411397	-0.105443	-0.385892	-0.078838	-0.183028	0.010844	NA	-0.343355	-0.112182	0.115153	-6.24588	0.037879	-0.001459	0.185621	-0.517017	-0.537569	0.532222	-0.095487	0.371248	-0.065774	0.122095
RPL24A	-3.545663	-0.705273	-0.036149	-0.400819	-1.761879	0.338038	-0.144486	1.886456	0.792813	-1.173732	0.6674	0.168591	-0.859768	0.267924	-0.267211	-0.092843	0.351605	-0.28037	0.297905	-0.121327	-0.920912	0.045311	NA	0.018958	NA	-0.506198	0.31371	-0.966172	-0.488989	0.711667	1.099902	0.465633	-0.869071	-0.006047	-0.80375
RPL2A	-1.32081	0.38708	-1.33754	-0.643735	0.384376	-0.537165	0.173454	1.295746	-0.179303	0.799268	0.623419	-0.035167	0.818537	-2.289003	-0.252486	-0.277908	-0.508162	1.068437	-0.143998	1.187931	-0.186104	-0.069867	NA	-0.070202	-5.496038	-0.123818	-0.190006	0.089949	-1.11862	-0.348704	0.686711	0.135241	-0.152969	0.084018	0.405655
RPL33B	NA	0.022479	0.599548	-0.079382	0.091453	-0.204367	-0.277611	0.785862	-0.104518	1.244347	0.326776	0.310082	0.746864	NA	-0.050498	-0.348383	0.226046	0.520141	-0.034419	0.881946	-0.170666	-0.033093	0.676943	0.232478	-3.810022	-0.120591	1.281034	-0.200033	-0.041957	-0.388009	0.42164	0.27962	-0.321742	0.001599	-0.719173
RPL35B	NA	0.416944	NA	0.83462	-0.606921	-0.436499	0.023461	-0.550562	0.146917	1.10467	-0.018505	0.532609	0.629635	-1.365004	-0.14421	-0.361405	-0.241919	0.462509	0.215604	0.844662	-0.846936	0.589895	0.552675	0.381554	NA	0.051237	0.488012	-1.079658	-0.537921	-0.454179	0.152165	0.081291	-0.278435	-0.370351	-0.746518
RPL41B	NA	NA	NA	-0.43978	-1.638275	-0.36865	-0.946763	-0.14329	0.321527	NA	0.542855	-0.97298	-0.115602	-1.290539	0.820145	-0.221685	0.269492	-0.515943	0.901708	-0.001568	0.347937	-0.508416	NA	-0.730635	1.637693	-0.029579	NA	0.351849	NA	-0.028132	-0.544289	0.13452	0.6752	0.215917	0.369834

RPL43A	NA	4.822024	NA	-0.675034	1.023529	-0.653552	-1.08478	0.842957	0.196668	NA	0.423977	0.153015	1.633158	-3.688724	-0.01644	-0.383733	-0.245566	0.491577	0.088668	-0.277133	NA	0.246729	NA	1.022921	-5.970966	2.675205	-2.044856	0.795398	NA	-0.312294	0.888494	-1.688599	0.14296	-0.778413	-0.679468
RPL4A	NA	-0.102287	0.619548	0.410137	-0.431788	-0.733024	-0.175214	-0.574634	-0.555977	NA	0.162947	-0.154584	-1.180015	NA	-0.440949	0.429572	0.455151	-0.046269	-0.032787	0.725771	-0.39155	0.386756	NA	-0.50611	1.486366	-1.153185	-0.284173	0.451237	-1.565787	0.471736	-1.245187	1.20298	0.675268	0.364754	0.734284
RPL8B	NA	0.841031	0.214364	0.174628	0.717412	0.20671	-0.654797	-0.352378	0.123661	0.259142	-1.054045	-0.221253	NA	-0.875074	0.203002	-0.280376	0.065855	2.51608	-0.482297	NA	2.313896	0.822764	0.667981	0.019029	NA	0.333857	NA	0.47173	-1.343474	-0.793584	-0.184931	0.621252	-0.429897	-0.004197	-0.600748
RPL9A	0.744782	0.900808	0.623173	-0.217464	-0.26822	-0.107912	0.145431	0.023355	-0.583551	NA	-0.174671	-0.504159	1.63337	NA	-0.397563	-0.818077	0.19092	1.651689	0.156699	0.972597	0.704483	-0.805887	NA	-0.429663	NA	0.440691	NA	NA	0.181229	0.15266	0.245916	-0.338805	0.184287	0.247259	0.171743
RPN10	NA	-6.794145	NA	-0.116156	NA	0.485	-0.864117	-0.965569	0.217244	-1.196488	-2.991785	-5.853869	NA	-1.376582	0.244597	-1.123181	0.460394	-4.028549	0.347443	-3.288644	-10.520739	0.284312	-3.716132	-2.384421	-2.84157	-0.957508	-6.515944	0.500816	0.258798	-0.072255	-0.886979	0.208872	-0.140735	-0.563594	0.596178
RPN13	NA	1.436989	-0.625817	0.746104	-1.105003	-0.003259	0.234118	-0.82704	-0.848761	1.310186	0.042866	-0.670869	0.942296	-0.059968	0.640875	-0.25343	-0.047261	0.182364	-0.267861	0.807736	1.752804	-0.155592	NA	-0.328722	NA	0.535558	NA	-0.197235	1.112566	0.053836	-0.707037	0.279698	-0.137223	-0.223145	-0.1091
RPN4	NA	-8.888792	NA	0.561442	NA	0.435225	1.202188	NA	0.26685	-7.035256	-1.139562	-2.325844	-2.326044	NA	NA	0.199079	0.178663	-1.89161	0.273565	-0.078731	0.574012	0.535764	-0.617944	-1.086016	NA	-0.086108	-4.86567	0.68501	0.849813	0.882627	NA	-2.650462	0.998321	0.250178	-0.621184
RPO21	NA	-0.089725	NA	-0.040182	-0.224439	0.332347	0.291764	0.640181	0.029887	0.646718	0.031506	-0.258999	-1.428025	-0.311656	0.538805	-0.023324	0.240065	NA	0.899859	-0.596635	-2.774108	0.404146	-0.973121	0.303317	NA	0.114013	-0.923257	0.023886	-0.103675	0.508353	-0.336053	0.292315	-0.071719	0.262311	-0.265735
RPO41	0.225468	-0.485825	-0.085405	0.729509	0.232416	0.426801	-0.197788	0.759326	-0.143176	NA	0.747401	0.927086	-2.94352	-0.747265	-1.044002	-0.407871	-0.817261	-0.25133	0.775139	1.058524	NA	-1.0859	-1.454283	-2.629847	NA	0.184476	-0.866824	0.343637	0.402571	-0.070906	1.140497	-1.467693	1.782511	0.04116	-1.072559
RPP1B	-0.065198	1.831709	NA	-0.459523	-0.037441	-0.068756	-0.694415	NA	0.174159	-1.023042	0.048632	0.536773	0.70253	0.501296	-0.476157	-0.934532	0.239355	0.151233	0.523773	0.234315	1.559552	0.595737	1.354699	-0.207892	NA	-0.52358	NA	0.116955	-0.525702	-0.592336	0.347393	0.062178	0.83566	-0.20156	-1.516188
RPP2B	4.616512	-0.246797	-0.004886	-0.628468	-1.676744	NA	-0.980716	NA	0.251782	NA	-0.77043	0.166612	NA	NA	-0.524165	-0.134564	-0.512073	1.39825	-0.131881	0.876353	0.912142	0.168948	2.026062	-0.09429	NA	0.355391	0.602715	0.313123	NA	-0.195305	NA	NA	0.412444	-0.44733	-0.673939
RPS0A	NA	NA	2.470798	-0.341926	-1.157157	-0.720667	NA	NA	0.054979	0.782908	0.262271	NA	NA	-1.740701	-0.64665	-0.829636	0.078791	0.106792	0.323474	0.833694	0.017369	-0.441607	-0.229757	0.182522	1.392627	0.104815	0.316493	0.278586	NA	-0.511841	NA	0.437234	0.570071	NA	0.422153
RPS10B	0.344745	0.553857	1.479828	-0.465961	-0.628861	-0.537409	-0.109214	1.076744	-0.747614	0.919829	-0.01519	0.28248	NA	-1.820428	-0.443376	-0.753598	0.196638	1.292856	0.122405	0.557257	-0.133743	-0.660635	NA	-0.074263	NA	-0.637667	0.808968	-0.435324	NA	NA	0.484537	1.098319	0.457649	-0.585243	NA
RPS11A	NA	NA	NA	0.797266	NA	-0.169349	-0.678146	NA	0.266775	NA	NA	0.746143	-0.455191	NA	NA	0.355211	0.63613	-1.045904	0.599692	-1.099671	NA	-0.690421	1.58299	-1.24548	NA	-0.228888	-1.480691	0.058413	0.967541	-0.628638	-0.031208	-0.852214	-1.053353	NA	-0.68036
RPS14A	NA	NA	NA	NA	0.866679	-0.538	-0.144563	1.721594	-0.036278	-0.118551	-0.299431	NA	-0.373199	-0.316867	0.306369	-0.423493	-0.23398	NA	-0.099476	0.927845	0.727081	-0.208305	0.597862	-0.381463	NA	0.863845	0.600994	0.337754	-0.016711	-0.432007	0.716437	-1.016369	-0.718389	-0.19522	0.396846
RPS16A	-1.60613	0.406149	NA	-0.297412	NA	-0.059063	-0.435923	1.987273	-0.206501	NA	-0.169399	0.503559	NA	-9.606658	0.148763	-0.043998	0.271879	1.294254	-0.082774	1.199618	NA	0.060522	1.114714	0.080256	-2.310435	0.00356	1.176716	-0.438779	NA	NA	NA	-0.020087	0.135035	-0.835121	-0.677848
RPS19B	NA	NA	NA	-0.169937	NA	-0.363287	-0.389313	NA	-0.032096	NA	-0.521738	0.571299	-0.830198	NA	-0.361171	NA	0.057073	NA	0.047442	NA	NA	0.08753	NA	NA	NA	-0.387822	-1.403456	-0.212355	0.244771	-0.2351	NA	0.173884	NA	-0.448075	-0.366031
RPS21B	-2.562388	NA	NA	0.102779	-2.424358	-0.162723	-0.776388	3.230824	-0.603323	-2.299589	-0.160765	-2.021423	-0.036254	2.126376	-0.08758	0.039169	-0.031007	1.024779	0.793162	1.275458	2.376762	-0.003257	NA	0.509805	NA	NA	1.298665	-1.191366	1.103522	0.278357	2.365916	-0.717375	-0.530258	-0.563483	-1.074158
RPS23A	NA	0.671171	-0.503217	-0.38935	0.217625	-0.207562	-0.794009	0.600901	-0.344411	-0.276297	-0.160537	0.612795	0.655797	NA	0.140464	-0.296177	0.077932	0.002353	0.37952	0.998986	1.134399	0.156097	NA	-0.863157	NA	-0.64171	0.064143	-0.437365	-0.592818	-0.206333	0.177265	-0.330125	-1.651843	-0.335811	-0.62988
RPS28B	NA	-0.318144	NA	-0.63723	0.273702	-0.990004	-0.671703	0.090487	-1.790801	0.728024	-0.359359	0.961255	NA	-1.378921	-1.144533	-0.947038	0.330586	0.081898	-0.487841	0.866691	NA	-0.124449	0.979827	-0.426234	NA	-0.223536	NA	0.132158	0.547453	-0.739662	-0.200673	1.696475	0.559925	-0.091003	0.412854
RPS29A	NA	1.359087	2.050681	-0.670851	-0.43752	-0.553355	0.156832	2.225897	0.504522	-0.73143	-0.495137	0.106932	1.290536	NA	-0.776961	-0.562326	-0.166405	0.220621	0.597794	1.170512	1.186963	-0.201442	NA	-0.175229	NA	0.109711	NA	0.290586	0.098231	-0.74595	NA	0.012942	0.004153	-0.255008	-0.383093
RPS29B	NA	0.745562	NA	-0.683901	-0.308574	-0.408477	-0.34954	NA	-0.076257	NA	-0.660787	0.519413	2.152912	NA	-0.11049	-1.058673	0.556478	0.770834	-0.516856	0.683529	1.306556	0.003876	NA	NA	NA	0.297954	NA	0.334202	-0.425759	-0.015908	1.471626	-0.088311	1.173167	-0.337165	-1.379691
RPS30A	NA	0.248609	1.59312	-0.398494	0.740326	-0.132958	-0.910597	1.428477	-0.247998	NA	0.527904	0.477882	0.701345	-2.34135	-0.934105	-1.039239	-0.092577	NA	0.558138	1.126083	0.087183	-0.53947	1.333011	-0.082557	NA	-0.500933	1.147599	0.128829	-1.037878	-0.021898	0.962986	0.515382	0.292887	-0.320538	-0.909524
RPS4A	NA	-0.366641	-1.59861	-0.292059	-3.727712	-0.359243	0.348593	-0.408533	0.255813	-1.995483	0.362387	-1.001794	NA	0.060316	0.589858	-0.408034	0.189164	-0.215174	0.528157	-0.80444	-2.075548	0.409426	0.164891	0.606445	0.04701	-0.202027	0.100558	0.70514	-1.206836	0.974945	0.498849	-1.567438	1.256058	0.05473	0.818312
RPS4B	NA	0.053394	1.984154	-0.878523	-0.956553	-0.249784	0.200201	NA	0.145421	0.350632	-0.08535	0.660733	-0.258308	NA	-0.440725	-1.247708	-0.39706	0.693993	-0.598177	0.929413	0.981747	-0.032281	1.573272	0.245897	NA	-0.085356	0.981516	0.110902	0.429094	0.217872	1.361332	0.948839	1.038636	-0.134893	-0.052914
RPS6A	NA	-1.788374	-0.354823	0.710442	NA	0.462869	-1.879415	0.93205	-0.364852	NA	NA	0.032978	0.194613	-0.440596	0.237001	0.046776	0.45045	-1.523824	0.938125	-0.3824	-0.87307	0.601095	1.005842	-1.730212	-2.170613	-0.838561	-2.374462	0.269137	0.049583	1.090084	NA	-1.274761	1.04054	0.783798	0.573321
RPS6B	NA	NA	NA	-0.444471	-0.304909	0.328624	0.291405	NA	0.779406	NA	NA	0.321784	NA	-5.223859	NA	0.104179	-0.56002	0.255658	0.299818	0.303835	NA	NA	1.520568	0.251286	NA	0.351665	-1.671386	-0.44333	NA	0.758421	NA	-0.385718	-0.425865	-0.097912	NA
RPS8A	-2.057743	0.278458	NA	0.995752	-3.252597	0.678165	-0.691369	-0.184663	0.252426	NA	-3.646155	-0.82717	-0.382747	-0.962403	0.78004	-0.274841	0.007885	NA	-0.496644	0.079348	NA	1.253727	0.930417	-1.138582	NA	-0.204296	-1.2985	0.287612	0.012145	-0.122172	NA	0.263785	1.449783	NA	1.515756
RRD1	NA	-0.764082	-1.419738	0.62746	0.088518	0.149427	0.531653	1.178599	0.709604	0.093298	1.793569	0.522423	-0.774616	1.223403	-0.164286	-0.509933	0.373385	0.646475	0.917762	0.321624	-2.570208	0.268891	0.398792	0.28419	NA	-1.328266	-1.63056	-0.00214	-0.496934	0.173072	0.410779	-0.240815	1.378677	-0.092976	-0.14669
RRD2	NA	-1.741928	0.255273	0.461766	NA	0.142851	0.095674	-0.313836	0.425316	-2.134786	1.607339	2.116438	-0.201862	NA	-0.2477	-0.313611	1.113776	-0.60669	0.410258	-1.749044	NA	0.213319	NA	-0.21926	NA	-1.618571	-2.382553	-0.861903	-2.031546	-0.38836	-0.569284	-0.11113	NA	-0.234319	0.15835
RRM3	NA	-7.677287	-1.216924	-0.371204	NA	-0.159597	0.592479	-1.604407	1.144796	0.423083	0.677124	NA	NA	NA	-3.371921	-1.726983	-0.068742	0.685186	-0.474522	-0.278104	-1.29899	-0.873788	NA	0.919925	-4.322739	-22.021402	NA	-0.740206	NA	0.312597	-0.522033	0.420076	0.431235	0.269207	0.160198
RRP6	NA	-1.303395	-1.66461	0.131152	0.06662	0.252124	NA	NA	NA	NA	-0.794413	-2.174728	1.119234	NA	0.29053	-0.153659	0.304883	0.116426	-0.203657	0.387826	0.353437	1.056535	NA	0.077047	NA	-1.595576	NA	0.724894	-1.676953	0.301861	1.092529	-9.241669	1.300542	0.2038	-1.269311
RRP8	NA	0.067079	2.394843	-0.693822	NA	-0.758661	-0.016163	NA	-0.190491	-0.344901	NA	-0.194864	1.099811	-0.883388	NA	-1.225551	-0.007626	1.236979	0.059185	0.718691	0.607725	0.341857	NA	0.953847	NA	-0.342733	1.096905	0.664198	-0.719713	0.946861	NA	-0.143	1.403679	NA	-0.040667
RSA3	NA	-0.314293	NA	0.228699	-0.054062	-1.268908	0.417469	1.567495	-0.411602	NA	NA	0.396755	NA	NA	-0.320032	0.55163	0.300429	0.747657	1.113941	0.959005	0.318013	-0.258142	NA	0.108369	NA	0.407863	-0.52663	-0.189756	-1.517737	-0.251303	0.30556	NA	-0.185673	-0.706008	-0.092218
RSC3	NA	NA	1.207572	-0.076778	0.938424	-0.524878	-2.238216	0.183831	-0.76817	-0.469244	0.126379	-1.314661	-0.631858	NA	-0.406484	-0.268159	-1.051418	NA	-0.492619	1.118141	-0.940219	NA	NA	-0.610662	NA	0.094315	0.404682	-1.482728	0.83418	-0.327488	0.668606	NA	-1.627022	0.196466	-0.591146
RSC4	-2.790374	-0.343342	0.822331	-0.162584	0.001474	-0.041687	-0.081925	0.661071	-0.839768	-1.016033	0.551822	0.147449	-2.584322	NA	0.209046	0.08114	-0.525509	-0.187368	0.365158	-0.573349	-1.818688	-0.506949	NA	-0.166056	-2.105006	0.052274	-0.35833	0.253107	-0.112738	0.207943	0.361574	0.416905	0.650208	-0.179145	0.355601
RSC58	-0.953395	0.380815	NA	-0.506232	-0.175162	-0.602809	-0.799629	1.045516	-0.644175	0.501898	-0.46317	-0.141552	0.826631	-0.305083	1.048957	0.315335	-0.297699	-0.35815	0.070268	NA	-0.276539	0.357271	-0.611556	-1.853903	NA	-0.30797	NA	-0.112407	0.144846	0.652653	-0.177426	0.016222	0.489607	0.118214	NA
RSP5	-0.780502	-1.015849	2.468873	-0.746106	-0.607398	0.123866	-0.543735	1.555428	-0.383423	NA	0.93468	0.473775	-1.809826	0.803676	-0.766129	-0.052613	-0.086892	0.229408	NA	0.74436	NA	-0.383343	NA	-1.152208	NA	-0.140787	0.723227	-0.352793	0.459757	-0.137254	NA	0.531242	-1.011914	-0.687033	0.151981
RTF1	NA	-3.662081	2.433502	0.303833	-7.503925	0.568294	-0.176652	NA	0.740141	NA	-5.384981	-6.545746	-1.450492	NA	0.19111	0.422704	0.616096	-4.274802	0.785982	-2.470968	-1.45786	0.840055	-0.074963	-7.893727	NA	0.838574	-6.373584	NA	-0.79147	0.614977	0.102804	NA	NA	-0.25912	-3.174789
RTG2	NA	-2.145838	NA	0.141863	NA	0.2224	0.610878	NA	0.449164	-0.794046	-1.722574	-1.715992	-1.345523	NA	0.273134	0.815481	0.45741	-1.881043	0.546645	-0.747151	-1.964725	-0.360548	NA	-1.070885	NA	0.143639	-0.858631	NA	-0.524979	0.837297	-3.103477	-0.197675	-0.044124	0.031123	0.220873
RTG3	NA	-0.497104	-2.497418	0.188393	-0.103338	0.76892	-0.147108	-0.870287	0.138562	-0.461597	-1.872961	-1.143853	-0.044098	-2.17929	0.7984	0.331165	0.37067	-1.009059	0.239187	-0.208796	0.675667	0.369484	-0.113673	-0.604894	NA	0.491944	-1.374269	0.139814	0.842688	0.687284	-0.809899	0.311108	0.082961	0.797361	-0.006751
RTK1	NA	-1.322829	NA	0.751817	-0.839907	-0.040523	0.299979	NA	0.833129	0.030117	-0.119934	-0.119717	0.75549	-1.1908	NA	0.4806	0.218676	0.326533	0.13363	-0.141481	-0.695284	0.205238	NA	-0.249067	-1.018689	-0.152524	-0.780267	0.280031	-0.852137	0.395253	-0.975971	0.266341	0.233639	0.525756	0.349065
RTN1	-0.217905	-0.076984	-0.0756	-0.236032	-0.24307	0.271118	-0.33124	-0.579049	0.367089	0.071059	0.471491	0.175933	-0.087521	-0.055749	0.226385	-0.45892	0.116724	0.224997	-0.128175	0.173455	0.827414	NA	NA	-0.47668	-5.648504	0.50192	0.478546	-0.502197	0.28948	0.426126	-0.652196	-0.381268	0.360817	-0.099329	-0.444247
RTN2	NA	-0.225478	-0.304508	-0.062331	0.134923	0.299734	-0.263321	-0.050811	0.39612	1.947205	0.070138	0.115613	-0.014184	-0.436393	-0.722263	0.013509	-0.131363	-0.141524	0.569642	-0.651689	-0.796513	0.111331	NA	0.289431	NA	0.607449	0.679601	0.299398	-0.198594	-0.272262	0.644294	-0.616368	-0.585561	0.390188	0.776062
RTR1	NA	-0.278293	-10.420476	0.605538	0.378339	0.32806	0.884894	1.920334	0.632599	-6.952055	-1.362168	0.063628	-0.625479	0.190966	0.262086	0.784362	-0.800938	-0.554253	NA	-1.986428	-1.183814	0.628113	-2.231644	0.660488	NA	0.358547	0.448177	-0.045648	-0.161026	1.0344	NA	-1.999046	0.833843	-0.020726	-0.038069
RTS1	NA	-4.647805	-8.336101	0.625711	NA	-0.187739	NA	2.797048	NA	NA	1.320304	0.148014	-0.104362	0.549262	-0.057773	0.407517	0.473159	0.234819	0.851607	-0.324962	-1.962212	0.92169	-0.134587	-1.464959	NA	-3.909448	-3.059736	0.439724	-0.147323	0.375097	1.889289	-0.48762	0.577907	-0.432516	-0.491752
RTT10	NA	NA	NA	0.39498	NA	0.056933	-0.001168	1.446975	0.495562	0.489412	-0.354762	0.274539	-0.503923	NA	0.333084	-0.336723	-1.795538	-0.69081	-0.261445	0.140969	NA	0.3494	-0.736774	0.065551	NA	0.139097	0.308492	0.082606	-0.907819	-0.65804	0.659709	-0.356267	-0.607578	-0.403483	-0.495417
RTT101	NA	NA	0.247846	1.760076	NA	1.100214	0.167247	0.702427	NA	NA	0.577481	2.249792	NA	NA	-2.147699	NA	NA	0.439775	-0.544032	NA	NA	0.364745	NA	0.05103	-0.949962	NA	NA	-0.002741	-0.381259	-0.251867	0.200382	0.63105	1.107581	-0.103664	NA
RTT102	0.83106	0.61817	-0.493021	0.314957	0.433409	0.176875	-0.28215	0.945469	0.28408	-0.603744	0.42247	-0.57345	0.342292	-0.818622	-0.186637	0.068622	0.426774	-0.02967	-0.161877	-0.494816	-0.711804	-0.371598	NA	0.720051	NA	-0.153601	-0.243343	-0.020081	-0.095087	0.268897	0.231962	-0.662621	0.301805	-0.118827	0.197786
RTT103	NA	-1.466202	-20.210562	0.459342	0.867482	0.393923	1.006329	-2.280748	0.110087	-4.929774	-0.195266	0.310832	-0.503076	0.984105	-0.151647	-0.230843	0.908463	0.305273	0.056809	-0.303261	0.749768	NA	0.607687	-0.701913	NA	-0.224616	-1.692378	-0.729051	-1.143745	-0.1287	NA	NA	-0.319296	0.407092	0.086981
RTT106	NA	-0.684542	NA	-0.021858	0.514324	0.300501	-0.158505	-3.451284	-0.115793	0.291613	0.002652	-0.114293	-1.664221	NA	-0.445929	NA	0.339558	0.597788	0.516483	-0.012729	-0.075669	0.545707	NA	0.106537	NA	-0.202683	0.683351	-0.284677	-0.492449	0.191769	-3.582787	0.052241	NA	-0.464108	-0.24326
RTT107	-0.128577	0.148936	0.240308	-1.509111	-0.831269	0.849544	0.646202	-1.759729	2.193781	0.680708	1.345516	2.635086	-3.944308	-4.919689	1.0428	0.618698	-1.67508	-1.196848	-1.320147	-0.878233	0.973154	0.920848	NA	0.601763	NA	-2.278125	-0.009998	1.250283	-3.721482	-0.115299	-1.949773	0.928238	2.075126	0.540931	1.342841
RTT109	NA	3.330074	-2.176936	2.024819	NA	1.106614	0.028824	-2.294856	NA	NA	-1.457255	2.525699	NA	NA	-0.167326	NA	NA	0.156439	-1.123278	NA	NA	-0.345361	-2.272115	0.189385	-2.20935	1.880905	NA	0.96942	0.659013	0.071031	-3.897601	-0.635012	2.6108	0.696381	NA
RUD3	NA	-1.39462	-10.420221	0.416224	0.245162	-0.355102	0.477469	0.016637	0.48238	0.365082	-0.440526	0.31797	0.095018	-2.228101	0.04583	-0.002768	0.603249	-1.572386	1.293067	-0.465997	-0.791938	0.743605	NA	-0.292853	-3.016904	-0.920397	-2.485769	0.323914	-0.664616	0.915709	1.070188	0.0095	-0.090011	0.481823	0.159127
RVS161	-0.662139	-3.946717	-2.419675	NA	-2.259673	-0.007213	-0.267316	0.331131	0.71871	-0.893769	0.506939	NA	-0.1935	-1.000092	-0.005834	0.135841	0.604754	NA	-0.079594	-0.409951	-1.457705	-0.352602	-0.593417	0.716389	-7.411321	-0.412849	-3.508179	0.12424	-1.476879	-0.067841	0.542902	-0.258234	0.278806	-0.130541	0.007579
RVS167	NA	-2.344553	-0.10347	-0.003765	0.643763	NA	0.393602	-0.126437	0.212607	-0.078535	NA	0.290784	NA	NA	-0.954954	0.026149	0.344824	NA	0.150063	0.219467	NA	-0.406717	-0.376314	-1.112728	NA	-0.877197	0.015064	-1.066516	-0.814994	0.076379	0.313167	NA	NA	-0.803246	-0.946668
RXT2	NA	-6.735437	-19.268881	0.63728	-0.612721	0.152263	0.505154	-0.284736	0.665182	NA	NA	0.091132	-0.475363	-2.755845	0.197402	-0.388704	1.191293	-2.14889	0.864933	-3.139181	-3.995668	0.863794	NA	-0.352535	NA	-1.505055	-7.061616	0.401816	-2.118331	0.102729	-0.572842	NA	0.344269	0.377535	0.263077
RXT3	NA	-1.225656	NA	0.153626	-0.650813	-0.049223	0.280244	NA	0.73345	0.908905	-0.074311	0.411634	-0.26547	-0.110287	0.206666	-0.162724	0.453918	-0.505204	0.727865	0.044881	-2.916136	0.376081	-0.16893	0.389443	NA	-0.560961	-1.233081	0.018961	-0.795199	0.042158	0.866363	0.30987	-0.133146	0.115679	0.204317
SAC1	NA	-1.039257	1.867077	0.630122	-0.370513	0.11257	-0.00325	NA	0.651252	-0.202879	-0.571109	0.121138	-0.804768	NA	0.284743	0.843527	1.207047	-1.917261	0.618427	NA	-2.193185	0.222209	0.094653	-0.856724	NA	-1.538387	-0.094978	0.355518	NA	0.322573	2.13442	-0.276809	NA	-0.124221	0.419784
SAC3	3.774271	-4.088837	-0.253909	0.024671	-4.653805	-0.51412	0.224671	NA	0.831914	NA	-7.373173	-1.013479	-4.896838	NA	NA	-0.321076	-0.182772	-1.02517	0.402275	-0.605814	NA	NA	NA	0.130679	NA	-0.974034	-3.563964	-0.031813	-0.849956	-0.134158	-3.28191	-6.458118	0.201854	NA	-0.307675
SAC7	-2.676175	-1.272311	-1.349865	0.526356	-0.213033	NA	0.645169	-2.874443	0.398617	-0.029187	-0.683346	-2.089668	0.584976	-2.958776	0.405178	-0.092261	0.528848	0.382409	0.91637	0.301278	0.840197	0.836517	1.313129	0.35783	NA	-0.06209	-0.848036	0.010374	-1.821837	0.10649	-1.469525	NA	-0.251489	-1.172335	0.10835
SAE2	0.980719	NA	1.323435	1.125242	NA	0.065738	0.208723	1.113658	NA	NA	0.843342	0.546321	NA	NA	-2.260832	NA	NA	0.565814	0.390795	NA	NA	0.450459	NA	-0.051383	-2.359315	NA	NA	NA	NA	0.549708	1.479208	0.203367	NA	-0.143791	NA
SAF1	0.946081	0.171153	NA	0.393443	1.048513	-0.209665	-0.363223	-0.792302	-0.395155	0.81226	-0.006514	-0.01535	1.327164	0.977125	-0.179233	-0.140162	-0.497179	NA	-0.329999	-0.09974	NA	-0.505022	NA	-0.296657	NA	0.480239	0.653089	-0.028154	-0.312561	-0.7528	0.00991	0.71183	0.033699	0.262912	-0.404459
SAK1	-0.547298	1.359737	0.985719	-0.669676	-0.755681	0.385408	0.175512	-0.160259	0.881845	0.191494	-0.476267	-0.164763	0.019546	1.074331	-0.389039	-0.171679	-0.820345	NA	NA	0.246778	NA	-0.206367	NA	0.096427	NA	0.623636	0.112218	-0.150032	3.748802	0.12414	NA	0.692955	-0.2768	0.494755	0.017738
SAM1	NA	0.675842	-0.610568	0.38437	-0.142737	-0.452168	-0.555641	-0.425651	-0.318881	NA	0.006882	0.202312	0.522797	NA	-0.446056	0.112226	0.092163	0.700874	0.132416	0.303811	NA	0.323456	NA	0.44292	-1.518356	0.411423	0.573939	-0.295138	0.053628	-0.765579	0.594549	0.17167	0.08037	-0.135282	0.522132
SAM37	NA	-2.973855	-3.218846	0.448064	-2.838674	0.564743	0.227708	-0.784113	0.836295	NA	-3.01846	-1.328337	-2.286656	-1.949833	-0.518588	-0.719392	0.496256	-0.104535	0.654094	0.693445	NA	1.21061	NA	NA	NA	0.313193	-2.600637	-0.019922	0.445293	1.631968	NA	-2.884623	0.899331	0.224969	1.11711
SAP155	NA	-0.2512	-1.443067	-1.062414	-0.683324	-0.018724	-0.448851	0.777935	0.215814	0.090995	0.0335	-0.429656	1.053656	-1.500385	0.29097	0.125829	0.084256	0.786473	-0.372426	0.445995	1.771626	-0.773651	0.790252	-0.154002	NA	0.137051	1.990347	0.207877	-0.596774	-0.005292	0.683549	-0.110999	0.527577	0.554416	-0.480736
SAP185	-1.308769	NA	0.786735	-0.289207	0.797295	0.316167	0.093476	1.880668	-0.296502	1.490717	-0.138573	0.240718	-0.479232	0.783162	-0.411887	-0.067557	-0.012191	1.001637	-0.393639	-0.342875	1.488677	-0.554087	0.153173	0.198597	NA	NA	0.963862	0.956641	0.263031	0.118336	0.371396	-0.123747	1.789926	0.061958	0.181029
SAP190	5.433142	1.063741	-0.57481	-0.019373	1.467346	-0.195076	-1.533402	-1.180616	-0.613339	-0.155278	-2.008612	0.42184	1.968909	NA	0.193237	0.844022	-0.099576	0.49539	0.05739	0.531019	2.026174	0.245387	0.21524	-0.975767	2.017329	0.344366	0.093105	-1.102616	-0.01514	-0.114836	-0.994534	0.627443	NA	-0.647381	0.058953
SAP30	NA	-10.561673	NA	0.020206	-0.589104	-0.227751	-0.35613	-1.150158	0.019668	NA	0.277158	-0.589837	NA	NA	0.083429	-0.80943	0.513786	-3.058573	0.911882	-3.092747	-4.002004	0.815412	NA	0.975856	NA	-2.83132	-9.741488	-0.29338	NA	NA	-1.62943	NA	0.595925	1.043672	NA
SAS2	0.124905	-3.35373	-12.354382	-0.177526	0.244148	0.239107	0.368087	1.16007	0.186213	-3.029718	-2.561744	-3.624077	NA	1.12695	-0.095096	-0.068008	-0.234353	0.348395	0.49546	-0.657374	0.730555	0.539893	0.48718	0.258753	NA	0.712462	-0.097166	0.605311	NA	NA	0.690786	-0.251155	NA	0.448923	-0.058925
SAS3	-6.935737	-3.569126	-1.442966	0.501142	-0.222317	0.204356	0.352897	1.989046	0.170548	-0.524919	-1.731508	-0.061527	-1.117705	NA	0.738517	0.690182	0.466493	-0.445658	0.428445	-1.157551	-2.330291	0.786293	-0.129972	0.222942	-5.187344	-0.286478	NA	NA	0.398368	0.4863	0.165327	-1.336706	NA	-0.347344	0.272534
SAS4	NA	-3.419367	-14.322864	-0.336464	NA	0.32974	0.251994	0.818568	0.013491	NA	-4.028625	-4.64528	NA	NA	0.682237	-0.470102	0.246101	0.869765	0.443321	0.733666	NA	NA	0.438594	0.654306	NA	0.784307	-0.5317	-0.558619	-0.979817	-0.24327	NA	-0.120492	-2.24967	NA	-0.188078
SAS5	NA	-1.779371	-17.501729	-0.039483	-0.374103	0.62216	0.561685	1.596113	0.294226	-2.059913	-1.933633	-3.18149	NA	NA	0.604957	0.345272	0.604429	0.448703	-0.532762	0.576677	0.518843	-0.017352	NA	0.511496	NA	1.376333	0.897246	0.194488	-0.434325	-0.13569	0.499147	-0.874958	-0.143537	-0.675361	-0.509895
SAT4	3.679188	-1.715708	-2.947972	NA	NA	-0.767866	0.703983	-0.675383	0.004173	2.286698	0.075262	NA	-0.770615	-1.193931	-0.315933	0.521955	-0.040732	NA	0.209888	0.00716	-0.262967	0.045491	NA	NA	NA	-0.395184	-0.715594	-0.851767	-1.213008	0.485092	NA	-0.432345	0.186534	-0.582968	-0.182069
SAW1	-4.081588	0.752844	0.025012	0.207058	-0.146425	0.464022	-0.180506	-2.247357	0.243732	0.506072	0.241851	-1.042703	1.020424	-0.947686	-0.095087	0.167316	-0.106975	-1.548674	0.032754	-1.603359	0.398952	-0.477243	NA	0.158376	-0.522982	-0.314927	0.921576	0.656028	-0.564516	0.242603	0.282345	-0.273585	0.309928	-0.08165	0.859212
SCD6	0.418311	NA	1.548135	-0.308031	-0.299413	0.046116	-0.282082	0.119338	-0.418811	0.323806	0.037218	-0.379064	1.402012	NA	0.171891	-0.231976	-0.438677	1.475492	-0.051739	0.553478	1.853759	-0.528271	NA	0.563944	NA	0.626966	1.328075	0.084196	0.11056	-0.382541	0.227877	0.653838	-0.7547	-0.23622	-0.011494
SCJ1	NA	-1.54775	0.784828	0.535848	-1.101224	0.205292	-0.203517	-0.968723	0.306701	NA	-1.440359	-0.684607	NA	-0.354393	0.325089	0.271823	0.544849	-0.995606	0.675227	0.742151	0.781881	0.679412	0.880274	-0.461568	NA	-1.045429	-1.005489	0.727627	NA	NA	-1.943177	0.420045	-0.349552	0.293036	NA
SCS2	4.593105	-1.133386	NA	-0.320388	-1.992248	0.016621	0.657546	-0.943799	0.061997	NA	NA	-0.096155	0.113936	NA	0.647267	0.052306	0.379094	-0.838066	NA	-0.006439	NA	-0.081823	NA	0.745202	NA	-1.07981	-1.732322	NA	NA	1.114306	NA	0.680524	NA	0.021165	0.482622
SCS3	-2.448781	-0.672716	NA	0.635716	0.007253	0.009962	0.511479	-3.372158	-0.069486	0.535182	NA	-0.996285	-1.03566	NA	-0.416158	0.203711	-0.041032	-0.497512	0.479945	-0.13528	-0.174116	-0.077034	NA	0.226296	-4.252944	0.696816	-1.338408	NA	-1.230216	0.296869	-1.563394	-0.826257	-0.212622	0.413012	0.465004
SCS7	-8.820492	-1.811725	-13.558961	0.119994	-0.242973	0.304377	0.893416	-2.584405	0.403234	-2.528721	-0.386988	0.571312	NA	NA	-0.04676	0.320277	0.358802	-2.040625	0.612619	-1.061406	-1.457595	0.940111	NA	0.195742	NA	-0.010948	-0.459573	0.218686	NA	NA	-3.721088	-1.202041	0.440231	-1.253605	NA
SCT1	0.463066	0.572749	1.712886	-0.425195	-0.000789	-0.028613	-0.258913	-0.068529	-0.815841	0.162082	-0.085381	-0.016868	-0.157373	1.309748	-0.152319	-0.004594	-0.536729	0.81581	-0.004787	-0.221984	-0.210692	-0.323752	-0.682247	-0.450562	NA	0.533813	0.219413	-0.054396	1.823837	0.498936	0.092395	0.775718	-0.142253	0.008325	-0.20813
SDC1	-3.542035	-7.147967	2.358828	0.36017	-4.367034	NA	0.010804	-10.86299	0.64176	NA	-2.494148	-0.601206	-6.444105	NA	0.573227	0.519171	0.396459	-1.89057	0.523266	-2.064495	-6.576572	0.576365	-1.123343	-0.712129	NA	-1.090491	-3.006022	0.098514	-0.118075	0.24906	-2.666654	-6.156984	1.207206	-0.026669	-0.088557
SDS3	-2.064535	0.694641	-0.144637	0.652031	NA	-0.059659	0.071189	0.216579	0.313744	1.304579	-1.000768	-0.294533	0.631695	-0.684293	0.642941	-0.422496	-0.558057	0.453104	0.43494	-0.056522	0.785671	0.232246	NA	-0.961659	-2.521475	0.15707	NA	-0.79752	-0.888309	-0.559305	0.587061	-0.111553	-0.880032	0.194128	0.577972
SEC22	NA	NA	NA	0.800346	-0.259602	0.135777	-0.525954	-1.061284	0.665598	-5.059597	-1.354185	-1.704883	-2.175228	NA	0.41395	0.121048	0.922271	-0.742233	0.97271	-2.415766	-1.436755	0.036151	-1.465329	NA	NA	-0.144346	-3.115085	-0.592603	-0.663639	0.72424	-0.431098	NA	NA	0.52473	0.18211
SEC28	NA	NA	NA	0.592967	2.057605	0.401997	0.200151	-1.042769	0.911898	NA	-0.220781	1.583573	-0.123204	-4.897188	-1.022025	-1.141084	0.670835	NA	0.612328	-0.042066	-0.96177	0.385349	-2.989999	-1.763087	NA	-0.891549	-0.085921	-0.229836	-0.242486	-0.43261	-0.553286	-2.827664	0.250698	0.200081	0.443199
SEC66	NA	-5.125538	0.347998	0.392318	-0.389201	0.423214	0.152707	1.346568	0.209103	-1.884385	NA	-2.282836	0.295591	-0.475466	-0.030241	0.212833	0.746079	-1.031278	0.784907	-0.913168	-0.309549	0.910469	0.039728	-0.073388	NA	-2.206621	-1.62737	-0.587321	-1.634293	0.61872	0.54574	-0.213054	-1.304063	0.377068	0.202861
SEC72	-1.659086	-1.431819	0.166111	0.243471	0.250788	-0.24941	0.256061	-0.871937	-0.518496	-0.174769	-0.650438	-1.940693	-0.578147	-0.261827	0.38802	0.838009	0.593525	-1.208187	0.102086	0.035714	1.056505	0.899145	0.494126	0.34009	NA	-0.744488	-0.905444	0.33323	-0.08826	0.468955	-0.331107	0.107576	-0.285078	0.090983	0.504318
SED4	NA	0.969851	-1.058554	NA	0.301701	0.214676	-0.350303	-0.579955	-0.406666	0.859068	0.330893	-0.015064	0.366682	-0.257623	0.412164	0.393029	0.622942	NA	-0.229877	-0.401918	0.34667	0.192252	0.416099	-0.447667	NA	-0.231335	0.524604	-0.169455	0.34194	0.231263	0.220696	-0.272738	0.500897	0.036691	-0.024692
SEF1	NA	0.830663	-0.910688	-0.185984	-0.282997	-0.219505	-0.13645	-0.382917	0.083365	2.095366	0.620849	0.858994	-0.221515	-1.617128	-0.587827	0.129875	0.371267	0.177226	0.452202	0.249802	-1.986544	0.028115	NA	-0.176908	NA	-0.38854	-0.290893	-0.341051	0.414947	0.342463	-0.674662	0.062426	-0.740497	-0.71846	-0.620621
SEM1	NA	-2.184639	-2.649819	-0.004779	-1.196837	NA	-0.216836	-0.369157	0.625413	NA	-10.816872	-1.187358	-0.507561	NA	-0.259465	-1.289653	-0.404122	0.862439	0.34791	0.879048	-4.208625	0.491117	-1.519974	1.164459	NA	-0.402417	-2.030951	0.52869	0.853995	0.122072	-0.533545	NA	0.377305	-0.012716	-1.488984
SER1	NA	0.549071	0.710722	-0.702887	0.433502	0.111776	-0.389773	-0.196698	-0.562304	0.518565	0.408991	0.247837	0.385442	-1.703083	-0.221715	-0.513228	-0.093026	-0.520272	0.084611	-0.172378	0.72842	0.088071	NA	-0.381163	NA	0.000705	1.077121	-0.534198	0.875519	-0.229809	0.149751	-0.452066	0.681508	0.103951	-0.10822
SER2	NA	-0.956997	-1.462597	-0.590845	-0.113731	-0.461987	-0.424167	-0.141759	0.65832	-2.192642	0.625886	0.195635	-0.611942	0.951098	-0.373134	0.614368	0.507755	-1.717575	-0.015083	-0.704115	-0.27763	-0.408664	NA	0.522169	NA	0.726803	0.350395	0.214035	-0.463455	-0.126895	0.561766	0.135308	-1.154024	0.008756	0.187994
SET2	NA	NA	-4.295533	0.041075	-0.666647	-0.277499	0.312287	NA	-0.1626	NA	-3.683972	-2.797991	NA	NA	0.115249	0.189912	-0.331765	1.371385	0.446506	NA	0.356326	0.106269	1.332084	NA	NA	0.037161	-0.980286	-0.612053	0.358517	0.226082	NA	-3.783163	-1.776655	-0.271489	0.080997
SET3	NA	0.15922	-0.89872	-0.780778	0.371512	-0.070099	1.200042	0.475683	0.395655	NA	NA	-0.975926	-0.149463	NA	0.306713	0.006857	-0.273523	NA	-0.261329	0.195597	-0.588972	0.310214	NA	NA	NA	0.657725	-0.1236	0.49022	0.164295	0.179495	NA	-5.480763	0.378894	-0.177621	0.484744
SET4	0.320637	NA	-0.088815	-0.07383	-0.330137	-0.421863	0.33485	0.570564	-0.033322	0.08036	-0.092032	-0.342967	0.208379	0.757521	0.640502	0.345303	0.108548	0.203089	-0.349552	-0.134695	0.129469	-0.202151	NA	-0.92574	NA	NA	0.195492	-0.318282	1.424805	0.63573	0.127389	-0.299432	-0.41939	-0.178453	0.537524
SET5	NA	0.620773	NA	-0.527393	0.622498	-0.214143	0.953124	-0.455212	0.056979	2.047817	-0.464364	0.037372	1.007355	0.392118	-0.10267	0.015098	-0.310065	0.642283	-0.681724	-0.122461	1.469831	-0.702203	NA	-0.365289	NA	0.595489	0.995371	-0.826444	0.242287	-0.912411	0.967207	0.283241	-0.841158	0.472835	-0.215635

SET6	0.960146	0.844441	-0.281359	0.523776	NA	0.149699	-0.144022	1.244885	-0.527202	0.076793	0.631277	0.037693	0.459473	0.251348	-0.396997	-0.095463	0.091696	0.076369	0.193819	-0.143119	0.891194	0.038744	NA	-0.063347	NA	-0.086739	0.747963	-0.14357	0.174855	0.200066	1.04758	0.110946	-0.748877	0.16596	-0.91847
SEY1	NA	0.219053	-0.322304	-0.04657	0.075308	-0.028268	0.006375	-1.34878	0.986739	1.500725	0.09037	0.09206	-1.025603	0.002917	0.019303	-0.003243	-0.151634	-2.564909	-0.078156	-0.559743	-0.99611	0.419259	0.727248	-0.006541	NA	0.529465	-0.195447	0.476962	-0.172957	0.120415	0.243201	-0.24415	0.416858	0.283365	0.110188
SFB2	NA	-0.645086	-0.63061	-0.19511	0.428899	0.053095	-0.032946	0.041802	-0.056986	-1.843853	-0.149773	0.25666	0.586066	NA	-0.024167	0.214388	0.303636	0.595281	0.669866	-0.907916	NA	-0.333055	NA	-0.154259	NA	-0.659216	-0.110204	-0.016049	-0.166544	-0.330689	-0.021583	-0.089974	0.806729	-0.035088	-0.068623
SFL1	NA	-2.453536	NA	0.112564	-0.1613	-0.080003	NA	-0.315552	0.084875	NA	NA	-0.24887	-0.226097	-1.740837	0.064962	-0.047759	-0.759799	NA	0.088433	-0.560218	0.483444	-0.617255	NA	0.465287	NA	-0.220758	-2.055827	-0.803112	0.160764	-0.147801	0.108898	0.518952	-1.424558	0.568252	0.511075
SGF11	NA	-0.742861	1.707756	0.25203	-2.550149	0.002361	-0.119084	0.604859	-1.274147	-0.03064	1.316725	0.19999	1.419675	-2.167647	0.312228	0.009862	-0.684852	0.017786	-0.087679	-0.293262	0.947911	-0.56209	0.830391	0.475707	NA	-0.93547	1.498957	-0.46368	0.773693	0.027604	1.054168	-0.494704	-0.462763	-0.477368	0.322687
SGF29	NA	NA	0.803192	NA	NA	-0.250577	0.431202	-2.795597	-0.182019	-0.824413	0.046758	NA	-3.303785	-1.308848	0.781223	0.003159	0.643366	NA	0.708546	-1.027929	-3.900019	0.2651	0.513526	0.461675	NA	-0.178893	-2.264104	0.937388	-0.253443	0.552765	-1.37446	-0.509795	1.1844	0.018895	-0.159591
SGF73	NA	-0.062769	-4.518151	0.924243	-2.079683	0.250494	-0.159699	NA	-1.36394	-2.446765	2.60532	0.784517	-0.470163	-3.891592	-0.102053	-0.243193	0.876233	-1.41747	1.264855	-0.36045	-0.572152	0.539941	0.3204	0.504446	NA	-0.335311	-0.05169	0.686985	0.138085	1.196013	1.291027	-0.107792	-1.340624	0.286395	0.371428
SGM1	0.674972	0.89872	0.460661	-0.247631	0.376842	-0.336641	0.104568	-0.706567	0.003137	0.609536	-0.711843	-0.587384	NA	0.162821	0.335774	-0.080613	0.085362	0.484256	0.780914	-0.102923	1.355025	-0.002433	-1.384114	-0.171372	-5.764954	0.605943	0.274796	-0.313453	0.084761	0.012926	-0.376267	-0.159259	0.07254	-0.021573	-0.5
SGN1	-0.317704	-2.051011	-0.466137	0.159067	-1.43507	0.108603	-0.09299	NA	-0.262685	0.664757	1.278281	0.417898	-1.269775	NA	-0.022308	0.131139	0.581089	-1.17948	0.630676	-1.247948	0.148911	0.152353	-0.317138	-0.326358	NA	-0.326948	-1.305758	0.402384	NA	0.725299	0.258002	0.762373	0.279864	-0.42136	0.638901
SGS1	NA	NA	-1.659008	-0.582325	0.622186	-0.492361	-0.245488	-0.244893	0.372184	1.561154	0.295925	-0.267618	NA	-1.174862	0.263448	0.349291	-0.518	0.585281	0.749658	0.150904	-0.359717	0.072786	NA	-0.373598	NA	0.49239	0.292036	0.067511	NA	NA	-0.230111	-0.053522	-0.165531	0.654588	NA
SGT1	NA	NA	NA	0.361479	-0.568859	0.402376	NA	0.60632	NA	NA	0.021665	-0.126684	-1.345509	0.178225	-0.408477	-0.30359	-0.088142	-0.332732	0.381785	-0.004704	-1.794641	0.26062	NA	-0.158228	NA	-0.709776	-1.746271	0.090126	0.969498	0.225547	0.472159	-0.120222	0.559865	-0.372262	0.419366
SHB17	0.432038	0.669444	-0.101141	-0.192598	0.108709	0.068324	-0.51296	0.022535	-0.331796	1.126941	-0.133129	0.319167	-0.231502	NA	0.097647	0.36793	-0.036508	0.153026	0.126246	-0.275949	0.249833	-0.068517	-0.649462	0.201104	NA	0.1487	0.337763	-1.215833	NA	-0.392931	-0.026229	0.510545	-1.790187	-0.124341	0.130633
SHE10	NA	0.120685	-0.239893	0.823895	-0.937449	-0.313404	-0.70619	-1.522626	1.110516	-0.251518	0.445895	-0.694591	-0.223618	-2.101876	0.557397	0.0677	0.427016	-0.376524	0.451854	-0.139978	-1.470328	-0.089512	1.311392	0.524513	-0.183668	-1.207734	-0.896262	NA	-0.047201	0.60351	-0.634095	0.270422	0.492394	0.775788	0.981132
SHE4	NA	-5.614128	0.3779	0.373339	-0.41342	0.458399	NA	-3.714023	NA	NA	0.062167	0.699261	-2.733341	-2.149534	-0.361758	0.608203	0.209584	-4.834887	1.363204	-0.746045	-2.248547	0.681834	NA	3.542665	NA	-2.551679	-4.304215	0.46177	-2.84976	1.608171	NA	0.715471	1.379098	-1.076536	-0.159906
SHE9	NA	0.53161	0.879022	-0.151722	0.086362	NA	-0.163619	-1.19073	0.088891	0.653453	-0.694034	0.491962	0.759947	-1.11042	-0.955752	-0.361508	0.032804	1.047311	-0.444331	0.911711	NA	0.162426	-0.120758	-0.221412	NA	0.526652	1.652911	-0.041824	-0.134615	-0.301246	0.95268	NA	0.452186	-0.092579	-0.829938
SIC1	NA	-0.551979	-1.337331	-1.189368	NA	0.185535	0.311272	0.326007	NA	NA	-0.792547	-2.735356	-0.607149	NA	-0.191394	-0.561706	-1.79578	0.903716	-1.368954	NA	-0.35152	-1.202945	-0.882599	0.72504	1.415809	0.973622	NA	0.959476	1.343285	0.978381	NA	-0.175101	1.228944	0.119059	1.140266
SIF2	NA	-0.364238	-0.214157	-0.405071	-0.298586	0.327145	0.403825	-0.180053	1.773556	NA	NA	-1.190896	-0.475897	0.419571	0.54932	0.46495	0.261186	-0.629086	0.06622	-0.062597	NA	-0.562711	NA	-1.516877	NA	-0.065433	-1.541675	-0.520784	-0.105375	0.568231	-0.029899	-3.942218	-0.851695	0.10701	0.606039
SIL1	NA	1.28848	0.352153	0.294872	-0.061149	-0.050545	NA	0.430326	NA	NA	0.234257	-0.114884	0.905762	-1.295836	-0.338464	-0.311077	-0.045622	-0.16061	0.218972	-0.18436	1.201982	0.460467	NA	-0.417568	NA	0.494771	0.651832	0.051087	0.767833	0.254242	-0.017472	-0.373425	-0.314438	0.05157	-0.558298
SIN3	NA	-8.569128	NA	0.256966	-2.866142	-0.914514	NA	-0.863502	NA	NA	0.097661	-0.418628	-1.369552	0.68307	0.478362	0.541018	0.368322	-1.447694	0.669038	-1.084789	-5.247696	0.132779	NA	2.020587	NA	-0.072014	-2.732379	0.014235	0.889906	0.534736	-0.306403	NA	0.258615	0.60949	0.0481
SIN4	NA	0.177352	NA	0.038434	-0.320527	0.149718	NA	-1.29328	0.143577	0.395494	-0.177685	0.364448	1.019538	NA	-0.312753	NA	0.38178	0.32534	0.264388	0.28293	0.609989	-0.836421	NA	NA	NA	-0.881895	NA	-0.07143	0.04171	-0.11732	NA	0.376808	NA	0.206817	NA
SIP1	NA	1.064625	NA	-0.069825	0.74784	NA	-0.279492	NA	0.015256	-0.073351	NA	-0.020977	-0.253449	NA	0.151445	-0.569994	0.203493	0.576496	0.421702	0.23192	NA	0.196029	-0.037003	0.40337	NA	0.610582	0.76023	-0.214206	0.759528	-0.388523	-0.334206	NA	NA	-0.38819	-0.377971
SIR1	NA	-9.336007	-11.896252	0.183385	-1.09102	NA	0.000212	-4.525495	-0.439028	0.203066	-2.17356	-5.030953	NA	NA	0.814565	1.072613	0.777117	0.075279	-0.05158	0.674337	-0.894831	0.82731	-1.081789	0.244471	-1.659982	0.182146	1.0286	0.376791	-0.294214	0.17578	NA	-0.401427	-0.094521	0.452275	1.253115
SIS2	1.09133	-2.009707	-3.413272	-0.191838	-0.979741	0.040637	-0.266876	-0.488658	0.131861	-1.236469	0.665428	0.16707	0.738349	NA	0.103594	0.085987	0.310991	0.388082	0.392953	-0.367525	-0.061986	0.045243	0.696887	0.454089	NA	-0.022979	0.354109	-0.612329	-1.206289	-0.130524	0.262335	-0.52163	-0.323469	-0.372168	-0.349995
SIZ1	NA	NA	-1.840689	0.199149	0.156691	NA	0.706165	NA	-0.581562	1.918785	NA	-1.450827	-3.213715	NA	0.501675	0.102226	-0.065921	NA	1.300497	3.671931	-2.354787	0.40123	NA	0.044419	NA	-0.049264	-2.705967	-0.416152	-2.948562	0.088786	NA	NA	-0.082971	-1.366314	-1.079148
SKG1	NA	1.098489	0.082146	-0.748665	0.402607	-0.100863	0.194694	0.418067	-0.016002	-0.697346	-0.309003	0.050732	1.11637	NA	-0.319316	0.334523	-0.807777	0.541266	-0.65959	0.191776	NA	-0.146172	NA	0.63503	NA	-0.118384	0.458701	0.352856	2.006038	0.041702	0.395707	0.342285	-0.354365	0.062059	-0.379679
SKI2	NA	-1.423021	NA	-0.199178	NA	-0.402999	0.623323	-1.116878	0.128243	0.012526	1.887231	-0.175123	NA	0.093051	-0.711239	0.052381	0.75593	NA	-0.236178	-0.558119	0.478193	0.228287	NA	-0.571515	NA	0.347278	1.444221	-0.038555	0.274041	0.555831	-0.047922	0.764321	0.236794	0.339597	-0.571896
SKI3	NA	NA	NA	-1.321923	-0.919212	-0.220721	-0.937802	-0.357369	-0.252587	2.380221	0.483708	0.045061	1.342258	-5.719813	-0.349845	-0.265149	0.646419	-0.268589	-0.428743	0.841554	NA	0.160521	1.357167	-0.050389	NA	0.630529	NA	0.286163	0.702626	0.041083	0.255265	0.414401	0.820765	-0.425426	-0.218011
SKI7	NA	NA	1.261942	-0.371111	0.519738	-0.209468	NA	0.292046	NA	NA	1.363707	-0.070066	1.790934	1.035663	-1.216152	-0.491252	-0.016417	1.589437	-0.019953	1.027323	NA	-0.199953	0.921334	0.140779	NA	0.151091	1.616964	-0.183672	-0.514011	-0.67897	-0.796939	0.6974	-0.202854	0.233243	-0.114419
SKN7	-0.056851	NA	0.002694	-0.290076	0.53603	0.180373	0.416114	-2.376872	-0.062007	-0.185171	0.905281	0.327153	-8.410823	1.242274	0.230462	0.064909	-0.088431	-5.282917	0.214462	-2.580273	-12.882746	0.079841	NA	-0.61641	NA	-0.545817	-1.841518	0.678718	-0.174787	0.596384	-1.017831	-0.589817	0.79638	0.025987	0.487863
SKO1	-1.116788	1.387752	2.083376	-1.067198	0.23709	-0.132711	-0.487359	1.466588	0.003769	-0.604975	-3.077289	0.463428	1.093874	-0.398454	-0.224338	NA	-0.087897	0.94358	0.168923	0.529076	NA	-0.62721	-0.016827	0.314584	NA	0.771756	2.390566	NA	-0.724125	0.056415	0.53388	-0.012703	NA	-0.98282	-0.228369
SKP2	NA	NA	-0.498748	0.469659	-0.169108	-0.035882	0.115015	-0.127253	-0.581406	0.202147	0.094163	-0.390533	1.102371	0.853532	0.116396	0.099841	-0.389513	0.598423	-0.092408	0.943778	NA	0.15131	NA	NA	NA	-0.073683	0.571541	-1.054857	-0.158921	0.048388	-0.040794	-0.544954	NA	-0.295557	0.288332
SKT5	NA	-0.828965	0.238721	0.415882	0.271859	0.459869	-0.151458	-0.303437	0.071666	0.626753	NA	0.125218	NA	1.601126	0.513114	0.035675	0.185027	-1.568954	0.404646	-1.51256	-3.869628	0.490715	NA	-0.441222	-2.405149	-0.113789	-0.459809	-0.643383	-1.751762	-0.337491	0.357926	0.571368	-1.375574	0.980212	-0.206761
SKY1	NA	0.266502	-0.230039	0.401029	0.559755	0.209594	0.499834	-3.337129	0.736717	NA	NA	0.066032	NA	0.581474	0.808103	0.619859	0.218507	-1.360957	0.921884	-1.590167	NA	0.231869	NA	-0.299229	1.549215	0.059583	-1.911357	0.4912	NA	NA	-1.666547	-0.241214	1.016886	0.929157	NA
SLA1	NA	-6.683363	NA	0.220693	-0.614319	0.545421	0.468947	-1.457836	0.74843	NA	-0.314761	-1.553626	-1.613493	-0.201007	-0.241123	0.251738	1.079535	-3.239707	0.632034	-1.749435	-2.776859	0.28903	-0.931029	-1.391408	NA	-3.767651	-4.063916	-1.329903	-4.550895	0.020515	NA	-0.278389	-0.589704	-1.873768	NA
SLC1	1.576163	1.272459	NA	-0.911233	0.778105	0.262656	-0.165454	NA	-0.155563	0.343888	-0.440769	0.242095	1.918124	2.064375	-0.411387	-0.448163	-0.938496	0.659437	-0.299915	-0.027861	1.916496	0.040119	NA	0.396444	NA	0.471531	1.083863	-0.129935	0.322343	-0.149391	0.404119	-0.282614	-0.099652	-0.221175	-0.371493
SLG1	NA	NA	-0.793789	1.068908	-0.072928	0.157457	NA	-0.663117	NA	NA	-0.077233	0.088186	-2.349204	-0.427996	-0.04519	0.045307	-0.013505	-0.05297	0.843551	0.060482	-1.066666	0.669342	NA	-1.160796	-2.345807	0.411781	-1.106656	-0.669945	-0.632866	0.731635	-0.396196	0.618243	-1.231833	0.291776	0.189768
SLI15	1.272582	-0.513647	-0.409624	0.460026	0.649056	0.015864	-0.553076	1.307009	-0.27604	0.886324	NA	NA	0.0264	NA	0.348859	-0.144194	0.334125	0.214777	0.401255	0.099941	NA	-0.158299	0.048937	-0.601727	NA	0.013404	0.726202	-0.190684	0.000279	-0.00159	0.279207	0.202063	-0.113913	-0.238373	-0.184867
SLK19	NA	-1.04309	-3.10837	-0.388994	-2.39802	0.34427	0.37442	2.456345	0.179164	-0.602797	0.277339	-0.188784	0.833426	NA	-0.478276	0.171159	0.44535	NA	0.427865	-0.161082	NA	0.078759	0.110575	-0.74999	NA	-0.026619	0.265692	-1.02276	1.294418	-0.208966	0.874533	-0.038514	NA	0.284807	-0.542089
SLM1	NA	0.658189	-0.495848	0.991531	0.273335	0.400646	0.181116	-0.224952	0.539878	NA	0.059865	NA	-0.109327	NA	0.129321	0.766797	0.628114	-0.032312	0.199519	-0.339384	0.329371	-0.516596	-0.740453	-0.404519	NA	0.487251	0.247801	-0.362056	0.345372	0.092324	0.06678	NA	-0.786121	0.4848	-0.011398
SLM6	-0.30491	-0.765567	NA	-0.493997	0.405215	-0.115641	-0.215824	1.939634	-0.271717	-1.870948	NA	0.778516	0.40867	NA	-0.623324	-0.939145	-0.396089	NA	-1.524704	0.101205	NA	0.839527	NA	0.519207	-2.88718	-4.62929	0.242284	0.34749	-0.016232	0.562388	0.359723	NA	0.816907	0.31328	-1.030568
SLP1	NA	-0.299318	-0.133214	0.049516	0.215471	0.532026	-0.199358	0.157474	-0.179903	0.425348	-0.073019	0.145784	0.726907	-3.68273	-0.396493	-0.100094	-0.236854	-0.024362	0.677918	-0.337337	0.825537	-0.551363	NA	0.799282	NA	-0.039457	0.218389	-0.514317	-0.392048	0.166674	0.168913	0.344774	-0.381466	0.67672	0.879542
SLT2	NA	-3.779773	-6.607465	0.279422	-0.23424	0.230175	0.074133	-0.382226	0.714902	-1.024865	-0.564602	-0.444128	-4.140935	1.011106	0.07506	0.495829	0.775529	-2.878686	0.497362	-1.416621	-7.48978	0.283473	-4.784977	1.362483	-5.341885	-0.556141	-4.2831	-0.092905	-2.966352	0.906022	0.187957	0.012046	0.448405	-0.168391	-0.032894
SLX1	NA	NA	NA	0.354619	0.04016	-1.155972	0.57516	-1.868552	-0.191255	0.522005	NA	0.305253	NA	NA	0.405188	0.353254	-0.357802	0.11083	0.371534	-0.403834	1.326279	0.315747	NA	-2.053789	NA	1.159622	1.197245	-0.397306	NA	NA	NA	-1.804062	-0.157093	-0.408052	0.242525
SLX8	-3.593625	NA	-2.903194	0.02272	NA	0.830245	1.210172	4.17093	NA	NA	-1.3677	-1.42013	NA	NA	0.386721	NA	NA	-0.37504	NA	NA	NA	0.55451	-3.11423	-3.219451	-2.732027	NA	NA	NA	NA	NA	NA	-0.375946	-0.030538	0.856428	NA
SLX9	NA	NA	NA	-0.299418	0.546907	-1.757821	-0.716224	-1.363502	-0.010822	NA	NA	0.6081	NA	NA	0.493548	0.504017	-0.003436	NA	0.452008	1.534026	1.048729	NA	0.791408	NA	NA	0.27346	0.730286	-0.550732	-1.080482	0.122169	NA	0.795381	-0.272043	-0.291993	0.343204
SLY41	NA	-0.692135	-0.086851	0.04077	0.180249	-0.003606	-0.09901	-1.716608	-0.648556	0.668337	0.832342	-0.25981	0.924838	0.026866	-0.601008	-0.071075	NA	0.328879	0.278852	0.297673	1.996899	-0.228846	NA	-0.701981	NA	NA	NA	NA	0.137586	0.477885	NA	0.803883	-1.855026	0.314152	0.308252
SMA2	NA	NA	NA	0.061195	NA	0.139543	-0.025814	0.162219	-0.508853	0.31309	-0.312148	-0.390915	0.688196	NA	0.100385	-0.114548	-0.002298	NA	-1.431642	0.632611	NA	-0.091858	NA	-0.421662	NA	0.773245	1.56331	-0.117007	0.427314	0.23331	-0.042467	0.080175	-0.299645	-0.707419	-0.826676
SMI1	-3.216442	-0.817165	-0.746209	0.10819	NA	0.283463	-0.213875	-2.336162	0.311608	NA	0.241808	-0.72491	-3.126689	-3.410724	0.518505	0.508228	0.688503	-4.512729	0.231651	-1.459537	NA	0.510783	-0.827121	-0.397772	NA	-1.016354	NA	-0.191592	-0.179983	0.025341	-3.236076	0.398029	1.336152	0.142607	0.496943
SMK1	NA	-1.36608	-2.788313	1.191466	-2.365377	0.07408	1.020139	-1.250681	-0.198853	NA	0.089109	-0.718476	0.133474	-2.024313	0.060884	0.315369	0.26091	NA	0.295097	-1.193282	NA	-0.096859	NA	0.535915	NA	0.156044	-1.818021	0.49699	-0.241931	0.245373	-0.792947	0.242583	0.738015	0.311146	0.747897
SMT3	NA	-7.211785	-2.839747	0.516225	-0.836749	NA	0.018454	NA	0.356668	-1.584338	0.34743	0.606449	NA	-0.017697	-0.26931	0.040908	0.605174	2.230478	1.095742	2.033151	-3.546893	-0.116593	1.009605	-2.594269	-0.444539	-0.819055	-3.916015	-1.292718	-1.337514	0.148958	NA	0.09181	0.159619	-0.176838	-0.357866
SMY1	NA	NA	0.204138	-0.099668	1.152464	-0.239771	0.625914	0.009937	0.43778	-0.31181	-0.360776	-0.364511	0.246123	NA	0.499431	-0.054362	-0.146745	0.090944	-0.327976	-0.6242	-0.016359	0.089434	-1.704303	0.623128	NA	0.235885	-0.074158	-0.417202	NA	-0.012221	0.341513	-0.522321	-0.800642	0.060962	0.633135
SNC2	NA	0.179248	-0.740593	-0.528793	0.443485	-0.118605	-0.080337	-0.611578	-0.000431	NA	-0.123824	0.129923	-0.548232	NA	0.493727	0.232139	NA	-1.008994	0.411054	-0.032581	0.849135	-0.454394	NA	-0.628428	NA	-0.753573	-0.530297	-0.215122	-0.264724	0.425327	0.318276	0.311598	-0.362603	-0.802357	NA
SNF1	NA	NA	2.032521	0.674906	NA	NA	-0.684347	0.119969	-0.553476	-0.691612	0.520371	0.234785	1.030021	NA	-1.134612	-0.764891	-0.564749	-0.169571	0.381507	0.49744	2.031692	-1.387495	0.454834	0.176385	NA	-0.243105	0.282972	0.156201	0.550093	0.249012	-0.418735	0.342816	-0.561194	-0.445505	0.241853
SNF11	0.18386	-0.075884	0.152652	-0.227655	-0.116019	0.481734	0.574051	NA	-0.074225	0.744136	-0.255803	-0.101845	NA	NA	NA	-0.212822	0.051333	-0.593277	0.415716	-0.563919	-1.901844	0.097622	NA	0.442791	NA	0.078606	-0.254788	0.267033	1.074633	0.190248	-0.390983	0.304899	0.078375	NA	0.831404
SNF3	NA	NA	0.020877	0.494117	-1.043261	-0.115085	0.207746	0.036194	-0.354013	0.23463	-0.297883	0.797961	0.558378	-2.104219	0.111439	-0.148296	0.258549	0.104092	0.568285	0.272079	0.478762	0.552851	0.026662	0.401308	NA	NA	-0.057324	-0.180257	NA	-0.554833	NA	-0.132609	NA	-0.257257	0.116707
SNF4	-0.137414	1.243818	0.49739	-0.00361	0.826895	-0.980564	-0.509902	-0.991254	0.063411	0.462852	0.641166	0.505881	NA	NA	-0.371368	-0.724518	-0.098833	0.090426	0.201763	-0.220285	1.628646	-0.445328	1.051673	-0.484929	-2.985491	0.531125	0.83069	NA	0.400548	0.022635	-0.606786	-0.254154	-0.345183	0.169185	-0.335183
SNF5	NA	NA	NA	0.514175	-0.043831	0.186787	0.407978	NA	0.952337	NA	-0.758279	0.115494	-0.337578	0.483688	-0.028227	-0.015473	0.395497	NA	0.507829	0.54097	NA	0.376696	NA	-0.485502	NA	-1.43981	NA	NA	NA	0.747874	NA	-0.55603	NA	1.076409	-0.467041
SNF6	NA	-1.060257	NA	0.794415	NA	0.689486	1.046505	1.469724	1.32813	NA	-2.206563	-0.347048	-0.131724	NA	1.028119	0.071444	0.331437	-0.807456	0.444125	-1.710346	NA	0.781064	NA	0.989051	NA	NA	0.566689	1.490646	-0.313427	0.009066	NA	-0.282289	2.919596	1.284846	0.222389
SNG1	NA	-1.21867	-0.920944	0.103153	-0.123242	0.171956	0.527271	-0.582645	0.122731	NA	0.370433	0.212146	-0.89192	NA	0.346126	0.914374	0.715344	-0.802779	0.277712	-0.372762	-0.441816	-0.147557	NA	1.198647	NA	0.266467	-0.141478	0.043285	-0.498581	0.485945	-1.180726	-0.046223	-0.026238	0.331	0.107955
SNN1	-0.55511	NA	0.725356	-0.43956	-0.444466	0.244963	-0.286157	0.041249	0.291896	0.292958	0.611994	0.354391	-1.049746	NA	0.308762	0.035132	-0.193957	-0.378217	0.043519	-0.475662	-0.273859	0.13811	NA	0.64175	-4.11391	0.343144	-0.243514	-1.363044	-1.043817	0.347837	-0.010188	0.249745	NA	0.004531	0.030462
SNT2	-1.811067	0.438865	NA	-0.339047	-0.948728	0.016705	-0.149433	1.373744	0.178947	-1.59945	-1.283539	0.971696	0.138716	1.483745	-0.32166	0.07424	0.339562	NA	0.313533	0.61583	0.168061	0.153009	0.695259	0.184096	NA	-0.09313	-0.274311	NA	-0.042866	-0.044422	-0.649209	0.332834	0.123333	-0.821208	-1.176212
SNU66	NA	0.65213	-4.348693	0.399735	0.337014	0.382104	0.276545	0.714537	-0.476854	-15.583691	0.315069	0.422319	0.736085	1.577143	-0.361681	-0.304494	NA	0.622891	-0.419826	0.536208	0.685457	-0.409443	0.208525	-0.867474	-1.344368	-0.334166	0.915893	-1.288858	NA	0.301741	0.273979	-11.842969	NA	-0.403685	0.095404
SNX4	NA	NA	-1.496717	0.599332	0.106369	0.314739	0.688163	-1.249995	-0.358622	-0.254207	0.215039	0.03672	0.395822	0.54599	0.54611	-0.492387	0.213592	0.299888	0.32863	-1.460909	-2.042887	-0.251954	NA	0.593321	-4.038997	NA	0.521606	0.818996	-0.095842	0.23159	0.137757	-0.596389	0.814727	-0.175251	0.214992
SOK2	NA	-4.196005	NA	0.761727	-1.586794	0.244974	-0.345014	-0.079968	0.724224	NA	-0.458978	-1.040477	NA	NA	0.494255	0.593757	0.703266	-1.979289	0.47384	-1.476146	NA	-0.004	-0.429786	0.090343	NA	NA	-2.643026	1.092326	-0.428169	0.503709	0.806534	0.380275	1.628722	0.547112	0.470278
SPA2	NA	NA	-1.912359	0.58775	0.003559	0.506693	0.577533	-1.204233	0.247143	NA	-1.037989	0.011715	NA	-1.463642	0.74984	-0.112956	0.223485	-2.247017	0.190118	NA	-3.272149	0.449072	NA	0.016497	NA	-0.434214	NA	0.435934	-0.558456	0.255267	0.287529	-1.366974	-0.40129	0.034784	0.712325
SPC1	NA	0.404292	0.456055	0.372039	-0.345721	-0.090429	-0.686421	0.437067	-0.254515	0.751913	-0.387916	-0.020774	0.442942	NA	0.119041	-0.42218	0.484218	0.902797	0.41723	1.054275	0.584552	0.054691	NA	-0.720709	NA	NA	0.74761	-0.346274	-0.240194	-0.130639	-0.754562	0.514676	-1.122296	0.192775	0.393915
SPC2	NA	1.524883	-0.171974	-0.770594	-0.104199	-0.028803	0.065638	-0.812239	0.184165	-1.122857	-0.302736	0.315461	0.438474	0.23595	0.043068	-0.130651	0.430914	0.109454	0.850971	1.041807	NA	0.335696	0.64133	0.249018	-2.363606	0.74408	0.592056	-0.219266	-0.154183	0.375559	-0.74544	-0.808728	-0.885094	-0.461142	-0.257027
SPE3	NA	-0.091448	-0.845666	0.022754	0.206765	-0.105809	-0.055016	1.868188	0.059542	-0.690087	1.006323	0.094672	-1.076777	-0.06039	-0.287056	-0.585485	-0.054645	0.733593	0.059129	0.09688	-1.251143	-0.347368	-0.331886	-0.343628	NA	0.331772	1.005073	0.87169	0.701121	0.380853	1.529201	-0.790339	NA	0.51253	-0.091166
SPE4	NA	-1.464256	-0.535045	0.25629	0.43908	0.586141	-0.640801	-0.489445	-0.009743	0.57744	0.038993	-1.043251	-0.744604	NA	-0.038775	-0.169405	0.642279	-0.002581	-0.104322	-0.119599	-2.018331	-0.207771	0.702966	0.045645	NA	0.542436	-1.509352	0.297664	0.220792	-0.108527	0.009096	-0.40587	-0.002264	0.247373	0.135171
SPP1	NA	-2.11042	1.689091	0.466329	NA	0.346005	0.371381	-0.313378	0.446847	-1.430203	-1.778312	-0.159592	0.295309	-0.660673	1.039619	0.721915	0.275257	0.060901	0.377047	-0.831267	-0.841771	0.393713	NA	0.858573	NA	0.232127	0.533305	0.526323	0.862931	0.389127	-1.322394	-0.455242	0.351697	0.048823	0.658326
SPT2	NA	-11.676292	-2.360143	-1.698702	-1.876193	-0.365951	-0.81415	-1.330329	-0.282541	-0.192884	0.373225	-1.322896	0.384491	-1.815634	0.282199	-0.139558	0.33059	NA	NA	1.007956	NA	0.141696	1.927807	1.030653	NA	0.792562	0.808078	0.149389	-3.357743	-0.143596	NA	-0.172099	0.877967	0.012039	0.021012
SPT21	NA	-2.790878	0.822083	-0.213476	-4.051386	0.273517	-0.223778	-5.495918	-0.485418	-3.458393	-3.859864	-0.416177	NA	-1.941621	0.185476	0.785704	-0.533756	0.104584	-0.104465	0.133346	NA	0.391388	-1.502525	-1.238744	NA	-0.765984	-3.772841	-0.253551	NA	NA	NA	-0.728534	-2.187519	0.718216	-0.017035
SPT23	NA	0.692505	-0.454778	0.280998	-0.273536	0.290754	0.234825	0.110337	0.462659	0.959702	NA	-0.529906	0.693217	NA	-0.166788	-0.094012	0.892194	-0.135922	0.298419	0.484574	-0.644474	-0.060119	-0.94471	-0.200473	0.510609	0.185965	-0.089713	-0.306646	0.362202	0.029458	-0.020665	0.712552	-0.50912	-0.133684	0.152931
SPT8	NA	-3.115999	-5.877164	0.817884	0.39712	0.166878	0.41135	NA	0.262467	3.22509	NA	-0.952997	-0.64826	NA	-0.138691	-0.234258	NA	-0.172398	0.07795	NA	-2.03345	0.136562	NA	3.278486	2.165372	-0.615721	NA	1.023304	-0.489476	0.742557	NA	NA	NA	0.428124	NA
SQS1	NA	0.808538	NA	1.015225	NA	0.520251	0.049079	-2.141014	-0.250139	-1.619268	0.503405	0.337076	NA	NA	-0.272508	NA	0.598567	NA	0.698322	-0.092757	NA	0.157167	-0.909996	-1.209631	NA	-0.630063	0.268287	-1.601725	NA	0.542345	-0.993859	0.369688	NA	-0.308323	-0.153599
SRB2	NA	NA	NA	-0.11137	-0.629314	-1.159242	0.538188	2.08518	1.474642	4.156981	NA	-1.201649	-0.308403	NA	NA	1.688085	0.424076	-1.408072	0.710359	NA	-0.506231	1.144369	NA	NA	NA	0.349982	NA	1.28322	-0.448919	NA	NA	NA	NA	0.391935	0.771533
SRB4	NA	-0.837389	0.105692	-0.320794	0.741909	-0.265841	-0.194958	0.902256	-0.402373	0.866762	0.612194	0.044141	0.046199	0.533198	-0.145228	-0.2539	0.504214	0.221164	0.041126	-0.07848	-1.416301	-0.350231	NA	-0.440838	NA	0.098018	-1.181401	-0.787378	0.314746	-0.147982	NA	0.235158	-1.181588	-0.657318	-0.07481
SRB7	NA	-3.638899	NA	0.768524	-3.564947	0.352806	-0.181141	1.403415	0.457981	NA	0.442355	-3.739237	NA	-4.722842	-0.028055	-0.105259	0.607898	-3.591491	1.10976	-1.231153	-4.868863	NA	-4.140501	-3.431501	NA	-0.321637	-8.620803	1.165715	-1.366387	0.753498	0.894497	NA	1.194804	0.34715	0.039242
SRC1	NA	-3.981026	-1.444126	-0.211801	-0.991984	0.451808	0.36077	-2.076321	0.808397	NA	-0.866416	-1.546944	-0.874974	-8.640114	0.591045	0.26884	0.14721	-1.440279	0.468887	-0.184796	NA	-0.127492	NA	-1.023871	NA	-0.314826	-1.999175	0.120896	-4.97581	0.195753	-3.532609	-9.252129	0.393862	0.535487	0.953064
SRL2	NA	-0.341468	-1.019345	0.502341	-0.371684	0.340546	0.073527	-0.34666	-0.446707	-1.079237	-0.38114	-0.0459	-0.127308	NA	0.264439	-0.133312	0.252421	0.055302	0.673398	NA	0.180287	-0.166518	NA	0.214969	NA	-0.148724	NA	-0.203436	-0.529246	0.527782	-0.688614	0.511225	0.292005	0.293572	0.171875
SRN2	-11.056082	-4.215212	NA	0.489117	NA	-0.046065	-0.009682	NA	-0.616759	-1.361803	0.247071	-1.765532	-2.860553	1.037875	0.533875	-0.577013	0.017735	-0.734023	0.361589	NA	NA	0.316334	NA	-0.499563	-4.515929	-0.606324	-1.554297	-0.014746	0.259178	0.221564	-0.528815	0.345144	-0.425657	0.021023	1.030077
SRP40	-1.041894	-0.637858	0.716732	0.091065	-1.506542	-0.52259	-0.876679	0.174712	0.197563	-2.051414	NA	1.403291	-0.233436	NA	-0.660689	-0.192641	0.175055	0.659138	0.332536	0.104175	0.440189	-0.159015	0.932433	-0.011452	-4.833431	0.096909	0.47626	0.288105	0.242823	-0.424848	0.250305	-0.603502	0.310582	-0.75626	-0.476373
SSA2	0.764436	0.964962	-1.424184	0.161082	0.106165	-0.139454	0.271766	-0.458181	1.321653	-0.566235	-0.380323	0.399123	0.658127	0.423148	-0.502009	-0.427726	-0.548962	0.259106	0.550752	NA	0.112575	0.248081	NA	0.401695	NA	0.147644	NA	-0.178002	-0.121585	0.370319	-1.337632	0.116708	-0.401512	0.475914	0.673702
SSA3	NA	0.613757	-0.348299	-0.048632	-0.091676	0.081992	-0.014006	-0.764529	-0.119732	1.087561	0.267283	0.122453	-0.148819	1.782464	-0.060746	0.027948	0.434579	0.207882	0.907526	-0.260505	-0.812615	-0.16365	NA	-0.224652	NA	-0.042746	1.191662	-0.399391	-0.226927	-0.012886	1.715739	0.075072	NA	-0.157462	-0.144272
SSD1	NA	-4.581428	NA	-0.130107	0.739847	-1.320583	0.190933	NA	-0.451243	-2.419819	-1.020836	-0.044229	NA	NA	-1.025941	-2.773955	-0.390595	NA	0.049383	-1.803	-3.446697	NA	-3.998963	NA	NA	-0.413117	NA	-0.231309	NA	1.14184	1.54863	NA	-0.179205	1.041007	0.160368
SSE1	NA	-2.141004	-6.423445	-0.35311	NA	0.076588	-0.187967	-4.893118	1.100039	NA	NA	0.212202	-0.155312	-2.991745	-0.217384	-0.336763	-1.019094	0.091741	0.312863	0.777278	NA	-0.601086	NA	1.263101	NA	0.863959	-0.749269	0.971202	0.511156	0.447508	NA	-0.5634	0.757331	0.504215	0.758018
SSF2	0.143931	0.228747	0.081652	0.18552	0.674548	-0.435543	-0.215919	0.379624	0.223361	-0.594595	0.082224	0.021908	0.085537	-1.048824	-0.093581	0.018507	-0.260248	-0.013404	0.388745	-0.508608	1.159309	NA	0.581005	0.508691	-3.52761	0.461312	0.180406	-0.170813	0.055701	0.391564	-0.101061	NA	-1.035714	0.02775	0.181084
SSH1	NA	0.671583	NA	-0.754511	-1.293049	-0.670168	0.01352	1.459932	-0.162589	0.222696	-1.446	0.36849	NA	NA	0.181284	-0.374134	-0.342139	0.607837	0.039828	-0.203677	0.679698	0.587682	NA	0.00627	-0.576791	-0.351992	-0.285177	0.0645	-0.512477	-0.279819	-1.214146	0.111616	-0.809274	-0.591558	-0.25303
SSK1	0.93413	NA	0.908263	-0.034445	-0.370369	0.27452	-0.016197	0.080155	-0.103617	0.45464	0.50869	-0.63365	-0.993698	-3.286337	0.138265	-0.04331	0.277702	-0.76139	0.454237	NA	-0.641061	0.02206	-0.679093	0.294431	-1.856917	-0.269337	NA	0.541069	0.254477	-0.064387	-0.351498	-0.45644	0.83385	-0.064462	0.605849
SSK2	NA	0.239015	-0.218384	0.850192	0.492998	0.545985	0.205762	-1.353121	0.181188	-0.275336	0.614636	-0.35308	-0.398548	NA	0.693985	0.157326	0.782212	-1.500801	-0.291348	-0.494508	-1.89492	-0.032406	-0.370189	0.143447	NA	0.849802	-0.734999	0.610937	-0.059919	-0.160223	-0.65585	-1.292028	0.984558	0.119797	-0.579431
SSM4	NA	-0.380046	-1.675788	0.075384	0.36632	-0.535061	0.097393	0.48101	-0.349584	1.157387	-0.352589	0.433449	1.505815	NA	-0.523654	-0.395547	0.566277	-0.318835	0.434975	-0.642015	2.073312	0.203303	0.635773	0.450671	NA	0.067743	0.574934	-0.3352	-0.316567	-0.145839	-0.118059	-0.215403	-0.144877	-0.759714	0.31198
SST2	NA	-0.567712	-0.079863	0.42491	-2.529383	0.452204	-0.439241	-2.655097	0.461175	1.18408	0.203622	0.235556	NA	-5.016059	0.128235	0.326145	1.267434	-2.985553	1.436791	-1.437583	-1.747163	0.923606	-0.493935	-1.027413	NA	-0.088503	-1.716503	1.032439	-1.212862	-0.19238	-2.798638	-0.063416	1.085084	0.156847	1.269819
STB1	NA	NA	-1.082554	-0.571876	-0.115998	0.509246	0.39894	-0.026814	0.652494	NA	-2.100676	-0.775566	-0.279213	1.491218	0.252409	-0.108247	-0.024632	0.008533	-0.715709	0.478238	0.67464	-0.204155	-1.891998	NA	NA	0.333355	0.659152	-0.641956	0.888136	0.220107	0.814737	0.155179	NA	-0.133521	-0.419645
STB5	2.736308	0.792076	1.892745	0.826491	-1.123552	-0.035704	0.017115	-1.324815	0.546425	-1.02461	-0.334707	0.759399	-1.981603	1.633552	0.134847	0.13066	0.473967	-0.376542	0.650502	-0.947966	-0.801871	0.302484	-1.177379	2.315882	NA	-0.606228	0.568852	0.111399	-0.643557	0.693035	-0.588557	0.438732	1.064779	-0.488487	0.142774
STD1	NA	1.062011	-0.64235	-0.13544	0.051241	-0.277473	NA	-1.106775	NA	NA	-0.370541	0.655659	0.167391	-0.32363	0.769875	0.031011	-0.057751	0.00192	0.320818	-0.099016	NA	0.54604	-0.381843	-0.319749	NA	0.13723	0.004591	-0.422454	0.487044	0.094851	-0.598106	-0.145571	-0.392012	0.071242	0.681664
STE24	NA	0.654714	-4.300719	0.591127	-0.212786	0.169126	0.205068	-0.422634	-0.529287	0.102594	-0.652076	-0.405524	-0.748129	1.157733	0.223438	-0.161055	0.299853	-0.679806	0.670471	-0.35942	NA	0.994786	NA	-0.828687	NA	-0.294034	-0.340692	0.113214	-0.499395	-0.003265	-0.32515	0.30529	-0.150545	0.33176	0.093071
STE50	NA	-1.15176	NA	NA	-2.133967	-0.661767	-0.192209	NA	0.605978	-1.082735	-0.593313	NA	-0.153293	NA	0.538249	-0.909526	0.767763	NA	0.968137	0.236505	-0.246809	-0.282725	-0.67657	0.303355	NA	-0.774849	-0.776228	0.460784	0.38635	-0.050066	-1.805937	-0.673492	-0.393373	-0.633477	-2.164125



UBA4	NA	0.008113	-13.013879	-0.566627	-0.1903	-0.693199	-0.213287	0.018921	0.014173	NA	-3.566467	0.159817	NA	NA	0.336745	0.07019	0.015129	1.203091	0.848326	0.564319	0.484285	0.598016	0.741446	NA	NA	-0.165172	-0.004895	0.886758	-0.425396	-0.227043	NA	0.407442	-0.272743	0.358605	-0.166962
UBC1	-0.637865	-1.080853	-0.83525	0.109653	-0.073227	0.03805	0.39271	0.000205	-0.138907	0.154922	0.781	-0.166001	-0.380862	1.421273	0.153906	-0.290502	-0.231441	0.280223	0.150149	0.301123	-1.012244	NA	NA	0.41224	NA	-0.201778	-0.349403	-0.104333	1.004177	0.119905	-0.006118	0.506142	0.154719	NA	-0.078332
UBC11	-1.377912	0.284627	0.287619	-0.337074	-0.800391	0.289194	0.078851	-0.048465	-0.187011	-0.079869	-1.025917	0.712816	1.446242	0.147454	-0.29393	0.196325	NA	1.447601	-0.051678	0.269892	NA	0.327949	NA	-0.282067	NA	-0.29846	-0.025237	-1.476242	NA	-0.012259	NA	1.29866	-1.72973	0.022992	0.433954
UBC12	0.717125	-0.128684	-0.132324	-0.060064	-0.052699	-0.244843	-0.073116	0.209742	0.098926	1.265794	-0.143697	0.44458	-0.346752	NA	-0.19405	-0.193887	0.309871	0.588774	-0.296867	0.818524	1.072348	-0.597999	NA	0.296097	-2.383382	0.610557	-0.322125	-0.742744	0.192355	-0.150342	0.5475	0.180893	-0.917289	-0.13957	-0.28558
UBC5	1.403132	1.382511	0.087361	0.062797	0.07745	0.088762	-0.247816	NA	-0.913936	0.486838	0.176627	-0.269337	0.910057	NA	NA	-0.107093	0.01603	NA	-0.710972	0.565201	1.187348	-0.319413	NA	0.715098	NA	0.793924	NA	-0.36924	0.812163	-0.510347	0.452795	0.030231	-0.89356	NA	-0.401519
UBC7	0.540581	NA	0.449544	-0.39374	-0.685101	-0.323859	-0.143258	-0.451807	-0.776516	NA	0.004182	0.006004	1.479579	1.903795	-0.07375	0.071083	-1.19257	0.493361	0.259901	0.791539	NA	-1.026209	-0.306431	0.708786	NA	0.120995	1.002551	-0.065187	-0.097591	-0.154605	0.909438	0.287199	-0.38516	-0.182803	-0.650134
UBC8	NA	-0.703664	NA	-0.910122	-0.233759	-0.054513	0.301614	-1.912158	-0.103065	NA	NA	-0.795351	0.145992	1.759361	NA	0.462878	0.670153	-0.867643	0.261352	-0.840503	NA	0.462251	-0.45714	-0.320244	1.024121	-0.190144	-3.248522	0.327548	0.298463	0.282831	-0.799943	-0.203892	-0.046375	0.007281	-0.127462
UBI4	NA	-0.673562	-0.823079	0.074706	NA	-0.363606	-0.265264	-3.569198	-0.217322	NA	-1.439344	-0.892674	-0.404792	0.444401	0.160924	-0.114984	-0.141717	-0.85587	0.347141	NA	NA	0.214641	-2.53309	-0.802205	NA	0.918843	NA	0.410589	NA	-1.098595	-0.989479	-0.514856	NA	-0.053541	0.947582
UBP1	NA	-0.371217	NA	0.572461	-0.206513	0.177542	-0.15164	NA	-0.274542	NA	-0.376393	0.24667	0.059653	NA	0.178574	0.510451	-0.100913	0.130792	0.484233	-0.188234	-1.140821	-0.719826	-0.480432	-1.465226	NA	0.297381	0.628739	NA	0.401936	1.134112	-0.773307	0.252676	0.110471	-0.029533	-0.035872
UBP12	NA	NA	0.798809	-0.095543	1.582101	0.363146	0.839441	-0.900823	-0.078773	NA	-0.856214	-0.190983	0.136295	-2.647455	-0.442935	0.069255	0.016953	0.852048	-0.21376	-0.644989	1.11611	0.42886	-1.075356	0.383425	-2.865746	0.446235	0.130635	0.348121	0.774954	0.104352	-1.122839	-0.230357	0.150433	-0.382207	0.318891
UBP13	NA	0.466563	NA	-0.80383	0.788999	-0.155729	0.054583	-1.275617	0.140724	-0.577942	-0.925305	0.426392	1.374519	0.640583	-0.966137	-0.352202	0.254235	0.186286	-0.089338	0.325799	-0.728135	-0.180183	-0.217567	-0.930008	NA	0.395252	-0.136737	0.036226	0.962856	-0.13424	-1.523365	0.377745	-0.821846	0.790181	0.850714
UBP14	-17.478285	-7.965024	-6.757593	0.635824	-1.25003	-0.029212	0.42695	-0.554163	-0.487848	NA	NA	-1.825719	-9.427308	-3.946736	-0.035103	-1.167048	0.416625	-0.751247	0.251413	-0.130685	-3.706246	-0.142518	-2.391443	-0.970617	NA	-0.579536	-5.935666	0.304476	1.42718	0.916342	0.511549	-1.647765	0.270073	0.070817	-0.195721
UBP15	NA	-0.380952	-2.861518	0.751805	-1.219822	-0.422493	0.724398	-1.985347	0.776891	-1.236707	0.099634	-0.567981	NA	NA	0.648851	0.238546	1.001934	-0.34571	0.491036	-0.398249	0.316822	0.654688	NA	-1.846063	NA	0.490781	-0.462927	-0.739201	NA	0.452175	-1.637311	-0.46167	-0.463892	0.949449	NA
UBP16	NA	0.385269	-0.567788	0.337516	-0.596687	-0.105832	-0.421237	-1.198073	0.008161	-0.136962	0.420208	-0.357215	-0.931581	NA	0.015848	0.597313	0.466536	-1.27836	1.104884	-0.652508	NA	0.499532	-1.035596	0.43785	NA	1.577167	NA	-0.683201	-0.191569	-0.007038	-0.582457	0.351783	-1.228563	0.43859	0.506966
UBP2	NA	-1.427101	1.974676	0.15166	-1.024728	0.359248	NA	-0.994138	NA	NA	0.322887	-0.298105	-0.050857	NA	0.103322	0.266403	0.238183	-0.556237	0.438812	-0.915716	0.645704	0.659531	-0.405881	0.007878	NA	0.328812	-1.536641	-0.130452	-0.014537	0.594783	-0.797871	-0.57679	0.192019	-0.441837	-0.140784
UBP3	3.979527	0.693188	NA	0.116288	-0.934794	-0.33047	-0.092939	1.724669	0.389137	NA	-1.511881	-2.87009	NA	-5.39556	-0.611918	-1.173515	0.461374	0.935959	NA	1.665921	1.14754	-0.121758	0.177909	NA	NA	0.357745	0.338781	-0.852163	-5.104811	0.732772	NA	-12.18223	-0.107475	-1.856218	0.827273
UBP5	NA	-0.850811	-0.447057	0.403157	-1.822681	0.463195	0.034472	-0.482606	0.723384	NA	-0.38164	-0.056899	0.141836	-2.922115	0.480926	0.266413	-0.185935	NA	NA	-1.106288	NA	-0.309981	NA	0.196554	-3.582672	0.126587	-0.724687	-0.381683	-0.4317	0.654329	NA	0.612467	1.222271	0.728764	0.631834
UBP7	NA	2.165724	-0.639657	0.051362	1.112693	-0.389347	-0.539549	0.241823	-0.641719	1.034911	-0.414346	0.598551	1.213397	1.401206	-0.140121	-0.37586	0.0088	0.630699	-0.374388	0.452556	1.367019	-0.009094	NA	0.488032	NA	0.695108	0.208056	-0.215309	0.37953	-0.361979	NA	0.858411	-1.126906	-0.395364	-0.414658
UBP8	NA	-0.438844	1.805502	0.508578	-2.394794	0.047244	-0.177265	0.762261	0.101541	0.867021	0.965871	0.120324	NA	-1.379422	0.346753	-0.217222	0.15918	-0.450926	0.273553	-0.986999	0.006326	-0.412536	0.764761	0.696058	NA	-0.611856	-0.538465	0.034732	NA	NA	0.550979	-0.070486	0.815094	-0.697683	NA
UBP9	NA	0.513905	-0.299903	0.080291	-0.747488	-0.207668	0.250871	-1.318779	0.110243	1.586474	-0.017397	-0.542696	0.113144	0.774741	0.112549	0.047769	0.276514	0.490893	NA	-0.379029	-0.041868	-0.189365	0.199772	0.226905	NA	-0.47563	NA	-0.285663	-0.112135	0.08436	NA	0.384207	0.359689	-0.25049	1.108737
UBR1	NA	-0.425473	-0.430006	-0.818189	-2.189685	-0.595268	0.167573	0.682875	0.56886	1.377741	0.359124	-0.944142	0.139679	0.362064	-0.202279	-0.558001	0.245459	1.137347	0.202935	-0.055818	0.747304	-0.195807	-1.930456	-0.184393	0.074474	-1.06819	0.53306	0.938741	0.994616	0.107582	0.109946	0.77419	-0.337745	-0.015065	-0.460774
UBR2	-2.124654	0.318792	-2.182906	-0.010852	-0.721172	0.280763	0.682183	2.399767	0.356585	-3.114007	NA	0.609198	0.259467	-1.139296	-0.023767	-0.267326	-0.353495	-2.509725	1.002804	NA	NA	0.419292	-1.10958	1.161241	NA	-0.89797	NA	0.748358	-0.006342	0.455737	1.321587	-1.353585	0.808633	-0.15053	0.007017
UBX2	-0.399422	0.77969	NA	-0.349824	-1.162841	-0.255729	0.002666	-1.240537	-0.584469	-0.758585	-0.04656	-0.196548	1.378796	0.646563	-0.135133	0.232121	-0.058354	0.381599	-0.117352	-0.266714	NA	-0.281742	0.324268	0.79094	-2.244868	0.238401	0.026132	0.140209	0.18644	0.27566	0.557037	0.582933	-0.511352	-0.117252	0.069657
UBX3	NA	-1.418362	NA	0.056286	0.34061	-0.175356	-0.021393	NA	0.103431	1.112415	0.167352	0.052575	0.321901	1.37546	0.44339	0.249034	0.390937	0.084231	-0.303673	0.586453	0.518058	-0.690967	-0.13699	-0.57499	NA	0.365304	1.140689	-0.057587	-0.510271	-0.049276	0.559982	-0.329898	0.214043	-0.383827	-0.39364
UBX4	NA	NA	-16.090911	-0.00917	-0.452051	-0.058787	0.050012	1.004897	0.19552	0.209207	0.384467	0.104709	-0.469916	-0.8101	0.028051	-0.538223	0.039905	-0.203024	-0.355616	0.004602	NA	0.232131	NA	0.819202	NA	0.082537	-0.981254	-0.368171	-1.851526	0.823857	0.257484	0.269525	-0.451964	0.324369	-0.399046
UBX6	-0.428224	NA	0.010484	-0.052479	0.34092	0.383081	-0.273072	0.504682	-0.189738	0.663974	0.290461	-0.248298	0.283135	1.580089	-0.179018	0.491244	0.209556	NA	-0.095478	-0.16837	1.399654	0.26854	0.447349	0.609631	NA	NA	1.076938	0.106996	0.128654	-0.032247	-0.014921	0.113739	-0.425895	-0.070617	-0.005424
UBX7	NA	0.741513	1.181343	-0.697807	0.019022	0.451918	-0.118828	0.103509	-1.147402	1.028267	-1.579056	-0.599556	1.575808	NA	0.053975	-0.526886	-0.268515	0.974157	-0.656776	0.139911	NA	0.25344	-1.397413	-0.742436	NA	-0.652172	0.176877	-0.75864	0.278713	0.352368	0.934314	0.060307	-1.011891	-0.286154	-0.036311
UFD2	NA	NA	-4.078212	0.426223	NA	-0.345413	-0.161198	-0.896145	NA	NA	NA	-0.349543	NA	NA	NA	0.592165	0.490455	-2.837719	0.143658	0.067419	NA	-1.068052	NA	NA	1.600235	0.166061	NA	0.684582	NA	1.230377	NA	NA	0.599001	-0.052924	NA
UGA1	4.296155	0.170816	NA	0.516682	-1.078774	-0.627593	0.309837	-1.308561	0.249294	1.393841	NA	-0.312659	-1.717165	NA	-0.388241	0.369595	-0.35955	NA	0.943876	-0.3425	-1.875104	-0.134183	NA	1.412893	NA	-1.085041	0.084066	-0.461973	NA	-0.185788	NA	0.759644	0.431012	0.181677	NA
UGA3	NA	-0.735023	NA	0.370924	-0.383917	-0.061066	0.419566	-0.538263	0.193123	1.041725	-0.107373	-0.67602	-0.503106	-2.009708	0.186752	0.349759	0.128325	0.038067	0.498035	0.354136	-0.167092	0.116611	0.546987	-0.340922	NA	-0.02753	0.152665	0.227485	0.000997	0.701888	-0.453229	0.154824	0.261024	-0.134876	0.627185
ULS1	NA	-1.045287	1.726162	-0.402849	0.05288	0.2557	0.390605	-7.12024	-0.257183	-2.663212	0.9313	-0.209723	-2.52749	0.776416	-0.220237	-0.142799	-0.23837	-0.448719	0.377284	0.194299	-6.083029	-0.545758	NA	1.408688	1.176879	-0.325197	-0.687651	-0.999674	2.169702	0.097778	NA	0.522348	-1.114969	0.504708	-0.023129
UME1	NA	-0.725868	-2.507006	-0.020044	NA	0.110962	-0.493178	0.481701	-0.634681	-3.169723	0.962696	0.569651	0.087933	-1.073257	-0.237755	-0.393375	0.530552	-0.052934	0.419285	-0.00302	-0.807347	0.64935	NA	0.341467	NA	-1.357098	-2.132831	0.184368	0.25645	0.25055	0.799566	-1.823074	0.263394	0.609591	-0.083516
UME6	-5.586159	-0.947457	NA	-0.046974	-0.641199	-0.547693	NA	-9.016498	1.055843	NA	0.279972	0.602048	-0.821261	NA	0.083981	0.008486	0.664446	-1.991344	0.655807	-0.434578	-1.890854	NA	-2.612847	2.106864	NA	-2.088209	-0.089073	0.683531	-0.83552	0.008342	NA	NA	1.648325	0.467469	-1.001927
UPF3	0.07652	1.962597	-1.686132	0.463878	0.793581	-0.214406	-0.52483	0.003252	0.049755	-1.674153	-1.05572	-0.215214	1.454086	-1.19118	0.187232	-0.487679	0.305436	2.114235	0.023029	2.187975	1.018652	0.542799	NA	0.96989	NA	0.628993	0.986964	-0.291083	-6.501566	-0.368633	-0.230515	-0.066161	0.064629	0.585916	-1.022951
URE2	NA	-2.68479	-7.209771	0.178041	-0.126076	-0.397998	-0.261167	-0.486292	0.217958	-1.741677	0.911724	0.822107	NA	NA	-0.005009	NA	0.345774	-2.52659	1.138559	-1.507841	-0.289946	0.718495	1.097025	NA	NA	0.007186	0.150702	0.167597	0.404681	0.104961	0.287369	-0.230229	NA	-0.230581	-0.370598
URM1	NA	0.291369	-14.241708	-0.350067	-0.473376	-0.522184	-0.469998	1.809401	0.093349	-1.591064	-2.376641	1.087514	2.237291	-8.280185	-0.531932	-0.454851	0.221115	1.209517	0.189187	0.948385	1.178394	0.541146	NA	-2.434504	NA	0.674183	0.145945	0.665462	-0.448153	-0.267321	0.237877	-0.413208	1.259638	0.238043	-0.745002
URN1	NA	-0.120638	1.299365	-0.173189	0.849069	-0.480221	-0.400959	-0.084867	-0.312494	-2.525032	0.440821	0.214237	1.075108	-0.796285	-0.012766	-0.505577	1.016811	0.383133	-0.195232	1.016169	0.577142	-0.090282	NA	0.53648	NA	0.903588	0.83795	-1.016626	0.919697	0.53983	0.220435	-0.049859	-1.694174	-1.035736	-0.633105
USA1	NA	-0.6529	0.00362	0.238148	-0.555499	0.099335	0.71101	-0.848486	0.507624	0.838185	-0.157616	-0.144354	-0.069808	-1.09508	0.161829	0.648626	-0.145554	0.214199	0.937766	-0.054282	NA	0.195048	0.153293	0.10921	NA	-0.188138	-1.19707	-0.017611	0.184537	0.071445	-0.15343	-0.315979	-0.455576	-0.028749	0.4779
UTH1	NA	NA	NA	1.497446	NA	0.426816	NA	1.601563	NA	3.705466	NA	-0.90128	NA	NA	NA	0.624906	0.365557	0.167845	NA	1.203644	NA	-0.000208	NA	4.222754	NA	1.493274	NA	NA	0.075226	3.564278	NA	3.658957	NA	NA	0.258184
VAC14	NA	NA	1.890206	0.03293	1.094582	-0.496217	-0.032257	-0.549702	-0.95208	1.399727	1.000142	0.045255	0.567511	-0.4881	-0.375746	-0.014484	0.065713	1.179995	-0.825522	0.722257	1.970773	0.163938	NA	-1.456653	NA	0.411043	NA	-0.872158	0.971885	0.256893	NA	0.431687	NA	-0.610178	-0.398597
VAC7	-0.175675	-1.121238	0.574972	0.130982	-0.629429	0.287751	-0.161898	-0.693432	-0.049463	0.88056	-0.145297	-0.52486	0.11131	NA	-0.130041	-0.350755	-0.252246	-0.241203	0.455373	0.603617	0.182833	0.430199	NA	-0.365763	NA	0.027021	0.597057	-0.990512	NA	-0.394313	-0.083365	0.282347	-0.232381	-0.144338	NA
VAC8	NA	1.246412	-1.88238	-0.297414	0.212666	0.055735	-0.133061	-1.770511	-0.514635	NA	-5.597821	-0.331571	-0.86104	-1.833556	-0.73058	-0.366024	1.168583	-0.142208	0.461993	-0.238277	-0.775718	0.636931	0.151638	-1.225021	NA	0.055493	-1.132822	0.767538	-0.646723	0.579608	NA	-0.097348	1.327036	0.005239	-0.230749
VAM10	NA	-1.932858	-12.273863	0.365817	-0.266602	-0.117217	NA	-1.707825	NA	NA	0.384663	-0.687686	-0.862189	0.115034	-0.020724	0.442995	0.749497	-0.088574	0.490102	-0.286588	NA	0.394754	NA	0.92126	NA	-0.1637	-0.128862	0.450796	-2.065061	0.399881	-1.131184	0.429197	-0.188316	-1.865999	0.386313
VAM3	NA	-1.880958	-1.292957	-0.269343	-0.647131	-0.394874	NA	-1.883181	NA	NA	NA	-0.641605	-0.951954	1.390069	0.25064	-0.265504	-0.529947	0.086262	0.210875	1.172441	-0.458227	0.016356	NA	0.919492	1.290432	0.653782	-1.271208	0.117357	0.712802	0.156666	NA	1.239238	0.892869	-0.933674	-0.8143
VAM7	NA	-2.294774	-0.546512	-0.343559	0.021956	0.037195	-0.129978	-2.517036	-0.112949	-0.492888	-0.019011	-0.891278	0.15767	NA	0.354467	0.272513	0.356054	0.902565	-0.53733	1.315953	NA	-0.272317	NA	-0.072526	NA	-0.969069	0.449983	NA	0.099928	0.291817	-3.199069	0.448531	0.327703	-0.167558	-0.347821
VHR2	NA	-1.732789	-1.788979	-0.239656	-0.13427	0.575166	-0.041347	-0.185364	0.846421	-2.340121	0.056324	0.406849	0.066873	NA	0.545209	0.157538	0.306149	0.12347	0.922621	-0.403289	NA	-0.245411	NA	-0.2592	NA	0.481679	-0.574169	-0.639785	0.083521	0.396231	NA	-0.472098	-0.989165	0.20574	-0.284962
VID22	NA	-0.477021	-2.488366	-0.706076	NA	0.265557	-0.352888	-2.567371	0.547176	-3.147509	0.911225	NA	-1.412091	-2.036036	0.227856	0.298438	-0.080206	NA	0.616044	-0.871534	-2.733691	0.536862	-0.514879	0.565134	0.762438	-0.796824	NA	0.896707	-2.984623	0.297624	-1.722518	-0.025164	1.165173	0.196783	-0.167029
VIK1	NA	NA	NA	0.199924	NA	0.402755	0.327954	-0.667514	0.46587	-2.202711	0.232501	0.761584	1.11226	-0.932194	-0.059473	-0.115961	-0.017653	0.602879	-0.178692	0.267231	NA	0.949073	NA	-0.308421	NA	-0.177534	0.015651	-0.13941	0.035261	0.146612	-0.046451	-0.910593	0.128613	-0.130973	-0.561275
VIP1	NA	-2.172702	0.563697	-0.146164	-0.479764	0.408091	0.129617	2.192731	0.083582	NA	0.477117	-5.539845	-2.389993	-0.220781	-0.403383	-0.484042	0.246369	-0.09324	-0.29809	-1.095507	-0.60385	0.510585	NA	0.70556	-3.471693	0.376188	NA	-0.32312	-1.566524	0.604595	1.405435	-0.15156	NA	0.097846	0.158874
VMS1	-8.66926	-0.310847	-4.236812	0.487906	-0.799561	0.642981	0.325812	NA	0.082822	-1.685665	-0.60255	-0.518923	0.921863	0.826394	NA	1.354758	0.627538	-0.877056	0.821383	-0.283801	-0.15114	0.596977	-0.557211	-0.663618	NA	-0.461618	-0.604817	-0.073265	-3.500112	0.513961	0.309975	0.161322	-0.809006	NA	-0.092559
VPS1	-1.483733	0.879028	NA	0.020294	-0.057031	0.171481	-0.794445	1.855123	0.05746	-3.133945	-0.611206	-0.245634	2.292211	NA	0.174346	0.244604	0.206956	-0.126764	0.71364	0.954331	3.199407	-0.152882	NA	-0.98836	-9.492841	0.845069	0.814275	-0.935594	-0.195255	-0.225962	NA	-3.737937	NA	-0.137569	-0.623782
VPS13	NA	0.943384	-0.992207	-0.258602	-0.144303	-0.063711	-0.229636	0.258581	-0.138132	NA	0.393579	0.178441	1.37829	0.976562	-0.417825	-0.634919	-0.300452	0.394222	-0.380116	NA	1.225174	0.246242	NA	0.492199	NA	-0.166453	NA	-0.621468	0.3819	-0.14547	-0.146773	0.391443	-0.945305	-0.388887	0.12686
VPS17	NA	NA	NA	0.280677	NA	0.029577	NA	NA	NA	NA	NA	-1.333951	-1.612031	NA	0.289036	-0.351245	-0.099703	NA	0.712748	0.161277	NA	0.344377	0.458784	0.961537	-0.040463	-0.76539	-3.270557	0.07298	-1.677728	0.270519	NA	0.162523	0.80794	-1.155055	-0.227278
VPS21	NA	-0.42272	NA	1.02566	-1.221676	-0.143543	NA	2.8744	NA	NA	0.274103	-0.922965	-1.103897	NA	-0.015565	0.370321	0.27223	-0.364457	0.393725	0.806044	1.576731	-0.141063	-0.398106	0.98127	NA	-0.344927	NA	-1.034573	0.076378	-0.003928	2.420048	-1.147323	-0.43196	-0.165466	1.074664
VPS24	-0.721942	NA	1.578497	0.310755	-0.273612	0.427668	NA	NA	0.49084	-5.183447	-0.631298	-1.297491	-2.526659	-2.471706	-0.08556	-0.153915	0.445499	0.112148	0.703939	-0.41669	-1.046312	1.014608	NA	0.618044	-2.550393	-0.959655	NA	0.241258	-3.247545	0.604031	NA	-0.953549	0.988797	0.746688	-0.011097
VPS27	NA	-3.554238	NA	0.797972	-0.454479	-0.978972	-0.756634	0.347046	0.269841	NA	0.579859	-1.670637	-1.034226	-0.26142	-0.489138	0.15546	0.679685	-0.381635	0.159877	-0.320293	NA	0.478598	NA	-0.179845	NA	NA	-3.687532	0.611355	-0.220461	0.196752	-2.114444	-0.106761	0.52279	0.423834	0.254045
VPS29	-5.416025	-3.121902	-5.389717	0.060899	-0.86745	0.144823	0.509091	-0.752303	0.312808	-0.304609	-0.437133	-1.600379	-0.248628	2.065115	0.453751	0.059431	0.546152	-0.342495	-0.260885	-0.855589	NA	0.163752	NA	-0.017159	-3.020815	-1.277074	-0.636125	0.525421	-0.411499	-0.306059	NA	1.262963	0.856906	-0.401859	0.711644
VPS30	NA	NA	-2.444895	-0.257349	NA	-0.290713	-0.201943	0.234555	0.392377	-0.392813	0.582465	-0.309129	1.665023	0.911276	-0.024192	-0.481042	0.162847	-0.712237	-0.119117	0.343159	1.603502	-0.345234	0.405631	-0.168801	NA	-0.363868	0.389059	-0.449726	0.250788	0.267739	1.22233	0.203277	NA	-0.310197	-0.023913
VPS35	-2.984733	NA	-3.555968	0.268784	0.857275	0.282552	-0.161917	-0.360498	-0.083367	0.704326	NA	-1.241624	-0.742159	NA	0.038951	0.441821	0.595694	-0.201597	0.457403	0.095923	1.691343	0.525914	-0.08666	-0.217758	-4.021377	-1.513773	0.03437	0.37884	-1.655466	-0.300902	0.108489	0.734845	0.254886	-0.468414	-0.53063
VPS38	NA	1.009086	1.019194	-0.001572	0.967837	0.260195	-0.913581	1.173632	-0.696948	NA	0.312661	-0.402222	0.401602	NA	-0.543695	-0.455537	0.05866	-0.253311	0.020841	0.885558	2.504632	-0.348573	0.644273	1.166677	NA	-0.739925	NA	-0.282212	0.590753	0.436981	NA	0.838728	-0.349016	-0.99509	0.239407
VPS41	NA	NA	-4.642455	-0.248593	-0.63505	-0.5852	-1.722161	NA	0.640572	3.705436	NA	-0.274426	1.141365	NA	NA	0.186551	-0.285814	0.37657	-0.226249	0.275016	NA	-0.901319	1.214987	NA	NA	0.320044	0.352844	-0.776892	0.061153	1.138746	NA	NA	-0.169402	NA	-0.814147
VPS5	NA	-0.158848	NA	0.440179	0.20627	0.636701	NA	0.728073	NA	NA	-1.448556	0.391737	0.224489	-1.33608	0.183823	0.090135	0.179826	-1.997999	0.190342	-0.169044	NA	0.648728	NA	-0.328197	NA	-1.099183	-1.761419	-0.938588	-0.71711	0.038481	-0.065927	-0.238719	1.02802	-0.759758	-0.394826
VPS51	NA	0.233228	-2.31665	-0.023185	NA	-0.730168	-0.006152	NA	-0.042963	NA	0.88654	0.123085	NA	NA	-1.031502	-0.606745	-0.094561	NA	-0.081231	1.290605	1.433642	-1.174883	1.94299	-0.423716	NA	-0.705735	NA	-0.180115	0.615622	0.08909	-0.822103	-1.37088	0.118482	-0.508639	0.726873
VPS53	NA	NA	NA	-0.450866	NA	-0.698589	-0.334835	NA	0.49505	-2.018436	0.03248	-1.661956	NA	-2.49912	-0.362975	0.001022	0.299592	0.395648	0.827274	1.368442	NA	0.14958	1.246009	-0.146679	1.519449	NA	-0.997211	0.650363	0.238371	0.319643	-0.00652	-0.338159	0.741286	-1.862148	0.468605
VPS70	0.054307	-0.570242	NA	0.051416	-1.810913	0.220676	-0.440269	-0.737455	0.569475	0.095104	-0.296693	-0.698535	-0.140527	-0.177977	0.085512	0.051446	0.723132	-0.177754	0.416837	-0.500526	-0.2875	-0.150339	0.176085	0.463207	NA	0.678548	-0.441255	0.412572	-0.294507	-0.574146	-0.024185	0.251782	0.726794	-0.049073	-0.312173
VPS71	NA	-2.675763	NA	-0.097522	-1.993511	-0.449884	0.345317	-4.650302	NA	3.677538	NA	-6.52169	NA	NA	-0.175347	0.725237	-0.515108	-1.414347	-1.185426	-1.459553	NA	-1.691754	-7.095611	NA	NA	-0.130566	-0.863011	0.398728	0.553941	0.753726	NA	1.458772	NA	NA	0.757359
VPS74	-1.193356	-0.120128	0.195971	-0.00428	0.612333	NA	-0.705704	0.299774	-0.532332	0.619842	-0.132074	0.815359	1.137828	-0.627736	-0.575804	-0.07461	-0.00091	-0.766162	0.600782	0.01759	1.669289	0.821357	NA	-0.212054	NA	-0.50518	0.691421	-0.063448	-0.168189	-0.118228	-0.361394	NA	NA	-0.014992	-0.941843
VPS75	NA	NA	0.469719	-0.517395	-1.304383	-0.002442	-0.250996	1.466784	1.209947	-0.810969	0.526574	0.759915	-0.104935	NA	0.911535	NA	0.23042	0.600216	0.415329	-0.45724	NA	0.405248	-0.427881	NA	-6.264883	0.7557	NA	0.476483	-0.284972	0.561197	1.613019	-0.77917	NA	0.320239	0.594767
VPS8	NA	-4.155737	NA	0.60128	-0.770682	0.023349	0.113497	-2.098174	0.75131	-3.559456	-0.347912	-2.917691	0.218872	NA	0.281876	0.197411	0.395851	-2.338492	0.715975	-1.422206	NA	0.732077	NA	1.197968	NA	-1.126267	NA	-0.264206	-1.645637	0.345172	0.531501	-0.51708	0.124751	-1.943811	0.121963
VPS9	-1.255863	-7.892342	NA	1.043614	-0.773734	0.335084	-0.00062	-3.84469	-0.09958	-1.883785	-0.012336	-1.790605	-1.308704	0.981038	0.768382	0.87734	0.263998	-1.309983	0.264705	-2.340107	NA	0.379023	-3.840891	1.075498	NA	-1.901355	-2.523906	0.771917	-2.0316	0.999395	-1.520479	0.744897	0.501202	-2.34186	0.890234
VRP1	NA	-2.088777	NA	1.184356	-1.321364	-0.050265	-1.012522	-2.219247	0.642712	1.963572	0.993497	-1.593944	0.116087	NA	-3.251186	-0.295206	1.244574	-0.955322	1.070027	-1.335944	1.707049	NA	-1.637496	-2.078085	NA	-1.433797	NA	-1.615173	-2.138836	0.304103	-0.033933	1.101599	-1.388023	-1.219868	NA
VTA1	-0.40242	1.569121	2.670719	-0.545094	0.723847	-0.58169	-0.642308	1.610868	0.126437	NA	NA	0.744599	0.277827	1.20856	-0.903106	-0.464735	-0.413669	0.507325	0.171682	0.736442	1.044234	0.084624	NA	0.511305	NA	0.561998	0.33619	-0.26643	-0.035366	-0.349621	1.009581	0.744762	-0.614272	-0.40778	-0.397141
VTC1	-0.536496	-0.295679	-1.411568	0.161035	0.93149	0.324733	0.243819	0.134953	0.228693	-0.722679	-0.191769	-0.217751	0.857642	NA	0.362092	0.042467	0.805101	-0.184743	0.520977	-0.165173	-1.010699	1.027677	NA	-0.297725	NA	0.25386	1.674667	NA	0.002734	-0.450551	NA	1.518801	NA	0.476643	0.098465
WHI2	NA	-1.36378	-1.20317	0.324573	-0.716104	0.007305	NA	-2.513619	NA	NA	0.273196	-0.676963	-0.806422	-2.774806	0.58342	0.416068	-0.073029	-1.210774	0.853544	NA	-0.006893	0.80269	1.2812	0.672844	NA	-0.379449	-0.376128	0.730616	-0.638398	-0.119178	NA	-0.090798	0.500622	-0.274427	0.248054
WHI4	NA	NA	1.357434	0.520694	NA	0.237193	0.050496	NA	0.415791	0.917573	-2.717156	-1.605031	NA	-1.889235	0.918925	-0.151517	-0.181325	0.810945	0.529369	0.761209	NA	-0.542407	NA	0.748896	2.376389	1.384745	0.983743	0.310766	-0.245475	0.16183	-0.695598	-1.078017	0.03684	-0.154967	0.395833
WHI5	NA	0.916836	0.529347	-1.167128	-0.713691	0.455714	NA	-0.934944	NA	NA	-1.26306	-1.253425	0.054419	-3.222333	0.781616	0.495511	-0.662785	-0.087097	0.333421	0.167265	0.463284	-0.905645	1.371694	0.046322	NA	1.140501	1.513532	0.430549	1.254483	0.887291	NA	-0.939693	-0.949962	0.803251	0.575816
WSS1	-0.475658	-0.931283	-1.277444	0.528743	-0.423848	0.024191	-0.061511	2.43589	0.862338	0.032495	0.22666	0.877773	-0.641329	-0.147863	0.030305	0.332179	-0.012119	0.366645	-0.192809	-0.496343	-1.276643	0.104264	-1.262059	-0.53038	-0.687522	0.370349	-0.571559	0.4946	NA	-3.220873	1.693207	0.310761	1.311706	0.326935	0.304707
XRS2	-1.015967	-1.04011	NA	0.705128	-2.499053	NA	-0.591011	NA	1.219066	0.079678	-3.323069	-3.75464	2.930399	NA	-0.053716	0.629586	-0.3698	0.116888	0.708085	-0.114317	NA	1.570293	-1.190878	0.390348	NA	-0.676583	-0.114657	1.648743	-1.383754	1.352377	NA	NA	NA	1.182731	0.916465
YAP1	NA	-0.833561	0.106399	0.389712	0.257723	-0.07592	-0.141866	-2.885488	0.482479	-1.421419	0.589444	0.864325	-5.788836	NA	-0.116704	0.316582	-0.256346	-2.718776	0.553834	-1.21884	NA	0.175587	-1.767191	0.329423	-3.755326	-0.259226	-0.535487	0.655482	0.241303	0.511492	-1.247632	-0.540133	1.036409	-0.535645	-0.004688
YAP3	NA	-0.365015	0.032317	0.406401	-0.304025	-0.137487	1.107593	-0.891406	-0.198804	NA	-0.48726	-0.657148	0.558205	-0.054561	-0.110097	0.517132	0.322393	NA	-0.232007	-0.054846	-0.80158	0.364387	NA	1.951387	NA	0.61869	-0.023852	0.060397	0.333647	0.188586	-0.570227	1.332193	-0.082402	0.650478	0.45226
YAP5	0.383798	-0.850245	-0.820662	0.293915	NA	0.117448	0.274144	-1.971699	0.387372	0.950418	-0.422207	-0.162292	-1.213589	0.413839	0.822424	0.379965	0.485661	0.023583	0.694946	-0.368388	-1.076919	0.214056	-0.103207	0.125806	NA	0.166331	-0.824966	0.49512	0.26647	0.069143	-0.295521	-0.294385	-0.044817	0.503721	0.614052
YAR1	NA	0.578702	1.871504	-0.862406	NA	-0.06939	-0.592338	2.001328	-1.160851	NA	-0.117477	-0.011395	1.356777	0.759042	-0.292157	-0.596514	-1.364058	1.232699	-0.21154	0.46199	1.738879	0.525109	1.208915	0.056769	NA	0.643348	1.163357	0.197488	NA	0.154427	0.632131	-0.422008	-0.123829	-0.441983	-0.928744
YBL036C	NA	0.204774	NA	0.244915	-0.433068	0.126573	0.412819	-0.0967	-0.040957	0.624087	0.041426	0.23008	-1.19912	NA	0.103363	-0.006681	-0.058893	-0.337088	0.197535	-0.416113	-0.557424	0.00621	0.002215	0.968292	-2.205825	0.379291	0.093801	0.123204	-0.425058	-0.197911	-0.011762	0.132107	-0.317012	0.066924	-0.458581
YBL081W	NA	NA	NA	-0.01516	-1.393177	0.558142	0.657282	NA	1.336095	-1.381589	-0.887405	-1.969844	-0.657111	-1.023648	0.660453	0.562153	-0.120619	-0.597956	0.704333	-0.350463	0.240685	0.019367	NA	0.40905	NA	0.343083	NA	0.9772	0.653769	0.087325	NA	0.429228	0.762268	-0.137351	0.799394
YBL086C	0.573508	-0.593397	0.820896	-0.197621	0.403665	-0.254977	-0.394521	-0.478479	-0.635064	2.106955	0.361071	0.125893	-0.392752	0.797966	0.298381	0.033286	0.459511	-2.004941	-0.220483	-0.2109	0.032393	0.402164	-0.583714	0.470976	NA	0.6885	0.845401	0.20884	-0.650344	0.177941	-0.144661	0.463089	0.152146	-0.033371	-0.411855
YBP2	NA	-0.229495	NA	0.169547	0.037269	-0.243452	-0.294332	NA	0.162497	-0.000298	-0.006252	-0.365733	1.081657	NA	-0.229319	-0.272728	0.368266	-0.855353	-0.013769	0.320982	1.800315	0.324953	-0.030369	0.420679	-2.398648	0.301316	1.484375	0.210085	0.433884	-0.4575	0.727953	0.585899	-0.662345	-0.802028	-0.277084
YBR141C	-0.113229	0.06271	0.019899	-0.015276	-0.282344	0.198643	-0.106349	0.863519	0.172347	0.390738	NA	-0.110751	-0.166525	NA	0.175869	0.18479	0.387071	-0.491238	0.290854	-0.543356	0.254676	-0.201154	NA	0.563611	NA	-0.41967	-0.20067	-0.49419	0.382641	0.147212	0.103185	0.792149	-0.106503	-0.353735	0.470518
YBR238C	4.640825	-2.699163	0.017986	0.220646	NA	NA	-0.628114	-0.784359	0.076788	2.677941	NA	-0.189382	NA	NA	-0.43306	-0.647746	0.143551	-0.253294	NA	0.393749	NA	0.06807	0.106235	-0.850997	NA	-0.28623	NA	0.152553	0.679558	-0.122401	NA	1.042988	NA	-0.173909	-0.354674
YCH1	0.327779	0.507357	0.955365	0.08956	-0.192167	-0.443037	-0.039768	0.826962	0.261974	-0.633352	-0.037492	-0.176956	0.936542	-0.068466	-0.064063	0.253776	-0.371845	0.524127	-0.115962	-0.482377	0.337388	0.140479	0.033804	0.051525	NA	-0.150163	0.727524	-0.058446	1.092447	0.129891	-0.200585	-0.0128	-1.139636	-0.112673	-0.279471
YCK1	NA	0.013889	0.95401	0.430228	0.36834	-0.124172	-0.164431	-0.196544	-0.57853	-0.362698	0.349189	0.265307	0.318056	-0.688821	-0.198173	-0.093102	-0.191639	-0.528522	0.548857	-0.074068	1.063812	0.032176	0.424717	0.238809	-1.090686	0.533906	0.364255	0.293264	-0.323338	0.253319	NA	0.749094	NA	-0.017643	-0.229747
YCK2	-1.321624	-1.177544	0.765975	0.45159	0.39301	-0.115104	-0.043882	-1.372797	-0.405031	0.05809	NA	-0.03092	0.685938	-0.047232	0.210379	NA	0.072342	0.098996	-0.056985	-0.248823	0.765124	-0.126206	0.314849	0.241138	NA	-0.099453	0.388665	-0.374584	-0.329946	-3.80E-05	-0.811526	0.510916	0.148855	0.013308	-0.214476
YCK3	-0.684203	0.717653	0.969799	0.193452	0.602884	0.06854	-0.42681	-1.92882	-0.70299	0.542669	-0.333147	0.350834	-0.023418	-3.779934	0.133797	-0.278587	-0.530045	0.510684	NA	0.074571	1.816371	-0.630154	0.088454	-1.308672	NA	0.233311	0.892705	NA	NA	-0.05109	NA	1.180876	NA	0.155618	-0.502548
YCL001W-A	NA	NA	0.509948	NA	NA	-0.64701	0.190853	0.888934	-0.42297	1.972654	NA	NA	-0.687194	1.405811	-0.592172	0.572864	-0.478999	NA	0.394399	0.197973	-0.395735	-0.283466	-0.234463	0.087683	NA	0.280908	-0.167729	-0.048195	0.623179	0.104627	0.928877	-0.101978	-0.584798	-0.089362	-1.183739
YCR050C	0.608521	0.994331	0.567862	NA	0.174305	0.094645	-0.175155	1.453701	-0.239855	0.528776	-0.443039	NA	0.463671	NA	0.175421	-0.078488	-0.456644	NA	-0.1862	-0.265212	0.822386	0.346877	0.846914	0.257567	NA	0.437344	0.794693	-0.0902	0.40107	-0.196453	1.045651	0.287827	-0.160126	-0.350672	-1.687566
YCR061W	0.379168	0.22423	0.059748	NA	-0.403377	-0.189804	-0.30354	-0.247794	-0.191573	0.129144	0.244294	0.261952	-0.19503	NA	0.389123	-0.393867	-0.227567	NA	-0.095163	-0.114112	NA	-0.506717	-0.536711	0.567259	NA	0.384675	0.293583	-0.956761	0.030122	-0.190242	0.295983	-0.258425	-1.787097	0.038547	0.557428
YDJ1	NA	-1.086964	NA	-6.181418	-9.667213	0.741305	0.367471	-4.424871	0.999517	-1.872583	-9.567169	-8.061172	-0.043463	0.185248	0.969528	0.790118	-5.778053	-1.809791	-4.767572	-1.00714	-2.749707	-0.118529	-9.958826	0.628831	-2.359764	-0.98344	-1.714744	0.655044	-0.783784	1.183347	-3.638792	0.235213	-1.903432	-0.165268	NA
YDL176W	NA	NA	NA	-1.032801	1.122883	0.188022	0.148534	0.265098	-1.217489	-0.124493	-0.132764	0.695693	0.767314	1.442494	-0.464179	-0.037905	-0.072365	0.716647	0.13507	0.716766	2.191842	-0.118128	NA	0.112517	NA	-0.014543	0.711617	-0.324919	-1.425361	0.002059	-0.596996	-0.624885	0.079008	-0.323054	-0.865934

YDR061W	NA	-0.391123	-0.676853	0.002837	0.139545	0.389297	0.082625	NA	0.230877	1.597783	-0.305468	-0.903287	-1.82235	-0.431318	NA	0.278753	0.031118	-0.161906	0.56647	-0.966554	NA	0.334502	-0.645435	0.303371	1.161663	1.044085	0.89585	0.196605	0.064485	0.147527	0.194142	-0.002522	-0.589618	NA	0.391501
YDR131C	NA	NA	0.286761	-1.009413	-2.016368	-0.028212	-0.682583	-0.604597	0.055081	3.388776	NA	0.293964	NA	NA	NA	-0.29611	0.400095	NA	0.0806	0.173471	0.481905	NA	NA	NA	NA	-0.655353	NA	-1.02955	NA	-0.122782	NA	1.330741	0.115731	NA	-0.128982
YDR161W	NA	-2.146109	-0.145538	0.465577	-1.20715	-0.165256	-0.287757	-1.4832	0.924109	NA	-0.121296	0.134927	NA	-1.453972	NA	-0.183055	0.138758	0.925117	0.907825	0.27962	NA	NA	NA	0.668986	NA	-0.053165	0.318085	0.378846	-1.882052	0.220539	NA	0.39582	0.962089	NA	-0.585929
YDR306C	NA	NA	1.133928	-0.967702	-0.104121	0.355449	-1.038715	-1.133433	-0.688161	0.262538	-0.254909	-0.211102	0.496546	-0.686768	0.006641	-0.677801	0.704664	0.570323	-0.531727	-0.011558	1.070477	NA	-0.371	-0.104377	NA	-0.099793	0.427239	0.240524	0.088989	0.207737	0.125318	NA	NA	0.247898	-0.728639
YEF1	NA	-0.915521	NA	-0.272063	0.766036	-0.297884	-0.09366	-0.130009	-0.830074	0.500264	-0.035398	0.277946	1.07509	NA	-0.390488	-0.06934	0.072827	-0.518825	0.382085	-0.098296	0.391117	-0.529753	0.094379	-0.961211	NA	0.469246	0.331805	-0.363939	-0.80268	-0.76132	NA	0.851977	1.018243	-0.086259	-1.190921
YEL043W	NA	-1.737682	-1.956506	-0.161098	-0.848522	-0.203795	-0.381626	-1.020745	0.120523	-1.173772	1.085617	-0.674569	0.704092	1.628972	0.231017	0.111263	0.767228	0.855221	0.978394	0.798647	NA	0.208294	0.018917	-0.64881	NA	-0.592812	-0.07726	0.271363	-0.891241	0.04264	0.695417	-1.506067	0.7245	-0.376279	-0.50618
YER156C	NA	NA	-0.40079	NA	NA	NA	-0.415501	NA	NA	NA	NA	0.836179	NA	NA	-0.620602	-0.708089	-0.076572	-0.378563	NA	0.220229	NA	-0.2038	NA	-1.83265	NA	0.597532	NA	NA	NA	-0.228794	NA	0.891355	-0.220746	-0.407157	NA
YGL081W	-1.758365	1.068825	NA	-0.611401	-0.961855	0.321553	-0.487	-0.740906	-0.553343	-1.530905	-0.59765	-0.097201	1.506619	NA	0.059386	0.413201	-1.213629	1.035033	-0.584836	1.059533	NA	-1.742771	NA	-0.707552	NA	-0.253487	0.048628	NA	3.460858	0.068078	-1.232334	-0.517333	0.152307	0.343512	-0.16312
YGL242C	0.048434	0.514358	0.776822	-0.014639	NA	0.755608	-0.512526	NA	-0.463964	0.005106	-0.606788	-0.229827	0.914201	-0.46531	0.115377	-0.015123	-0.01645	0.173817	-0.307729	-0.346711	0.329226	-0.306617	0.807047	0.49908	-7.146966	0.52716	0.350481	NA	0.357805	-0.260613	0.168964	0.097456	NA	0.038387	0.1275
YGR054W	NA	NA	NA	0.173834	-0.334637	0.062469	-0.163748	-0.420187	0.75891	-0.959884	-0.658269	0.652503	NA	-1.785017	0.452367	0.364435	0.432868	0.44272	0.292582	0.63022	1.257014	NA	NA	1.001488	NA	-1.246284	1.145118	-0.212267	-0.970142	-0.652462	-0.4299	-0.859166	-0.523128	-0.222268	0.124687
YGR122W	NA	NA	NA	0.941157	-0.586983	-0.530939	0.469639	1.071685	-1.245744	4.129214	1.122319	-1.85366	NA	NA	0.77282	0.273317	0.127071	-2.379173	0.635517	-1.150442	NA	0.572468	NA	-2.148889	NA	0.373656	-1.070286	0.726146	0.700026	-0.333939	NA	-2.570228	1.5151	0.289632	0.285631
YGR237C	NA	-1.137515	-4.171125	0.667085	-0.303075	-0.014117	-0.571236	0.783235	-0.291351	0.703274	0.418444	0.204451	-0.499723	-0.144118	-0.242609	-0.449585	0.255534	0.225352	0.319075	0.130566	-1.631117	0.199202	NA	0.603006	NA	0.44594	-0.873924	0.251571	-0.139076	-0.322107	NA	-0.212652	0.218982	-0.118497	-0.163753
YHP1	NA	-1.273929	-0.327842	0.417604	-1.637333	NA	-0.298664	-1.501499	1.079505	2.458126	-0.117902	0.279378	-0.612964	-3.794524	0.842063	0.475075	-0.19136	0.386142	-0.165098	-0.812348	-1.892288	0.383478	NA	-0.60359	-4.683701	0.384221	-0.893706	-0.143757	0.57514	-0.16236	-1.242142	-0.478391	0.278195	0.14335	0.934108
YHR078W	NA	0.621271	-0.741728	0.168019	0.504304	-0.362761	0.115851	-0.856517	-0.263929	3.052705	0.126212	0.627535	0.031908	0.664078	0.534732	0.076447	-0.05428	0.094625	-0.114613	0.537551	0.738225	-0.173176	NA	-0.333032	1.09457	0.653919	NA	NA	0.96058	-0.261723	NA	0.804042	NA	0.072102	-0.156464
YIL029C	4.643178	-1.411158	-0.017556	0.223426	-0.730865	0.200769	-0.280852	-1.142804	0.474054	NA	NA	0.313713	0.648132	-1.59528	-0.253883	-0.053978	0.201105	-0.243381	0.091848	-0.741808	-0.121314	-0.019672	0.56289	0.670617	NA	0.068126	0.45199	0.493638	-0.586539	0.653709	3.639643	-0.012268	0.417003	-0.461422	0.360136
YIP3	NA	NA	-0.607805	-0.035757	-0.223748	-0.40417	-0.454298	0.959605	-0.281356	1.575267	0.629205	0.239138	1.136785	NA	-0.543869	-0.222901	-0.163968	0.172335	0.187157	0.268917	1.020951	-0.337632	0.378073	-0.240237	NA	0.475489	-0.160548	-0.343624	-0.568386	-0.256265	-0.311501	0.636204	-0.458105	0.276325	-0.445822
YIP5	NA	-2.895488	-0.015697	-1.204128	-0.275451	-0.235934	-0.050682	-1.128926	0.250879	NA	0.063518	-0.379031	NA	-2.457619	-0.111909	0.365111	-0.06674	0.458502	0.499532	0.679539	NA	-0.256991	-0.195775	0.692487	NA	-0.542354	-0.641721	NA	-0.29927	0.271996	-1.72072	0.959948	-0.275461	-0.376432	0.044252
YJL055W	NA	NA	0.647807	NA	NA	0.050314	1.344741	-1.422399	-1.098534	5.163612	NA	0.172517	NA	NA	0.568499	0.477452	-0.47055	NA	0.079006	NA	NA	0.573787	NA	NA	2.811571	NA	-0.796497	0.663893	0.426836	0.25588	NA	0.917674	-0.356726	-0.168568	NA
YKE2	NA	-1.263488	-2.952262	-0.664964	-7.917854	0.347769	-0.58616	0.876098	0.771485	NA	-1.090217	0.476026	-0.592602	-2.557838	0.569362	-0.096324	0.060888	-1.756587	0.219509	-1.359581	-1.175933	0.265893	-0.06897	-0.714006	-3.044527	-0.443433	NA	0.33187	0.34462	0.194665	0.786454	NA	0.098182	0.164113	-0.163184
YKL023W	NA	NA	0.489915	0.078069	NA	-0.702322	0.539809	NA	-0.045191	NA	NA	-0.674384	NA	NA	-0.330961	-0.984737	-0.108996	NA	-0.484959	-0.104801	-1.534158	-0.390082	NA	0.952928	NA	-0.843996	NA	-0.076393	-0.236362	0.047315	NA	-1.361278	NA	0.271901	NA
YKU70	NA	NA	-0.399051	1.2566	NA	0.525673	0.456232	1.264645	NA	NA	1.185546	0.940435	NA	NA	-0.21803	NA	NA	-0.002128	0.562156	1.737819	-0.622385	0.703767	-0.922323	0.551455	-1.667076	0.604485	0.472229	0.812361	NA	NA	1.133753	0.526618	-1.292658	0.422434	NA
YKU80	0.559	-2.42599	-3.699586	0.777697	-0.653019	0.523302	1.300009	-1.145531	0.864196	0.244856	0.446545	-0.288099	0.391243	-1.467067	-0.541061	-0.697842	1.376387	-2.031721	1.544193	-0.909547	NA	-0.014833	1.421576	0.338132	NA	-0.290624	-1.457381	-0.418569	NA	NA	0.453973	-0.579977	NA	0.271192	-0.500475
YLR177W	-0.271221	-1.43484	0.452863	-0.291895	-2.274346	0.381095	-0.371597	-1.674888	0.044376	1.059276	0.323771	-0.634919	-1.070613	-1.411843	0.695251	-0.000741	0.272328	-1.706484	-0.036993	-0.001524	-0.377797	-0.197169	NA	0.587643	-5.313786	0.206302	-0.25708	0.413074	-1.192109	0.697819	NA	0.040852	0.937758	0.120731	-0.648102
YLR224W	NA	-0.391308	-2.856175	0.338424	1.387672	0.316867	0.025636	0.367053	0.07046	-0.369452	0.217875	-0.597397	-0.385253	0.589015	-0.382611	-0.583513	0.019623	-0.470693	0.547795	0.168176	-1.093867	0.635472	NA	-0.074361	NA	-0.242833	-0.497102	0.820976	1.026402	0.096447	-0.16123	0.575068	0.156212	0.409372	-0.622785
YLR278C	4.612434	0.148684	0.24848	-1.187661	0.206372	-0.095768	0.316308	-0.082496	-0.269511	2.665961	NA	-0.065783	1.198812	0.241452	0.363824	-0.186767	-0.302413	-0.16783	0.238154	-0.109386	-0.355176	-0.367409	0.505131	-0.163466	NA	0.18651	1.276923	-0.230311	1.054325	-0.515295	NA	-0.432831	-0.158048	-0.016484	0.035524
YLR287C	0.067613	-0.066398	-0.378285	0.410444	-0.464448	0.134841	0.199926	-0.792227	0.713507	0.848295	-0.206744	-0.164926	-0.553891	0.121083	0.423121	0.491634	0.739332	-0.646104	0.432304	-0.012661	NA	-0.175279	0.476119	0.059183	NA	0.008652	-0.379623	-0.330516	-0.684323	0.141397	-1.208234	0.154807	-1.009608	0.43041	0.28143
YMD8	0.317413	0.606423	-1.066954	-0.408934	0.908933	0.010128	-0.562863	0.070652	-0.124211	-1.135078	-0.338494	-0.19106	-0.659565	0.333976	-0.116977	0.325899	0.33769	-0.470468	-0.148865	0.057748	NA	0.155514	0.113704	0.77873	NA	0.555349	-0.660072	-0.042803	-0.611554	0.421839	-0.80321	0.272638	-0.356905	0.006486	-0.260072
YME1	NA	-1.187794	-1.023422	0.148466	-1.37041	-0.42299	-0.006229	-1.667959	0.303762	-5.086406	-0.219292	-0.08883	0.710702	-0.173675	0.568621	0.40104	-0.030084	0.325312	0.565189	-0.244859	-0.499233	0.23226	0.846261	-1.457573	NA	-0.800831	-2.647261	0.266776	0.441651	-0.57723	NA	-4.48496	0.638159	0.323806	-0.195288
YML108W	NA	0.057696	0.357605	0.061181	0.707548	-0.332131	0.522145	-0.04151	0.27804	0.935098	-0.177509	-0.283068	NA	1.687625	-0.156873	-0.321751	0.277886	-0.005765	0.045508	-0.396031	NA	0.320859	NA	-0.137361	NA	0.236951	0.536099	-0.332638	-0.315824	0.262993	-0.011243	0.835614	0.436655	0.102152	-0.541517
YML119W	NA	NA	0.349047	-0.075515	0.697448	-0.624495	0.031875	-0.615743	-0.088199	-0.10571	0.090913	-0.044166	0.227902	0.235421	0.122487	0.360384	0.152357	0.401508	0.536016	0.21217	NA	0.100218	-0.255254	0.178401	NA	0.371207	0.343739	-0.307495	-0.553618	-0.354889	-1.386906	-0.501818	0.459148	-0.2687	-0.498801
YMR010W	NA	-0.144483	-0.890579	0.345477	-0.208696	0.134409	-0.721299	-1.955099	0.424807	-0.801454	-0.449947	0.447257	-0.832863	-0.924137	0.101064	-0.076981	-0.332154	1.00036	0.309227	0.125327	NA	0.707061	1.218573	0.920789	NA	-0.056025	0.474827	-0.174707	0.030565	0.449702	-1.012094	-0.037866	-0.302911	-0.366228	0.447114
YMR102C	NA	0.870667	1.463893	-0.433919	0.017192	-0.431641	-0.471988	0.925615	-0.319907	0.450619	-0.309067	-0.309158	1.659018	1.240608	-0.25329	-0.105089	-0.052786	1.298082	0.108504	0.261778	1.990381	-0.753967	-0.003974	0.814346	NA	1.037417	1.176432	-0.138768	NA	NA	0.485005	0.302287	-0.441311	0.935898	-0.095301
YMR111C	NA	-0.272024	-6.037837	0.216293	-0.761939	0.457562	0.356184	0.993692	0.197162	-5.246144	-0.664332	-0.149469	-0.119484	NA	0.279993	0.126378	0.141641	-0.478649	-0.122289	0.02236	NA	1.011402	-0.836994	-0.461292	NA	0.987621	-0.346624	-0.181877	NA	NA	0.615651	-1.947665	0.541703	-0.071942	0.53392
YMR209C	NA	-0.48768	-0.709718	0.280783	-0.370872	0.082097	-0.555479	-1.077541	-0.495305	NA	0.719481	0.202041	NA	0.205252	0.388923	0.127895	0.125117	-0.746046	0.507311	-0.374477	-0.899776	0.84492	0.657406	0.565149	NA	-0.261841	-0.536497	0.257322	NA	NA		-0.320058	0.852541	0.359882	NA
YND1	NA	1.010509	NA	0.079117	NA	-0.152576	-0.261486	0.109207	0.586337	1.729143	NA	-1.452109	NA	NA	0.704836	0.916651	-0.053042	-0.934422	0.490155	-1.087674	-1.328695	-0.292938	-0.059054	1.226719	NA	0.714078	-0.739726	0.173092	-1.624078	-0.620629	NA	-1.039968	-0.217959	-0.74199	NA
YNG1	NA	-0.818614	0.285311	0.09882	-0.13526	0.338043	NA	0.155091	NA	NA	-0.856161	-0.05483	1.004785	-1.032245	0.252002	0.221311	0.03185	0.223232	0.122995	-0.003202	0.178718	0.153221	NA	0.662014	-7.707541	0.443031	-0.550626	-0.567502	-0.302994	-0.017121	0.235952	-0.213571	-0.844364	0.50954	0.099759
YOR342C	-0.473073	-0.282309	-0.442394	0.635901	0.870921	-0.79106	0.417637	-0.484664	0.590134	-0.222032	0.051032	-0.693995	-0.331502	NA	-0.237269	-0.525507	NA	0.105072	0.580966	0.348866	0.318263	0.257254	1.192377	-0.286515	-0.753889	-0.065448	-0.29378	0.362585	0.521077	-0.281954	-1.15994	-0.054512	0.086102	0.047093	-0.070165
YOS9	NA	1.09196	-0.172519	0.001857	0.398287	-0.197719	-0.469619	NA	-0.416412	1.8384	0.553915	0.036649	1.543379	0.910853	NA	-0.375646	-0.330245	1.111038	-0.36789	0.287446	NA	-0.61796	-0.183759	0.50547	NA	0.72132	0.09086	0.050949	0.290076	-0.227433	0.15708	0.922381	-0.48708	NA	-0.134551
YPL041C	NA	-0.368911	-0.277813	-0.335061	1.285288	-0.15468	0.680984	-0.448549	-0.183053	0.636633	0.159191	0.056245	-0.485965	1.253699	0.261454	0.139746	-0.852058	0.12481	-0.125017	0.902898	0.396422	-0.398327	-1.520509	-0.405416	NA	-0.853455	1.02999	-0.264478	2.678509	0.88259	0.163126	-0.20597	-0.625267	0.210205	0.364291
YPL068C	NA	-0.708591	1.087537	-0.181342	-1.490593	0.072467	0.212848	1.491309	0.373385	-1.80785	0.472445	-0.115804	1.069335	1.577312	-0.177683	-0.215358	0.071804	0.399078	-0.144208	0.125784	0.721958	0.38899	NA	0.006609	-3.611705	0.516999	-0.052232	-0.045077	0.58918	0.219386	-0.014392	-0.513572	-0.310038	-0.431756	0.056562
YPL113C	NA	NA	-0.405926	0.224197	NA	0.124938	-0.150429	-0.038679	0.18423	-0.955072	-0.229391	-0.076661	0.216569	NA	-0.125361	0.249648	-0.079808	-0.809983	0.260238	0.154767	-0.618469	0.090191	NA	0.802738	NA	-0.093546	-0.508717	0.00847	0.748816	-0.277143	NA	0.375569	-0.477017	0.342523	0.848355
YPL150W	-1.75835	0.383336	-0.533736	0.036385	NA	0.082375	-0.369469	0.988857	0.62983	-4.926909	0.568257	0.536814	0.440846	0.441382	0.152985	5.90E-05	-0.092574	0.39167	0.488057	-0.163583	NA	0.154525	NA	0.592009	-4.790103	-0.408195	0.565231	-0.408693	-0.20404	0.088365	0.574627	-0.503495	-0.852373	-0.541074	-0.185724
YPR022C	NA	-0.102604	-0.373101	0.044066	0.319426	0.046603	-0.666649	-0.338909	-1.031485	0.616342	-0.310986	-0.598048	-0.131654	NA	0.013419	-0.078181	-0.799313	-0.161933	-0.091775	0.701309	1.612756	0.139579	0.027424	0.484157	NA	-0.052439	0.486381	-0.550671	0.365263	0.250525	0.406036	0.244739	-2.065575	-0.091437	0.510968
YPR063C	NA	-0.685377	-0.142219	-0.786198	0.745154	-0.496715	-0.281129	0.913364	0.432019	NA	0.208031	0.283831	0.188864	-1.815404	-0.105867	0.173546	-0.232296	0.267257	0.033886	-0.150904	-1.096607	-0.113779	NA	0.847847	NA	-0.108656	-1.000177	-0.080448	NA	-0.961009	0.624901	-0.443873	-0.455246	-0.139587	0.131101
YPR174C	NA	-0.378916	-0.226534	0.761892	-0.220953	0.042739	-0.077781	-2.988537	0.937369	1.212587	-0.359781	-0.914678	-0.530226	-1.352233	0.456702	-0.116889	0.67432	-0.43614	0.493983	-0.390763	NA	0.059841	NA	0.250855	NA	0.375332	NA	-0.131695	0.826571	-0.075781	-1.81718	-0.260102	-1.501199	0.091714	-0.317581
YPT31	NA	-1.274328	-2.770067	-0.011588	-0.697171	-0.168414	0.283548	1.045325	0.121984	-4.00477	-0.013019	0.107058	0.57425	-0.30587	0.562318	0.121424	-0.073481	NA	-0.032065	-0.308647	1.051856	0.33532	NA	-0.650349	NA	-0.015775	-0.204848	-0.0847	-0.849512	0.2153	NA	-0.66838	-0.448269	-0.462958	0.219409
YPT6	NA	-0.783666	-17.920705	-0.089609	-0.147977	0.261137	-0.645593	-0.098155	-0.033766	-1.980297	0.130094	0.132772	1.714873	NA	-0.359599	0.811065	0.557917	0.534863	-0.368302	0.719147	2.66497	-2.479056	NA	-0.853843	NA	-0.980728	0.945415	-0.221065	-0.057898	-0.069776	NA	-2.242499	0.584166	-0.61637	0.136939
YPT7	-4.214706	-1.533492	-3.802049	-0.330874	-0.189194	0.42201	0.221398	-1.609739	0.496048	NA	-1.085485	-0.389187	-0.15749	NA	0.191256	-0.127688	-0.368255	0.106264	-0.211081	-0.333311	NA	0.942935	0.361029	0.330212	NA	-0.068514	-0.991252	0.008143	-1.030969	0.862627	-0.757143	0.060432	0.718682	0.08453	-0.394191
YSN1	NA	0.176725	NA	-0.3882	-0.485274	-0.317338	0.183997	-0.416455	-0.107214	NA	0.260656	0.657467	-0.052146	-0.930416	0.10101	0.271484	0.610629	0.225137	0.612793	0.4697	NA	-0.645517	-0.934835	0.178577	NA	0.696985	0.207067	-0.443271	0.897939	-0.508665	-0.093282	0.048367	-1.607938	-0.358112	-0.832806
YSY6	-0.962983	0.006406	0.725229	-0.344328	-1.448477	-0.200954	0.174294	0.40151	-0.463915	-0.771328	NA	0.211223	-0.274995	-1.569146	-0.430776	-0.330627	-0.35885	0.37023	0.243678	1.22586	-0.056659	-0.086207	-1.910392	0.9011	NA	-0.548502	-0.224028	-0.087817	NA	0.327207	-0.179822	-0.181491	-0.113994	0.386758	0.519805
YTA7	NA	-1.11758	NA	-0.805612	-0.864505	-0.351526	0.417033	1.017295	-0.380338	3.828833	NA	-0.268311	0.639185	1.036306	1.482999	1.130889	-1.373103	0.520699	-1.471613	-0.118415	-2.148882	-2.22299	0.779354	NA	NA	0.556887	-6.053149	0.921385	-0.779113	-0.113151	NA	NA	NA	0.014676	0.01886
YUR1	-1.427429	NA	-0.027295	0.688706	0.785237	0.571267	0.389438	0.539413	1.266597	-0.500612	-0.002351	NA	-0.512316	-0.950141	0.401023	1.122647	0.714008	-0.454969	0.631884	-1.530547	-0.436454	1.174708	NA	-1.032963	NA	NA	-1.33588	0.447205	-0.407935	0.202896	-0.925828	-0.455136	-0.040091	-0.148617	0.39836
ZDS1	NA	-0.833559	-1.747861	0.784805	-0.215102	-0.164121	0.063637	0.916665	0.289381	-1.49023	0.010915	0.434723	NA	NA	0.24385	0.381984	0.592694	-0.598067	-0.263349	-0.607534	0.539043	0.481904	0.067168	-1.373402	NA	0.810887	2.96919	0.492229	NA	NA	1.134914	0.040742	-1.264829	-0.125479	NA

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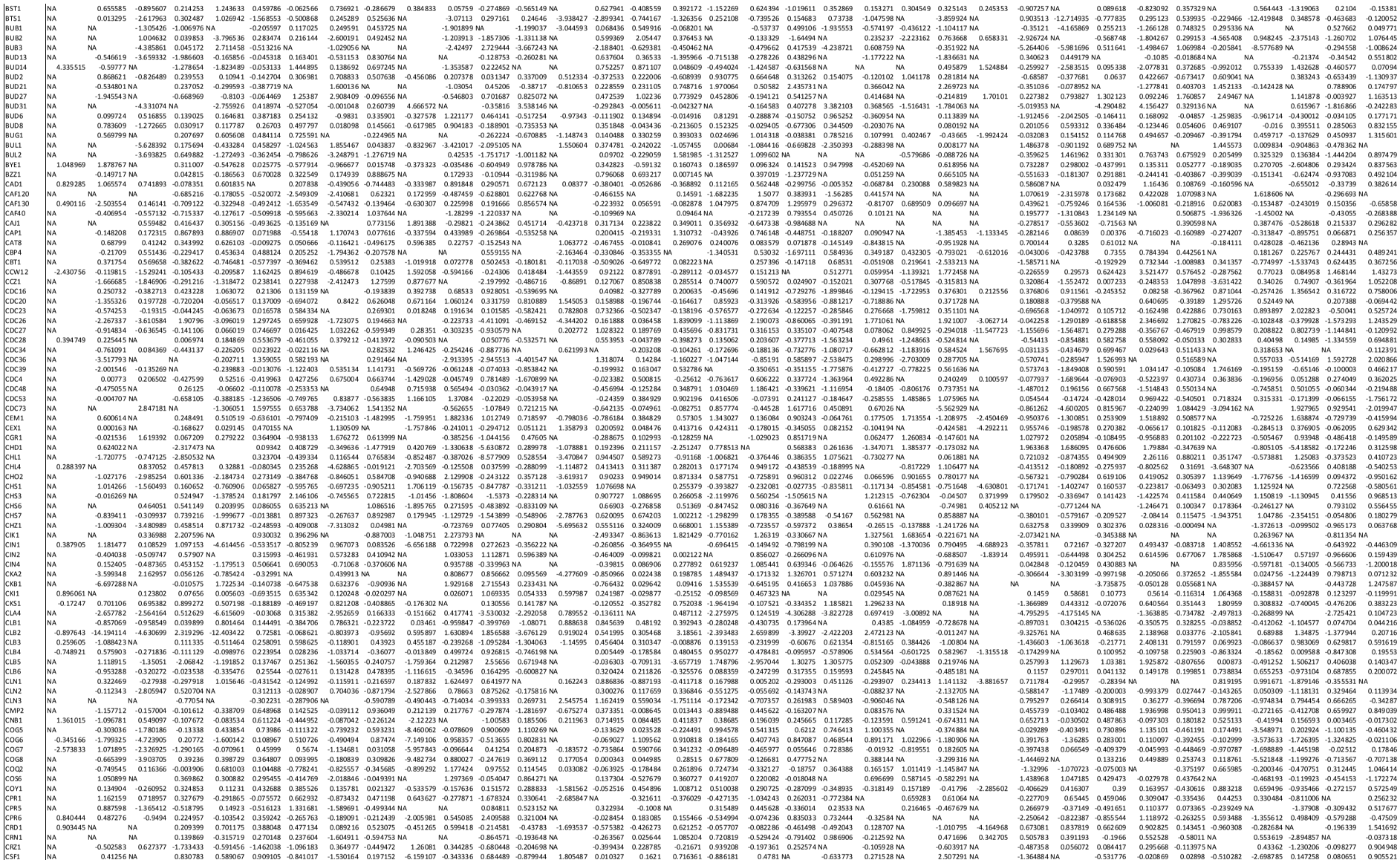
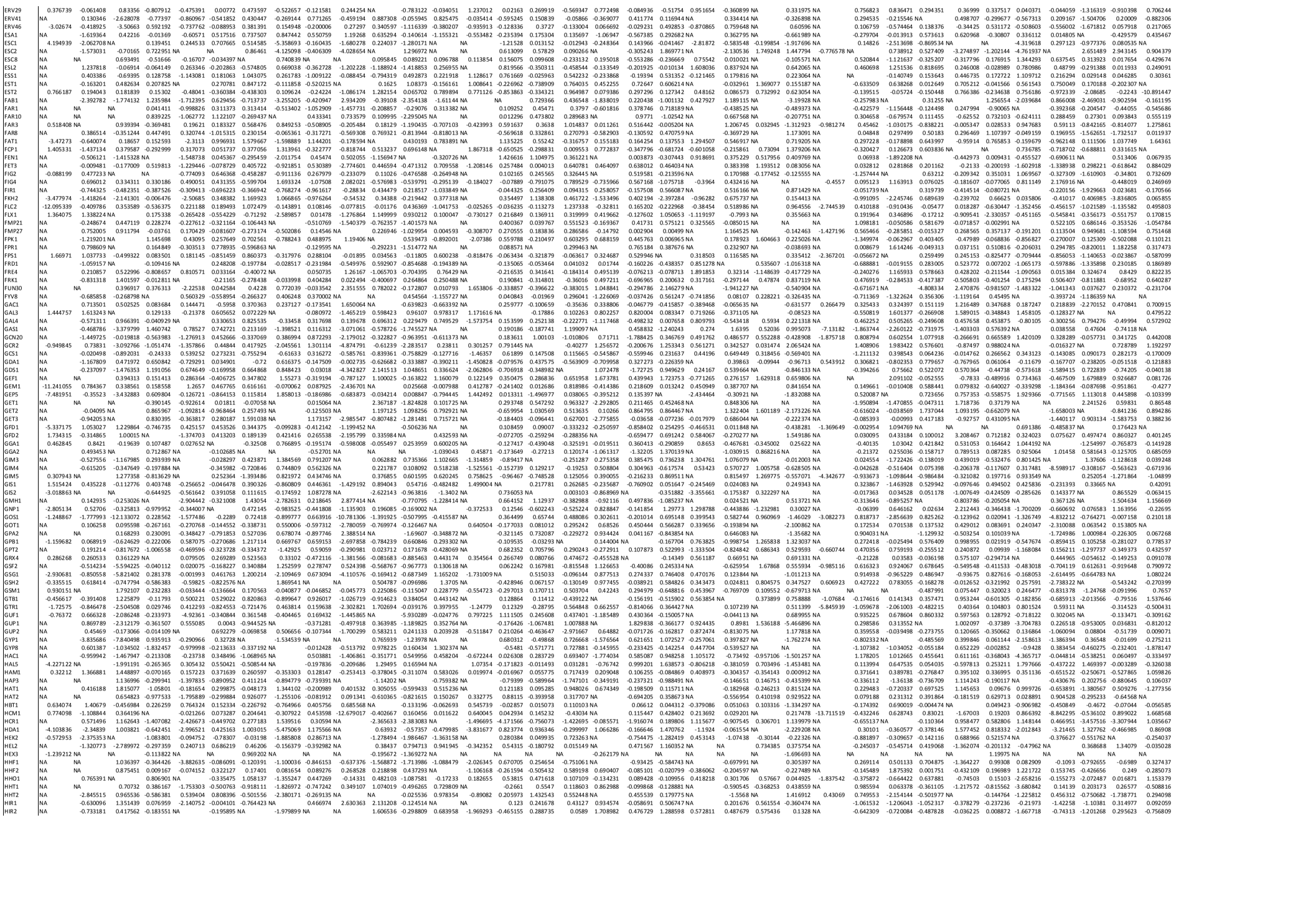
Gene	ARP8	ASF1	BRE1	DCC1	DDC1	DOT1	EXO1	HEX3	HST3	HTZ1	MEC1	MRC1	MRE11	NUP133	PPH3	PSY2	RAD17	RAD18
AAD4	NA	-0.594423	-0.707581	-0.008246	0.423999	0.681915	-0.197897	0.238132	0.191123	-2.148973	0.086813	-1.228943	-0.12673	-0.120241	-0.011042	-0.570941	-0.272679	1.236926
ABP1	NA	NA	-0.027532	NA	0.240443	-0.107937	-0.877136	-0.351913	-0.10172	-1.264937	0.170381	-0.70492	-1.43953	-2.667905	0.610718	0.407717	0.053317	NA
ACB1	2.350108	0.558944	-0.271346	0.026034	0.330648	-0.344358	0.207462	-0.312687	-0.382366	-0.45833	-0.957844	0.485767	0.265015	NA	0.389498	0.073571	-0.143457	0.308189
ACE2	NA	-0.483101	1.727018	0.401417	0.437491	0.694812	0.538229	2.424292	0.81978	NA	NA	-0.414713	-0.963609	NA	2.227659	0.782744	0.0306	NA
ACK1	1.086157	0.776401	NA	-0.242664	-0.592548	-0.714444	-0.013461	-0.378739	-0.301968	-0.445266	0.101677	-0.031038	0.513918	0.469212	-0.283636	0.025191	0.762634	NA
ADD66	NA	1.927374	0.799265	-0.823813	-0.616832	-1.493656	0.045102	1.796325	-0.510208	NA	-0.411205	0.849839	0.232851	NA	-0.795739	-0.417231	-1.113151	0.308245
AGE2	NA	0.115658	0.367654	0.275802	-0.080441	0.306491	0.371929	-0.559296	-0.013405	0.093791	1.320373	-0.185772	0.785308	NA	0.91722	0.612592	0.527417	-0.042949
AGP2	1.231917	0.804583	1.010702	-0.164453	0.914085	0.463902	-0.128523	-0.66795	0.187014	-0.967718	NA	0.128035	0.683858	-1.019744	-0.973542	-0.283744	0.911541	0.711212
AGX1	NA	0.390041	0.174707	0.305822	0.219227	0.111748	0.623087	NA	0.003022	1.336085	-0.721707	-0.979456	NA	-3.339482	0.549305	-0.24271	-0.313211	0.218225
AHC1	NA	NA	-0.283186	-0.591423	-0.862245	0.59248	NA	-2.22036	NA	NA	-3.173048	-2.844304	-0.623579	-3.077143	0.764208	0.362692	-0.444172	0.010879
AHC2	-1.139338	-0.355243	-1.01723	NA	-0.154321	0.306273	0.035457	-3.431955	0.814181	-4.970141	-2.719847	-1.466768	0.614287	-0.732879	1.218986	0.226091	-0.061854	NA
AIM21	1.387459	0.063865	0.593274	-0.051832	0.123315	-0.463686	-0.652854	1.022853	-0.77524	0.448682	-0.149291	0.318409	0.898789	1.088349	-0.064022	-0.744471	0.133592	0.685901
AIM22	NA	NA	1.109543	0.083777	0.270414	-0.057669	0.502387	-0.420473	0.108207	-1.415958	1.153764	0.977922	1.336635	-1.778714	0.105851	-0.312602	0.095416	0.547363
AIM26	0.897217	0.746792	1.068444	-0.634884	0.543157	-0.591914	-0.29612	0.162811	-0.829355	0.387778	0.047868	-1.42557	-0.200593	-0.175433	-0.335477	-0.05943	0.224994	0.332028
AIM29	-1.944591	0.288161	-0.641267	-0.616832	-3.420637	0.020799	-0.056292	-0.450243	0.401067	-3.038034	0.669169	-0.672853	0.302501	NA	0.749921	0.329949	-0.377416	-0.993786
AIM3	0.994748	NA	0.881622	0.437994	0.737789	-0.367355	0.357548	0.399284	-0.690951	-1.673684	NA	0.495367	NA	1.354687	0.13309	-0.362776	0.645726	-0.704103
AIM32	NA	-0.099348	0.648712	0.161987	-0.604625	0.696038	0.255745	0.060877	-0.195281	-0.668453	0.889703	0.088772	0.413164	0.005292	0.192409	0.15052	-0.033935	0.276487
AIM34	-1.111491	1.192504	-0.174001	-0.710672	0.400219	-0.048218	0.624961	-1.13988	0.937061	-3.030295	-0.417891	0.32268	-0.545291	NA	-0.207407	-0.126344	0.222844	-1.303594
AIM4	NA	NA	-0.048493	-0.465972	0.878763	-0.167225	-0.364503	NA	-0.847013	1.004214	NA	-0.46259	-0.994725	NA	-0.654835	-0.1421	0.149709	1.487452
AIM44	NA	-5.693106	NA	-1.349957	NA	0.052828	-1.262312	-0.210755	-0.72743	0.161391	-1.300813	-1.546816	-3.429945	-0.230172	0.104021	-0.135323	-1.54997	-2.500283
AIP1	NA	0.110645	NA	0.226074	-0.467887	0.132392	0.912489	-2.877049	-0.351233	NA	-0.690677	-0.884883	NA	NA	0.625156	0.416498	0.134434	NA
AIR1	NA	0.800059	0.813012	-0.915817	0.657659	-0.424197	-0.491778	0.978031	-0.433968	-1.630521	-0.376863	-0.371426	0.507228	-0.127711	-0.300533	-0.080052	-0.478579	0.269714
AIR2	-0.577883	0.562491	NA	-0.499496	-0.340968	0.253633	0.55318	-0.841677	1.525633	-0.184308	0.628815	0.167055	0.174739	NA	0.555674	-0.652273	-1.124131	0.558512
AKR2	NA	-0.84566	NA	0.378051	-1.762181	-0.759429	NA	-0.867355	NA	NA	0.402728	-1.777659	0.246128	-3.050698	-0.197363	0.274671	0.868517	-0.776226
ALB1	-2.102739	NA	NA	-0.225117	-0.368013	0.832156	-2.084726	0.086226	0.929956	-0.584383	-0.616619	0.851108	1.609934	NA	0.681561	0.240037	-0.19299	0.71852
ALG12	NA	1.59576	1.771958	0.268758	0.457869	0.072189	-0.007379	-0.628615	0.963126	-0.321739	-1.739113	0.626448	0.184874	1.301017	-0.005632	-0.249485	0.390126	0.020092
ALG3	NA	0.080319	1.645367	-1.528784	1.454935	0.108725	-0.040632	NA	0.094216	NA	NA	0.963783	NA	NA	-0.201819	-0.008796	-0.334783	NA
ALG5	0.344196	0.223301	NA	-0.133498	NA	0.089325	0.393292	0.359664	-0.252068	-0.192502	-0.118326	-0.138031	0.503042	0.902531	-0.120256	-0.490341	0.00493	0.170885
ALG6	NA	NA	-2.19693	-0.669414	1.570206	0.689161	NA	0.027165	NA	NA	-0.493178	-0.95378	NA	1.467964	-0.110632	-0.296474	0.132807	0.201418
ALG8	NA	1.062132	-0.433781	-0.565731	0.263642	-0.203506	NA	-0.641253	NA	NA	0.025172	-0.804801	0.110947	NA	0.536503	0.007069	-0.379166	0.523087
ALT1	-1.894242	-1.028847	-1.196197	0.443172	0.360593	-0.127135	-0.035804	1.256603	-0.398478	-0.078136	1.046639	0.946811	0.437829	NA	-0.27116	0.532548	0.760575	1.285191
AMD1	NA	0.172867	0.375116	0.035018	-1.013863	-0.411106	0.277933	1.033011	0.256637	NA	-0.310543	-1.755081	-0.14603	1.480067	0.23441	-0.161812	-0.286631	0.499125
APA1	-0.210464	0.713208	0.579754	NA	-0.081844	-0.167531	-0.352609	-0.724129	-0.103454	-1.332041	NA	NA	0.023481	1.983485	-0.144189	-0.066567	0.129808	NA
APC1	NA	NA	0.087123	0.617599	0.236692	0.506997	1.0752	1.186021	-0.042681	-1.158828	0.478273	-1.124321	-0.09743	NA	0.424914	NA	0.057267	-0.973306
APC11	NA	0.606783	NA	0.747148	-0.477744	0.136825	-1.604355	NA	-0.515556	NA	1.821564	-0.363658	-1.176907	-0.257302	NA	0.287611	0.490057	-0.813634
APC4	NA	-1.30281	0.46672	0.214161	0.284849	0.421288	0.200918	0.726056	0.058829	0.287821	0.56703	0.533776	0.029216	-0.39198	NA	-0.552699	0.451424	-0.556083
APC5	0.600458	-1.156897	0.174892	-0.918146	-0.525552	-0.392324	-0.227077	1.257471	-0.063241	-1.294275	NA	0.028187	-1.089775	0.160871	-0.461087	-0.675735	0.332707	0.650231
APC9	NA	-0.418661	-0.61984	1.700761	-0.879968	0.483106	0.480584	0.032523	0.976157	-1.490285	NA	0.277516	0.277262	-2.43759	0.693996	0.1447	1.789405	-2.216658
APE3	NA	-0.628644	NA	0.440586	-1.245253	0.007461	-0.01124	0.162117	0.897279	NA	1.183059	-1.703516	-0.194082	0.544206	-0.567439	0.430247	0.130862	-1.186601
APL5	NA	NA	-0.558759	-0.269768	NA	-0.544208	-0.008193	0.613496	0.093394	NA	-5.719095	-2.633946	-0.06423	-1.403092	0.324472	-0.21753	NA	NA
APL6	NA	0.799481	NA	-0.586158	-0.406192	0.489583	0.557718	-1.215424	0.198468	-0.620814	-1.205832	-0.833302	0.31709	NA	0.663271	0.038308	-0.219762	NA
APM3	NA	-0.045312	-0.79237	-0.100654	-0.236173	-0.268836	1.126881	-0.30705	0.856861	0.031216	-0.504224	-0.769598	0.665975	0.256618	-0.052393	0.199491	0.072294	NA
APM4	1.185277	NA	0.174292	0.237931	0.45254	0.151438	NA	-0.208878	NA	NA	-0.186544	-0.074685	0.677179	NA	-0.05231	-0.265321	-0.146248	0.466101
APQ12	3.365582	-0.219792	-4.421378	0.088327	-0.674549	-0.509356	0.931813	-3.427347	1.096057	NA	0.7749	-1.372868	0.325079	NA	0.192075	0.300132	-0.630134	0.065284
APS3	NA	NA	0.285163	-0.220155	0.215963	0.498084	-0.497885	-0.477717	-0.476331	0.186239	-0.657103	-0.154711	-0.455954	NA	-0.139506	-0.096701	-0.096581	0.338055
APT1	NA	NA	NA	-0.983355	-0.756903	-0.366766	0.757517	-0.32733	-1.499502	-0.464554	NA	-0.377158	-0.876252	0.707799	0.041289	0.266351	-1.075427	-0.890875
ARC1	NA	0.450852	-0.626915	-0.49684	-1.668621	-0.446039	-0.079544	NA	-0.541524	NA	NA	0.491692	NA	1.379954	0.19882	-0.378674	0.411147	1.018986
ARG80	-0.502965	-0.148592	NA	0.169976	1.158131	0.08068	0.295236	-0.188655	0.236576	0.102676	-0.326606	1.009391	-1.175169	1.126626	1.071497	0.102875	-0.446847	0.063396
ARL1	NA	-0.13997	-3.193192	0.374291	-0.679214	0.410181	0.510968	-0.349691	-0.201474	NA	NA	0.350078	0.558249	-4.386492	-0.287927	-0.097249	0.557442	1.492468
ARO1	NA	-2.319423	-2.044209	1.046645	-2.771699	1.171546	-3.081365	-0.378616	-3.105505	NA	-2.461147	NA	-2.084659	2.355349	NA	0.316496	-0.403484	-2.983991
ARP1	NA	-2.812506	2.006706	-0.596145	0.865764	0.281095	0.26208	-0.083613	0.134536	NA	-0.927982	0.529888	-0.459595	-0.611123	1.33387	0.775594	-0.867135	-0.373985
ARP4	NA	NA	-5.90653	0.078498	-1.804493	0.714312	0.174956	-2.938567	-1.62899	1.149121	1.565164	-1.659038	1.377413	-3.546271	0.427537	0.432296	0.290215	1.337276
ARP6	NA	NA	NA	NA	NA	-0.112487	0.84342	NA	-1.176172	3.41848	NA	NA	NA	NA	NA	-1.281168	-1.66145	0.101783
ARP7	-2.908387	0.3606	-1.761935	0.07896	-0.106259	0.458096	1.000135	NA	0.210405	NA	-0.188504	0.503448	0.261273	NA	0.460275	0.525708	0.017704	-2.086209
ARV1	NA	NA	-3.661154	0.889241	NA	0.685212	0.264417	-0.428089	0.131147	-2.324519	-0.144862	-0.347872	0.355325	NA	-0.099578	0.20122	0.747936	-0.253524
ARX1	4.391934	0.695634	1.217484	0.35968	0.079412	-0.606513	-1.358977	0.720149	-0.420944	1.431108	-0.060862	0.185515	-0.282427	NA	NA	-0.422632	0.98048	0.39531
ASF1	NA	NA	0.171906	1.572571	NA	2.042681	0.325445	-3.792723	NA	NA	1.622462	2.847707	NA	NA	-1.046083	NA	NA	1.332153
ASH1	NA	1.525676	0.123326	0.295307	-0.502761	0.174783	0.170116	0.301805	-0.263817	0.513439	0.234377	-0.322604	-0.114378	NA	0.237562	-0.231657	0.227985	0.411689
ASI1	NA	0.44365	0.235094	0.308428	-0.099393	0.095208	0.850142	-0.244395	0.528412	0.997872	1.073636	-0.289131	0.547091	-0.973141	-0.189694	0.182411	0.930547	0.126014
ASI3	1.036807	0.215739	NA	0.001131	0.644288	0.134256	0.282351	-0.329743	-0.397264	-0.06592	0.617493	0.218644	0.294442	-0.841171	-0.585171	-0.028817	-0.039814	0.268533
ASK10	2.342096	1.410777	1.680381	0.249546	0.780322	0.557858	-0.596437	0.827973	0.031974	-1.474807	-0.107461	-1.124153	0.414714	1.397414	-0.72724	-0.27726	-0.726097	0.135404
ASM4	1.286879	-0.491187	NA	-0.284654	0.007144	0.266751	0.642966	NA	0.818389	-2.789243	-0.252895	-0.655504	0.481714	-14.791303	NA	0.433662	-0.334009	NA
ASR1	NA	-1.987921	0.009574	0.224434	-0.756937	-0.657152	0.761017	NA	-0.05061	0.226058	0.566432	-0.847356	NA	NA	-0.281989	-0.210526	0.438647	0.05406
ATG21	NA	-0.548679	-1.952019	-0.295029	NA	-0.320247	-1.409407	-0.714824	0.826606	0.039986	0.957497	0.125877	1.326224	NA	0.67121	0.109077	0.52305	0.869097
ATG8	NA	NA	0.556238	0.32403	0.435207	-0.338317	-0.329897	-0.339371	-0.628251	-1.135231	-1.031738	-0.31254	0.175311	1.669252	-0.562133	-0.851218	0.185872	0.920308
ATP23	1.725137	1.688058	0.47614	-0.758358	0.313905	-1.069666	0.782053	-0.418445	-0.003793	-2.692027	-1.728297	1.455842	1.104747	-1.742934	0.861253	0.533151	-1.912224	0.5211
ATS1	NA	-0.310746	-0.835534	-0.057958	-0.249155	-0.759851	-1.139587	-0.265701	-0.210407	0.041279	1.79634	1.003274	-0.233252	-0.107364	0.208051	-0.368216	-0.035284	-0.021489
AVL9	NA	0.731226	-5.167362	0.649641	-0.770756	0.249177	0.618355	-0.17598	-0.087788	0.700256	0.194994	-1.98698	0.322258	-0.955253	-0.170519	-0.206691	0.775559	-1.88315
AVO2	NA	-0.168083	0.164443	-0.171688	1.17917	0.269022	0.485742	-0.456769	-0.581066	NA	0.052265	0.748247	NA	-1.546229	-0.235545	0.083709	0.198267	-0.322504
AZF1	NA	-0.196792	0.138736	0.120092	-0.405909	0.352923	NA	-0.026126	NA	0.630988	1.403012	-0.565642	0.377155	-1.384222	0.088097	0.105576	0.307027	0.387731
BAS1	NA	1.282776	1.226325	-0.666259	0.458871	-0.100305	-0.676646	1.194675	-0.453918	-0.291795	1.597714	1.484661	1.797741	NA	-1.523245	-0.796794	-0.0357	1.609708
BBC1	NA	0.302244	0.034924	0.022588	0.527414	0.241805	-0.158704	0.192578	-1.126199	0.013671	0.762384	-0.200279	0.855903	NA	-0.427761	-0.32425	0.131359	0.047393
BCK1	0.091637	NA	-2.835688	0.815006	-2.508482	0.45892	0.806858	-0.650789	0.473934	-1.013209	-0.112238	-0.996973	-1.241162	1.536974	0.310369	0.988913	0.82776	-3.163386
BCK2	NA	0.402139	-3.240826	-1.46019	-0.030945	-0.359038	-0.466911	0.53042	0.157319	-1.353524	0.421809	-0.004552	0.735771	0.961426	0.726667	0.203791	0.205724	0.931246
BDF2	-4.867013	NA	NA	0.312253	1.005545	0.267039	-1.247507	NA	-0.045466	-6.887703	-1.212815	0.198499	1.085446	NA	0.655663	0.014076	-0.843493	1.21585
BEM2	NA	-2.484978	0.614662	-0.591722	-0.638327	0.886224	1.334622	-0.360313	0.012221	-0.134879	-0.564589	-0.216033	0.261204	NA	0.399653	0.733152	0.13477	0.022602
BEM3	-1.29425	-0.291074	0.504276	0.101358	NA	1.061121	1.239238	-0.762904	0.878181	0.764716	0.129522	-0.849059	-0.445011	-1.889084	0.348732	0.153729	0.186304	-0.337675
BEM4	NA	0.199581	-2.073115	-0.427885	NA	0.377576	0.378359	1.368301	0.399153	-2.975074	0.538149	-0.304372	0.273517	0.304336	-0.91612	-0.884727	-0.577787	0.538705
BFA1	NA	-8.40862	0.616955	-0.864141	-2.618052	0.736064	0.604359	-2.085235	0.564738	NA	-0.900808	-3.117172	-3.684768	-0.010344	1.171059	0.227106	0.600314	-6.994296
BIK1	NA	0.641953	-1.956551	NA	0.557659	0.218077	-0.44758	1.30906	0.825422	-4.609622	-0.936041	NA	-0.062317	NA	-0.674373	-0.440462	-0.089717	NA
BIM1	NA	-3.121999	1.36721	1.656227	NA	0.373842	0.367667	0.373183	0.182467	NA	0.965845	-8.215446	-0.532371	NA	-3.199977	-1.226546	1.6199	-1.229935
BIT2	NA	-0.682069	-0.065847	0.459814	1.312997	0.702119	-0.583021	-0.176579	0.541998	NA	-0.663061	0.640389	0.170831	0.889574	0.452483	0.83029	-0.634164	-0.503688
BLM10	NA	1.433827	0.279009	-1.682776	0.863492	0.280573	-1.730111	0.255992	-0.44867	NA	NA	-2.288615	0.431513	-1.541393	0.467596	0.110854	-0.305287	0.47924
BMH1	NA	NA	-0.942149	-1.877254	-0.405551	-0.183509	-0.285816	0.224925	-0.028171	-2.359012	-0.676188	-1.422597	1.902948	0.762432	1.205916	0.704701	-1.242863	0.240888
BMH2	NA	-0.839251	0.288265	-1.792928	-1.274512	-0.150566	0.844574	-0.486905	0.121421	NA	0.178218	-1.434016	0.631162	NA	NA	-0.301758	-0.995708	0.182768
BNI5	NA	0.894159	0.624256	-0.339035	0.636078	-0.08808	0.325679	0.126519	-0.437404	-0.346038	-1.137084	-0.072693	-0.117814	-0.657554	0.694782	NA	-0.330912	0.178927
BOI1	0.248408	-0.761994	0.984232	0.229516	-0.297706	0.469327	-0.318614	0.595861	0.301573	-1.441651	NA	-0.416812	-0.544755	-0.620587	-0.194541	-0.538992	-0.462133	-0.757287
BOI2	-0.39024	-0.229848	-0.772445	0.209381	0.061483	1.333302	0.841799	-0.75949	0.798413	NA	-1.149763	-1.14993	-0.545615	1.6039	1.207719	0.982787	0.940108	-2.135288
BOP2	1.134389	-0.99356	-0.418609	0.095251	-0.395049	0.518162	-0.60055	NA	0.010014	-3.01734	0.165844	-0.232274	0.075405	NA	-0.607359	0.558211	0.184376	-0.540769
BRE1	3.237553	NA	NA	0.505062	NA	0.21974	0.358979	NA	NA	NA	0.572923	-5.282391	NA	NA	NA	NA	NA	1.25335
BRE2	-3.420507	-2.993208	2.222397	0.403495	-2.378274	0.286536	0.51975	0.311809	0.766495	NA	0.300832	0.650757	NA	-7.364642	0.554153	-0.425762	0.897389	-0.049287
BRE5	NA	0.351539	-0.784454	0.582625	-4.188366	-1.097968	-0.558002	1.417084	-1.063746	NA	-1.194198	-5.165999	-0.333143	NA	-1.132586	-1.379376	0.776369	0.531944
BRR1	NA	1.631002	NA	-1.426214	-1.389346	0.481429	-0.503738	-0.592591	-0.524875	-9.477087	-1.573675	-1.269241	0.78042	-0.48941	0.369806	0.232816	0.758271	1.198456
BSD2	NA	-1.597943	-2.907591	0.382216	0.471334	0.189245	0.072065	0.196051	0.279919	-0.829177	0.599832	-1.1992	-0.559471	0.79901	0.087904	0.210672	0.252583	-0.488267

Gene	RAD24	RAD5	RAD52	RAD9	RFA1	RPD3	RSC1	RTT101	RTT109	SAE2	SGS1--NULL	SGS1--PM	SLX8	SWR1	TOF1	UBC13	YKU70
AAD4	0.097597	0.493083	0.609283	-1.176147	NA	0.733469	-4.99187	-0.613866	0.75745	0.167343	4.106644	0.514098	-1.482504	0.019501	-0.17762	1.103584	0.70612
ABP1	-0.03275	-0.763684	0.440912	-0.397728	NA	0.300011	NA	0.141869	0.898665	0.697599	-0.795809	0.68784	-0.53168	0.026667	-0.989547	0.089878	0.523509
ACB1	-0.731452	0.2875	NA	0.637083	NA	1.000767	NA	0.956295	-0.230058	0.419038	0.350456	0.031476	0.319078	0.386286	-0.640613	-0.207799	-0.748901
ACE2	0.008189	NA	-0.073639	0.000886	-0.156433	0.524486	NA	2.343019	-0.964612	0.772595	-0.640012	0.887034	1.822201	0.786665	0.38765	2.280314	1.292291
ACK1	0.307223	0.400626	0.053819	-0.21648	NA	1.047169	-2.299466	0.298885	-0.342926	-0.397288	-0.177429	-0.46716	0.681518	-0.156746	-0.483678	-0.340173	-0.52029
ADD66	-0.02595	1.205405	NA	0.032054	-0.020741	1.095147	NA	-1.231354	0.84042	0.218709	-0.248778	-0.822487	0.774124	-0.961961	-0.026899	0.505542	-0.774999
AGE2	-0.190426	1.01303	1.347293	0.812917	0.038952	-1.130071	NA	-0.351099	-0.408605	-0.595529	0.215011	0.448739	-1.449022	0.204204	1.630325	0.106887	-1.0681
AGP2	0.228944	-0.320899	0.437258	-0.923953	NA	-1.131644	-2.537973	-1.451955	0.643265	-0.136908	0.36131	0.298095	NA	-0.772933	0.023493	-0.866139	0.684677
AGX1	-0.414598	-0.11161	0.687219	0.320885	1.138267	-0.230004	NA	0.236304	0.48374	-0.287213	0.932198	0.434228	NA	-0.456612	-3.071267	-1.093035	-0.228868
AHC1	-0.175798	0.30528	-0.390111	0.012824	NA	-0.29038	NA	-0.68539	-0.135237	0.760092	0.037516	0.234389	-2.193605	-0.186307	-2.557635	0.654465	0.91816
AHC2	-0.743505	-0.199895	1.178387	0.446497	-0.032244	0.880791	NA	-0.149586	-0.116518	0.91036	-1.2171	-0.102374	-2.573428	-1.826057	-0.039484	1.110421	1.332514
AIM21	-0.330453	0.557777	0.683551	-0.321097	NA	-0.198299	-1.496764	-0.453451	0.365057	-0.246596	0.617507	0.136105	NA	-0.254161	-1.420514	0.236904	0.70324
AIM22	0.09991	0.900174	0.588807	-0.624544	NA	-0.467226	NA	NA	-1.661322	0.097838	1.423861	-0.520535	0.827626	-0.122471	1.846488	-0.704434	-0.14664
AIM26	0.242045	-0.289847	-0.481466	0.398116	0.668999	-0.138839	NA	-0.685136	0.438374	-0.897435	0.543402	0.318203	0.531361	-0.089403	-2.062399	-0.317132	-0.329607
AIM29	-0.611219	-0.012005	-0.101302	0.520532	NA	1.13744	NA	0.880462	0.213655	-0.052605	0.33886	0.340964	-0.358335	0.220345	-1.37353	-0.505281	0.455445
AIM3	0.618007	-0.901934	-0.038302	0.710999	0.151841	-0.402476	NA	-0.231768	1.311792	-0.057788	-0.583839	-0.04923	0.730499	0.229398	-0.868023	-0.170205	0.072919
AIM32	0.80961	0.578441	NA	-0.303648	0.868773	-0.0175	NA	-0.766896	-0.034975	0.51134	1.302212	-0.045923	-2.536613	-1.118771	0.219166	-0.572587	0.465934
AIM34	-0.096193	0.935345	NA	-0.889879	0.052518	-0.287692	-4.590424	-0.80495	0.182997	0.023455	NA	0.200317	-0.57921	-0.308321	-0.233574	0.32303	1.271823
AIM4	-0.181598	-0.326492	NA	-0.07611	-0.173434	-0.408289	NA	-0.330957	NA	-0.277096	NA	0.323226	NA	0.779485	0.286928	-0.28141	NA
AIM44	-0.559816	-1.130893	-3.538215	-0.32416	-1.935483	1.244012	-9.81088	0.237937	-3.380194	-0.050248	-0.918848	-0.112012	-0.873371	0.641965	-0.109738	0.208636	0.534505
AIP1	0.184947	-0.052781	NA	0.662943	-0.543403	-0.435182	NA	NA	-0.79819	-0.371264	NA	NA	NA	-0.012946	NA	-0.885793	0.249721
AIR1	-0.900414	-0.619962	0.813234	0.485777	NA	0.178779	-4.458348	1.09061	-0.250718	0.477042	-0.021015	-0.057675	0.755883	-0.692446	-1.032732	-0.27769	0.719471
AIR2	-0.120732	0.759145	-0.263994	-0.790051	NA	0.676382	NA	0.354814	0.193563	-0.228295	3.394568	0.678887	-0.984348	-0.887459	-0.95953	0.666773	1.298718
AKR2	0.903168	0.47125	-0.490636	0.462742	0.867668	0.231833	NA	1.113108	-0.090443	0.457035	-0.347195	0.122935	-1.400729	-1.830928	0.057282	-2.389116	-0.201604
ALB1	-0.125414	0.79913	NA	-0.162652	NA	-0.156655	NA	NA	-0.428879	0.214084	-0.602722	0.693375	1.056312	0.157597	-0.375968	0.37264	0.398332
ALG12	-0.383692	0.439146	0.168395	-0.424077	-0.668253	-1.372126	-1.073603	0.007653	1.154422	0.259377	0.471252	-0.04764	-0.365669	-0.24723	-1.790257	-0.741616	0.571429
ALG3	-0.41879	-0.676696	NA	-0.781851	NA	-0.007536	-0.426001	-0.752139	NA	0.425632	0.057385	0.036043	3.572451	0.046041	-0.598426	-0.238274	0.233066
ALG5	-0.025993	-0.724143	0.469242	0.116886	0.54125	-0.030739	-2.249957	-0.522985	0.643339	-0.409195	0.049253	0.11169	0.15652	0.084584	NA	-0.078064	-0.281303
ALG6	-0.437118	0.223066	1.210388	-0.329234	0.399268	-0.879603	NA	-0.259336	0.711205	0.210783	0.661134	-0.013703	-0.261224	-1.054501	NA	0.184842	-0.228836
ALG8	-0.32212	0.416574	-0.015382	-0.125162	0.896323	0.111078	NA	0.336174	0.338575	0.093279	3.786846	0.360785	0.271859	-0.234171	-1.052093	0.47773	0.161401
ALT1	0.486102	NA	0.107224	1.36007	1.11863	0.79606	NA	-0.477503	NA	0.063986	0.153797	0.094604	1.184187	-0.6248	-0.105627	0.689236	0.471859
AMD1	0.91479	0.882744	NA	-0.514897	-0.025206	-0.052492	-0.459792	1.035103	1.321629	0.1771	-0.186982	0.098726	-0.362445	0.463945	-2.854746	0.467968	-0.234941
APA1	0.179299	-0.795873	0.2676	-0.641837	NA	0.672766	-3.949707	-0.565168	1.487812	0.273542	-0.02424	0.360856	0.344347	-0.324719	0.454559	0.039029	-0.108797
APC1	-0.393717	-0.036769	0.052031	0.018462	-0.817732	-0.686936	NA	-0.481245	-2.917548	0.50843	1.167893	0.152535	1.355142	0.512173	NA	0.275385	0.243409
APC11	0.221655	-0.091085	NA	-0.063567	NA	0.32973	NA	-0.947108	NA	0.237653	0.144907	0.447338	NA	-0.457059	0.792247	NA	-0.113428
APC4	0.204786	0.566642	-0.277609	-0.530768	NA	-0.490789	NA	-1.251641	-0.299883	0.627962	-0.488133	-0.027263	1.371175	0.23105	-1.638332	NA	0.923174
APC5	0.465703	0.771153	NA	-0.449183	NA	-0.104579	NA	-0.300225	0.243314	-0.402632	0.629841	-0.890905	1.474544	0.12452	-1.538409	0.036032	0.084168
APC9	1.77619	NA	NA	0.76046	0.374954	1.479883	-0.198551	-0.607289	NA	-0.460082	1.764465	0.814023	-0.598849	0.307856	-0.472103	-1.158877	-0.222336
APE3	-0.104232	-0.257566	0.162787	-0.290388	0.071209	0.197893	NA	0.231751	-0.4295	0.759334	0.042915	-0.743982	-2.479707	0.072643	-1.252865	-0.714157	0.214861
APL5	0.424853	-0.887139	-0.066547	0.134479	-0.446869	-0.661785	NA	-0.034367	1.697327	0.456778	0.805662	-0.432705	-1.058723	0.450512	-3.183552	0.50969	-0.336469
APL6	-0.938424	-0.203191	0.167099	-0.189868	-0.442889	-1.164518	NA	0.30565	0.396262	0.074255	NA	0.191193	0.482771	0.179173	NA	0.459185	0.313369
APM3	0.288285	-0.427839	-1.197057	-0.159418	NA	0.180001	NA	-0.059509	-0.15541	-0.096912	-1.388416	-0.171676	0.03235	0.890063	-0.457615	NA	0.228306
APM4	-0.295297	-0.14736	NA	0.175878	0.2669	0.446096	NA	0.201828	0.378368	0.445927	NA	-0.080152	0.138239	0.203027	-0.818813	-0.341925	0.241584
APQ12	-0.319684	0.299653	0.258481	0.852318	0.582898	2.079763	NA	0.281854	-2.374108	0.206141	-0.906056	0.799654	-1.887796	-5.781648	-1.935634	-0.657873	1.198422
APS3	-0.458866	0.04154	0.461004	0.248689	-1.14877	-0.542452	NA	NA	0.519219	0.153498	0.304488	-0.439692	0.373775	0.356553	-0.852002	0.77565	0.81842
APT1	0.541787	-0.696414	NA	0.56074	0.687921	-0.56113	NA	0.511284	-0.729528	NA	-0.082852	-0.700055	-0.637897	-0.518226	NA	-0.728939	-2.191494
ARC1	-0.136687	NA	0.280459	-0.723833	1.283318	NA	NA	0.97303	-1.152084	NA	-1.187019	0.068419	NA	0.181624	0.190887	-0.054984	-1.745
ARG80	0.271261	0.284395	NA	0.955256	NA	-0.385288	-1.189911	0.364388	-0.264521	0.066023	0.003611	0.124958	0.461044	0.378538	-0.131172	-0.179887	1.262644
ARL1	0.556679	0.762538	0.879926	0.056641	1.531165	-0.141695	NA	-0.1905	0.50466	0.164678	0.743649	-0.229241	NA	-0.475182	NA	0.706284	0.144412
ARO1	0.542509	-0.481834	NA	NA	-2.558762	2.259092	NA	1.379841	2.16959	0.63681	-0.638128	1.754573	-1.434035	-3.007002	NA	NA	0.834554
ARP1	-0.371981	-0.811435	NA	0.283485	NA	-0.07777	NA	-0.351054	-1.688144	0.396671	0.830571	0.400221	0.493262	-0.821349	1.304518	0.80812	0.202114
ARP4	1.185689	1.357686	1.613036	0.802896	-0.166136	-1.081447	NA	NA	-1.233143	-0.462198	0.568062	-0.189325	-7.131208	-0.360744	0.770848	-0.507672	-0.378088
ARP6	-1.766768	NA	NA	0.58124	-2.16412	-0.488614	NA	-0.19243	NA	-1.371294	0.35688	1.656289	NA	1.960514	-0.486089	0.205879	-0.975886
ARP7	-0.041013	-1.221201	NA	0.646352	-1.043794	-1.009221	-1.222844	0.526089	0.814981	0.264128	-0.186353	-0.276933	0.622833	-0.638463	-1.28312	0.862947	0.32889
ARV1	0.934005	-0.749628	0.116943	-0.324731	NA	-2.598073	NA	-0.380367	0.275123	-0.392241	-0.082568	-0.240549	-1.265497	0.147361	-1.523188	0.112726	0.336392
ARX1	0.42358	0.533351	0.635741	0.035925	NA	-0.265455	NA	1.138529	NA	-0.422055	-0.244137	-0.835033	NA	0.318818	0.008792	NA	0.1475
ASF1	-1.99679	NA	NA	0.071614	NA	-0.997004	-4.219172	NA	NA	0.596553	0.424634	0.139474	-7.944155	-3.590219	1.839814	0.442047	0.041631
ASH1	0.036478	-0.488048	NA	0.137415	NA	-0.232683	NA	0.083069	NA	-0.275081	0.972268	0.146042	1.47552	-0.478208	-0.518956	-0.348913	0.021388
ASI1	0.345015	0.637905	-0.77109	0.627573	-0.30853	0.515875	NA	0.325403	-0.038024	0.172711	NA	NA	-0.658141	-0.286893	0.199099	-0.244734	0.927374
ASI3	0.194194	-0.012073	0.290821	-0.391021	-0.316742	-0.042137	NA	0.352604	0.281853	-0.358346	0.393169	-0.210719	-0.274593	-0.491303	-0.413548	-0.448008	0.950218
ASK10	-0.079892	0.703543	0.996648	0.325148	0.490825	-0.542721	NA	-0.659502	0.471252	0.021566	0.862574	-0.11758	0.558079	0.419498	-0.276062	-0.527919	-0.411333
ASM4	0.167943	-0.145967	0.779422	0.623256	0.356436	1.167147	NA	0.128678	0.683339	-0.004354	NA	0.203682	-0.247312	0.208616	0.402123	-0.096253	0.879068
ASR1	-0.033145	0.042451	-0.671261	1.038381	-0.266025	-0.034711	NA	-0.633475	NA	0.235611	-0.250773	-0.016265	-0.379218	-0.396644	-1.662248	0.209165	-0.04736
ATG21	0.091881	-0.088026	NA	-0.314638	NA	0.33934	NA	-0.777794	-0.504105	-0.061367	-0.737004	-0.466324	-0.715977	0.481674	0.279129	-0.840022	-0.939643
ATG8	-0.57964	0.384351	NA	-0.762754	0.42337	-0.06722	NA	0.149102	0.510213	-0.932792	0.094889	-0.351947	0.817625	-0.322307	-1.807806	-0.27361	0.189627
ATP23	-1.401241	0.502322	1.982893	-1.511764	NA	-0.999248	NA	0.161491	1.224989	-0.11309	0.281501	0.042714	0.230745	-0.92355	0.332598	0.642318	0.071502
ATS1	0.265212	0.758456	-1.10033	0.203569	NA	0.685776	NA	-1.283509	-0.520269	-0.158612	0.59093	-0.337372	-0.640707	-1.044116	-0.934428	0.633578	0.501297
AVL9	0.695309	NA	0.717319	0.050724	-0.459203	0.732335	NA	-0.242628	NA	-0.964744	-0.256182	0.628749	-0.117755	0.777283	-0.105052	0.200928	0.256312
AVO2	0.061824	0.372377	NA	-0.429471	0.29521	-1.275717	NA	0.641762	0.950347	-0.378891	0.055675	-0.402307	0.610176	-0.016247	-1.053252	-0.141008	0.026249
AZF1	0.067874	0.42164	0.437134	-0.008808	0.80024	0.752789	NA	-0.605287	-0.037895	-0.12068	-0.215477	-0.286517	-0.632498	-0.948521	0.176587	-1.424952	-0.315168
BAS1	-0.040572	2.145587	2.034394	-1.531938	NA	0.151023	NA	1.068433	1.385697	0.098448	0.959104	-0.54879	1.316202	-0.905202	2.274303	0.022769	-0.419499
BBC1	1.46594	0.335744	0.117078	-0.700972	NA	0.402327	NA	NA	-0.091839	-0.182739	0.232125	-0.325869	1.208632	-0.058347	-0.449713	0.144059	-0.165118
BCK1	0.719172	-2.535287	-3.948813	0.529658	-0.897526	2.323011	NA	NA	-4.792815	-0.479009	-2.491335	1.193104	-1.041643	0.271688	-0.230689	-0.548504	0.328947
BCK2	NA	-0.356622	0.252531	-0.011582	NA	0.358864	-2.955923	-0.285275	0.410135	0.152106	-0.396657	-0.393689	NA	-0.277409	-0.718769	0.386589	-0.233359
BDF2	0.02766	-0.623347	0.687962	0.214256	NA	-0.515791	-0.690064	0.697348	1.641004	0.121179	0.882851	-0.478494	1.784508	-0.372558	0.532721	0.525712	-0.459803
BEM2	NA	-0.838558	-1.288695	0.912302	NA	1.785967	NA	-1.64168	-1.716382	0.378275	-2.429948	1.009726	NA	-0.626952	0.990123	0.844132	0.19739
BEM3	0.294408	0.235079	-1.21334	0.174688	1.438267	0.628407	NA	0.161862	-0.520142	1.324478	0.281576	0.914172	-0.328994	0.196159	-0.796596	-0.191437	0.792634
BEM4	0.684253	0.079205	0.854161	0.635854	0.131067	-1.158371	NA	-1.361232	-0.035685	0.494981	0.990067	0.578795	0.847466	-0.136007	1.241257	-0.577602	-0.253545
BFA1	0.668894	-4.788917	-4.556668	-0.759233	-2.734897	0.560029	NA	NA	-11.141481	-0.370299	-2.759359	0.375382	NA	-0.051076	0.30945	-1.152745	0.289811
BIK1	-0.217555	-0.418599	0.253234	-0.07482	-1.514322	-0.178353	NA	0.793314	2.022646	0.348207	0.418894	-0.256166	0.546873	0.837736	0.555662	-0.042235	0.22819
BIM1	1.673778	-1.756103	-0.779809	0.961907	NA	0.316789	NA	-0.723478	-2.174691	-0.956729	1.794871	-0.140301	-0.197383	-4.702926	NA	-2.493861	0.317483
BIT2	-0.259962	-0.732659	0.412172	-0.334312	-0.390201	0.630836	NA	-0.230642	0.30033	-0.434571	0.27133	-0.488762	0.348861	0.603629	-0.739692	-0.015714	-0.006991
BLM10	-0.974201	0.256528	0.40166	-0.611398	-0.072227	1.774094	NA	-0.165036	1.085059	-0.1362	-0.86556	0.344672	-2.064234	0.18384	-0.388449	0.16962	-0.008739
BMH1	NA	2.256867	NA	-0.557179	NA	-0.471366	NA	1.754556	1.507527	0.60772	-0.786482	0.176478	NA	-1.255233	-0.632344	0.647195	0.043472
BMH2	-0.910352	1.11586	0.17715	-1.646549	NA	0.104499	NA	0.075006	-0.734973	0.600675	3.612474	0.527431	-0.652809	-0.032727	NA	NA	NA
BNI5	-0.588297	0.088332	0.636549	NA	1.01725	0.245973	-0.558666	0.161479	0.065222	0.332168	0.290554	0.291303	0.02069	0.604151	NA	-0.163707	0.955819
BOI1	-0.51144	-0.053891	NA	-0.311927	-0.163619	0.386062	-2.458124	-0.400314	-0.128726	0.026148	-0.448854	0.413164	-0.326601	0.31237	0.230987	-0.804366	1.042984
BOI2	NA	-1.405461	NA	0.211236	-1.190752	0.701669	-0.231879	-0.768232	-1.71118	0.86503	-0.973679	0.192319	NA	0.552956	0.85274	-0.551978	1.413017
BOP2	0.036588	0.075388	-1.038326	-0.234689	NA	-1.137255	NA	0.37254	0.103729	0.116597	0.185865	-0.47005	0.911509	-2.298025	-1.048969	0.559086	0.031976
BRE1	NA	NA	NA	NA	0.686038	-2.518036	NA	NA	NA	NA	0.168404	0.811536	NA	NA	NA	-0.959082	NA
BRE2	0.618115	NA	-0.271931	1.401154	0.144375	1.97118	-8.465184	-0.39733	NA	-0.408489	-0.134688	0.112909	-3.049885	-8.756666	2.11304	-1.356148	-0.059236
BRE5	0.304148	1.485537	0.580061	0.492509	0.881829	NA	0.999772	1.672897	1.763495	-0.403768	-2.722232	0.381126	NA	-5.652471	-1.457556	-2.759598	0.368398
BRR1	0.818029	1.33722	-0.959131	0.715905	0.002085	1.386644	NA	0.901472	2.175566	0.245868	NA	0.577028	-0.689403	-0.565847	0.001493	0.014589	1.319661
BSD2	0.138895	-0.187418	-0.071992	0.817894	0.063311	0.930488	NA	0.291093	-1.826686	-0.392967	-2.073356	0.150481	NA	0.203194	-0.350977	-0.359246	0.976353



CTK3	NA	-2.505524	NA	-4.103675	-2.833629	-0.44082	NA	NA	-1.072091	NA	NA	-7.375971	0.309346	1.332015	-0.890103	0.241624	-2.950231	NA	-2.190705	1.845264	NA	-0.505148	NA	-2.003637	1.44374	-0.606212	-5.43694	-1.139702	-1.865459	0.728529	NA	NA	NA	-1.203365	-0.806623
CTP1	1.347919	0.147484	-0.762854	-0.358669	0.114559	-1.355297	-0.110088	0.379154	0.171875	0.960921	-1.320196	0.424293	-0.111952	1.896792	-0.380969	-0.206145	-0.778279	0.869504	-1.072084	1.261105	NA	0.560757	NA	-2.828516	NA	0.673367	0.962418	1.395071	-0.375414	-0.702908	-0.154541	-0.568244	0.208141	0.282767	-0.96916
CUE1	NA	0.738352	-1.330168	0.379825	-0.193072	-0.174154	0.255108	-0.219586	-0.984655	1.785586	1.828754	0.462014	NA	0.268754	0.221505	0.343307	-0.152661	-0.159493	0.003365	0.210134	-0.30073	-0.571896	1.793663	0.462908	NA	-0.532682	0.397121	-0.542052	NA	NA	-0.465835	0.073968	NA	-1.07415	NA
CUE2	NA	NA	-0.601758	-0.292798	-0.221716	-0.182303	-0.594476	-0.384644	-0.675696	-1.476143	0.693568	1.039698	NA	1.354963	-0.406562	-0.023732	0.094692	0.287673	-0.116736	0.363755	0.058188	-0.728754	1.073701	0.043696	NA	-0.066055	1.005676	0.081938	0.256796	-0.751459	0.417169	-1.016621	0.349815	-0.696626	0.208391
CUE3	-4.750531	1.26821	-0.688787	0.262163	0.741718	0.1141	-0.123	NA	-0.327883	-1.531156	-0.947434	-0.841742	0.263141	NA	0.38133	-0.462182	0.735065	-0.547198	0.569737	0.383203	0.989839	0.341576	NA	-0.075107	-2.568507	0.294634	1.484109	NA	-0.735268	0.245954	-0.976118	0.202435	NA	0.513145	0.206669
CUE4	NA	1.027514	NA	-0.028932	-2.489168	0.034654	0.305692	-0.858856	0.764674	0.192893	-0.546093	-0.395373	0.0231	1.563517	-0.165528	-0.399251	0.45602	0.377584	1.108582	0.728236	NA	1.033063	0.526292	-0.033832	NA	0.027224	-1.177109	0.098213	0.394635	-0.839625	0.485756	0.416613	-0.226994	1.099064	-0.340547
CUE5	NA	-0.216956	0.411427	0.417292	0.664679	0.045258	NA	-0.635184	NA	NA	1.580162	0.184067	0.773569	NA	0.355154	0.048346	-0.497788	-0.189296	-0.450209	0.134848	0.972429	0.13523	NA	-0.00122	-5.110667	-0.503578	1.016071	0.794581	2.16226	0.158903	-0.215566	-0.414042	0.780467	-0.218999	0.396293
CUL3	NA	NA	0.393483	-0.754057	NA	0.177188	0.009673	NA	-0.652011	-2.287617	-0.249048	-0.722884	NA	NA	0.134815	-0.341811	-0.461427	0.897615	0.10921	0.331729	NA	-3.528166	NA	-0.748128	NA	-0.118486	NA	-0.61051	NA	0.297926	-0.258881	0.259853	-0.711901	0.094156	-0.364412
CUP9	NA	0.234812	-0.979964	-1.292425	NA	-0.439066	0.044227	1.933227	0.032656	NA	-0.29179	-1.463601	0.051238	NA	0.451178	0.652955	-4.219497	0.657828	-0.529215	-0.496219	NA	-0.446301	0.812023	0.053655	NA	0.436881	0.260489	-0.11196	0.711084	0.194411	0.728472	-0.468487	-1.798966	0.311792	-1.642536
CWC15	-1.861149	0.712679	1.535036	0.446076	NA	0.451707	0.806911	-1.286095	0.578106	-0.104513	-0.945386	-1.007183	0.524276	-1.940891	NA	0.451211	-0.231927	0.031997	0.499917	-0.165954	0.192667	NA	NA	0.3959	NA	0.803696	-0.153863	0.525065	-0.300558	0.353125	-0.214447	-0.073949	-0.357184	NA	1.300286
CWC21	-3.794513	-0.18093	-1.702766	-0.702983	0.92886	NA	0.324509	0.667556	0.024918	-4.022182	-0.492398	-0.112779	1.052139	NA	-0.151753	0.048618	-0.252393	1.226242	-0.075591	-0.451559	1.065715	0.934411	NA	-0.470298	NA	0.168079	0.459408	-0.767337	-0.464442	0.427233	0.258273	-1.860539	0.215909	-0.211017	1.909288
CWH41	NA	0.212067	1.819802	-0.030767	0.31393	0.620893	0.634351	-1.78251	0.682726	NA	0.516467	-0.802451	0.798678	-1.232941	0.817885	0.202258	-0.369521	-0.88368	0.173814	0.13267	0.49256	0.025715	NA	1.504158	NA	0.133777	0.502719	-0.582196	-0.612859	0.172723	-0.921174	0.228017	0.105041	0.083403	0.261557
CWH43	NA	-0.681002	-0.917264	NA	-0.84526	0.212342	-0.656549	1.150921	0.069378	-0.125772	-0.160153	NA	0.137974	NA	0.096983	0.106366	-0.129867	NA	-0.178631	-1.161337	0.588848	0.409825	NA	0.612311	-1.601215	-0.259688	0.460641	-0.383222	-0.510653	0.602894	1.076962	0.322035	-0.530452	0.424816	0.704375
CYK3	NA	-1.037449	NA	0.350494	-1.754903	-0.098826	0.724401	NA	0.352616	1.081702	-1.382441	-0.030804	-2.009054	NA	-0.272423	0.377439	-0.15487	-2.401464	-0.358683	-0.507985	-1.554581	0.24888	0.982032	-1.590859	NA	-1.163847	-1.331719	0.94804	-2.028079	0.038651	0.744196	0.342321	NA	0.991686	0.668015
CYT1	NA	0.318408	-0.034809	-0.080733	0.83816	0.133226	NA	-0.391116	NA	NA	0.364892	0.411479	-0.216812	-0.607787	-0.494534	-0.5404	0.077823	-0.186917	0.737172	0.091555	0.358019	-0.242914	NA	0.035436	NA	-1.04248	0.184616	-0.164539	1.180536	-0.48546	-0.294269	-0.419738	NA	0.881799	0.307209
DAL81	NA	0.007761	NA	-1.936124	0.173592	1.354802	0.504603	-0.306961	0.179029	-0.160047	0.180416	NA	0.099836	-1.733753	0.882193	0.240516	-2.549691	0.541927	-1.351869	1.147555	1.064538	-2.843387	NA	1.757914	NA	0.583154	1.984997	-0.062797	3.13173	0.34776	-0.371602	-1.40593	1.638547	1.384051	-0.66044
DAS1	NA	NA	0.011724	0.689293	0.258876	0.028392	0.786823	0.399844	-0.390665	0.358652	1.095666	-1.813569	-0.613806	NA	-0.272557	0.24531	-0.478248	-0.826167	0.068418	-0.358076	0.330622	0.266833	0.849717	-1.234039	NA	-0.123764	-0.460248	-0.040754	-0.35462	0.540417	1.216017	-0.405244	NA	-0.122034	0.197106
DBF2	NA	NA	-5.295336	0.418536	NA	0.350211	-0.400241	-0.991462	0.094462	0.020319	-0.745489	-1.279068	-1.059448	-0.537728	-1.16649	0.163176	0.266493	-0.025536	-0.197625	0.085091	NA	-0.608013	0.100209	-0.232703	NA	0.993156	0.878767	0.827687	-0.997619	1.534166	-0.30059	1.337262	-0.270138	-0.382078	1.182923
DBP1	NA	0.001143	NA	-1.124529	NA	-0.265757	-0.887913	0.830091	0.563764	NA	0.335164	0.230543	NA	-0.225576	0.182106	0.172435	-0.237923	0.816737	0.478155	0.355184	0.133337	-1.242169	NA	0.222845	NA	0.944544	-0.679752	-0.926493	-0.591688	0.127313	-1.536813	-0.424887	0.253771	0.047606	-0.973865
DBP3	NA	0.745887	NA	-0.730175	-0.784913	0.390868	-0.07809	1.094192	-0.337475	NA	-0.223797	0.205073	0.910983	NA	0.096244	-0.575375	-0.203526	0.106929	-0.559539	1.412805	-1.827442	0.014708	NA	0.477775	NA	0.880601	0.742611	NA	-0.970394	-0.21451	-0.600995	0.395343	0.59879	0.306684	-0.285701
DBR1	NA	1.479193	-0.078086	-0.844445	0.236876	-0.63028	0.503625	-1.670317	0.848915	-1.661963	1.170462	0.457107	0.757627	NA	0.839448	0.741561	-0.054197	0.937533	0.105573	0.038987	0.375014	-0.112272	NA	0.013447	NA	0.642484	-0.818175	0.265144	-1.12301	0.688784	-0.097061	0.407699	-0.293872	0.397589	0.746624
DCC1	-1.746698	NA	NA	NA	NA	NA	1.08039	NA	NA	NA	-1.791336	NA	NA	NA	NA	NA	NA	NA	-6.863889	NA	NA	NA	NA	1.049876	NA	NA	NA	NA	1.433113	1.26126	NA	NA	NA	-0.630102	NA
DCN1	NA	-2.727541	NA	-0.190529	NA	-0.753701	-0.931761	0.99076	-1.240835	-1.20024	NA	0.363056	-0.248685	NA	-0.721788	-0.578793	-0.120266	-0.911209	-1.14151	NA	0.928823	0.10298	NA	-0.575204	NA	0.304828	0.173727	-0.844332	-0.272664	-0.918418	2.153387	0.23494	0.203024	0.309711	-0.051266
DCR2	0.356028	0.906689	-0.590601	0.405718	0.141986	0.385983	0.128218	0.78663	0.441116	-0.212214	-0.15259	-0.1522	0.041707	NA	-0.228583	-0.221153	0.143526	0.640599	-0.203605	-0.789215	0.478483	-0.549893	NA	-0.507065	NA	0.413569	0.871505	0.518691	-0.482447	0.550606	0.682977	0.486515	-0.15343	-0.038944	0.230722
DDC1	-0.860603	0.305329	0.442716	2.313759	NA	0.762172	1.052461	-1.632659	0.298094	-0.806395	NA	NA	0.325869	1.613085	2.412856	2.06508	NA	-0.549113	2.658879	-1.770079	-0.145403	-0.23262	NA	0.9525	NA	2.103165	0.575898	1.738567	-0.020675	0.716787	-1.99283	-0.69762	NA	-2.305108	1.600617
DEG1	0.983837	-2.055764	-3.788565	0.749671	-0.863501	0.143929	-0.694633	-2.59076	-1.187284	-5.211253	3.199568	1.1876	1.25312	0.100645	0.095732	-0.354688	1.314778	1.107201	1.854849	0.011586	0.668222	0.859352	0.470358	0.105504	NA	-3.125378	-0.70106	-2.496987	0.569739	-0.086631	-2.930246	-2.776878	1.193266	-0.430709	0.442276
DEP1	NA	-3.204714	NA	1.066745	-1.106162	-0.168203	-0.197418	NA	1.024308	NA	-0.418996	-0.218003	-2.294935	3.087443	0.154579	0.201391	1.077249	-1.412317	1.068726	-0.918201	-2.727501	1.176282	NA	2.534522	NA	-0.875326	-5.686298	-0.705188	0.241717	1.104166	-8.108162	NA	1.907177	-1.76451	-0.30822
DGK1	NA	-1.308577	0.566884	NA	-0.461973	-0.250803	-0.450542	-0.176483	-1.060101	3.976554	NA	0.209274	-0.381201	NA	0.366972	0.148698	NA	NA	-2.142018	-0.440009	NA	-0.435006	NA	-0.187842	NA	0.817049	-0.862611	-0.139678	-1.142501	0.125477	NA	0.461829	-0.953705	-0.566178	0.203399
DGR2	NA	0.419406	-0.056126	-0.358229	-1.328074	0.380785	0.983295	-0.167768	0.328568	1.180334	-0.012529	-0.445992	0.05763	-0.305333	0.010553	-0.10239	0.195054	-0.326824	0.8396	0.08959	-0.468513	-0.331922	0.347046	-0.929883	NA	0.167621	0.266919	0.474926	0.877523	-0.231667	-1.091736	0.067771	-0.08689	-0.559231	0.522766
DIA2	NA	-2.6568	-1.771583	-3.714014	0.008623	1.615118	NA	NA	NA	NA	0.949058	NA	NA	NA	-5.397665	-1.647088	-5.158986	NA	-3.490763	1.685888	NA	0.263284	-1.151518	1.301244	NA	3.184113	1.617182	-3.465638	NA	2.163016	NA	-0.946912	NA	0.998036	-0.623409
DIE2	NA	1.214738	NA	0.546505	-0.231894	-0.262026	-0.442249	0.963669	-0.468139	0.577874	-0.649766	-0.209288	NA	0.362541	-1.123303	0.211573	0.591498	0.892043	0.618963	-0.17342	0.902832	-0.66982	NA	-1.448456	NA	-0.107305	0.817479	-0.38758	0.608179	-0.376379	0.598182	0.322242	-0.97206	-0.200293	-0.69483
DJP1	NA	-0.091001	0.704285	0.361453	-1.751733	-0.219725	0.381561	-1.306316	0.650796	NA	-1.171712	-0.200749	0.770707	-2.477205	0.390931	0.34313	-0.58363	0.707708	0.317781	0.912402	NA	0.425852	0.042296	-0.219166	NA	-0.317261	0.934581	0.108727	0.08783	-0.076139	-0.754583	-0.090018	-0.131691	0.050708	-0.122435
DMA1	NA	-0.527265	0.402058	0.244357	-0.347452	0.151599	0.521262	-4.30E-05	0.66368	1.106238	-0.764777	-1.379391	0.147291	1.508499	0.469693	0.751908	-0.081692	0.611169	-0.098445	-0.0472	NA	0.101692	0.743635	-0.284545	-0.329262	-0.344706	-0.674957	0.447473	-0.401638	1.023788	-0.81981	0.850617	0.748877	-0.500189	0.049532
DMA2	-2.211782	-1.290055	-0.018524	0.121527	1.267366	0.774169	0.330283	1.032983	1.571113	-3.157492	-1.290525	-1.286773	NA	-2.117315	0.603581	NA	-0.016733	-1.5143	-0.228109	-0.124579	NA	1.038798	NA	-0.486166	NA	0.82482	-2.001413	0.804309	-1.468604	0.283549	1.639861	0.342923	-0.631877	-0.179879	1.3908
DNF1	NA	NA	0.144621	-1.469383	-0.17303	NA	0.277283	NA	-0.330552	NA	-0.073514	-0.903306	NA	NA	0.897942	-0.218194	0.077217	NA	NA	-1.203393	-1.219995	-1.29405	NA	-1.017377	NA	0.028111	-1.091426	0.305298	0.229671	0.78376	NA	0.852528	0.174709	0.496367	0.505346
DNM1	0.673315	1.712348	0.954987	-0.219978	0.265728	0.332915	0.000947	0.905605	-0.376702	-0.796362	0.075242	0.228653	0.625821	NA	0.2187	0.440853	0.003837	0.020659	-0.27443	NA	NA	0.111363	0.647954	-1.135572	NA	0.325047	NA	0.293717	0.717949	0.14483	0.280328	-0.531498	-1.072253	0.24431	0.687372
DOA1	NA	NA	-2.153182	-0.201754	-4.844579	1.213435	-0.085074	NA	0.759874	NA	-1.069182	-3.16644	-1.911347	-2.68112	1.103699	0.736454	-0.036957	-0.195716	-0.21334	-0.160276	-1.717864	1.208198	-2.514119	2.846311	NA	0.441524	NA	0.00625	0.378312	0.784815	NA	-5.111397	NA	-2.379923	0.899915
DOC1	NA	NA	NA	1.063131	NA	0.793476	-0.871441	-2.495852	1.231685	-2.113216	-0.631739	-3.861506	-2.787402	NA	0.656974	0.709211	1.129673	-2.003214	1.121583	-1.185504	NA	2.284773	-2.887074	1.336171	NA	-0.882483	-6.057047	NA	2.222208	0.184236	-1.883113	0.605185	NA	-2.782698	-0.446558
DOM34	NA	NA	-0.806096	0.33845	1.540565	-0.362249	-0.320874	0.648853	-0.112873	NA	1.906447	0.866016	-0.421876	-1.18959	0.042287	-0.846584	0.080012	0.936615	0.12549	0.863142	NA	-0.494313	NA	-1.358232	NA	1.412723	2.134199	0.000839	0.410777	-0.6447	-0.522641	0.921729	NA	0.221008	1.1054
DOT1	0.289718	NA	NA	-0.332112	NA	NA	-0.753376	1.131496	NA	NA	NA	-1.989438	NA	NA	0.353979	NA	NA	1.447086	NA	NA	NA	0.620276	NA	-2.532982	NA	NA	NA	NA	-2.863584	0.282315	NA	0.043074	-2.383119	-0.526388	NA
DOT6	0.422327	0.276097	0.569378	-0.385491	-0.073807	0.531696	-1.101378	0.14886	0.335131	-0.80048	NA	1.287356	0.812646	0.882501	-0.203139	-0.473436	0.201786	NA	0.546865	-0.322266	-1.662353	-0.889774	-0.455859	0.719411	NA	-0.491274	-0.888407	0.192528	-0.280612	-0.231879	NA	0.316654	NA	1.103232	-0.103991
DPB11	NA	NA	0.495631	0.378521	-0.345355	0.031218	0.706972	1.650486	-0.055246	NA	-3.395443	-2.810507	-1.290138	NA	-0.171448	0.167582	-0.369199	-1.451637	0.556651	0.039078	-1.194404	-0.230829	NA	-0.085623	NA	NA	0.371077	0.526392	-0.210546	0.326899	1.086314	NA	1.077422	-0.33668	0.49748
DPB2	NA	-0.627307	-0.282349	0.330317	0.454009	0.157343	-1.134767	2.331202	0.242421	-8.217378	0.249311	0.136482	-0.548925	-0.854254	-0.289494	0.427015	0.361764	-0.917725	-0.193503	0.403273	-0.853852	-0.386968	NA	-0.832992	NA	-0.376854	-1.400783	NA	0.041141	0.176331	2.350439	-4.056994	NA	0.50037	0.462859
DPB3	-0.888364	0.795034	1.551009	-1.108491	-0.769523	0.716848	0.050015	-1.175921	-0.925407	-5.191098	0.073881	0.055467	NA	NA	-0.084435	0.139163	-0.70881	1.348656	-1.50686	0.624547	1.030081	-0.109533	NA	0.599169	NA	2.893203	0.217161	0.972693	1.938628	1.463912	-2.516613	-1.403006	-0.596481	1.465293	1.075628
DPB4	NA	NA	0.973432	-3.895598	-0.371891	0.027111	0.836827	-2.525736	-1.299093	-7.128332	-0.57379	0.468049	0.67036	-4.578959	NA	0.376515	-2.450911	0.478227	-1.696631	1.125819	NA	-0.826474	0.23402	0.668799	NA	2.788437	0.43047	0.651323	0.498184	1.048622	-0.069035	-0.752675	1.081424	NA	0.102024
DPL1	NA	0.196988	0.812263	-0.122749	0.492448	0.461966	0.317475	-0.120391	0.399901	-1.044952	-1.312967	0.183378	-1.083283	-1.421865	0.240268	-0.17314	-0.241638	1.017744	0.004298	-0.110788	NA	NA	0.164755	0.348175	NA	0.51613	0.096526	0.319351	-0.941213	0.592913	0.223136	NA	-1.198215	0.387455	1.047443
DRS2	0.71972	NA	-5.050495	0.084617	-0.015403	0.340596	-0.276514	-0.439811	-0.099078	0.045708	0.887049	0.363062	1.005483	-0.151721	-1.093564	-0.439433	-0.54521	-0.65994	0.529592	0.047185	-1.118193	-0.497302	NA	-1.058182	NA	-0.994356	-0.003514	-0.370006	0.883466	0.014615	-0.513904	-0.263812	-0.457361	-0.456394	-0.014718
DSD1	1.142724	0.288396	0.519931	0.162544	0.1957	0.683042	0.442069	-0.943932	0.075737	-0.452012	-0.141951	-0.522789	0.345065	NA	-0.652011	0.130532	0.137283	-0.037385	0.128328	-0.001431	-0.003458	0.003359	NA	-0.303772	NA	-0.916123	0.018383	NA	0.187426	-0.033401	-0.370954	-0.550155	0.541239	-0.421455	0.212339
DSE3	4.30327	1.134471	0.694391	-0.435617	0.348592	-0.241637	-0.505353	0.134513	-0.901757	-2.030887	-0.424853	0.975522	-0.324621	NA	-0.509012	0.208745	0.264957	-0.442062	0.696588	-0.273411	0.699931	0.315489	-0.38956	0.582825	1.394929	0.076356	1.5028	0.370109	-0.638848	0.539117	0.926322	0.027339	0.512261	-0.582521	0.104318
DSS4	1.101759	-0.008115	NA	0.767369	0.148581	-0.534171	-0.239586	-0.448167	-0.685045	0.70315	0.114639	-0.059607	-0.060027	NA	1.109642	0.304563	0.240311	0.063397	-0.71822	-0.584109	0.913881	0.542656	NA	-0.041702	NA	-0.603653	-0.361885	0.378446	-0.622237	0.745631	0.020037	0.654341	-0.633169	0.050346	-0.377151
DST1	NA	-4.05574	-5.118287	0.796815	-3.579741	-0.221285	0.090149	NA	0.209025	3.766677	NA	-1.939957	NA	NA	0.496448	0.931245	-0.629342	0.058572	-0.188152	1.109335	NA	0.721412	NA	2.250648	NA	-3.378131	NA	0.318934	-0.469009	1.490301	NA	NA	-2.464409	0.119824	-0.775784
DUG2	-4.841813	0.756268	1.210505	0.283646	0.932389	-0.09595	0.989047	0.539661	-0.06375	NA	NA	0.456578	0.403975	2.572416	-0.956142	-0.442647	0.149988	-0.919856	-0.677725	0.170882	-0.259549	0.029494	0.231013	0.289835	1.649305	0.079919	1.043588	0.396903	0.543155	0.234	0.285455	0.271762	1.687783	-0.1447	0.598837
DUS3	NA	0.403208	0.946678	-0.421024	0.692133	-0.064315	-0.257463	0.501196	0.637331	-0.332905	-1.16491	-0.267044	0.598165	NA	0.32617	-0.01889	0.075918	0.476198	0.270195	-0.32158	NA	0.135684	NA	0.09754	NA	-0.37233	-0.212871	-0.024882	0.426326	0.314207	-0.239793	0.549031	-0.227638	-0.158228	-0.064294
DYN1	NA	-0.738452	-0.133008	-0.769478	-0.10529	-0.082807	-0.725132	-0.130586	0.184064	NA	NA	0.576686	-1.347071	NA	-0.373028	0.829679	-0.8962	-2.39709	-0.325379	-0.163682	NA	-0.590278	NA	0.205643	NA	0.277805	-1.141092	0.299657	-0.327236	-0.033197	-1.918445	-0.344151	0.742077	-0.296803	0.42767
DYN2	NA	NA	0.470992	0.52958	-0.415049	NA	0.990565	0.38357	-0.04839	0.788605	0.096379	0.494841	0.312515	-1.152752	-0.248892	-0.305749	0.243195	-0.541617	0.753101	-0.296318	0.39025	-0.493263	NA	0.660337	NA	-0.028354	-0.845976	-0.300222	-0.184175	0.414104	0.319827	NA	-0.492375	-0.635531	-0.51921
DYN3	NA	-3.264128	1.066673	-0.201878	0.803651	-0.079866	-0.165877	-0.410631	-0.232846	NA	-1.126697	0.133342	NA	NA	0.894623	0.748952	0.148301	-0.063243	0.105799	-0.842682	-1.551195	-0.814209	0.46713	-0.195123	NA	-0.362834	-1.309232	-0.072755	-0.669146	0.11064	NA	-0.443419	0.425353	-0.285942	NA
EAF3	NA	-4.717111	NA	-0.559157	-2.535672	-0.344066	0.264627	NA	0.413128	-3.133398	-1.182845	-2.414461	0.612758	-6.996317	0.144923	1.089403	-0.169741	0.733887	-0.412463	0.707958	0.469124	0.584513	1.715565	-0.277523	NA	0.934776	-0.001278	1.10196	0.269246	-0.340381	NA	-2.075554	-0.81701	-1.003998	-0.262921
EAF6	NA	-1.737395	-0.441837	1.021159	0.580447	-0.58974	0.016751	-4.531345	-0.965733	NA	2.327212	0.434686	0.969841	-0.474754	-0.218831	0.166198	1.195999	0.535789	0.594928	0.409981	NA	-0.381309	1.056758	0.594177	NA	-0.155076	-0.028242	-0.395051	0.072839	-1.145171	NA	-3.452595	0.127024	-1.314957	-0.677977
EAF7	NA	NA	-3.791082	1.88618	-0.879064	-0.1595	-0.428005	NA	-0.963998	4.489344	NA	0.860913	NA	NA	0.503765	NA	1.687596	1.323762	1.58121	0.520748	-0.8963	0.9268	NA	NA	NA	-0.587254	NA	-0.21724	NA	-0.601153	1.846089	-5.238765	0.345542	-0.244306	0.231046
EAP1	NA	NA	NA	0.934541	NA	-0.380474	0.641915	NA	0.842829	4.96326	NA	-1.740719	-1.128828	NA	1.910304	2.525014	-0.162425	1.112444	0.009752	0.951078	NA	0.276788	NA	NA	NA	-1.960078	NA	-0.297113	-0.167755	1.550451	-0.260765	NA	NA	-0.332383	-0.775322
ECM18	0.834681	0.791949	0.881854	0.248103	NA	-0.003307	0.56501	0.00884	0.94579	-0.312355	1.31277	0.503113	-0.366232	NA	NA	-0.03139	-0.277125	0.12372	0.440026	0.040099	0.046049	NA	NA	-0.454195	NA	-0.35376	0.432424	-0.383183	0.031383	-0.145865	0.270059	0.411847	-1.59569	NA	0.214392
ECM2	NA	-0.68932	-1.020276	0.654988	0.774659	-0.446483	0.213185	0.165765	-0.026726	0.870837	NA	0.599489	NA	NA	0.140291	-0.348711	0.117617	-1.057238	-0.011768	-0.030866	NA	0.679784	NA	0.788271	1.517147	0.079741	-0.781343	-1.337751	-0.117011	-0.058418	-0.461881	-0.440589	-0.094649	-0.179685	-0.096802
ECM21	NA	2.241144	1.104043	0.014812	0.168413	0.13453	-0.137687	-0.679493	0.220059	2.416194	-1.094799	-0.615925	0.82096	1.41818	-0.291403	0.408284	0.11342	-0.424168	-0.019493	-0.428706	-0.6808	-0.173927	-0.4564	-0.750143	NA	-0.046761	0.818743	0.190992	NA	0.344943	-0.327729	-0.377634	-1.635428	0.262338	0.469909
ECM22	2.919991	NA	0.604576	-0.04584	0.616725	0.996435	0.23904	-0.785308	0.189581	-0.473216	-0.327893	0.162098	0.640672	-0.691459	-1.060813	-0.857383	0.160935	0.4845	-0.159678	-0.553779	0.466084	0.578895	NA	0.227339	NA	-0.645943	0.287505	-0.202737	1.500299	-0.202705	0.289475	-0.893092	-0.176828	-0.078104	0.355718
ECM30	NA	0.918361	0.014255	0.193016	-0.264125	-0.114288	0.989668	-0.467833	0.46234	-1.301325	1.761625	0.871205	1.36797	0.152695	-0.452516	0.056166	-0.324342	1.318271	0.094834	1.009246	0.984612	0.640123	1.259422	-0.730209	NA	-0.479772	0.640866	0.271106	0.91964	-0.002973	-0.392652	-1.179453	NA	0.16799	-0.547455
ECM33	NA	-0.44907	0.178912	-0.081184	0.962832	0.574785	-0.758113	-0.119153	1.030733	0.605191	NA	-1.043111	-1.605796	0.12252	0.712904	-0.275611	0.361437	0.012032	-0.052789	-0.180773	-0.69102	0.023157	NA	1.07623	NA	-0.32753	0.027275	-0.7503	-0.971918	0.170513	-0.993664	0.154684	-0.819811	0.603713	0.78534
ECM5	NA	0.138923	NA	-0.293077	-0.397176	-0.156691	0.298921	0.004156	-0.016463	0.153303	-0.934244	-0.201171	NA	-0.430354	0.101383	0.547191	0.053131	-0.451716	0.093034	0.186919	-0.759963	-0.394826	0.233253	-0.849811	NA	-0.470706	0.111454	-0.047319	NA	NA	0.6534	0.256861	-0.345978	-0.914774	0.113699
ECM8	NA	1.176808	-0.192494	-0.070871	0.736248	-0.37977	0.075016	NA	-0.311712	-0.034941	NA	0.704673	0.369249	NA	-0.173582	-0.522282	0.038153	-0.039063	0.323766	-0.772627	NA	-0.370422	0.525196	0.36116	0.601255	-0.605278	1.727636	-0.375726	NA	0.277558	NA	-0.281107	-1.161158	0.137284	-0.033776
EDC3	-0.321402	0.41422	-0.352388	-0.132074	-0.979238	0.444851	0.063405	-0.853745	0.227343	-1.212663	0.669521	0.429656	0.211039	-2.631522	0.550889	0.186822	0.605208	0.0236	0.200594	-0.888705	-1.525375	-1.338772	0.358582	1.176142	NA	-0.391358	1.001246	0.187309	-0.578837	0.122869	-1.011318	0.327658	0.206644	0.61513	0.230324
EDE1	-0.885197	-1.45311	2.714746	-0.040678	-0.357577	0.730051	0.154418	-1.369844	1.240994	0.081478	0.305878	-1.385554	-1.252235	-1.593326	0.521928	0.810111	0.802855	-1.07814	1.335157	-0.440131	-3.064319	1.078899	-0.753922	1.434156	-3.856081	-0.587882	-1.337899	0.517946	-1.648842	1.170086	-2.888788	1.367671	0.618244	-1.855864	1.325874
EGD1	1.109499	1.669231	-0.604305	1.259047	1.096111	-0.257872	-0.338695	-0.933418	-0.760079	0.71805	2.671757	1.693293	0.578879	-0.069942	0.121587	-0.769476	2.25389	1.219305	0.931121	0.599873	0.677529	0.71739	NA	-1.092122	-2.753362	-0.528783	0.534223	-0.427611	0.516698	0.181284	-2.087565	0.10687	-0.186196	0.100785	0.242971
ELA1	-2.693649	0.355323	NA	-0.224968	0.405032	0.69564	-0.430987	-1.291748	0.374584	-2.155835	NA	0.217638	0.720369	NA	0.131899	NA	-0.996174	0.397685	0.130941	0.528275	-1.032954	-0.345164	0.514714	NA	-3.007887	0.09963	-0.332492	0.276511	-0.513169	0.103171	0.521944	0.11242	NA	-0.516692	-0.116259
ELC1	NA	0.502396	0.507399	-0.747134	-1.310562	-0.454058	-0.253946	-1.47965	0.546511	1.940704	-1.094725	-0.615966	-0.364178	NA	0.760741	0.210073	-0.60592	-0.622618	-1.133524	-0.760404	-0.182058	0.662097	NA	0.915368	0.024963	0.311452	0.230609	-0.504047	1.03797	0.643569	0.041379	0.39258	0.043079	-0.516409	0.103495
ELF1	NA	-0.538976	0.234821	-0.29325	-2.445975	0.161012	0.610192	-0.305188	0.133441	-2.543397	0.403447	0.009418	1.585066	-1.187546	0.089636	0.345933	-0.406686	1.094593	0.066944	0.726002	NA	0.289459	NA	0.255419	NA	0.083134	1.807304	-0.038282	-0.063425	0.142076	-0.484558	-2.041514	0.996605	-1.084916	1.045384
ELG1	NA	-2.614197	0.560078	-2.484715	-1.688455	0.082779	1.000029	-7.364634	-0.262942	-0.810476	-1.727547	-6.731585	-8.438567	-8.802366	-0.146022	0.614289	-3.14644	-0.047315	-2.169732	0.727824	-4.181915	-2.568899	NA	-1.818875	0.081567	1.10771	0.242487	0.541349	-4.028697	0.38862	-5.221014	-0.22177	0.411189	0.255672	1.317283
ELP2	NA	1.152381	NA	0.651957	-0.844358	0.379265	-0.070986	-1.599855	-0.417345	-6.430303	1.517184	2.078274	1.93387	-5.186919	-0.408808	-0.151053	0.635199	1.232414	0.22535	2.056609	0.773042	1.119853	1.418018	-0.32343	-8.211564	-0.929397	0.565563	0.765456	0.50441	-0.825043	0.54842	-1.533893	2.050385	1.488071	-0.954302
ELP3	NA	0.487244	NA	-1.228697	-0.848383	-1.189162	-0.808714	0.283169	-0.597483	-4.927667	1.352247	1.606823	1.386476	-5.762301	-0.912735	-0.854168	0.530771	1.462463	-0.415123	1.83495	0.463172	-0.855887	0.172208	-1.85071	-8.41074	-0.134986	-0.023384	-0.205264	-0.28629	-0.173284	-0.369544	-3.047927	1.024904	0.751525	-0.532717
ELP4	NA	0.665624	NA	0.030363	NA	-0.13464	0.011051	0.098174	-0.629997	-4.569999	2.00233	1.946541	1.922133	-0.621799	-0.334596	0.36913	0.50687	1.998195	0.501037	2.166823	-0.134024	0.599685	1.321365	0.413995	NA	-0.987859	-0.07345	1.027769	0.228888	-0.314648	-0.364478	-2.45033	0.907841	1.225605	-0.768799
ELP6	-5.232355	-0.136452	NA	0.324855	-1.797225	-0.490955	0.284348	-0.056018	-0.438302	-5.548069	1.365328	1.249696	NA	-4.787089	0.084274	0.471128	0.968403	1.343043	0.580548	1.697452	0.757934	0.225742	1.779291	-2.366014	-5.175368	-0.971726	-0.147646	0.169392	-0.52289	-0.627524	NA	-2.573487	1.630754	0.310517	NA
EMC1	NA	-1.12113	-1.469185	NA	0.102093	-0.326372	0.729345	0.365186	0.8277	NA	-0.192543	NA	-0.16069	NA	-0.616348	-0.085086	0.202372	NA	0.562085	0.087473	1.469222	0.040207	0.55134	1.0283	NA	0.436329	0.13485	0.219445	0.146177	-0.431629	-0.22219	0.037692	NA	-1.151091	0.095293
EMC2	NA	0.248956	NA	1.583692	-1.231374	-0.825022	-0.276575	NA	-0.488446	2.81215	-0.114415	-0.668443	NA	3.143468	0.358142	-0.233867	-0.616251	NA	1.461618	-0.235569	NA	-0.834094	0.978772	1.271003	NA	0.323912	-0.213414	0.587993	0.820774	0.175654	NA	1.148188	0.167245	-1.523585	-1.453947
EMI1	NA	0.839772	0.229212	-1.070074	1.219992	NA	-0.575697	-0.942086	-0.53827	NA	NA	1.507195	0.571742	NA	-0.19847	-0.444468	-0.110535	0.334277	-0.823703	0.968295	1.777383	-1.999333	NA	0.365656	NA	-0.681849	-1.465606	-0.026318	0.342585	-0.117221	NA	-1.110675	0.754494	0.30852	0.125237
EMP70	0.76469	0.262453	-0.088854	-0.114058	-0.39522	-0.112065	-0.073424	-0.663348	-0.22041	-0.463344	-0.281694	-0.341376	0.530473	-0.19223	-0.109583	-0.255246	0.38203	0.126576	-0.020296	NA	1.136484	0.562361	0.31954	0.468644	NA	0.655411	NA	-0.027856	0.149119	-0.164011	NA	-0.368296	NA	-0.812911	0.493744
ENT2	NA	0.290513	0.373568	0.344233	-0.314614	0.348237	0.33266	0.552654	0.533969	0.580824	-1.172739	-0.232412	-0.411232	0.2001	0.688319	0.102901	0.18393	-0.311557	-0.092509	0.049956	NA	-0.372092	NA	0.049165	NA	-0.410263	-0.221002	0.1483	-0.195054	-0.047622	NA	-0.435564	-0.256712	-0.296259	-0.97066
ENT3	NA	0.70183	1.649856	0.087601	-0.231801	-0.124031	0.00877	-0.120088	0.538997	-1.942895	0.847773	0.180926	0.474558	-0.117544	-0.711686	-0.253595	0.154408	0.898441	0.098792	0.207275	0.995808	-0.248464	NA	0.969412	-3.680615	-0.600676	0.171153	-0.628808	0.697634	0.045144	0.099903	-0.893868	-1.367634	-0.447474	0.567411
ENT4	NA	NA	-0.215308	0.699276	1.129287	0.365565	0.039466	1.862588	0.599293	-0.776848	-0.65226	-0.774003	-0.356367	NA	-0.464489	-0.230361	-0.397444	-0.120676	-0.11405	NA	0.585283	-0.164523	NA	-0.166134	0.096435	0.006898	NA	0.087865	-0.639155	0.45563	-2.070636	-0.033451	-1.855063	-1.912198	0.263868
ENT5	NA	1.266357	0.993689	0.412937	0.859848	-0.138179	-0.030041	0.507458	-1.613376	NA	0.34943	0.698408	-0.502433	NA	NA	-0.473307	-0.339123	0.647969	0.133107	0.064881	1.205907	NA	NA	0.267155	NA	-0.340648	0.383678	-0.539582	0.610321	0.009197	0.890773	-0.644362	-0.763331	NA	-0.148131
ENV11	NA	0.961517	0.088596	0.638857	1.837571	-0.547386	-0.008418	-1.088006	0.578216	-3.920176	1.406693	1.666109	0.171188	0.595034	0.122474	0.556385	-0.118393	-0.075576	-0.38214	-0.259351	0.051619	-0.605095	NA	-0.087312	NA	0.253825	-0.025436	0.550274	-0.187251	0.012134	-1.559387	-0.340597	-0.328809	0.004245	0.541832
EPL1	NA	-0.983561	0.354216	-0.162588	NA	0.085471	-0.027365	1.519609	-0.50356	0.321056	NA	0.34878	-1.818191	NA	0.285566	-0.255618	0.440799	-1.758652	-0.205991	-0.787304	NA	-0.023569	-1.705445	1.476844	NA	0.1969	0.912451	-0.241574	-0.171562	0.761172	1.832458	1.02875	0.84352	1.305975	0.000787
ERD1	NA	-0.387051	-1.283038	-0.46446	2.487528	NA	0.225455	0.834727	-0.515645	1.622936	-2.669198	0.36172	-2.943811	NA	0.885459	-0.591801	-0.238536	-0.316171	-1.492938	-2.224227	-1.768324	0.530714	-0.901456	-3.83656	NA	-0.367702	-0.833021	0.363094	-3.080915	0.062702	0.421917	NA	NA	-0.722024	1.364745
ERG3	-1.224419	0.662526	1.231365	0.327313	-0.925301	0.027085	0.37211	-0.316823	-0.797169	-2.533094	2.034161	1.229438	1.999004	-1.603965	-0.516398	0.04971	0.121321	1.754048	-0.189308	NA	1.467247	0.067828	1.887926	-0.822856	NA	0.144437	NA	NA	0.988769	-0.644067	-0.348153	-2.705808	NA	-0.641785	0.29486
ERG5	NA	0.341062	-0.586371	-0.016352	-0.278065	-0.127859	-0.518797	-0.80372	0.314966	-5.60917	0.286521	0.242808	1.456036	-2.687116	0.074849	-0.051039	0.404319	1.084802	-0.392347	1.299264	NA	-0.147341	NA	0.039422	NA	0.901949	-0.642044	0.550002	0.749818	0.365711	-0.35278	-3.495184	1.388011	0.918518	-0.443314
ERJ5	0.905143	-0.442988	1.845255	-0.094086	-0.855171	0.216755	0.28214	0.628654	0.053451	NA	1.557172	0.51234	1.810655	-1.681238	-0.773071	0.039711	-0.398566	1.566559	0.020691	1.457006	2.035778	NA	1.457111	-1.203466	NA	0.433176	-0.318682	0.703949	1.028252	0.539426	-0.503156	-2.247643	NA	0.084506	-0.126004
ERM6	NA	0.994108	-0.037967	0.088422	0.558089	0.453831	-0.583481	-1.878633	0.352923	NA	-0.148822	1.325097	-0.914808	1.195874	0.02046	-0.488442	-0.070909	NA	-0.457976	0.586928	-0.210747	0.624266	NA	-0.186843	NA	NA	-0.758141	-0.180858	-1.272754	0.233449	0.133555	-0.156856	-0.743447	-0.208993	0.075496
ERP1	NA	0.777359	-0.13256	0.168155	NA	-0.235284	0.794673	-0.177405	0.940164	1.987381	-0.672123	-0.6794	0.101142	-1.852769	-0.016968	0.548565	-0.285526	-0.453851	0.140597	-0.507265	-0.16677	-0.213841	NA	0.108202	NA	-0.033261	0.320077	0.466429	0.060751	0.859197	NA	-0.390922	NA	-0.951297	-1.169276
ERP2	0.482919	0.512474	0.310488	0.339366	0.844393	-0.119608	-0.499535	0.832279	-0.448164	0.03961	-1.018482	0.09963	-0.148518	1.491838	-0.119893	0.29929	-0.05874	0.269658	-0.342209	0.229797	NA	-0.122396	NA	-0.362877	NA	0.162965	-0.174566	0.722822	-0.349722	-0.255147	NA	0.58719	-0.323837	-0.19614	0.703236
ERP4	NA	0.108836	0.480591	0.159871	-0.144371	-0.108016	NA	-0.051764	NA	NA	0.231918	-1.152543	0.097784	NA	-0.163322	0.173317	0.711843	0.314319	-0.453888	0.177509	NA	0.304864	NA	0.812172	NA	-0.062605	-0.95565	0.637404	-0.168784	0.034762	NA	-0.586625	NA	0.155012	0.723089
ERV14	NA	-2.682322	-6.987096	0.970678	-0.033933	-0.293221	-0.331972	1.923989	-0.512633	NA	-0.637952	1.004399	0.669424	1.75448	0.244885	-0.77185	1.204577	-0.69511	0.861688	0.052501	-0.357323	-0.306164	1.078359	NA	-1.116873	-0.388782	-2.219397	-0.308857	-1.219426	0.612855	1.758219	-3.669208	NA	0.512491	-0.870898
ERV25	NA	-0.721804	0.667058	-1.024521	0.772279	-0.065063	-0.644625	0.476173	0.398603	-0.200708	-0.556052	-0.328009	-0.072449	NA	0.838295	-0.030019	-0.45766	0.95509	-0.258851	-0.07849	NA	-1.115709	0.434416	-0.895321	NA	1.345315	-0.158043	-0.199089	2.0493	0.794875	-0.651964	0.350485	-0.56106	-0.344408	-0.861341



HIR3	-6.50874	0.213944	-1.526108	-0.347294	-1.397637	-0.434786	-0.878515	-2.851938	0.583778	-1.594467	1.95337	0.296962	0.545243	-2.870298	0.11724	0.176704	0.091172	0.693124	0.4471	0.843343	-0.257704	0.551857	NA	0.083092	NA	-1.092775	-0.048315	-0.607618	-0.869234	0.113952	-1.353904	-0.003203	1.189918	0.158958	-0.432489
HKR1	0.016237	-0.41148	0.252241	0.429558	0.506162	NA	0.543999	-0.565238	-0.247237	-2.336907	-1.000363	0.497243	0.123789	NA	-0.45263	0.012491	1.041345	-0.879755	0.738048	-0.385247	-0.000694	-0.598733	NA	1.808957	NA	0.531867	0.912131	0.352242	0.546717	0.170436	0.237697	NA	-0.122182	0.155333	0.160216
HLJ1	-0.280297	-0.009911	-0.379609	0.067706	0.584764	0.503293	0.689708	0.549274	-0.095408	0.191782	-0.063804	0.843676	NA	-2.188685	0.420607	0.45267	0.562546	0.452968	0.083985	-0.144757	0.227803	0.362487	NA	1.653262	-2.738224	-0.158011	1.196642	-0.727485	NA	NA	0.586093	0.172515	-0.584629	-0.276577	-0.295743
HMG1	NA	NA	-0.661966	1.092887	-0.414987	NA	0.880647	NA	0.980382	NA	-0.565479	-1.166821	-1.379644	NA	0.384889	-0.035642	0.124824	NA	-0.29309	-0.194673	NA	-0.837716	0.159366	-0.725233	0.68398	0.84058	0.536785	-0.906799	-1.033565	0.396061	NA	-1.528319	-0.450949	NA	0.911444
HMG2	NA	-0.425588	-1.455442	-0.339257	-0.839553	-0.156195	0.524657	0.28342	0.294648	0.280779	0.390479	-1.399752	-0.015431	-1.056861	-0.135824	-0.128659	0.135115	0.14415	0.055528	0.747916	0.657929	-1.000361	0.595452	0.390005	NA	-0.124591	0.488529	0.480992	-0.50202	0.032626	-0.105623	-0.468748	0.335098	-1.032158	0.126708
HMO1	NA	-0.784104	NA	-1.850648	NA	-0.411229	-1.147292	NA	-0.577217	NA	-4.93214	-5.023819	-2.038746	NA	-0.435278	0.185365	-1.827051	-0.351984	-1.374657	NA	-4.634143	NA	NA	-0.07854	NA	0.647967	NA	-0.000111	NA	0.504809	NA	-1.369015	NA	NA	-0.420072
HMT1	NA	-1.560827	0.116532	-0.915039	-0.064502	0.852179	0.08982	NA	1.332989	1.555727	NA	-1.19959	-0.917279	NA	-0.693691	0.028153	-0.225245	0.686596	0.147202	0.614986	0.923972	1.206679	NA	0.564165	NA	0.483414	-0.695179	0.465684	1.089784	-0.105192	NA	-0.430751	-2.511395	-0.913588	-0.136952
HNT1	-0.892485	-1.315464	NA	0.319453	-0.714687	0.213055	0.897686	NA	1.115512	-0.948229	0.039422	0.207867	NA	0.92069	1.059832	0.563387	-0.472571	-0.072321	0.459612	0.337511	NA	1.317681	-1.379073	1.358721	NA	-0.832125	-2.540519	0.418724	2.683337	0.655026	0.160954	-0.369576	0.237158	0.201154	-0.501096
HOC1	NA	-2.864866	-3.293208	1.020333	-1.35358	0.166468	2.517206	0.794194	1.719809	NA	NA	-0.235606	-0.875841	-0.903386	2.028018	1.099557	1.581575	-1.140303	1.967113	0.131032	-1.747458	3.068047	-0.44979	0.770765	NA	-0.638094	-2.549614	0.29329	-1.055814	0.884301	NA	1.77608	0.53964	0.025928	0.735061
HOG1	1.345712	0.570107	-0.203579	0.01772	-0.844969	0.670923	0.538806	-1.282682	0.202833	-3.616269	0.853844	-0.219474	0.100288	-2.383349	-0.013342	-0.111964	0.994996	-0.151052	0.461798	NA	NA	0.218372	0.701989	-0.313719	NA	0.189143	-0.593556	-0.45886	1.232817	0.023903	-1.226962	-0.318345	0.716666	-0.632014	0.189859
HOM3	1.180823	0.288478	0.587311	0.490567	0.444741	-0.137321	-0.418964	-0.115255	0.511822	-2.20134	NA	0.716459	0.202307	0.038685	-0.364434	0.344777	0.123512	0.641155	-0.266221	0.661918	0.43211	0.033931	NA	0.563109	NA	-0.318312	-0.12416	-0.042608	0.720484	-0.094211	NA	-0.297349	-0.583453	-0.153796	0.45047
HOM6	NA	0.546888	NA	-2.178635	NA	-0.964972	-1.608952	0.125238	0.128202	-0.601302	-0.50196	0.881238	-0.462704	0.57649	0.389572	-0.095821	0.716888	0.225888	-0.27558	-0.132282	-0.284904	-0.285499	-0.168873	-0.519031	NA	-0.157956	NA	0.127836	NA	-0.360874	-0.787306	0.041909	0.597153	0.517336	-0.692181
HOS1	NA	0.351207	0.358277	-1.08989	-1.43877	0.766287	-0.223206	1.000541	-0.057654	-0.699415	-0.120591	-0.351427	-0.175426	-1.547832	0.345241	0.378453	-0.525026	-0.767475	-0.680471	-0.145893	NA	-0.061611	0.609036	1.18279	NA	-0.352715	-0.008236	0.455368	1.097805	0.092056	1.420919	0.066875	0.053204	0.534493	0.584698
HOS2	NA	0.177255	0.456106	-1.76131	-0.032516	0.61098	0.448173	-0.142386	1.549448	-10.84419	-2.361622	-3.690732	-0.995751	0.05951	0.07699	0.330543	-1.425454	0.475066	-1.050482	0.208953	0.269579	-0.804014	-1.99746	-0.278181	-0.894957	1.230481	-0.445553	NA	0.09578	0.689515	-1.250581	-0.398192	-1.196804	0.919368	1.357391
HOS3	NA	-0.98828	0.286228	-0.131122	NA	0.086797	0.351125	0.283956	0.691981	-2.075629	0.648165	0.128802	-0.311074	NA	0.636025	0.488325	-0.074069	0.823999	0.691214	0.213828	0.147518	0.393662	0.91794	0.148399	NA	0.832248	0.726236	0.418723	0.465815	-0.879095	-1.505473	0.580304	-0.199442	-0.652538	-0.30987
HOS4	-0.065391	1.250732	-1.253004	-0.026911	0.429719	-0.40333	-0.339755	1.250073	0.612136	-2.392493	0.236759	0.056987	0.294331	1.420121	-0.212715	-0.261236	0.218458	-0.140479	-0.313541	0.939232	0.252412	-0.561962	0.906398	-2.018301	-0.969498	0.033159	-0.160561	0.839667	0.866921	0.050793	1.236214	-0.974469	-0.453463	0.471005	0.439201
HOT1	0.590507	-0.276975	0.060579	1.034404	-0.682554	-0.02104	0.325399	-1.390289	0.725385	0.320512	0.150238	-0.692965	NA	0.612956	-0.053372	-0.270569	0.489758	0.316685	-0.110778	-0.014886	0.777395	-0.071631	NA	0.880404	NA	-0.264023	0.472718	-0.643162	NA	NA	-0.305483	-0.135531	0.912713	0.283371	0.027895
HPC2	NA	-0.695558	0.241446	-0.19839	-0.685744	-0.071049	0.864287	-2.753576	0.823848	-1.129135	NA	0.589854	0.206046	-2.149988	-0.495733	0.590546	0.135383	1.435069	0.636876	0.890639	NA	0.820196	0.243634	0.517703	-2.774254	-0.786887	0.954248	0.056042	0.097404	0.19571	-1.060823	-0.695704	0.295028	-0.90429	-0.939095
HPR5	NA	NA	0.500958	0.784685	NA	-0.239321	0.040064	-3.89859	0.484164	-0.807663	-1.630238	NA	-4.064614	-6.776884	-2.523259	-1.786909	1.342556	3.519001	0.837938	NA	1.80085	-3.591213	2.596961	1.819448	NA	NA	-5.100621	-1.000579	NA	1.608206	-4.609285	-0.091154	NA	1.57279	-1.21705
HRD1	1.797478	1.805322	1.401871	-0.838232	-0.117346	-0.22912	NA	-1.167644	NA	NA	0.162736	-0.047011	0.750203	0.739877	0.087937	0.096234	-0.120393	1.072207	-0.201318	0.473309	-0.187219	-0.120265	1.134142	0.747064	NA	-1.081172	-0.341649	0.154814	0.970699	-0.229083	-1.390257	0.260784	-0.746863	-0.31338	-0.154157
HRD3	NA	0.702244	-0.844516	-0.04058	0.692119	-1.188171	0.846117	-0.458276	-0.940194	0.381291	1.088388	1.010828	0.97338	-1.018006	-0.510846	0.077238	-0.769619	0.095633	-0.005358	-0.057784	NA	0.935852	0.124785	NA	-3.763599	-0.111405	1.039874	0.021692	0.86153	0.158568	0.113182	0.322745	0.343587	-0.640679	1.020628
HRT1	-4.477769	-2.260183	-1.992723	-0.314936	-1.309054	0.1116	-0.601034	1.761374	1.358401	-2.551443	0.899421	-0.177366	-1.636738	0.626846	0.590756	0.918855	-0.225094	NA	-0.065653	0.636251	-1.940741	-0.092439	NA	-0.167401	NA	0.08309	-1.347657	0.930561	1.107228	0.397327	2.569808	-2.196742	-1.125749	-0.54364	-0.070048
HRT3	NA	-0.336755	0.152668	0.531611	-0.306781	0.258608	0.466348	-0.702377	0.477237	0.826007	NA	-1.225321	0.17225	-2.909395	0.131043	0.244922	0.299338	-0.44837	0.676815	NA	0.846255	-0.085176	0.942458	-0.635296	NA	-0.373498	NA	-0.172027	0.096611	-0.046628	NA	0.024149	-0.163129	0.277827	0.583461
HSC82	NA	-3.00614	-0.637327	-0.141426	NA	-0.292693	0.24689	-5.011218	0.747639	1.677182	-1.553903	-1.486519	NA	NA	-0.33483	0.742962	-0.581427	0.657267	-1.653502	-0.259544	-1.424881	0.61539	NA	-1.635478	NA	NA	-0.865515	-0.350864	NA	NA	NA	0.118555	0.831696	-0.123719	-0.720379
HSE1	NA	NA	NA	0.490365	-0.085414	0.358605	0.238873	-0.059133	0.883898	-2.962842	-0.856902	-0.925794	-0.804905	NA	0.573627	0.342051	0.320422	0.954934	-0.310526	-0.600454	NA	0.341296	-0.134357	-0.244033	NA	1.047482	-0.680793	0.270071	-0.062186	0.459321	-0.881062	-0.15123	-0.202118	-0.331611	0.019417
HSL1	NA	-7.759144	-3.166233	1.678937	-9.473646	-0.352861	-0.627857	-2.430652	-3.003061	-7.531372	-0.014428	-4.035725	-3.470847	-4.882846	-0.392918	-0.781563	2.132443	-4.417625	1.957858	-5.102286	NA	1.337656	-0.32913	1.026142	NA	-4.856827	NA	0.513735	1.43959	0.133777	-2.621634	-0.566942	-0.343997	-4.123577	-0.758558
HSM3	1.326968	1.051463	0.121371	-0.080235	-0.076654	-1.294862	0.078919	1.515632	-0.730474	-1.515901	-0.189651	0.206182	-0.026329	NA	0.303734	-1.223944	-0.162293	-0.434511	0.626848	0.548915	NA	0.031731	NA	0.44116	NA	0.192219	0.137676	0.164069	-0.431238	-0.828262	1.953767	-0.507232	0.004537	0.007164	-0.622854
HSP42	NA	1.12228	-0.772519	-0.558796	-0.014965	0.416112	0.13578	0.327022	0.687139	-1.119256	0.047924	-0.412411	0.426243	1.093275	-0.133971	0.043974	0.307323	1.142445	0.514265	-0.471249	0.38693	NA	-0.081657	1.760383	NA	-0.089838	0.699516	0.086687	0.851295	0.584614	-0.882498	-0.797349	0.671503	NA	0.749275
HST1	-5.247564	-1.084442	2.373206	-0.189188	-1.527185	0.344158	NA	0.994301	NA	NA	0.101382	-0.015454	0.386421	NA	0.213896	0.064151	-0.500585	1.017119	-0.833647	0.821664	-1.409192	0.404995	-0.011847	1.056503	NA	-0.217979	-1.356422	-0.359887	0.79167	0.64242	0.180867	0.065022	-0.383009	-0.03527	0.9518
HST3	-0.462999	1.180935	0.955831	0.988477	NA	0.109938	NA	0.886126	NA	NA	NA	NA	0.667048	-0.452542	-0.600026	-0.024258	NA	0.8295	0.206415	1.43825	-0.744209	-1.646524	2.051376	1.443675	-2.991994	2.89594	1.685393	-0.755468	-6.765161	1.209685	0.690134	-0.150959	-3.884798	0.046933	1.590853
HST4	1.731335	1.007703	NA	-0.235703	0.173671	-0.097369	-0.21362	0.779649	NA	-1.144691	1.377052	-2.501334	0.388356	NA	-0.705997	-0.009876	-0.430935	0.326036	0.061276	1.03494	NA	NA	NA	0.99159	NA	1.048462	-0.910834	0.046627	-0.340157	-0.429028	-0.666793	0.718249	-1.871501	0.499461	-0.791826
HSV2	NA	NA	NA	0.041768	-1.463208	-0.431284	-0.986621	-1.050236	-0.476841	1.040751	0.28879	-0.602347	0.061081	0.25954	-0.300721	0.627038	-0.625782	-0.657166	-0.235639	-0.015078	0.937027	-0.31655	0.209617	0.512643	NA	0.234864	-0.450987	0.451575	0.864856	0.408994	NA	1.148319	0.755208	0.10686	-0.375928
HTA1	NA	NA	0.93813	0.00096	-5.583375	-0.618323	-0.397569	-3.380833	0.060429	-5.12453	0.633877	-1.860411	-0.5129	-1.405334	0.94492	0.162546	1.023204	NA	-0.639328	0.382274	NA	NA	NA	0.04632	NA	0.047974	0.596783	0.872885	-0.407259	0.738697	-1.08655	-0.354122	-0.320861	0.638312	0.196936
HTD2	0.829621	1.617927	0.659609	-0.623936	-0.224685	-0.697219	-2.066814	-0.178136	-0.744462	-1.395581	1.430613	0.758209	0.683398	0.058121	-0.154227	-0.818824	0.014583	0.940655	-0.354845	0.86469	NA	0.038662	NA	-0.53923	NA	0.440457	-0.453036	-1.124424	1.785822	-0.129283	0.251974	-0.44636	1.141755	-0.912565	-0.912815
HTZ1	NA	-5.68931	NA	-0.760892	NA	-0.197981	NA	-3.321311	NA	NA	-1.369605	-2.462272	0.744874	NA	0.306659	2.640377	NA	0.480635	0.048187	0.237783	0.753401	0.187876	-3.102029	NA	NA	0.387097	-3.955826	-0.240952	-0.026931	0.048281	-5.515023	2.9722	-0.335133	-0.113058	0.734216
HUA2	-0.638911	0.353114	0.765974	0.507203	-0.602863	0.076436	0.278531	0.474554	1.331992	NA	-0.531	-0.382594	0.207833	NA	0.464758	0.366363	NA	-0.537569	0.034109	0.183632	0.422095	-0.390367	NA	-0.769937	NA	0.148438	0.33441	0.480272	0.058613	0.620656	0.368163	-0.138263	-2.844456	0.43674	0.896412
HUL4	NA	0.437402	0.868388	-0.720061	-0.052157	-0.656865	-0.509709	0.64294	0.527845	-0.202252	-0.133252	-0.188256	0.721926	NA	0.243219	-0.153038	0.599807	0.603566	-0.47802	0.317502	-0.233621	0.209645	0.305875	0.51306	NA	NA	0.608566	0.10859	0.022968	-0.001035	0.029219	0.111533	-0.366016	0.439136	-0.297113
HUL5	NA	-0.169916	-0.069919	0.434824	-0.322133	-0.330142	0.600336	0.329751	0.758507	0.929941	0.476992	-0.255127	-0.082402	NA	0.005293	0.324153	0.06545	-0.276015	-0.167029	-0.284883	-0.447879	0.703939	1.629867	1.074892	NA	-1.038761	-1.152631	NA	-0.04258	0.443557	0.005234	0.182578	1.166313	0.02034	0.005719
HUR1	-1.023087	NA	1.663808	1.361237	-4.670486	0.422974	-0.099032	-4.033391	1.013666	-7.22966	3.100431	-0.14074	-3.047255	NA	-2.875949	-2.767399	1.677021	-1.696745	1.541065	-0.492322	-1.989882	2.413349	-0.680285	-0.239284	-4.041252	-6.716304	NA	NA	-0.733394	0.342535	-1.398216	-3.320728	1.388435	-3.129756	NA
HUT1	NA	0.92906	0.341966	0.073669	NA	-0.224906	0.812116	0.157745	0.264304	0.484836	0.198823	0.487326	0.187845	-2.427927	0.579557	0.024301	0.145298	-0.384722	0.726843	0.291105	0.22093	0.848622	NA	0.853743	-2.303422	-0.017084	0.417452	0.499027	0.77947	0.297936	0.496131	0.870175	0.526755	0.394523	0.49026
HXK1	NA	0.536952	-0.492379	0.560636	-1.390867	-0.135282	0.168247	-0.823683	-0.264999	0.831654	-1.294569	-0.094979	0.183914	NA	-0.303291	-0.367508	-0.111344	0.006798	0.825926	0.523577	NA	0.636813	0.731824	1.262235	NA	-0.420315	-0.511447	-0.197198	NA	0.254241	-0.38891	-0.737944	0.327682	-0.523957	0.382002
HXK2	-4.63286	0.592765	-1.216561	-0.07678	-1.978946	0.257598	0.688315	-0.144533	-0.649689	-3.639304	-0.898468	-0.869111	NA	NA	0.627183	0.486759	-0.08188	1.012346	0.07323	0.14831	NA	0.265132	0.780918	0.907482	-4.497936	1.210227	-0.120621	NA	0.307573	0.478002	0.753585	-0.969983	-1.16999	-0.965254	-1.015006
HXT10	-0.143353	-0.533835	0.37437	-0.501771	-0.380933	0.774861	0.559803	0.460718	-0.818277	-1.587887	0.855653	0.237445	1.068169	2.191876	-1.028473	-0.606206	0.069707	0.571147	-0.078387	-0.135013	NA	0.066445	0.181958	1.500218	NA	-0.285308	-0.026107	NA	1.259658	-0.589126	-0.256693	-0.368807	-1.786454	0.229541	0.335957
HXT17	NA	0.764069	0.074494	0.104616	-0.306138	0.481677	0.185189	-0.657597	-0.816993	-0.350783	-1.485237	-6.054867	NA	0.723365	-0.125727	0.279263	-7.522547	0.161113	-0.130818	-0.784642	-0.849283	0.265912	NA	0.3724	NA	0.386518	1.32652	-0.09382	0.095534	-0.015573	0.099523	-0.27357	-2.067061	0.324479	0.965707
IDH1	NA	-0.075542	-0.379045	-0.761354	-0.428605	0.52699	0.481558	-0.965525	0.264805	NA	0.879084	-0.774627	0.557208	-1.499345	0.243399	0.523603	-0.441275	-0.473621	0.498914	-0.024248	0.906178	-0.037578	-0.317471	-0.819801	NA	-0.423226	-0.309195	0.249149	0.951144	0.197314	-0.317186	-0.485286	-1.109802	0.209231	1.433157
IES1	NA	NA	-5.327287	1.149185	NA	0.534921	-0.759233	-0.974606	-0.137534	-6.442254	0.747934	-1.905959	-0.263855	NA	0.957109	-0.562632	1.407858	0.23191	-0.162296	0.5162	0.705618	0.291772	0.089276	0.227299	NA	-0.769362	-2.156654	0.104139	-0.41467	0.163551	-5.437206	-2.76778	-1.2306	-0.11377	-0.57906
IES2	NA	NA	-3.31933	-0.765819	-2.376029	0.268679	1.352771	-2.021831	2.099085	NA	-0.089861	-0.403433	0.387806	-3.779963	1.899854	NA	-0.706564	0.034742	-1.156365	0.941483	1.36993	-1.693387	0.079013	NA	NA	0.457496	-4.097535	-0.335082	0.380367	0.478164	-5.518844	0.22634	NA	0.430826	0.776441
IES4	NA	0.225491	NA	-0.631166	-0.168489	0.550755	0.546629	0.356671	0.32783	-1.215372	0.151744	-1.218778	1.280882	NA	1.050919	0.995268	0.362194	0.519564	-0.10028	0.332297	0.653166	-0.382181	0.385252	-0.466513	NA	1.302272	0.984707	0.961054	-0.233853	0.414701	0.300648	0.949533	-1.132111	-0.330711	-0.91953
IES5	NA	-3.704028	-2.719329	0.453732	-0.628697	0.857168	-0.756734	-1.125333	-0.178706	NA	0.237712	-0.550455	NA	NA	-0.108703	-0.927746	1.468333	1.188162	NA	1.231093	1.236832	1.436072	NA	1.670339	NA	1.419536	-1.002773	0.488862	0.091231	0.889579	NA	NA	-1.73552	0.765479	-0.091333
IKI3	NA	-0.48132	-5.942588	0.124291	-1.50686	-0.473204	-1.418678	0.893986	-0.709085	NA	1.120576	1.887425	1.898414	-3.1407	-0.258651	-0.280776	0.591544	1.659622	0.375631	1.660582	1.916538	0.541438	2.174252	-0.102774	1.414096	-0.561863	0.637947	-0.495906	0.312389	-0.490139	0.612955	-1.25626	1.619871	0.798988	-0.634252
ILM1	NA	-0.352425	-1.655154	0.248669	-2.917367	0.158978	-0.294967	-1.989467	0.546852	-3.302129	0.088382	-0.383964	-2.312221	NA	1.288711	0.839884	0.596013	-2.794728	0.069434	-0.53367	-1.640347	0.424422	NA	-0.765329	NA	-0.803455	-1.248122	0.011674	-0.595718	0.094183	-3.970594	-0.741511	0.951484	-0.340556	0.044992
IME1	0.43453	NA	0.23028	-0.694544	-0.398995	0.113619	-0.035163	-0.443519	-0.561518	-0.639119	-0.959386	0.556115	0.611326	-2.276434	-0.183853	-0.067357	-0.157534	-0.312927	-0.192511	-0.064173	0.076406	0.83197	NA	0.111489	NA	-0.21724	0.909255	-0.234679	0.510782	0.52505	0.719347	-0.160666	-1.397159	0.138971	0.659316
IMG2	NA	-0.0264	0.404606	NA	NA	-0.942056	-0.861711	1.006192	-0.446956	-3.822958	1.448703	0.771784	0.984511	1.048404	-3.037633	-1.371425	0.036103	NA	0.072236	1.14084	0.195159	-0.259714	0.786117	-1.097354	-1.806854	0.260115	0.876608	-0.377056	0.909377	-0.54429	0.978864	-2.528632	0.446794	0.309837	-0.225284
IML2	NA	NA	-0.123841	0.790967	-0.682585	-0.144598	-0.09883	-0.804006	0.549972	-0.120964	0.371362	0.097522	-0.465147	-3.136499	0.424018	0.540455	0.541287	-1.540483	0.389058	-0.202195	-2.111238	0.381892	0.180336	-0.085219	NA	NA	-2.931512	-0.225091	-0.705379	0.418074	-2.420871	-0.013586	0.280964	-4.719234	0.396308
IML3	NA	0.121128	0.518405	1.302195	-0.174695	0.511151	0.758918	-4.631158	-0.233716	-0.050588	NA	-0.528585	0.244765	-3.493859	1.00464	-0.270613	0.481601	-0.683569	0.105111	0.178398	-0.503559	0.635799	NA	0.562667	NA	0.382042	-0.287828	-0.087432	-1.174215	-0.198527	NA	-0.65783	0.719964	-0.540257	0.072611
IMP2	NA	-0.294904	0.158229	0.504779	-0.478634	-0.416404	0.975926	-3.021204	-0.895615	NA	1.521342	0.893381	0.400093	-0.970989	0.15627	-0.270245	0.886434	-0.422661	-0.033907	0.642655	NA	-0.557868	NA	-0.391767	NA	-1.644794	-0.522154	-0.908895	1.851172	-0.620167	NA	-0.678518	0.456939	0.323114	0.294466
INO4	3.810138	0.157863	-0.093403	-0.996769	-2.001757	-0.466179	0.53743	-1.42494	0.061438	NA	NA	-0.236141	-0.612636	-1.415843	-0.750998	0.471227	-0.872769	-0.170615	-1.195004	-1.185204	0.058054	0.083858	1.075122	0.057563	NA	0.072113	-0.78581	-0.142527	-0.56906	0.826921	NA	NA	-0.349108	0.548969	1.090056
INP51	0.812838	-0.567236	-0.881809	-1.012553	-0.99115	-0.032053	0.758323	0.249582	0.152013	0.619331	-0.236553	-0.947828	-0.498138	-1.495624	-0.074665	-0.151217	-0.106108	-0.723373	0.183266	0.080237	-0.781158	0.025109	NA	0.53161	NA	0.568803	0.706374	0.16487	0.193089	-0.388693	0.836963	-0.305023	-0.032768	-0.054117	-0.373528
INP52	NA	-0.968189	1.809982	0.08967	0.077152	0.442621	0.658214	0.377367	0.330707	0.425108	0.058539	-1.65486	-0.862489	-0.306552	0.101163	NA	0.40431	-0.068287	-0.079901	0.358972	0.147699	-0.117896	0.264875	0.053198	NA	0.717228	0.23698	0.258524	-0.186241	0.702955	-1.540541	0.432883	-1.919531	-0.681967	0.86347
INP53	NA	0.185993	-0.164389	-0.874618	-0.700945	-0.182267	NA	0.302672	NA	-3.083727	1.289242	0.390199	1.261303	-1.363799	-0.498989	0.362832	0.328052	0.337768	0.827238	1.239659	0.861449	-0.634368	1.742539	-0.486544	NA	-0.511139	0.790355	0.168737	1.632482	-0.523243	-0.239554	-0.855464	0.221163	-0.782929	-1.017815
INP54	NA	2.013834	1.332168	-0.034068	0.710166	0.331312	NA	0.641066	NA	NA	-1.16057	-0.483339	0.279018	NA	-0.402587	0.145675	-0.040129	0.814975	-0.501939	-0.157243	0.832541	-0.014981	-0.268126	0.052428	NA	0.179485	1.356864	-0.736396	0.465334	0.112944	NA	0.269106	-1.095248	-0.215083	-0.265814
IOC2	4.178808	-0.484304	-0.995661	0.29799	-0.001567	-0.22934	-0.227532	0.781476	-0.081933	0.367905	-1.723271	0.464571	0.683233	-0.095705	-0.121774	-0.104663	-0.298087	0.283527	0.156882	NA	0.855541	0.557894	NA	1.320998	-7.256071	0.437573	NA	-0.299072	1.09816	-0.008042	-0.815109	-0.957527	-0.290082	-0.779509	-0.697477
IOC3	NA	NA	NA	-0.226836	1.642891	0.613351	-0.496747	-9.775621	0.707883	NA	1.06946	-0.568557	-0.068526	NA	0.513197	0.387126	-0.629063	0.714076	-0.592753	0.178262	NA	-1.572431	NA	-0.76837	NA	0.938995	0.362903	-0.421347	-0.183629	-0.01421	NA	0.99293	-0.199333	0.379835	0.719993
IPT1	NA	-1.20269	1.364966	0.600361	-2.002568	0.14198	0.489602	NA	0.281654	0.528224	0.044241	-0.248704	0.115371	NA	NA	0.462708	0.09329	0.603927	0.216837	0.722192	-0.615504	-0.159805	1.557242	0.27808	NA	0.141408	-0.631315	0.550626	0.470845	0.183768	-0.379762	0.299614	0.35925	NA	0.332328
IRA2	NA	-1.069249	-1.776889	-0.124863	-1.028496	0.380971	0.86069	0.252951	NA	NA	0.182854	-0.361552	1.077347	-5.021923	0.513072	-0.041061	-0.597045	0.264703	0.073474	1.431317	1.168549	0.374214	1.015779	0.643001	-8.2798	0.511185	-0.808907	0.307374	-0.816657	0.792465	0.437546	-4.567097	1.622838	-0.715738	0.698448
IRC15	-0.38817	-0.199471	-0.616124	0.193932	0.383986	0.064703	0.297346	-3.35671	0.052706	-3.731599	-0.041656	0.585753	-0.25642	-3.888563	0.291079	0.319799	0.404153	0.398657	0.80377	0.517288	-0.364664	-0.550117	NA	0.864045	-1.499692	0.035803	NA	-0.516968	-0.862612	-0.114213	-1.850412	-1.211726	0.533842	-0.416876	0.187927
IRC21	-1.108466	NA	0.095662	1.730653	-1.472197	-0.342599	-1.689804	-0.137165	-0.63327	-0.288625	3.406834	1.402367	NA	NA	-0.557998	-0.310286	1.28968	1.8119	1.619038	1.238358	NA	0.934436	NA	0.341384	-4.409683	-2.392212	0.295249	-2.613091	-0.818483	0.299716	-2.126561	-0.812714	-0.098298	-1.251124	NA
IRC25	NA	-3.154743	0.283426	0.616741	-1.226955	0.371019	0.19815	1.643919	0.951326	NA	-0.246892	-0.540209	0.306281	0.439392	-0.878983	1.045153	-0.27175	0.975898	0.043888	NA	-1.414938	0.188049	0.143646	-0.212984	NA	-0.447623	NA	1.185648	0.187344	0.444701	NA	-0.606232	1.540709	-0.374621	-0.134552
IRE1	0.184641	0.296939	-0.466965	0.290499	-0.104804	-0.035046	0.17867	0.147631	-0.231852	NA	-0.5798	-0.136556	0.070949	1.016321	0.482129	0.386556	0.074989	-0.428795	0.964405	0.108619	0.929669	0.657512	NA	-0.134862	NA	0.038329	0.284676	-0.078716	-0.276153	-0.242754	-0.045482	-0.170284	-1.175464	0.404664	0.175988
IRS4	NA	-0.016259	-4.459217	0.311103	-0.51974	0.108873	1.071326	-0.577153	0.431239	1.150062	-0.327796	-1.433327	-0.881214	NA	-0.254643	-0.139485	0.055504	0.101653	0.260897	0.32461	NA	0.829321	NA	0.700574	NA	0.645371	-0.42907	0.226503	0.195236	-0.088536	-0.033695	-0.518578	NA	0.240429	1.027646
ISC1	4.032589	0.361348	NA	0.272857	-1.259527	0.077497	0.916461	-1.05074	-0.791367	-2.317447	-0.623779	0.560631	0.247297	0.961702	-0.292576	0.471123	0.4301	-0.556054	-0.397118	0.238317	0.579123	-0.651213	NA	0.053819	NA	NA	-0.51311	0.780568	-0.936163	-0.98	-0.363392	0.233134	0.845745	-0.921441	-0.338871
ISR1	NA	-0.179556	0.876689	0.638261	-0.826354	0.105864	0.416157	0.648509	-0.14287	-1.290991	-1.577606	0.039968	1.157451	NA	-0.264717	-0.030989	-0.149199	0.183909	0.501219	0.322159	0.657509	0.131966	0.192821	0.922534	NA	0.150704	0.580367	-0.074131	0.184742	-0.00082	-0.281992	-1.060904	-0.298261	-0.870135	0.555977
IST3	NA	0.387599	-6.597727	-0.557315	0.053584	0.280693	-1.008165	0.362708	0.284583	3.685039	NA	-0.384442	0.57	NA	0.664791	0.358677	-0.57812	-0.120834	-1.335977	0.065239	NA	-0.017277	NA	-0.890692	NA	-0.418023	-0.093458	-1.055702	0.442805	0.692977	1.845259	-8.567915	0.66753	0.53658	0.213498
ISW1	2.613668	0.492922	1.151439	-1.522296	0.340493	-0.201134	0.159163	-3.767602	0.383576	-0.529285	NA	-0.177597	-0.583617	NA	0.443349	0.753296	-2.701387	-0.229645	-2.935554	-0.023355	1.675989	-0.096866	1.456325	0.065127	NA	1.57222	0.513045	0.159598	1.002436	0.055566	-4.737487	-0.46151	0.314547	0.639485	0.553308
ISW2	NA	0.702179	0.332964	0.336128	-3.294141	-0.362434	-0.076664	-0.383135	-0.352094	-1.070296	-0.259912	-1.314054	0.961657	-0.074544	-0.201099	0.289605	NA	-0.825815	-0.040065	-0.151299	NA	-0.270167	NA	-1.181689	NA	-0.943199	-0.294495	0.163518	0.356722	0.803226	1.075749	0.635408	-1.134465	0.116299	0.039454
ITC1	NA	-0.700553	0.223508	0.481216	-1.360058	-0.268429	0.929897	-0.556106	0.577855	-1.295191	0.996198	-0.583602	-0.464581	NA	-0.193001	0.319018	0.050411	-1.434264	-0.222499	0.12422	0.011346	0.307526	0.739378	-0.681754	NA	-0.044349	0.597253	NA	-0.487397	-0.257832	-0.395666	-0.468507	0.704352	0.142002	-0.427038
ITR1	NA	NA	1.014122	-0.547265	0.114159	NA	-2.495739	0.09618	-0.043546	0.464187	0.999308	-0.042155	0.787305	NA	-0.673426	-0.340124	0.226223	0.409838	-0.382349	0.284046	NA	-0.889462	NA	0.985129	NA	-0.213389	0.570514	-0.06805	0.006455	-0.767364	0.311614	0.257088	-0.531099	-0.886645	-1.428956
IWR1	NA	-0.941076	NA	0.156068	-3.115784	1.867052	1.273515	NA	1.607462	NA	-1.255793	-1.513159	-0.593174	NA	0.116403	0.281405	-0.934926	-0.962086	-0.424931	-0.303541	0.560671	1.218349	-0.982005	2.693207	-5.200532	0.056059	-0.453003	0.768105	-0.907892	1.720919	0.318421	-4.549093	1.369099	-0.527973	1.557087
IXR1	NA	1.090644	NA	-1.27589	-0.62278	0.944475	1.229697	-0.255627	1.466899	NA	0.337342	0.337467	0.224148	-1.99031	1.132603	0.22029	-0.685135	0.766036	-0.811295	1.624145	-0.016528	0.138185	1.082463	NA	3.073028	0.413397	0.556025	0.429079	1.511209	NA	2.324317	-0.84299	NA	-0.515054	0.303285
JEM1	NA	NA	0.671166	-1.184608	-0.065161	-0.045744	0.074783	-0.146482	0.628871	0.203824	-0.357625	0.062487	0.138559	NA	0.47006	0.940673	-0.034012	0.134415	0.185158	-0.282377	0.119041	-0.559451	1.012069	-0.152196	NA	NA	0.27747	1.127074	0.302936	0.039246	-0.074585	0.512311	-0.466742	-0.237034	-0.033383
JHD1	NA	-0.491283	-1.100176	-0.612046	-1.062166	0.363624	-0.253498	-2.270945	0.290603	NA	-0.313338	0.28889	0.426947	NA	0.274713	0.079784	-0.116846	-0.886595	-0.36397	-0.000541	0.297693	-0.574884	NA	0.764179	NA	-0.817641	0.074032	-0.085388	-0.375132	0.912799	NA	0.803871	0.200333	1.374537	0.055067
JHD2	-0.528115	0.457244	-0.584437	-0.003059	0.184561	0.1161	-0.680114	NA	0.645963	0.4118	-1.404456	-0.553161	0.205418	-0.37582	0.285035	-0.008549	-0.168053	-0.117328	-0.288656	0.885388	NA	-0.157173	NA	-1.011131	NA	0.746404	1.04498	0.044419	4.236727	-0.207829	-1.03132	0.597238	-0.356414	1.03352	-0.098575
JJJ1	NA	NA	-0.537545	-0.415403	-0.101708	-0.302668	-0.376961	-0.46143	-0.166203	NA	0.476357	-0.639275	-1.017008	0.091313	-0.382093	NA	-0.006915	-1.352621	0.062514	-0.192683	-1.881281	NA	NA	-0.509723	NA	0.314804	0.232872	-0.583549	0.577436	0.10006	0.708205	-0.622875	NA	-0.241754	0.027207
JNM1	NA	NA	2.121889	-0.038584	1.011275	1.086917	-0.09072	0.227324	-0.49446	NA	NA	0.796581	NA	0.033901	1.508725	1.079861	-0.528415	-1.733514	-0.787725	-0.563042	-0.017194	0.099079	NA	-0.624243	NA	-0.174588	-0.96256	0.51405	-0.363487	0.373617	NA	-0.159785	0.621258	0.003083	NA
KAP120	NA	-1.515327	-0.14595	-0.077027	NA	-0.327516	0.44157	-0.356953	-0.734929	NA	0.635018	-0.189253	-0.962206	-4.455234	-1.028586	-0.381439	-0.135601	-0.210747	-0.283134	0.494073	-1.379731	-0.240935	0.402736	-0.430408	NA	-0.54381	-0.063148	0.311069	-0.501947	0.544557	-1.374555	0.473915	0.450767	0.274459	-1.511167
KAP122	NA	-3.184555	-3.31887	0.69229	-3.0172	-0.076046	-0.129388	-1.8789	-0.285874	NA	2.232572	-1.133712	-0.076618	NA	0.381765	0.713951	0.772579	0.259112	0.923071	-0.360985	NA	0.044304	1.509636	NA	NA	-0.938245	-0.920774	-0.244239	0.329345	0.170067	NA	NA	0.282288	-0.737839	-1.455874
KAR5	NA	-0.24415	0.299688	-0.329359	0.37605	0.120871	0.132629	-0.735392	-0.478075	3.165799	NA	0.233286	0.216886	NA	0.05648	0.505972	-0.31811	NA	-0.307069	-0.218385	NA	-0.039845	0.456293	0.605067	NA	0.116402	1.114192	0.143227	0.166854	0.045826	NA	-0.688047	-0.715331	-0.372873	0.733549
KAR9	4.32817	-0.175647	0.151897	0.374207	NA	-0.141394	1.370078	-0.242594	0.061805	1.014944	-0.233434	-0.779055	0.345165	-0.695765	-0.134324	-0.204006	0.877853	0.290467	0.423103	-0.144822	-0.412241	0.283147	0.817593	0.283794	NA	-0.315908	NA	0.374171	0.645352	-0.041814	-0.340607	0.178926	-1.521759	-0.835409	0.206738
KEL1	4.598354	0.06312	NA	-0.058195	NA	0.93682	1.077908	-0.123246	1.46791	1.857826	NA	-0.491036	0.01876	-1.309998	0.924001	2.053332	1.38123	-0.276289	0.361674	0.318676	0.02294	0.846079	NA	0.139964	NA	1.181745	0.566324	1.34374	0.17703	0.526732	-1.642681	0.881582	-1.216892	-0.885759	0.63063
KEM1	NA	-3.102898	NA	-0.598843	-8.853123	-0.24676	-0.065857	-4.579862	1.002252	NA	-0.474566	-0.293013	-0.797545	NA	1.125745	1.202898	0.193755	-0.764776	-0.060312	-0.138822	-2.208777	0.240598	NA	1.879348	NA	0.081883	-7.129974	NA	-2.685355	0.682855	NA	NA	-2.612059	-1.71849	-0.339209
KEX1	NA	0.936341	1.106978	0.196389	-0.48021	0.053471	-0.54198	-1.555767	-0.537575	0.74059	-1.600725	0.037063	0.810266	0.733657	-0.588193	0.433154	0.667309	-0.462033	-0.966693	-0.882841	0.380561	-0.156368	1.02098	0.332307	NA	-1.286001	-0.069607	NA	0.312802	0.635599	-1.679177	-0.504195	-0.758935	-0.794512	-0.263201
KEX2	-1.210644	0.044846	0.662452	0.652761	2.259772	0.9705	-0.244271	-1.278309	0.928406	-1.949742	-0.06275	0.948083	0.902412	1.134993	-0.047024	NA	1.018324	0.059042	0.276279	0.801519	NA	0.210478	NA	NA	NA	0.126903	-0.950095	0.980055	-1.13542	-0.37489	-1.070158	0.647596	NA	1.357299	0.172237
KIN1	1.4824	0.529074	1.753717	0.358891	0.084839	0.131447	0.614371	0.231073	0.117291	0.510914	-0.14978	0.224057	-0.237826	NA	NA	0.341173	0.17542	0.380632	-0.177486	-0.38062	0.132086	0.500299	NA	0.162463	NA	0.616851	0.780069	0.053197	0.044828	0.334109	-0.241348	-0.173005	-0.037759	NA	0.657006
KIN2	NA	0.554922	0.593278	-1.437195	-0.165178	-0.084939	-1.011416	0.45129	-0.770731	-0.766675	0.296806	0.226491	-0.089257	1.05249	-0.236681	0.221269	-0.370853	0.076577	-0.323255	NA	-0.259865	-1.169376	-0.078598	0.705847	NA	0.358397	NA	0.20055	0.476694	-0.410394	-0.4014	-0.22834	-0.315887	0.436257	-0.929087
KIN4	NA	-1.159106	-0.255552	-1.732749	-2.058095	-0.616813	-1.385572	0.234249	-0.762956	NA	1.42933	0.47051	0.774922	NA	-0.246163	0.409325	-0.008915	0.440148	0.129419	-0.156431	NA	-0.088516	-1.437086	0.062296	NA	0.912822	0.489543	-0.050401	0.319012	-0.252903	0.336332	-0.015675	-2.234766	-0.658047	-1.003192
KIP2	NA	0.210935	0.654288	0.864427	NA	-0.352235	0.049659	-1.303708	0.753514	-0.680461	-0.235906	0.847047	0.338834	-0.991365	-0.57678	-0.296148	-0.361673	-1.555914	-0.311708	0.405317	-0.492723	0.273966	0.761251	0.664123	NA	0.253192	-0.093646	0.291125	1.009294	0.068877	0.847841	-0.105668	0.533659	-0.245389	0.484221
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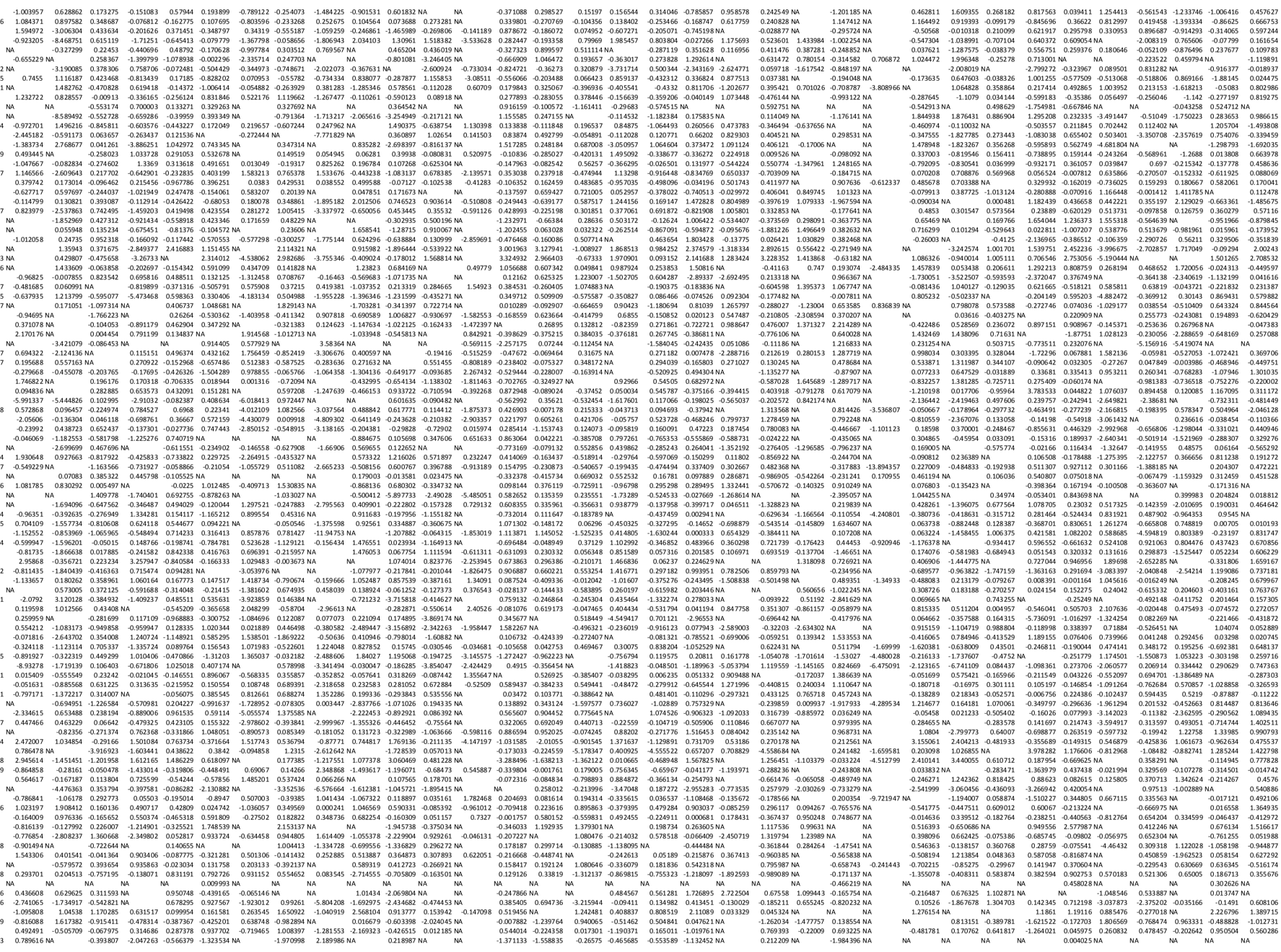
KNS1	NA	-1.24371	0.226698	-0.069884	-0.593982	0.18059	0.52735	-0.263105	0.155276	0.353174	-0.052073	0.717658	0.367324	-1.448289	-0.761681	-0.012463	0.125388	0.72973	-0.256626	NA	-0.060859	-0.030477	-0.645469	0.309128	NA	-0.777906	NA	0.112695	1.01951	-0.362958	0.987342	-0.51124	0.76133	-0.598351	0.391993
KRE1	NA	-2.100438	-0.753052	1.23859	-0.991592	1.0724	0.895268	-2.203381	0.87877	NA	0.418737	-1.592551	-1.406283	NA	-0.445036	0.497511	0.694445	NA	0.887352	-0.408866	NA	1.280323	NA	NA	NA	-0.923051	-0.965261	0.011188	-2.443645	0.778778	-4.584005	-1.20805	NA	-0.613138	0.329862



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MSG5 NA 0.815198 0.669442 -0.212835 0.75819 0.585724 0.546786 NA -0.640886 -2.353433 -0.734409 0.260028 0.831598 0.03056 -0.241342 0.341351 0.295344 NA 0.206228 1.963555 0.259578 0.188133 1.421849 -1.288722 NA -0.04824 -0.362313 NA -0.982068 -0.922178 -0.852597 -0.393333 -1.404265 0.349395 0.772019
MSH2 NA NA 0.955181 0.516362 -0.577909 NA NA NA 0.902077 NA NA -1.643368 -0.017852 NA -0.212303 -0.029461 0.221823 1.083727 -0.837279 0.930433 0.016527 1.202317 0.895097 NA NA -0.635097 NA 0.297553 0.700666 1.111213 NA NA 0.635229 1.631905 NA
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MSI1 -0.058974 NA -0.4297 -0.818805 -0.310986 0.937416 0.793898 -0.68946 0.936216 -1.117986 NA 0.152442 -2.276213 NA 0.538124 0.963266 -0.530853 0.985481 0.107446 -1.198665 0.570712 -0.142821 -1.854369 1.649227 -1.511641 1.529685 -0.324248 0.403844 0.760432 0.827192 NA 0.605565 -0.736844 -1.521788 2.196746
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NAM7 1.343897 1.187551 1.057315 -2.114298 0.225601 -0.42695 0.111151 0.24647 -0.068029 -1.746051 NA -1.032133 NA NA 0.35978 -0.487133 -2.593693 1.411663 -3.295902 2.29105 NA -0.101878 0.793002 0.317488 NA 1.413459 0.841441 1.057995 -3.398117 -0.187304 0.438521 1.024652 NA 0.917045 -1.473219
NAM8 NA -0.158803 -0.179211 -0.013067 -0.900796 -0.242735 -0.054734 0.620823 0.644693 -1.165609 -0.115778 -0.78029 0.576569 -1.402932 -0.410491 -0.302574 -0.002547 1.268689 0.10166 0.910833 NA 0.257942 NA -0.335133 NA 0.458904 0.477951 -0.645776 0.940111 -0.253381 0.899845 -0.989374 0.098348 -0.710371 -0.335636
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NBP2 NA -3.538656 NA 0.038654 -0.829512 -0.079331 0.052466 -1.128809 0.305158 -1.632365 0.134447 -1.39997 1.247668 -1.712376 NA 0.45025 -0.147144 0.914729 0.332349 0.591988 1.188561 NA NA 0.132116 NA 0.455285 -1.034969 0.448899 -0.397191 -0.107475 0.076054 -1.40176 1.081564 NA 0.86728
NCL1 NA -2.985214 0.227714 0.408228 -0.179008 0.12171 -0.169678 NA -0.608165 NA NA 1.076698 NA NA 0.873663 -0.504076 0.116627 -1.643563 0.524622 -1.545742 NA -0.328625 0.53026 1.273139 NA NA -0.208301 NA -1.0872 0.232041 NA -0.004932 NA 0.499071 0.730033
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NGR1 NA 0.341778 0.16538 -0.599278 -0.347699 0.597033 0.776821 -0.071831 -0.089013 -0.382229 NA -0.241155 0.555764 NA 0.329034 -0.137165 -0.224619 -0.052338 0.369853 -1.183427 NA -0.170073 NA 0.501467 NA 0.23454 -0.01569 0.208349 0.960905 0.282309 0.097792 0.598679 -0.515984 -0.196731 0.635883
NHP10 NA -2.808565 NA -0.281164 -1.253297 0.841607 0.544533 NA 0.468082 -0.895943 -0.247329 -0.754894 -0.16951 -1.217653 NA 0.552965 0.545198 -0.632928 0.356662 1.000701 -0.330427 0.17117 NA 2.005702 NA -0.292001 -1.086325 0.092647 0.224537 0.812644 -0.578395 -0.60274 2.097526 NA 0.309781
NHP6A NA -0.579953 NA 0.448161 -0.475018 1.139824 -0.205612 NA 0.69501 NA NA -0.049074 -0.513486 NA 0.360612 0.208973 -0.208859 1.110703 -0.497703 0.174924 NA -0.473495 NA 1.3253 NA -0.75565 -0.117044 1.25799 0.434596 -0.383798 2.192803 -0.066324 -0.947184 -0.136136 0.663955
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NKP1 1.85385 -1.34959 0.837759 -1.50201 0.437663 NA -1.302274 -0.804193 -0.272597 -0.760506 0.516343 0.340657 -0.192628 NA 0.04065 0.378675 0.016397 -0.800709 -1.164641 1.028528 1.06924 -0.159042 NA 0.669613 -4.390762 -0.301248 -1.688529 0.640526 -0.334652 -0.822304 -1.404451 NA -1.847283 0.063913 -0.348883
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NMD4 NA NA 0.248768 -0.324038 0.328069 -0.484945 -0.140673 0.62637 0.023895 0.626507 -0.383281 -0.403294 0.595739 NA 0.146034 -0.106344 0.252615 0.182804 -0.148866 0.311761 -0.501524 0.308761 NA -0.239301 NA 0.077032 1.049897 0.185549 -1.189124 -1.011379 -0.79425 -0.511025 0.263029 -1.334884 0.388434
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NOP12 NA NA 2.19189 -0.524843 -0.68361 -0.545868 NA 1.617514 NA NA -0.436592 -0.125254 0.677407 -0.150675 -0.235352 -0.484268 0.185581 1.439341 -0.065091 1.228613 -0.429392 -0.0759 NA 0.602162 NA 0.922169 1.531334 -0.168118 0.141123 -0.451476 NA 0.065418 NA -0.765312 0.311343
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NUT2 NA -0.462117 -0.302948 0.366956 -0.168162 0.426536 -0.38181 1.090993 1.269515 0.032827 NA -0.580381 -0.334433 0.579537 0.044985 0.304749 0.184857 -0.627611 0.779724 -0.240551 -0.279833 -0.232279 NA 0.628267 NA -0.370952 -0.927837 -0.058342 0.889244 -0.077141 1.555046 -0.15058 -0.655307 -0.039291 0.838732
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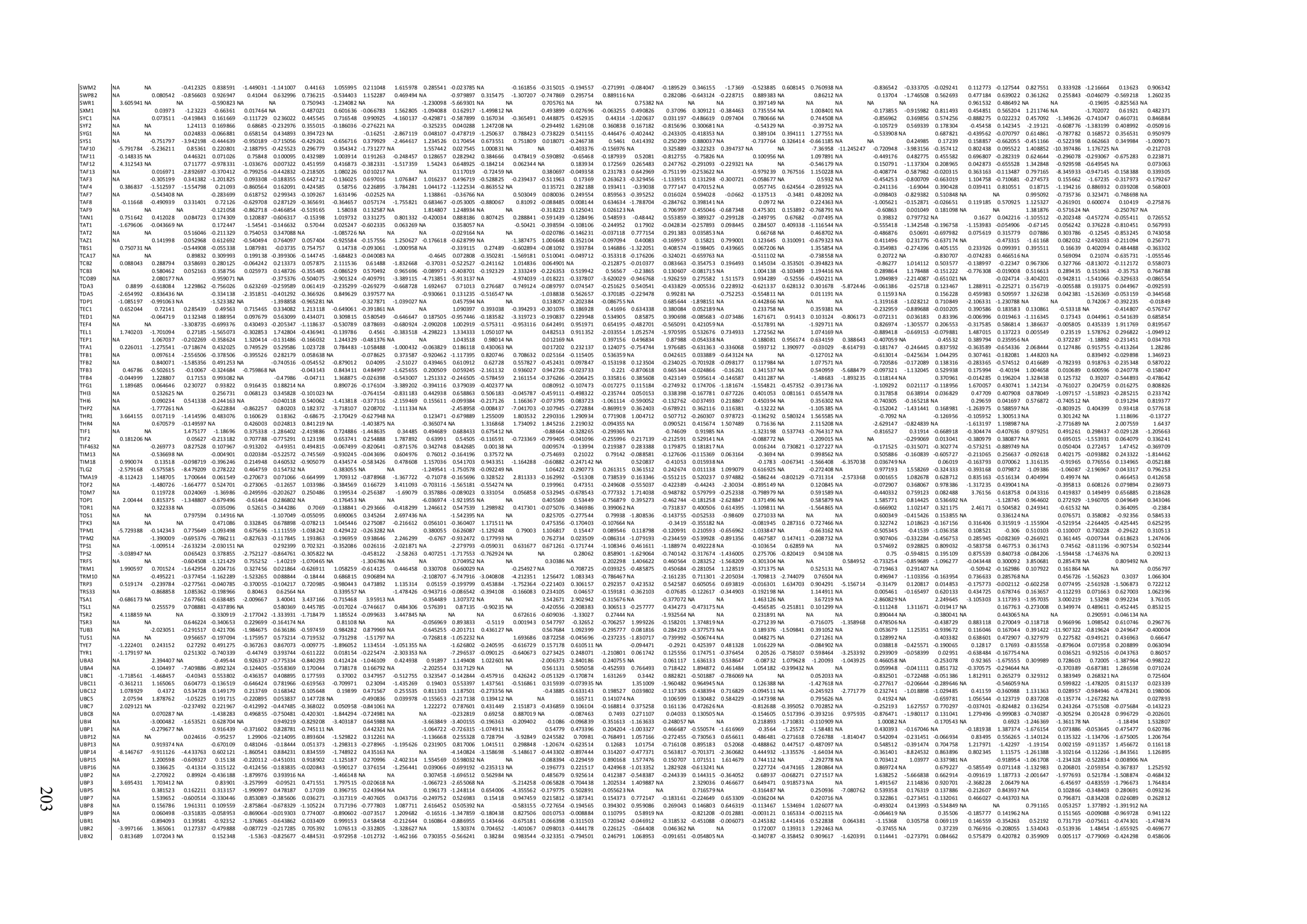
OPI1 -1.124637 -1.05845 0.621855 0.104201 1.837925 -0.353465 -0.848196 -1.214458 0.095357 -8.767438 1.472341 1.053173 1.005477 NA 0.20527 -0.218803 0.150833 1.177442 0.145519 0.453619 NA -0.211905 0.520791 -1.930687 NA -0.109072 -0.14379 0.376118 0.044572 -0.616829 -1.896428 -4.964541 1.827011 -0.801774 -0.08491
OPI10 NA -0.011939 0.179033 0.291603 -0.324029 0.185302 NA 0.465884 NA NA 0.114848 0.68446 0.415877 0.997114 0.272605 0.02114 0.35208 0.706286 -0.042547 -0.07777 0.263122 -0.384187 NA 0.960419 NA -0.151449 NA NA 0.830328 -0.263302 0.104417 0.709022 NA -0.457411 -0.56877
OPI3 NA -0.034765 NA 0.903704 0.82268 -0.367005 -0.396902 -1.168625 -0.10338 -3.313754 0.309501 0.12296 0.85866 -0.187698 0.588844 -0.734274 1.090542 -0.926249 0.711957 0.401683 0.830204 0.941703 1.355689 -0.829134 NA -1.429533 -0.716739 -0.482913 -1.557991 0.596008 -1.540984 0.316127 2.035178 0.235242 -0.592588
OPY2 NA 0.432712 -1.168231 0.058023 0.598717 1.050284 0.403405 -1.092601 -1.375584 -0.838497 -0.053358 0.598931 0.09638 NA 0.854592 0.429927 0.380437 -0.758503 0.111297 -0.459871 NA -0.587258 NA -1.48388 NA -0.95488 -0.512915 0.367978 -0.057411 0.297265 -1.797784 -0.453268 -0.442827 -0.978471 1.2388
ORC1 NA -0.024335 -0.368459 -0.877256 0.144107 0.559591 0.09857 NA 0.305869 0.905132 1.626093 0.344835 -0.732566 NA 0.202252 -0.19552 NA 0.529182 0.464169 0.229567 NA -1.720421 -1.195418 -0.277696 -2.633836 0.331619 0.190129 -0.227972 NA 0.278153 -0.62966 0.163789 0.334439 0.208951 NA
ORM1 NA NA 1.003498 -0.054253 0.293045 0.749664 0.441476 0.125451 -0.278121 -0.820671 -0.200304 -0.235633 0.076273 0.800411 0.345744 0.263772 -0.192525 -0.077801 -0.428479 -0.715029 0.415592 -0.276168 NA 0.76744 NA -0.096786 0.72877 -0.007454 0.002897 0.052443 0.183245 -0.221912 1.484429 -0.538776 0.429731
ORM2 NA NA NA -0.693423 0.843198 0.001783 0.878775 -0.073636 -0.807698 -0.557459 0.553749 1.124061 0.422455 NA -0.374001 0.074042 -0.151485 0.869701 0.655719 -0.140162 -0.471517 0.180969 NA 0.26692 NA 0.293664 1.019259 0.494308 0.032347 -0.329244 -1.609251 -1.29779 -0.512577 -0.166156 -1.283264
OST3 NA 0.920842 0.174394 -0.349629 0.359174 0.02359 NA 0.566084 NA NA -0.488359 0.031917 0.440941 0.865639 0.694695 -0.067962 0.44328 -0.383599 0.02375 -0.68646 1.03582 0.383636 NA -0.463558 -3.01388 -0.335241 0.444877 -0.105746 0.232656 0.814538 0.342189 0.507219 -0.842833 0.175159 -0.518497
OST5 NA 0.969943 0.530107 0.205138 0.858168 0.621611 0.349313 -0.421697 0.499115 -1.944676 -0.534722 0.089978 0.620677 0.371952 0.321192 0.459123 -0.02602 -0.323799 0.12608 -0.634342 0.226376 -0.238197 -0.531528 -0.018894 NA 0.154925 0.489057 NA 0.518746 -0.450921 -0.387557 0.135945 -1.622557 -0.205927 1.504429
OST6 NA 0.6471 NA -1.211828 -1.528899 -0.801466 -0.431894 0.430234 -0.588381 -0.324755 -0.176083 0.349152 NA 0.683761 -0.137951 -0.081502 -0.573677 0.115375 0.324363 -0.007345 NA -1.084318 NA 0.996122 -2.689694 0.760707 0.070634 -0.144635 NA -0.210031 -0.028233 -0.422278 0.599681 0.360174 -0.633235
OXR1 -0.918679 -0.688379 -1.252573 0.25346 NA -0.281768 0.665499 -0.074038 -0.081622 -0.765793 0.903397 0.156776 0.781339 1.371401 -1.224332 -0.416775 -4.30761 -1.128998 0.525146 0.054298 0.213091 -0.636557 1.330994 0.365176 NA -0.607739 -0.951347 0.062295 -0.492199 -0.124791 0.193381 0.029911 1.282756 0.478147 0.36838
OYE2 1.33467 0.343856 -1.14399 -0.187853 0.339345 0.015025 -0.41758 -0.164888 0.709481 -1.305379 0.199188 -0.005632 0.144152 NA 0.462915 -0.137008 -0.025226 0.084143 0.41467 0.766561 1.233437 0.554435 0.035923 0.44857 NA -0.233456 0.641319 -0.480089 0.812225 0.126247 -0.184978 0.098464 -0.310357 -0.722632 -0.00819
PAC1 NA -1.401295 0.61237 -0.819985 -0.630598 0.015665 0.286481 1.239727 0.140537 -1.628462 NA 0.997034 0.325378 -2.622612 0.261072 0.225331 NA -0.28188 -0.243258 -0.151991 NA -0.200181 -1.428613 -0.163219 NA 0.284433 -0.906021 -0.356781 3.502122 0.67364 -0.068449 -0.679972 0.545749 0.86774 0.379155
PAC10 NA -0.917945 -0.877664 -0.321033 1.349428 -0.050436 -0.232364 0.804925 -0.204861 NA -0.859532 1.371232 1.317493 -1.161056 -1.035728 -0.654874 0.004351 NA 0.491109 1.161289 1.633651 0.497665 NA -1.168064 NA -0.13918 -0.820401 -0.182312 0.743117 -0.351442 0.37365 -8.089441 1.41918 -0.668094 -0.426898
PAC11 NA -2.549211 0.879499 -1.240541 -0.619636 NA -0.944841 NA -0.358345 0.323493 -0.128989 0.692932 0.020155 1.644629 0.774042 0.597871 0.353123 -0.731791 -0.100125 -0.274891 -1.417411 0.714609 -0.589612 -0.17346 NA -1.089782 -2.204559 0.419507 -0.862587 0.864549 0.016061 0.619925 -2.207361 0.296173 -0.179807
PAC2 NA 1.410483 -0.34015 1.072103 -1.557236 -0.082198 0.076444 0.506187 -0.175576 -1.245131 0.949501 0.495442 -0.850566 -0.094278 0.339824 0.211507 -0.011476 -1.036903 0.180191 0.045197 NA 0.6108 -0.082453 -0.530093 NA -0.280589 -0.518142 0.334062 0.77107 0.397496 1.397255 -1.165062 0.201009 -0.576885 0.698858
PAN3 NA -0.11842 -0.894975 -0.710376 1.242035 0.608731 0.950578 -0.544662 0.097004 -0.288753 -1.083843 -0.418396 0.342032 1.11849 0.161463 0.480148 -0.535743 0.034071 -0.06429 0.145817 0.345518 0.084345 NA 0.519777 NA 0.213208 -0.638959 0.422407 0.887153 0.29765 -1.314362 -0.245333 -1.704492 -0.620265 1.721484
PAP2 0.888411 0.130372 0.895694 -0.097636 0.311845 -0.21854 -0.418472 0.5626 -1.114125 -0.076307 NA -0.082048 0.19692 0.62011 0.117888 -0.4818 0.334189 NA -0.273725 -0.614049 0.15238 -0.146725 NA 0.587377 NA -0.678276 -0.275623 -0.322566 0.106455 -0.188955 0.277155 -0.394645 -0.359477 0.243674 0.373434
PBP1 NA -0.842051 NA -0.418893 -2.30794 -0.554106 0.815426 -2.144164 0.180616 1.583043 -1.930398 -0.803097 -0.56801 -5.42449 0.344522 0.338456 -0.323371 0.110397 -0.157463 0.431027 -0.113125 0.033659 NA 0.444572 1.356144 0.317849 0.592488 0.860067 -0.759936 0.244041 -2.005637 -0.0945 -1.490499 -0.602948 -0.483867
PBS2 NA NA -0.307764 -0.096076 -0.661102 0.424002 0.86508 -1.983166 1.170622 -2.671147 0.063534 -0.963499 0.407888 -3.061292 0.761918 -0.138546 0.089347 1.194218 0.176523 0.184895 0.395241 -0.785453 1.177642 -0.611675 NA NA -1.352394 -0.143552 1.233061 0.179842 -1.095206 -1.184883 0.204344 -0.1486 0.32098
PCA1 NA NA 1.21601 -0.102384 0.035639 0.319581 -1.183353 0.424045 -0.228996 -1.504837 0.179443 -1.169327 NA 2.311599 -0.295597 0.016959 0.405969 0.180733 -0.236216 0.069469 0.020721 0.679375 NA 0.369816 NA 0.360568 NA -0.366539 0.027313 0.283733 -0.916801 -0.267045 -0.418018 0.010385 0.289678
PCH2 NA 0.464131 -0.321315 0.094533 0.339668 0.251751 0.090889 -0.029931 -0.255144 NA NA 0.8969 0.433174 -0.006745 0.171538 -0.051525 0.458601 0.217346 -0.672745 0.194977 0.919349 0.150024 0.127451 -0.458149 NA 0.311534 0.966222 0.695001 1.217099 -0.567654 0.83859 -0.256822 0.247392 0.135618 -0.326237
PCP1 NA -0.211296 1.025572 0.312155 0.750892 -0.570483 -0.696219 -0.638161 -0.102918 -1.583574 1.796974 1.00974 1.372517 0.517306 -0.054353 -0.809075 0.323028 0.427123 0.51445 1.728115 -0.048846 -0.548521 1.335972 -1.085638 NA -0.643234 -1.991088 0.007624 -0.276282 -0.808985 -0.305949 -0.244428 2.675783 0.973105 -0.439175
PCT1 NA 0.908385 0.857411 -0.027826 0.465546 -0.281843 -1.016764 0.250299 -0.539374 -2.944439 0.315679 -0.355796 0.760975 1.126881 -0.02322 -0.401645 -0.038985 0.18482 0.25037 0.859464 0.330409 -0.157796 NA 0.500503 -1.254154 -0.330702 NA 0.113094 0.451106 0.079284 -0.240013 -0.946789 -0.026663 0.105738 0.577584
PDA1 NA -0.478671 NA -1.531272 0.199955 -0.170739 -0.680466 -0.475189 -0.618852 3.766614 1.127769 NA NA NA NA -0.098102 -0.426486 -0.932876 NA NA NA 0.002644 NA NA NA 0.514906 0.941404 -0.630984 NA 0.730329 NA 0.270871 NA NA -1.675906
PDB1 -0.884792 -0.239562 1.623012 0.253634 -0.483406 -0.471545 0.120093 1.81631 -0.887386 -2.636212 NA -1.026182 1.026772 2.320964 -0.707617 -0.53137 -0.079923 1.303277 -0.061867 0.796093 0.223899 0.046493 -0.468045 -0.4797 NA -0.470331 0.172167 -0.488867 1.275212 -0.033297 1.692849 -0.269011 0.595764 -0.412202 -0.117583
PDC1 -1.582413 0.965219 -0.337736 -0.116885 0.036019 0.077402 -0.636957 NA 1.062973 0.246888 -0.414685 0.755102 NA NA 0.194428 0.390103 9.00E-05 NA -0.509332 NA -0.410033 -0.391308 NA -0.666554 -0.997683 0.284326 NA -0.324184 -0.076005 0.040352 -1.389759 0.099778 -0.257201 0.128361 0.56431
PDE2 -1.074061 -0.530237 -3.665385 -0.401558 -0.514326 0.043098 0.377936 0.308214 0.766174 -3.525221 NA 0.144309 0.629091 -0.485 -0.454131 -0.09384 NA -1.126495 -2.857533 0.080011 0.131899 0.77397 -0.162806 1.083034 NA -0.05937 -1.262924 0.358654 -0.1773 0.376035 0.630205 -0.994587 0.037856 -0.996081 0.437261

RAD10	0.30263	0.313013	-0.159485	-0.431449	-0.383941	0.498144	0.375671	-0.863624	0.360719	-2.590865	-0.872166	0.140622	0.047157	NA	-0.707588	0.37475	-0.860614	-7.954647	-0.382724	-4.57448	NA	-0.644325	NA	0.516274	NA	0.628399	-1.029984	0.141952	-1.673039	0.74871	-1.090215	-0.12441	0.044181	-3.129885	0.472681
RAD16	NA	NA	NA	-0.654577	-0.981097	0.230197	0.232085	-1.75512	-0.182664	NA	NA	-0.410438	0.582229	NA	0.574655	0.43842	-0.340226	-2.32294	0.328779	-1.814661	0.233952	-0.719805	NA	-0.702504	NA	0.93046	NA	0.538296	2.147234	0.372471	NA	0.896227	0.987568	-1.924324	-0.196891
RAD17	-0.533505	-1.617424	1.381955	3.114529	-8.957909	0.880347	1.942691	0.36135	1.246965	-0.014974	NA	NA	1.180922	-2.568977	3.110691	2.749143	NA	-0.442177	NA	-0.391503	1.184925	0.076134	-5.921721	1.912481	NA	0.874032	-1.767536	2.711078	-0.241446	1.505936	-0.200874	-0.304943	NA	-0.92114	2.14145
RAD18	1.006829	NA	NA	NA	NA	NA	-0.847963	NA	NA	NA	1.249616	0.547915	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.762198	-0.549231	-0.251943	NA	NA	NA	1.378668	0.950414	NA	NA	-0.299264	2.332203	NA
RAD23	NA	-0.897382	-1.650184	0.427369	-2.090426	0.633161	0.550861	-1.982831	0.28204	NA	-0.952638	-0.631633	-0.278203	-0.052708	0.70902	0.571762	0.320024	-5.374046	0.88383	-0.810611	0.795836	0.905982	NA	1.308661	NA	1.318326	0.322244	1.356602	0.268936	0.702713	-2.572686	-2.000166	-0.80235	-2.039963	0.440967
RAD24	NA	NA	0.409828	NA	NA	0.469497	1.690952	-0.326124	NA	NA	NA	NA	NA	NA	2.314307	NA	2.439846	-0.789686	NA	NA	NA	-0.571607	NA	-0.145953	NA	NA	NA	NA	-1.538053	0.737995	NA	-0.703627	NA	-2.268472	NA
RAD26	-0.248554	0.382112	0.703041	-0.303274	0.32243	0.350024	0.396706	0.968942	-0.378949	0.089377	-0.138642	0.597132	-0.533164	-0.338324	0.079172	-0.024592	0.539557	-0.696119	-0.410819	-1.817541	0.623981	-0.393437	NA	0.745958	-3.696676	NA	-1.148864	0.146075	0.980006	0.411177	-0.278471	0.890235	-0.52827	0.170587	-0.163758
RAD27	-0.028301	-5.099612	1.199091	-1.061648	2.252455	3.545644	0.194876	3.377035	-0.911417	-0.799751	-0.005305	-3.319711	NA	-0.905196	1.450922	2.953564	-0.508672	2.387765	-0.987003	2.612434	NA	-0.588349	NA	3.50411	NA	4.409521	NA	-2.509859	-3.170588	3.586294	3.589192	2.236968	2.026403	3.33472	3.743536
RAD5	1.034992	1.741424	0.645259	0.784682	NA	0.232151	2.256994	0.635617	NA	NA	0.260971	0.372829	NA	2.753598	1.114824	NA	NA	4.54652	-2.492551	NA	NA	-3.46694	1.657082	0.574959	NA	1.264445	NA	0.934612	3.305606	0.414877	0.178156	0.076575	2.784114	0.733639	NA
RAD51	0.002409	-0.063498	0.758456	-0.586989	-0.443628	0.344384	0.972415	-0.125729	0.474417	1.079827	-0.199424	-1.09855	-0.008507	-2.716196	0.056186	-0.379649	-0.10624	0.270478	NA	0.146836	0.281706	-1.088967	0.53342	0.498912	-3.914351	-0.247727	0.542732	0.143366	3.151533	0.097689	NA	0.075874	-0.662021	0.4047	0.446451
RAD52	1.537975	1.456633	0.530433	0.580469	NA	0.663354	-0.407631	-1.597529	NA	NA	NA	-1.408834	NA	NA	-0.962778	NA	NA	0.097103	0.230406	1.126164	NA	0.170277	0.616613	-0.231323	NA	1.399318	1.639326	1.029473	1.873228	-0.573741	-1.124287	-0.135214	NA	0.576632	NA
RAD54	0.831791	-0.469091	0.945114	0.586006	-1.108073	-0.240501	0.423633	-1.51678	0.24406	-1.487682	1.014922	1.519431	2.503931	NA	-0.498682	-0.548774	-0.021227	1.465987	0.325233	1.529639	2.80618	-0.347259	2.483496	-0.555361	NA	0.386862	0.585219	NA	2.580357	-0.192289	-0.824545	-0.474975	NA	-0.412697	0.013051
RAD55	0.277314	0.465424	0.173072	-0.390438	-2.970314	0.085896	0.809936	NA	0.075814	-1.135027	1.038631	-0.086857	2.243793	NA	NA	-0.470958	0.085253	0.20653	0.073585	0.746231	2.643239	-0.543858	1.884835	1.777595	NA	-0.601013	NA	0.111418	2.450799	0.258682	-2.275974	-0.907186	0.490861	NA	-0.762815
RAD57	-0.349549	0.633111	NA	0.442142	-0.966358	-1.058606	1.008739	NA	-0.410489	-0.007624	1.415758	1.661218	2.727187	NA	NA	-1.129392	0.009662	0.10383	0.505089	1.538833	NA	-1.204155	1.912774	-0.317335	-2.414677	1.358884	0.873189	0.54639	2.128846	-0.880491	-2.531479	0.265875	NA	NA	-0.963585
RAD59	NA	0.954834	NA	-2.484743	NA	1.016298	0.425545	NA	0.602431	-0.288684	-0.128012	-1.293824	1.349237	NA	0.152179	-0.23024	-3.306838	-0.039387	-3.154772	0.514603	1.682621	-1.739411	NA	1.196368	NA	-0.706147	0.710647	0.045979	2.834736	-0.13088	-0.209742	1.058244	1.381824	0.872059	0.725676
RAD61	NA	-1.80791	NA	0.020566	-1.323319	0.254014	-0.285321	NA	1.107577	NA	-0.474489	-1.201511	NA	0.737124	NA	0.661906	-1.395979	0.530807	0.143061	-0.987377	0.49931	-1.081854	-2.091314	-0.15306	-4.440706	0.097191	-0.706599	-1.46302	1.81353	0.284484	-0.046416	0.46292	0.005842	NA	-0.018824
RAD7	NA	1.672159	0.352688	-0.193566	0.439495	0.742031	1.021464	-0.357478	-0.299986	-0.43441	-0.795087	0.246456	-0.286387	-1.876769	-0.146456	0.138275	0.314542	-1.891388	-0.125864	-1.806865	NA	0.651493	NA	0.810257	NA	NA	NA	0.278741	1.417589	0.236888	0.196804	0.240027	-0.744744	-1.064993	0.484376
RAD9	NA	NA	1.011363	-0.876074	NA	NA	-0.235503	0.307035	NA	NA	-5.497961	NA	NA	NA	2.076729	NA	NA	0.848533	NA	NA	NA	NA	NA	0.810239	NA	NA	NA	NA	-7.702775	0.167422	NA	NA	NA	-4.749502	NA
RAS1	NA	NA	-1.203143	-0.439216	0.035032	0.379868	NA	-0.230149	NA	1.692823	0.592962	0.663925	-0.057521	NA	0.844568	0.783509	0.496341	NA	0.049031	0.769062	0.862044	2.045346	NA	0.835611	NA	0.380353	0.378061	1.139659	0.477661	0.539637	0.9791	0.330928	NA	-0.708571	-0.287267
RAS2	-2.838871	0.334957	0.151391	-0.779628	-1.019018	0.439263	-0.304593	-0.662922	0.854564	-1.642733	-0.614934	-1.719691	-0.452813	-1.379143	0.025743	NA	0.662611	-1.52691	-0.923789	0.668705	-1.129533	-1.54043	-2.705082	0.89811	NA	-2.523795	-0.235139	-0.075587	2.12835	0.883347	NA	-0.606425	0.026255	0.478937	0.997504
RAV1	-0.883597	-0.206471	NA	0.190414	-0.723747	-0.120716	-1.612215	0.003459	0.131141	-0.196062	0.029454	-0.136724	0.369168	0.614776	0.344885	1.214959	0.786932	NA	0.502328	0.427237	1.341585	-0.210353	1.104494	-0.276063	NA	NA	NA	0.308728	0.423182	-0.103153	0.124014	-0.654743	NA	0.369893	0.343911
RAV2	NA	0.347427	-0.511455	0.285571	1.092182	0.132702	-0.072088	0.517384	-0.617192	-1.074809	-0.099255	0.367291	0.546061	-0.130955	0.274389	0.008966	-0.036981	0.850009	-0.00218	0.307942	1.366275	NA	0.835436	0.051225	NA	0.237701	1.292425	0.173093	0.099289	-0.330494	0.213093	-0.450545	NA	0.057195	1.232567
RBA50	-1.30232	-0.832146	NA	-0.173117	0.36063	NA	0.617841	0.169159	-0.172432	-0.766236	-0.804598	-0.886177	-0.59987	0.972915	0.104967	0.359929	-0.087143	-0.454514	0.355944	-0.016032	-0.345242	-0.183806	-0.600765	-0.438401	-1.777968	0.221909	-1.113387	0.158574	0.60195	0.215542	1.100219	0.901558	0.300839	0.067654	0.664888
RBL2	1.034708	-1.124244	NA	-0.311115	0.970536	-0.972771	-2.118238	-1.459127	-0.292055	NA	1.039404	-0.035774	-1.183971	-0.252602	0.471594	0.198903	-0.273354	-0.702768	0.779253	-0.102954	0.343678	-0.269853	-2.353076	-0.556234	NA	-0.198999	NA	-0.186252	-1.540184	0.478453	-0.135163	0.877446	-1.720884	-0.161608	-0.359629
RCE1	NA	NA	-1.892344	0.341513	0.82082	-0.145225	-0.348469	NA	-0.414991	NA	0.182044	0.606965	NA	NA	-0.299816	-0.201757	1.642199	-0.160798	0.379427	0.664083	0.858709	0.272741	0.469968	-1.150383	0.598254	-0.294651	0.605712	-0.195734	NA	NA	NA	-3.775964	NA	-0.432766	NA
RCO1	NA	-2.424874	NA	-1.235673	-2.102169	-0.310892	-0.315872	-15.919278	-0.641823	-0.890683	-0.946648	-3.475181	0.930808	-7.368851	1.156186	0.856447	-1.109572	1.340192	-0.226541	1.766827	1.029421	0.256737	NA	-0.298545	NA	1.336501	1.006201	0.68913	-0.249931	-0.008407	NA	-0.196084	-0.782687	0.982581	-0.503569
RCS1	NA	-1.038374	NA	-0.917393	-1.066519	-0.357551	-0.97636	NA	-0.821384	NA	NA	-2.608636	NA	1.189665	NA	-0.181302	-1.762456	NA	-0.929793	0.401377	NA	-1.185029	0.803788	0.557199	NA	-1.381164	NA	NA	-0.528442	-0.018263	0.02446	-0.45186	1.084211	0.34698	-0.314922
RDH54	NA	-2.738591	0.275455	-0.028992	-0.666198	0.554364	0.933383	-0.700947	1.160758	-0.877676	NA	1.137428	-0.282812	-0.289029	1.047821	0.410558	-0.202917	-0.362133	0.683403	-1.465652	NA	1.185797	2.156125	1.965809	NA	-0.278873	NA	0.434268	0.448822	0.919744	-1.150855	0.521619	1.287794	-0.940968	0.153968
REC104	NA	-0.082954	NA	-0.100358	0.575008	-0.158841	-0.053058	-0.312303	0.361733	1.203733	0.772513	-0.338789	-0.088461	-0.107383	-0.103559	0.302751	-0.452094	-0.126006	-0.301577	-0.64681	-0.243988	0.200675	NA	0.222061	0.4883	0.624317	0.423241	0.448947	0.743026	0.043235	NA	0.318094	NA	-0.336689	0.452746
REC114	0.904737	NA	NA	0.556989	-0.548312	-0.740926	-0.823569	0.310929	0.222121	0.553228	0.523152	0.062123	NA	NA	0.732356	0.466246	-0.136692	-1.501678	0.260491	-0.323153	-0.137258	-0.677423	NA	0.72483	NA	0.413147	NA	0.103905	NA	NA	1.331138	0.406875	-0.146416	-1.702575	-0.536161
RER1	-1.951636	0.042245	-1.92501	NA	-1.564528	0.063397	0.170765	0.369056	-0.295109	-0.504104	-0.053781	NA	0.742319	-1.332864	0.494418	-0.067052	-0.18077	NA	-0.57285	0.326682	1.320277	0.020294	0.068234	1.342021	NA	0.027853	-0.072642	0.335517	0.441769	0.060103	0.107807	0.153949	0.203229	0.736688	-0.032992
REV1	-1.689853	0.247029	-0.212631	-1.257335	-0.359262	-0.229751	-1.448243	-0.327688	1.590058	0.921713	0.591953	-0.886346	0.432871	0.109878	0.697866	0.08813	NA	-1.377677	-3.650843	-1.765385	NA	-0.602229	-0.050532	0.764583	0.575564	0.61466	0.613836	0.714171	0.508836	0.439655	-0.897967	0.670747	-0.200303	-9.769859	0.191649
REV3	-0.429465	0.27978	1.005594	-1.044205	NA	0.50201	-1.34768	-0.362338	0.323697	NA	0.029043	-0.748735	0.681106	NA	0.164723	0.464119	-1.8591	-0.201286	-1.001752	-1.647134	-7.58453	-0.014485	0.719498	1.300601	NA	0.472737	-0.545458	0.203517	0.860999	1.015209	0.043995	-0.228781	1.066379	-8.082168	0.40421
REV7	1.223021	NA	0.831151	-1.065436	0.209502	1.587767	0.319473	NA	1.405705	NA	-0.701749	-1.23294	0.698198	0.862781	1.784852	1.750206	-1.039703	-1.241939	-1.247205	-3.40104	-7.838062	0.433939	NA	0.646497	-1.203297	0.627071	0.845356	1.005078	-0.133126	1.437967	-0.278762	0.713493	-0.629727	-9.249497	2.258429
REX4	NA	0.685472	NA	1.217893	0.982027	0.002808	-1.00547	NA	NA	NA	0.642823	0.867626	-0.274932	NA	0.125211	0.332907	-0.000997	NA	0.525929	-0.052183	-0.12279	1.1361	-0.05796	-0.35553	NA	0.857738	1.619393	0.70147	0.76057	-0.17277	-0.102531	-0.204901	1.130376	0.508857	0.689625
RGA1	NA	-1.432691	-0.193542	0.715955	-0.253651	0.840441	NA	-1.073667	NA	-0.994579	-0.239981	NA	0.670508	-0.690832	0.194289	0.634156	0.557939	-0.264532	0.260285	-1.179824	0.442162	-0.41666	-0.498228	0.455339	NA	-1.4251	-1.148191	0.375954	-1.553645	0.253038	-0.422458	-0.604536	NA	-0.361853	0.479973
RGD1	NA	0.267445	-0.679742	0.365744	0.094288	0.188038	-0.61557	-0.798688	-0.316891	0.639853	NA	0.219508	NA	-1.700545	0.117884	0.399591	-0.022589	0.300588	0.092394	0.159991	-0.27415	0.307864	0.672237	0.694946	NA	-0.022683	0.319454	-0.182467	0.029869	0.336385	-1.141611	0.166394	0.526762	0.207077	-0.493658
RGR1	NA	-0.013709	0.219766	-0.661473	0.149491	0.344524	0.465963	0.782488	-0.205456	-0.426908	0.897744	-0.06062	-0.492823	NA	0.308952	-0.289138	1.162223	0.175204	-0.204369	NA	-0.750808	-0.670982	0.033624	0.240278	NA	-0.198123	NA	0.244914	-0.683454	0.256636	0.745007	0.533217	-0.065907	-0.092911	0.428299
RHB1	NA	0.582204	-0.132117	NA	-0.174924	-0.259646	-0.494766	1.598461	-0.10337	-0.177824	-0.399782	NA	0.324905	2.836355	0.506393	-0.295406	-0.512996	NA	-0.078964	0.299188	NA	-0.22338	NA	-0.214833	NA	0.169334	-0.281894	0.56393	0.887611	-0.166715	1.248264	-0.209578	-1.881742	0.231907	1.213631
RHO4	NA	NA	0.897987	-1.325422	0.211821	0.047931	1.360285	NA	0.54374	1.793008	NA	0.368807	-0.752715	NA	0.730943	0.328748	0.481397	0.177348	0.243827	0.655835	NA	0.188876	NA	0.494328	NA	-0.464824	-0.898153	1.14598	0.112947	0.24779	-0.178585	0.871903	0.301095	-0.013458	-0.548105
RIC1	NA	-0.154634	-5.065303	0.734467	-2.281999	0.96017	-1.052863	-3.040237	0.440251	-6.416105	-0.534885	-1.01978	0.031101	NA	-0.567929	0.326607	0.39919	NA	-0.162633	NA	-0.487001	0.902295	NA	0.391601	NA	-1.049342	NA	0.07087	-0.459168	-0.546914	-1.859756	-6.866162	0.749702	-1.739744	-0.828248
RIF1	1.260102	-3.13739	0.073796	-1.259689	-0.373389	-0.67331	-0.112878	-4.801047	0.832375	-0.11616	-0.804094	-0.087627	-6.461698	-1.940551	-0.189178	0.349914	-0.948283	0.484634	-0.583025	0.099845	NA	-1.313143	0.583418	-0.126751	NA	-0.092481	-1.279667	0.128046	1.128344	-0.114002	-3.437389	0.667367	-0.67117	0.847833	0.151611
RIM1	0.865412	0.177431	0.723639	NA	0.503057	-0.361343	-0.566733	1.197534	-0.642176	-2.090674	1.77928	NA	-0.067092	-1.595383	-1.307563	-0.601154	-0.003718	NA	-0.057617	1.444022	0.200877	-0.411998	0.860404	-1.942068	NA	-0.262578	-0.096846	-0.627942	0.938515	-0.017753	0.718792	-1.147981	0.469149	0.562553	-0.233103
RIM101	3.358289	NA	NA	-0.645969	-2.583643	0.720075	0.009524	1.262272	-0.011441	NA	1.115556	-1.750252	NA	NA	0.541819	0.376119	-0.875358	0.120474	-0.566843	1.099743	-2.029792	-1.040219	0.949443	-0.161159	NA	1.017409	NA	-0.885166	0.962021	1.681023	1.528378	-3.907371	NA	0.210078	0.619688
RIM13	NA	-1.953402	NA	-0.954049	-1.917268	-0.909725	-0.621063	1.626077	-0.674592	NA	1.348667	-3.423266	NA	NA	0.2643	-0.349785	0.705343	0.512356	-0.609583	0.68664	NA	-0.694034	-0.248703	NA	NA	-0.092483	-1.89334	0.181562	NA	NA	NA	-1.969485	NA	-0.043003	-0.257382
RIM15	-7.46764	0.796166	-3.176411	0.87908	0.895088	0.372702	-0.663335	NA	-0.560154	0.554971	-0.65529	-0.022326	NA	NA	0.106153	1.027193	0.392202	0.975411	-0.045297	0.589801	NA	0.641206	0.174329	-0.167558	NA	-0.16845	0.930806	0.12624	0.622444	-0.036687	-0.464556	-0.043241	NA	-0.17287	1.007846
RIM20	NA	-1.450762	NA	-1.419072	-2.525216	1.03058	0.087079	0.500328	-0.644953	NA	0.334069	-1.624927	-1.841723	NA	0.579566	0.567367	NA	0.037979	-0.127872	0.689991	-1.797903	-1.225704	NA	0.447283	NA	-1.060922	-1.326007	-0.872182	2.161545	0.731217	0.315181	-3.358084	-1.467016	0.929993	1.170119
RIM21	NA	-4.252068	NA	-1.303097	-4.493436	0.668422	-0.106662	0.520951	-0.581077	-3.797713	-0.160693	NA	-1.17314	-4.840647	0.440628	NA	-0.047947	-1.152593	0.187734	0.008086	-1.749045	-1.203688	0.440174	NA	NA	0.275154	-0.672803	0.11673	1.004884	0.773311	0.943315	-2.547859	NA	-0.117491	0.908425
RIM8	NA	-2.565926	NA	-0.580502	NA	-0.409906	0.369151	1.462541	-0.306949	NA	1.358333	-1.784013	NA	-3.332009	1.205707	0.5506	-0.305481	NA	0.328378	-0.850446	NA	NA	NA	NA	NA	0.297902	NA	0.984246	1.468903	3.824936	NA	-2.044204	NA	NA	NA
RIT1	-0.005664	0.321772	-1.471598	0.466737	-0.482077	0.135738	0.879173	1.020414	0.854188	0.203294	-0.116724	-0.481978	NA	-0.178602	0.657909	-0.795224	0.401754	-0.543669	0.163841	-0.359824	0.610842	0.068001	0.250228	-0.911254	-1.995902	0.15861	0.112839	NA	NA	NA	0.177212	-0.102622	NA	0.65296	NA
RKM4	0.119481	-0.425173	0.562438	-0.013803	-0.111336	-0.213977	-0.627971	-0.159875	0.07232	-2.002593	-0.544296	-0.267484	0.499861	-0.653373	1.202125	-0.096004	-0.245077	0.313973	-0.211769	0.534764	1.108387	NA	4.405096	0.485692	NA	-0.173079	0.355243	0.58416	3.587188	0.913658	-0.120037	NA	0.54102	1.177676	0.614317
RKR1	1.638747	0.6873	-0.44689	-0.136531	-0.549579	-0.346627	0.570377	-1.382898	-0.287608	-0.696399	-0.809123	-0.476397	NA	NA	0.201885	0.228059	0.682996	0.024486	-0.124433	-0.380756	0.259283	1.609317	1.554673	1.642866	NA	0.007184	0.8072	2.135759	NA	NA	NA	0.008122	-0.490463	0.194381	NA
RLF2	NA	-7.013849	-1.75759	-1.143405	-3.043788	0.074326	-0.459769	-3.035189	0.354904	-0.749617	-1.03557	-1.082338	-3.714192	-5.159355	0.981567	0.939831	-0.106047	-0.150233	-0.663665	1.057532	-0.88665	-0.110605	NA	0.410245	NA	-0.179134	-1.136811	1.134499	0.791655	0.743345	-3.375304	0.204747	0.359795	-1.172228	0.394096
RLM1	NA	-0.323224	0.668731	1.459941	NA	0.272151	0.082688	0.011162	1.034476	-0.362764	-0.035005	-0.906041	0.319768	-1.359798	-0.434077	0.292964	-0.204224	-0.513417	0.210551	-0.626514	-0.021879	0.740887	0.00214	-0.543008	NA	-0.125829	-0.975031	0.379697	0.187666	-0.117062	-1.048513	-0.228775	-0.11725	-0.706148	1.039686
RMD11	NA	-0.528723	0.684397	-1.143471	-3.7834	-0.188401	0.446471	-2.118765	-0.000742	-1.549989	-3.819427	-3.87303	0.272841	-5.770372	0.087331	0.737018	-0.92722	-0.892383	-1.568065	-0.59944	NA	0.490403	0.545063	1.350968	NA	1.074056	0.537369	0.173329	0.280741	-0.000167	-2.392614	-0.024329	NA	-0.282317	0.342645
RMD5	NA	-0.374419	-1.53097	-0.100435	-0.112155	-0.553749	-0.091992	-0.896757	-0.771797	-0.089814	1.09692	0.692683	0.884174	-1.817737	-0.235157	-0.498456	0.178419	0.348208	0.874013	0.87554	1.158955	NA	NA	-0.458939	NA	-0.363101	0.421427	0.005406	0.016684	-0.640586	-0.753876	NA	0.620065	1.372948	0.458403
RMD8	NA	-0.756088	-0.495952	-0.77218	0.44698	0.42769	0.135032	-2.454006	0.409533	-0.542143	-0.888276	-0.102088	-0.790765	0.625024	-0.140681	0.667178	-0.022683	-0.193401	0.027776	-0.299598	0.438128	0.803161	-0.45765	0.325802	NA	0.177766	-0.852829	0.513329	-0.166076	0.70347	-2.611209	0.808746	0.731871	0.177199	0.157137
RMR1	NA	-0.78084	-0.040215	-0.161215	0.833389	0.117304	0.952545	-1.738281	0.064773	-1.258442	1.152889	-1.133476	0.562165	-3.882357	0.651683	0.594405	0.073635	-0.285217	1.756387	0.403936	0.489214	-0.646453	0.765671	0.401471	NA	1.203028	-0.005617	NA	-1.561715	-0.550726	1.377776	0.099998	0.694189	-1.432329	-0.52107
RNH201	1.680898	-6.595914	1.189123	-0.409482	0.299979	0.680387	0.412004	0.780878	-0.18852	-1.873878	-1.292566	0.578621	-4.794251	-0.712937	0.474676	0.348433	-0.854643	0.339073	-1.348596	0.166203	-4.679201	-1.638438	NA	0.509528	NA	-0.5657	-3.590124	0.68334	-6.081792	0.068961	0.240682	-0.086556	-1.390678	0.056405	0.740865
RNH202	-0.556725	-3.386402	NA	0.06111	0.52234	0.339018	-0.090858	0.284931	0.102334	-0.833924	0.525505	1.050846	-5.32139	-0.196454	-0.571429	-0.167173	0.226336	-0.188647	0.814532	-0.196417	-3.749535	NA	-0.970622	-0.392737	-4.295969	-0.95314	-4.163093	-0.182233	-8.495801	-0.664949	0.246054	NA	0.801492	-0.363358	-0.204888
RNH203	NA	-1.668879	-0.499747	-0.245366	0.314408	0.504939	0.766764	0.469709	0.265494	-2.318846	-0.349155	1.139732	-6.449777	NA	0.106333	0.687162	-0.248268	-0.653051	-0.218417	-0.032821	-6.334674	-0.217539	NA	0.656013	NA	-1.463439	NA	0.311975	-3.775348	0.424747	-0.731284	0.645939	0.770176	0.056763	0.948326
ROT2	NA	0.19877	1.693271	-0.369294	0.157947	-0.121792	0.104684	-0.31615	-0.021493	0.849582	NA	-0.00734	NA	NA	0.528375	-1.190923	0.507533	-0.741779	0.701548	0.22867	NA	-0.172756	NA	-2.514181	NA	-0.702626	0.534414	-0.487301	-0.687473	-0.596615	-0.57518	0.018712	NA	-0.617917	-0.623919
ROX1	NA	-0.073168	1.753373	0.065429	0.277746	0.028573	0.505298	-3.533031	-0.168007	-3.681982	-0.923216	1.019478	-0.097198	-1.294306	0.361957	0.30712	0.046812	0.029176	0.388765	0.947709	-0.619914	1.021751	NA	0.581048	NA	0.534005	-0.287091	0.116099	-0.492231	0.133565	-1.46241	-0.55157	2.215851	1.326161	1.128745
RPA14	NA	-3.626037	0.66814	-1.304532	-2.319406	1.110529	1.072211	-0.813813	1.439478	NA	NA	-4.157659	0.530635	-1.487511	NA	0.496895	-2.464368	-0.783522	-0.901019	-0.621699	NA	NA	-0.119324	NA	NA	-1.076877	-1.617012	-0.267909	-0.989549	0.614956	-0.904382	0.782168	-0.830769	NA	0.540162
RPA34	NA	NA	-0.440412	-0.529991	-4.587238	0.882815	-0.015018	0.337281	0.777159	-0.777785	-2.1456	-2.690213	-1.648541	-0.563128	0.249839	0.832142	-1.020827	0.310271	-0.784524	0.374543	0.708523	0.165136	-1.545368	-0.377467	NA	0.584836	-2.165761	0.707667	-0.529631	-1.094915	-1.869075	-0.903321	0.225661	0.102893	1.137109
RPB11	NA	1.297772	-2.196306	-0.358149	0.024376	0.757473	NA	1.089353	NA	NA	NA	-1.365623	0.604197	-2.524155	-0.221624	0.072689	0.004041	2.177184	-1.0703	1.803474	NA	-0.081503	1.090984	NA	NA	1.062859	0.510881	1.572562	-3.120687	-0.261299	1.440888	-3.175555	-0.493977	0.659824	-1.003876
RPB2	NA	NA	-0.166567	0.134558	0.168993	0.567987	0.120886	0.15811	0.567514	NA	0.307383	0.466148	-1.541195	1.561662	0.517783	0.492347	0.79235	0.125678	1.027858	-0.554592	NA	-0.296476	NA	-1.089064	NA	0.124914	-0.443944	0.540235	NA	-0.960953	0.197968	0.607818	-1.001813	0.453933	-0.109598
RPB3	-4.243564	-0.754944	-9.261635	-1.948322	-0.092386	0.361011	-0.47102	1.410705	-0.743312	-8.817043	-1.115132	0.59525	0.339958	1.857369	0.255896	-0.063431	-0.823088	-0.056281	-0.872554	NA	-0.159309	0.083224	-0.690139	-0.029058	-8.463223	-0.560342	-0.434054	0.904255	1.551781	1.10063	2.683262	-2.963916	1.150364	0.507301	-0.221365
RPB7	NA	1.109302	1.02396	-1.387406	-1.160638	NA	0.487857	0.538546	0.696032	0.557759	-1.408169	-0.831648	-0.331163	1.510915	0.591224	-0.48373	-1.087003	1.587255	-1.165178	2.126618	-0.065371	-0.291634	NA	-0.749536	-3.244144	1.685496	1.274971	0.510232	-3.647318	-0.094521	-0.5648	NA	NA	1.875537	-0.571117
RPB9	NA	-0.860836	NA	-0.421262	-2.544704	0.402165	0.618927	0.258853	0.636504	4.328234	-1.757378	-2.031026	-0.197998	-2.027538	0.487408	0.66287	-1.664623	1.119427	0.077005	1.068666	-0.190717	0.885243	NA	-2.742109	NA	-0.78622	-0.483879	1.010952	0.202835	0.542173	1.339488	NA	NA	0.271113	1.130948
RPI1	NA	-0.969232	0.047952	-0.177028	1.380604	-0.165559	0.211062	-0.527002	-0.477713	0.203393	0.062212	1.295736	-0.191633	-1.011715	0.035643	-0.441066	-0.189359	0.250611	0.439735	0.394669	-1.146306	0.095509	0.789111	-0.162284	NA	-0.046457	0.999844	0.013703	0.893611	0.11491	0.389846	-0.033491	NA	-0.348083	0.158499
RPL11B	NA	0.697338	NA	-1.303756	-0.435898	-0.333478	-1.192882	0.556411	1.094731	3.011064	-0.309343	-0.105821	1.064428	0.840624	-0.301465	0.488735	0.586066	-0.114615	-0.899057	2.07888	0.808962	0.412332	2.013666	0.17649	NA	0.276747	0.967041	0.246743	-0.116981	-0.106921	1.576282	1.373947	-0.279595	-0.497209	0.079234
RPL16A	NA	NA	NA	-0.140987	0.052906	-0.071835	-0.442543	NA	0.414987	NA	0.192368	-1.260776	-0.998101	-0.476635	-0.994069	-0.108324	0.04472	NA	0.470821	-0.304356	-0.755595	-0.299216	1.133985	-1.294575	NA	-0.175969	-1.233307	0.667046	-0.063356	-0.807752	-1.415982	-1.152676	-1.063614	0.15591	0.04079
RPL16B	NA	NA	1.602282	0.014648	NA	-0.402374	-0.017361	-13.898648	-0.49372	-2.781068	1.334207	-1.180038	0.720932	-12.726115	-0.145325	-0.410368	0.564962	2.114217	0.554105	2.259599	NA	-0.226753	1.241664	0.440931	NA	0.778468	0.180619	-0.347576	NA	-0.635703	NA	NA	-0.024081	0.715134	-0.834589
RPL17B	0.037604	NA	0.465181	0.140111	-2.387683	-0.618869	0.865519	NA	0.181181	0.548517	0.091397	-0.470193	-0.645404	3.345217	0.534199	-0.698544	0.011047	1.160994	-0.439813	-0.123783	NA	-0.277393	0.756371	-1.298387	NA	0.376263	-0.397684	-0.719201	0.388394	0.70071	1.127551	-0.198574	-2.041035	0.422381	0.117872
RPL19B	-5.749304	-0.256445	-3.099643	1.217925	-1.075862	1.126047	0.181602	0.730048	-1.386232	-0.617082	3.785827	0.38645	0.07695	NA	-0.664477	-0.016535	1.450985	0.458036	2.012391	1.105178	-1.661363	1.352696	2.045566	0.33613	-8.020023	-1.025529	-0.047804	-0.587501	2.260595	-0.410135	NA	-0.882408	1.481977	-0.184791	-0.934695
RPL23A	NA	-0.904709	1.160016	-0.845032	-1.011737	0.803531	-0.362447	0.576467	-0.719747	NA	-2.752927	-0.112189	NA	0.531491	-0.33363	0.39494	-0.264611	0.34385	-0.347532	0.61154	NA	-0.06245	0.135534	0.674553	-6.616096	0.503917	-0.090792	0.174618	-0.456927	-0.237868	0.063049	0.824582	0.166333	0.324466	0.560021
RPL24A	-2.575398	-1.154177	-0.806798	-0.027894	-2.306056	0.335273	-0.209123	1.469929	0.626025	0.306587	0.466952	-0.312069	-0.213612	0.682855	-0.415843	0.420538	0.197356	-0.337024	0.240716	0.002834	-1.239744	-0.107861	NA	0.518648	NA	-0.167382	0.117008	-0.443774	-0.062845	0.287355	1.301125	0.704209	-1.618107	0.200431	0.548841
RPL2A	-1.274315	0.36558	-2.296658	0.291209	0.60272	-0.454629	-0.289242	1.537368	-0.741001	0.125498	0.900643	-0.135684	0.598282	-2.017205	-0.418011	-0.156767	0.030355	0.558108	0.315708	1.584658	-0.270334	0.410281	NA	0.390334	-3.841695	-0.333036	-0.739565	0.046854	-0.985949	-0.218594	0.920061	-0.299266	-0.848443	0.299098	0.170438
RPL33B	NA	0.171935	1.107425	0.269987	-1.011286	-0.60518	-0.652751	0.335892	0.073327	0.640294	0.66235	0.229738	0.591566	NA	-0.394937	-0.348773	0.273778	0.864949	0.03872	0.646706	0.164097	0.6	0.387454	-0.085855	-1.784056	-0.108938	1.27726	-0.187879	-0.152814	-0.132564	0.76643	-0.244388	-0.627736	-0.077742	-1.022109
RPL35B	NA	0.716732	NA	0.195465	-1.021651	-0.161195	-0.009977	-0.169379	0.28232	1.18687	0.057715	-0.371568	-0.467094	0.401917	-0.027938	-0.212111	-0.073874	0.384217	0.291665	0.996667	-1.3788	1.051046	0.719108	0.566956	NA	0.450141	0.321217	-0.109636	-0.321897	-0.330426	-0.209755	0.060885	-0.886059	0.138681	-0.463272
RPL41B	NA	NA	NA	-0.022138	-1.925426	-0.310482	-0.667934	-0.026384	0.117883	NA	0.268609	-2.022268	-0.511771	-2.752318	0.844342	0.194397	0.154379	-0.054161	1.0199	-0.339481	0.7274	-0.547198	NA	-1.133402	0.30078	0.446615	NA	0.041252	NA	0.240375	-1.532867	-0.022509	0.012102	-0.214051	0.429308
RPL43A	NA	4.929623	NA	-0.754096	1.069068	-0.379872	-0.962091	-0.825747	-0.356428	NA	0.55544	1.196155	-0.560509	-5.108404	0.477187	-0.258104	0.133647	-0.467067	-0.557289	-0.374657	NA	0.772532	NA	0.030476	-9.514887	3.635239	-2.046977	0.424376	NA	-0.232784	0.237995	-2.380522	-0.014421	-0.697196	-0.050452
RPL4A	NA	-0.222092	0.769345	0.335718	-1.041568	-1.012446	0.286574	-0.120937	-0.428009	NA	-0.371751	-0.756532	-0.507343	NA	-0.841136	0.284376	0.138679	0.067964	-0.273661	1.051772	-0.622688	0.55151	NA	-0.432606	0.633755	-0.589563	0.450299	0.577739	-0.817009	-0.265379	-0.909481	0.639797	0.264532	0.137025	0.871651
RPL8B	NA	0.916874	0.620289	-0.249081	0.277385	0.049398	-0.198785	0.242111	-0.374003	0.594653	-1.207078	-0.572375	NA	0.153767	0.859469	-0.089628	-0.891302	2.302507	-0.318356	NA	0.656786	0.281348	-0.656135	-0.274028	NA	1.116619	NA	1.23021	-0.661085	-0.129478	0.277814	0.63571	-1.76681	1.118782	-0.194081
RPL9A	1.381185	0.979337	0.675938	0.278267	-0.652162	-0.375846	-0.224561	0.605454	0.110222	NA	-0.944716	-0.904665	0.695956	NA	-0.390366	-0.581773	0.032074	0.800728	0.222486	1.075191	-0.354243	-0.530053	NA	-0.653345	NA	0.352416	NA	NA	0.360199	0.699566	-0.046179	-0.655535	-1.512204	0.36139	0.644394
RPN10	NA	-4.316861	NA	0.442936	NA	0.968666	-0.647159	-1.149635	0.155199	-1.934381	-0.653183	-7.430413	NA	-1.998523	0.40269	-0.846878	0.938255	-5.10122	0.170801	-1.167654	-3.028957	1.228781	-2.922422	-1.31307	-3.109473	0.083005	-7.02258	0.076026	0.183797	0.492945	-1.806371	0.18044	0.227832	-1.48155	1.398694
RPN13	NA	0.299393	-0.533144	0.781699	-2.301479	0.213661	0.486064	-1.025059	-1.22541	0.096905	-0.880229	-1.496274	0.153717	-0.44432	0.212888	0.122478	-0.08187	-0.176447	-0.696711	0.021467	0.68558	0.066518	NA	-0.579945	NA	0.984248	NA	-0.369446	0.98282	0.352952	-0.454966	-0.274183	-0.487267	-0.066061	0.464914
RPN4	NA	-3.822274	NA	0.968525	NA	0.510294	1.291376	NA	0.927206	-7.63956	-0.909457	-2.491296	-0.446885	NA	NA	0.787717	0.076871	-0.941086	-0.079485	0.078701	0.341751	0.962937	0.128905	-1.604031	NA	-0.064192	-3.862018	-0.323387	0.942774	1.864156	NA	-2.650669	1.190694	-0.623924	-1.377614
RPO21	NA	-0.54902	NA	-0.004252	0.271743	0.079344	0.563335	0.364941	0.120267	-0.060325	0.007866	0.262256	0.043595	1.194201	0.185088	-0.163279	0.156062	NA	0.601687	-0.263368	-1.265625	0.111967	1.301371	0.493899	NA	-0.26044	-0.425066	0.445491	0.359244	0.113499	0.737919	-0.284481	0.622131	-0.288879	-0.496701
RPO41	0.374935	-1.692901	0.229605	0.950874	-0.310537	0.445038	-0.816907	0.675808	-0.484654	NA	1.888517	0.819632	-3.317936	-1.420795	-0.968949	-0.39265	-0.984234	-0.895248	0.490507	0.629924	NA	-1.121712	-1.267363	-2.376177	NA	0.296984	-1.737303	-1.072483	0.73964	0.012164	1.056896	-2.287053	0.574401	0.063192	-0.784274
RPP1B	-0.606486	1.936642	NA	-0.259246	0.778385	-0.683933	-0.636315	NA	-0.297698	-0.007948	-0.156001	0.333696	0.137867	0.919308	-0.211449	-0.631935	-0.295634	0.212254	0.39417	0.167598	0.412214	-0.305974	1.577947	0.220053	NA	-0.083639	NA	-1.027267	-0.33549	0.109553	0.891939	-0.318919	0.469944	0.415875	-0.736837
RPP2B	4.201929	-0.80618	-0.827516	-0.576631	-1.662002	NA	-1.626302	NA	-0.727391	NA	-1.758802	-0.575757	NA	NA	-0.110593	-0.354767	0.244483	1.228732	-0.417766	1.255319	-0.665885	-0.202767	0.996941	-0.746903	NA	0.358808	0.124188	-0.885598	NA	-0.144718	NA	NA	-1.151829	-0.730577	0.100124
RPS0A	NA	NA	1.685036	0.425365	-0.672347	-0.343651	NA	NA	0.122682	1.110942	-0.236407	NA	NA	-1.172651	-0.401757	-1.071044	0.354447	-1.45912	-0.292262	0.502702	-1.771389	-0.215985	-1.442017	-0.303646	0.832724	0.327882	0.207515	0.311245	NA	0.122943	NA	0.594116	-0.76137	NA	0.260341
RPS10B	-0.061785	-0.186936	0.799401	-0.042285	0.118313	-0.812049	-0.510297	0.789925	-0.85817	1.062638	-0.086031	-0.461375	NA	-0.77287	-0.198076	-0.500315	0.3314	0.766798	-0.031818	0.523278	-1.565624	-1.309792	NA	0.017464	NA	-0.75402	0.283575	0.097142	NA	NA	0.161383	0.901334	-1.39226	-0.470048	NA
RPS11A	NA	NA	NA	0.950917	NA	-0.62961	0.12569	NA	0.605412	NA	NA	0.960411	0.114943	NA	NA	0.712851	0.672366	-0.284572	0.322039	0.095328	NA	-0.517429	0.721991	-0.039548	NA	1.117111	-1.174157	-0.593529	0.772113	-1.590587	0.658088	0.255426	-2.049448	NA	-0.103861
RPS14A	NA	NA	NA	NA	-0.345329	0.225677	0.245802	1.563802	0.514757	-0.434239	-0.357475	NA	-1.07674	0.848506	0.999117	0.55731	0.080527	NA	0.148644	-0.726044	0.053415	-0.438019	0.74215	-0.168934	NA	0.885928	0.03904	1.579446	-0.376809	0.923044	1.403934	-0.133002	-0.967887	-0.04541	2.001234
RPS16A	-1.025079	0.414168	NA	-0.959446	NA	-0.577713	-0.734059	1.818133	-1.214175	NA	-0.58182	0.014615	NA	-6.59451	0.193433	0.114217	0.007992	1.099966	-1.069298	1.158661	NA	-0.25611	0.67562	-0.396548	-2.978761	0.606314	1.095824	-0.584992	NA	NA	NA	0.285472	-0.586264	0.01635	-0.903847
RPS19B	NA	NA	NA	-0.838593	NA	-0.946793	-1.090261	NA	-0.528304	NA	-1.608339	0.750075	-0.854495	NA	-0.040408	NA	-0.056125	NA	-0.591017	NA	NA	0.133737	NA	NA	NA	-0.580795	-2.113557	0.240755	-0.858405	0.517641	NA	0.132969	NA	-0.001819	-0.421737

SIN4	NA	0.081385	NA	0.614837	-0.145094	0.12191	NA	-0.77682	0.273214	-0.03799	0.283098	0.217952	0.366789	NA	-0.152579	NA	0.110514	0.434019	0.530825	0.126385	0.541754	-0.537209	NA	NA	NA	-0.961074	NA	-0.661498	0.384576	-0.079182	NA	-0.050896	NA	0.283003	NA
SIP1	NA	0.192587	NA	-0.113809	0.879316	NA	-0.194231	NA	0.252833	-0.896701	NA	-0.169787	0.094682	NA	0.603248	-0.308231	0.047777	0.390306	-0.499043	-0.120358	NA	-0.188581	-0.759105	-0.19986	NA	0.392317	0.284078	-0.04574	1.011203	0.017752	0.033957	NA	NA	0.912541	0.076834
SIR1	NA	-4.144889	-7.458189	0.118685	-1.761615	NA	0.6194	-4.039341	-0.337568	0.101429	-0.685795	-4.042969	NA	NA	-0.035752	1.213698	0.027926	1.284538	0.052083	1.423974	1.166839	1.169744	0.490165	0.768306	-3.038987	0.201464	-0.861472	0.615582	0.109096	0.393799	NA	-1.142454	0.419315	-0.000915	0.746054
SIS2	1.891477	-1.871751	-2.011248	0.28926	-1.223937	-0.485231	0.163819	-0.914521	-0.323379	-1.121068	1.299569	0.318148	0.677708	NA	0.010006	0.036313	0.280618	1.230491	0.570858	0.430231	0.003233	-0.77736	1.278986	0.569332	NA	-0.197862	0.714903	-1.026963	-1.231935	-0.540639	0.667058	-1.05731	0.444075	-0.20195	-0.861441
SIZ1	NA	NA	-1.173736	-0.097802	0.114462	NA	1.061186	NA	-0.261158	1.837933	NA	-1.308181	-2.814706	NA	0.18258	0.108963	-0.184111	NA	0.965221	4.559696	-0.831793	1.361146	NA	-0.312629	NA	-0.188895	-2.343566	-1.514418	-2.528692	0.411247	NA	NA	-0.388399	-1.917429	-0.998793
SKG1	NA	0.751831	0.443272	-0.140708	0.483261	0.158978	0.510174	0.555854	-0.223694	-0.918871	0.326	-0.141327	0.459506	NA	-0.085776	-0.398449	-0.593846	0.841299	-1.541471	-0.153629	NA	-0.683905	NA	0.760889	NA	-0.680896	0.545142	0.163785	2.059803	0.481119	0.112328	-0.286936	-1.029608	0.576918	-0.357079
SKI2	NA	-1.198682	NA	-0.198908	NA	-0.103416	0.387509	-0.750603	-0.409324	0.753285	2.973521	-0.635754	NA	1.79236	0.197652	0.496405	0.874378	NA	-0.464292	0.764776	0.167248	0.100284	NA	-0.764606	NA	1.447163	1.025224	1.065587	0.3241	0.249258	-0.396872	0.756169	-0.352764	0.010728	-0.412541
SKI3	NA	NA	NA	-0.6767	-0.204553	-0.33981	-1.567347	0.509855	-0.525798	3.507152	1.581665	-1.329387	1.186816	-5.921457	-0.145662	0.166328	0.896883	0.415419	-0.518963	1.608077	NA	0.06259	1.341262	-0.36134	NA	1.58049	NA	0.257916	1.123982	0.240131	0.305518	0.369896	1.259982	-0.500876	0.4002
SKI7	NA	NA	1.522966	-0.190241	1.474948	-0.371711	NA	0.08914	NA	NA	2.286026	0.14826	0.946235	1.598109	-0.63211	-0.537904	0.151819	1.676523	0.321539	1.122453	NA	-0.827012	0.574814	-0.508061	NA	1.046719	1.554773	0.146349	-0.778546	-0.653339	-0.477608	0.557647	-0.420869	-0.331364	0.836138
SKN7	0.095	NA	0.458617	0.090491	0.3728	0.578822	0.199531	-2.506597	-0.032881	-1.062744	2.142433	0.524704	-5.190255	0.863796	-0.420348	-0.094779	0.065083	-2.984931	0.395157	-1.948008	-5.680663	0.159406	NA	-0.146714	NA	-0.36534	-2.156378	0.47826	-0.750792	0.630497	-1.654603	-0.571554	1.368748	-0.093369	1.256614
SKO1	-0.207318	1.634177	1.453051	-0.202728	0.847901	-0.442219	-0.192168	1.750368	-0.043584	-2.370849	-2.993727	-0.179499	0.385076	-1.172075	0.823939	NA	-0.279902	0.359516	-0.191465	-0.446064	NA	-0.264162	-0.157949	0.110178	NA	1.481785	1.989143	NA	-1.273921	0.04255	0.732151	0.458671	NA	0.609361	-0.519392
SKP2	NA	NA	0.313358	0.408811	-0.371686	0.052629	0.160133	-0.473395	-0.086614	-0.25016	0.441954	-0.172394	0.35873	0.994907	0.005348	-0.048024	0.287509	0.816878	-0.685036	0.495417	NA	0.167153	NA	NA	NA	-0.273721	0.35664	-0.736311	0.17403	0.058913	0.600899	-0.948349	NA	-0.037239	0.560053
SKT5	NA	-0.959677	0.195229	0.393836	0.639158	0.751421	-0.716296	0.01001	0.952461	-2.147961	NA	-0.552106	NA	1.306742	0.485952	0.389523	-0.038635	-0.364091	0.762135	-0.351946	-0.931315	1.039924	NA	0.979702	-1.429282	0.046122	-0.315313	0.146743	-0.121868	0.157947	-0.475892	0.328395	-1.379551	0.533251	0.001383
SKY1	NA	1.621553	1.478629	-0.211301	1.169667	-0.07602	0.423244	-2.850413	-0.406429	NA	NA	0.825798	NA	-0.954388	-0.716964	0.669206	0.369176	0.661201	0.609179	0.663055	NA	-0.088594	NA	-0.139191	0.762117	-0.161239	-0.326502	-0.490564	NA	NA	-3.242485	-1.365627	1.405899	0.133837	NA
SLA1	NA	-10.654129	NA	0.303567	-5.904145	0.271208	0.11403	-3.296864	0.351127	NA	-1.259462	-4.765197	-1.777204	-2.561752	-0.341193	-0.389898	0.597156	-3.602784	0.43131	-1.826724	-3.536625	0.741476	-1.564331	-0.739624	NA	-4.769603	-5.422695	-3.150303	-4.567497	0.64631	NA	0.341021	-1.038119	-7.340124	NA
SLC1	1.876782	1.131437	NA	-0.670472	0.406259	-0.142523	-0.306372	NA	0.21333	-0.967069	-0.449052	0.423106	0.961357	2.170123	-0.336452	-0.459953	-0.191367	0.459263	-0.773039	-0.308281	0.621738	-0.354868	NA	0.145148	NA	0.566424	0.57999	0.155246	-0.114938	0.115864	0.509477	-1.110196	-0.678888	0.192342	0.332483
SLG1	NA	NA	-0.223415	0.322163	0.48292	-0.127154	NA	-0.693617	NA	NA	0.838813	0.15248	-5.947295	-1.062338	-0.281492	0.125005	0.382824	-0.214143	0.521209	0.18827	-0.911808	0.444835	NA	-0.743675	-3.127663	-0.591559	-0.593786	-0.300185	-0.307464	0.020542	-0.086566	-0.112186	-1.12827	0.534981	0.215234
SLI15	1.743865	-0.419168	-0.44598	0.607043	0.383465	0.135716	-0.702068	1.007704	-0.723599	-0.114879	NA	NA	-0.630599	NA	0.28713	-0.074005	0.219717	0.329947	0.811303	0.219343	NA	0.395365	-0.359659	-0.409021	NA	-0.255425	0.672348	-0.027015	0.375807	-0.018585	0.639691	-0.871398	0.091889	0.253402	0.201063
SLK19	NA	-1.643078	-2.826947	0.364442	-1.484749	0.608692	0.24622	1.971698	0.587349	-0.54455	0.952206	0.769558	0.842627	NA	-0.651586	-0.097069	0.823844	NA	1.049149	-1.049848	NA	1.03631	-1.016673	-1.811918	NA	-0.325664	0.038996	-0.490826	1.60418	0.175078	0.600642	-0.347869	NA	-0.067765	0.083134
SLM1	NA	-0.055582	0.438239	0.713856	-0.348236	0.594795	0.402449	0.214478	0.302834	NA	-0.787491	NA	-0.157255	NA	-0.379017	0.225044	0.487453	-0.395531	0.464259	-1.163204	-0.029863	0.340296	-0.363144	-0.422964	NA	-0.53945	-0.663573	0.279103	0.680619	-0.095068	-0.124938	NA	-0.868522	0.50045	0.777879
SLM6	-0.854812	-1.364135	NA	-0.478514	-0.158659	0.077544	-0.768271	0.612443	-0.282382	-0.705892	NA	0.03635	-1.066318	NA	-0.286504	0.001051	0.177443	NA	-0.767449	-0.03211	NA	0.31996	NA	1.001276	-2.113626	-3.42663	0.318565	-0.660636	0.080788	0.621009	0.334316	NA	0.252721	0.377522	-0.869547
SLP1	NA	-0.164983	-0.032707	-0.234854	0.274564	0.671915	-0.48276	0.103736	0.499579	-1.245799	-0.135817	0.202989	0.324872	-5.090506	-0.143914	0.122677	-0.098925	0.464134	-0.087591	0.104378	0.99521	-0.261936	NA	1.052048	NA	-0.28645	0.350015	-0.347967	-0.010396	0.389146	0.188964	-0.372516	-0.502897	0.752438	1.419903
SLT2	NA	-5.228141	-2.481449	0.667364	-0.711325	0.636567	0.670949	0.163021	0.800176	-2.660431	-0.485871	-0.639839	-0.90428	0.921717	0.691684	1.169868	1.10762	-1.386549	0.745808	-1.600472	-2.59039	0.64406	-2.121016	2.211824	-1.462557	-1.567138	-4.519378	0.129095	-2.121127	0.561836	0.396348	0.728614	0.413037	-0.529566	-0.129889
SLX1	NA	NA	NA	-0.101025	-0.048174	-0.676962	0.093041	-2.403535	-0.344846	-0.471115	NA	1.064598	NA	NA	-0.363946	-0.01619	-0.074573	0.230593	0.821327	-0.956297	0.966236	0.612153	NA	-2.046299	NA	0.481799	1.080559	-1.093373	NA	NA	NA	-1.605736	-0.408038	-0.780873	0.038624
SLX8	-2.104003	NA	-3.230012	-0.118145	NA	1.063493	1.54645	4.179358	NA	NA	-0.487541	-0.803117	NA	NA	0.402868	NA	NA	0.878852	NA	NA	NA	0.120811	-0.488642	-3.543745	-8.297932	NA	NA	NA	NA	NA	NA	-1.500685	0.539812	0.329602	NA
SLX9	NA	NA	NA	-0.792816	-2.115709	-1.238629	-0.871926	-2.0182	-0.12637	NA	NA	-0.83188	NA	NA	1.520962	0.946766	-0.511788	NA	-0.342197	0.527585	-0.3098	NA	-0.162407	NA	NA	0.428802	-0.509106	-0.921547	-1.405243	0.705403	NA	-0.160959	-0.987564	0.348173	1.093597
SLY41	NA	-0.665165	-0.099191	0.291643	0.039939	0.072124	-0.254342	-1.296888	-1.16821	0.105633	1.563697	0.462228	0.79397	0.365322	-0.282726	-0.232731	NA	0.046689	0.387337	0.065834	1.211587	0.021755	NA	-1.550845	NA	NA	NA	NA	0.390873	-0.021456	NA	0.144453	-2.049836	0.200893	0.670332
SMA2	NA	NA	NA	-0.313867	NA	0.365322	0.902892	0.280965	-0.958972	0.39794	-0.781777	-0.519165	0.2987	NA	0.577567	-0.34851	-0.195087	NA	-1.319996	-0.044316	NA	-0.14813	NA	-0.473971	NA	0.760128	1.389464	-0.02447	0.249249	0.151736	0.331309	-0.2232	-0.737905	-0.881795	-0.407727
SMI1	-3.834396	-0.585314	-1.286785	-0.059683	NA	-0.185515	-0.377713	-2.750371	0.260013	NA	0.550902	-0.721017	-1.54157	-5.210871	1.273022	0.730257	0.557563	-0.739398	-0.131669	0.068481	NA	0.401932	0.765349	-0.714848	NA	-0.758345	NA	-0.642082	0.304997	0.103572	-1.284229	0.16311	1.982708	0.300385	0.176834
SMK1	NA	-1.061923	-2.505286	0.711279	-1.786646	0.211106	0.923473	-0.960363	-0.132617	NA	0.14034	-0.99612	0.508224	-3.234302	-0.587851	0.280969	0.960529	NA	-0.175293	-0.452219	NA	0.501994	NA	0.55321	NA	-0.339803	-0.452183	-0.033671	0.413481	0.249572	-0.068625	0.361499	0.627257	-0.130538	0.905983
SMT3	NA	-6.831275	-2.105837	1.01651	-1.420199	NA	-0.072471	NA	0.094035	-3.850295	1.572753	0.491125	NA	-0.129395	-0.328025	-0.387804	0.756456	2.670921	0.692395	2.26207	-3.645486	-0.198312	1.024579	-3.366383	-0.877849	-1.623677	-4.071824	-3.582185	0.292513	-0.018022	NA	-0.609544	0.631158	-0.514655	-0.947737
SMY1	NA	NA	0.567285	-0.440492	1.174516	-0.041082	0.775936	0.270071	0.716371	-2.152099	-1.593997	-0.339082	-0.102676	NA	0.544075	0.228874	0.116899	-0.427391	-0.467444	-1.716399	-0.901155	0.332961	-1.964906	1.127068	NA	-0.393737	-0.758525	-0.757394	NA	0.760955	0.490051	-0.422256	-0.737388	0.240439	1.252271
SNC2	NA	-0.091573	-0.373577	-0.536702	0.440962	0.594296	0.639264	-0.069846	-0.543599	NA	0.601204	-0.291357	-0.931199	NA	0.620435	0.390723	NA	-1.280342	0.053747	-1.14748	-0.021188	-1.050503	NA	-0.68396	NA	-1.161324	-0.261322	0.456462	0.090118	0.439832	-0.073006	-0.366356	-0.172662	-1.005001	NA
SNF1	NA	NA	0.263444	1.002336	NA	NA	-1.934602	-0.103978	-1.60607	-1.115417	0.978566	0.199726	0.518331	NA	-0.958307	-0.763065	-0.492097	-0.617122	0.133459	0.73026	1.184824	-1.030356	0.116243	0.234491	NA	-0.033635	-0.500514	-1.050288	0.906463	-0.791724	-0.236724	-0.193685	0.750964	-1.453772	-0.277153
SNF11	-0.348494	-0.465642	0.018551	-0.717438	-0.362252	0.490735	1.066384	NA	0.265734	-1.840343	-0.838714	0.193441	NA	NA	NA	0.042818	0.019455	-0.30254	0.252347	-0.187663	-0.536013	0.069283	NA	0.86918	NA	0.069959	-0.214846	0.681646	1.231855	0.369087	0.361296	-0.024865	0.483393	NA	0.646747
SNF3	NA	NA	-0.002622	-0.076953	-1.136472	-0.385908	0.587615	-0.031661	0.018132	0.879331	-1.399176	0.241817	0.393867	-4.191446	0.284197	0.152602	0.334462	0.805235	0.434611	0.161385	1.025592	-0.052109	0.060906	0.989659	NA	NA	-0.37364	-0.746325	NA	-0.872337	NA	-0.126314	NA	-0.831724	-1.216042
SNF4	0.326287	1.670729	-0.65613	0.29396	1.041833	-0.79545	-0.762285	-0.279807	-0.584143	0.385184	0.973401	0.652789	NA	NA	-0.699695	-1.014027	0.318369	-0.107105	0.093022	0.119362	1.465363	-0.034938	1.458051	-1.543217	-3.893178	0.379199	1.088929	NA	0.800122	-0.196774	-1.215339	-0.04339	0.106086	-0.355361	-0.513306
SNF5	NA	NA	NA	0.60882	-0.745452	0.053966	0.886286	NA	0.88609	NA	0.80755	-0.565661	1.598704	-0.587523	-0.361088	0.908247	0.235191	NA	-0.140475	1.318111	NA	-0.242346	NA	0.049478	NA	-0.834901	NA	NA	NA	0.826526	NA	-0.719087	NA	0.203111	-0.656302
SNF6	NA	0.89974	NA	-0.156558	NA	0.627334	0.036764	1.26874	0.85	NA	0.216214	-0.61691	1.670242	NA	-0.132803	0.096753	-0.58759	-0.153684	-0.886565	0.566571	NA	0.468096	NA	1.574511	NA	NA	0.806086	0.590649	1.324299	-1.116824	NA	-0.660615	3.024795	-0.777587	-1.243288
SNG1	NA	-1.24773	-0.332232	-0.280523	-0.604401	-0.061335	0.775965	-0.735878	-0.234575	NA	-0.607375	0.254065	-0.267762	NA	0.402618	0.445009	0.441229	0.263599	-0.103186	-0.239038	1.112831	-0.048174	NA	1.258032	NA	0.126057	-0.008298	0.312777	0.114365	0.277537	-0.870947	-0.355279	0.299814	-0.205261	-0.076722
SNN1	-0.280697	NA	0.423295	-0.46746	-0.248184	0.345021	0.091614	-0.053136	0.525139	-1.167681	0.488009	0.193218	-0.28777	NA	0.135628	-0.086484	-0.575436	0.327022	0.244594	-0.579856	-0.097608	0.309152	NA	0.930903	-0.937582	0.202871	-0.772839	0.082062	-1.465052	0.169481	-0.350141	-0.489905	NA	0.340182	-0.051275
SNT2	-1.998147	0.405542	NA	-1.063672	-1.414755	-0.189922	-0.345741	0.486559	-0.380627	-0.885278	0.463982	1.502451	0.680375	2.280569	-0.032838	-0.561111	-0.512516	NA	0.925832	0.355403	0.861227	-0.460952	1.218115	0.476291	NA	-0.33298	-0.359205	NA	-0.289387	0.301072	0.26104	0.622386	0.769474	-0.525604	-0.685211
SNU66	NA	0.532546	-2.679173	0.331215	0.399593	0.306203	-0.135497	-0.252563	-0.275313	-12.31499	-0.143366	0.316745	-0.349094	1.129104	-0.408273	-0.137401	NA	0.676321	-0.384911	0.014456	-0.09097	0.111585	-0.595581	-1.825208	-1.458122	-0.525823	0.522425	-2.076099	NA	0.21334	0.22245	-7.650021	NA	-0.000136	0.953745
SNX4	NA	NA	-1.282598	0.121396	0.071608	0.294108	0.929355	-0.553981	-0.501144	-1.012051	1.024903	0.226994	0.828569	0.485668	0.343015	-0.424444	0.501246	0.839277	0.163309	0.00933	-0.037481	0.130382	NA	0.759559	-1.787691	NA	1.197634	0.47668	0.605377	0.446495	0.541665	-0.358905	1.012969	-0.498294	-0.099786
SOK2	NA	-1.798123	NA	0.340484	-1.345768	0.122135	-0.156241	0.681246	0.225022	NA	0.941389	-0.852706	NA	NA	0.36578	0.756102	0.113246	0.157445	0.045525	0.390455	NA	0.011279	0.806168	0.055041	NA	NA	-0.86679	0.647038	-0.066098	-0.067624	1.359828	0.593789	1.428415	0.294949	0.449428
SPA2	NA	NA	-0.181153	0.413132	0.400338	0.76818	0.77354	-1.171029	-0.016573	NA	-0.647754	0.17753	NA	-1.556781	0.10338	0.274897	0.353725	-0.824129	-0.380638	NA	-0.528167	0.740389	NA	0.076833	NA	-0.513108	NA	0.600543	-0.006353	0.257481	1.151588	-1.024439	-0.288045	-0.461773	0.065375
SPC1	NA	0.657597	0.472881	-0.028609	-0.836912	0.300917	-0.240776	0.07985	0.048663	0.580045	0.096092	-0.035876	-0.198026	NA	-0.228598	-0.631059	0.061505	0.752567	-0.183184	-0.373339	-0.926317	-0.061723	NA	-1.168619	NA	NA	-0.125746	0.355394	-0.562569	-0.210001	-0.425353	0.099061	-1.368797	0.25854	0.32371
SPC2	NA	1.60972	0.206639	-0.805166	0.213422	0.089673	1.064695	-0.295993	0.350628	-0.982827	0.362881	0.471491	-0.658511	1.085268	0.048209	-0.285777	0.639145	-0.145988	0.135879	0.993953	NA	1.117182	0.0023	0.775767	-1.425453	0.860095	0.99974	-0.415761	0.26008	-0.09596	-0.33753	-0.522732	-0.750501	-0.507538	0.175112
SPE3	NA	-0.24175	-2.484873	-0.724392	-0.602956	-0.582863	-0.125234	0.900316	-0.052686	-0.917026	-0.100035	0.346745	-0.663787	-0.220372	0.020953	-0.560191	-0.558095	0.433162	-0.954256	0.255165	-0.776195	-0.94427	-0.463715	-1.193381	NA	0.263463	0.314021	0.228402	1.058269	-0.072143	0.803045	-1.313231	NA	-0.143922	0.276872
SPE4	NA	-1.621675	-0.481485	0.037083	0.024444	0.166375	-0.472392	-0.571688	0.655601	1.072773	0.335405	-0.744738	0.149177	NA	-0.294243	-0.112894	0.305568	0.547905	-0.072444	0.254441	-1.438707	0.094061	0.803528	-1.251557	NA	0.175749	-1.177821	0.061157	0.553333	0.206789	-0.212729	-0.584269	-0.610398	-0.440646	0.73871
SPP1	NA	-2.565053	1.393519	0.395225	NA	0.590918	1.193967	-1.243676	0.184626	-7.309161	0.027359	-0.240239	0.285546	-0.882108	0.536072	0.398625	-0.040242	0.616378	0.444409	-0.228078	-0.367448	0.442683	NA	1.175848	NA	-0.094559	-0.440419	0.271296	0.965643	0.553303	-2.045532	-2.367725	0.033142	0.291382	-0.028995
SPT2	NA	-7.53782	-1.239167	-1.905929	-2.434816	-0.426984	-0.799612	-1.837185	-0.850619	0.857677	0.867646	-1.774251	0.949578	-2.024729	0.837504	0.021312	-0.120229	NA	NA	1.50977	NA	-0.198071	1.928284	0.144337	NA	1.682342	1.119811	-0.176872	-2.022347	-0.037521	NA	-0.088452	1.011453	-0.056496	-0.043615
SPT21	NA	-3.915998	0.299231	0.364035	-4.897128	0.822413	0.262641	-4.788473	-0.252262	-2.067984	-1.553739	-1.763521	NA	-2.082155	1.155761	1.318022	0.081806	0.522729	-0.241063	0.215075	NA	0.704272	0.190557	-1.472136	NA	-0.353757	-3.474245	0.361111	NA	NA	NA	0.450235	-2.334407	0.722015	-0.021586
SPT23	NA	0.622601	0.090546	0.268725	0.664751	0.263115	-0.216611	0.545975	-0.333287	0.391201	NA	-0.346912	0.477096	NA	-0.074989	0.098023	0.867584	-1.098758	0.072508	-0.43664	-0.345929	0.221425	-1.755212	0.094484	0.274841	-0.344957	-0.749789	0.12733	0.199025	-0.820495	-0.15702	-0.058113	-0.817315	0.095845	0.39253
SPT8	NA	-2.239172	-4.294432	-0.203562	-0.478103	0.174612	0.59364	NA	-0.228874	2.509601	NA	-0.655151	0.109631	NA	-0.029168	-0.063492	NA	0.538391	-0.077918	NA	-2.033427	-0.691337	NA	2.238788	2.112453	-1.084755	NA	-0.386369	-0.092247	1.120681	NA	NA	NA	0.175419	NA
SQS1	NA	1.137378	NA	0.188468	NA	0.541163	-0.53005	-2.374014	-0.299422	-1.149743	0.250851	0.397159	NA	NA	0.104867	NA	-0.232792	NA	0.051548	-0.766746	NA	-0.313207	-2.02328	-1.368209	NA	-0.740469	0.49596	-0.305913	NA	0.162079	0.464293	0.573034	NA	-0.525718	0.225369
SRB2	NA	NA	NA	-0.523205	-1.546621	-2.055901	-0.38429	1.89751	0.255628	5.039956	NA	-0.119985	1.080361	NA	NA	0.768529	-0.522717	0.664693	-0.399291	NA	0.886607	0.701654	NA	NA	NA	0.742568	NA	0.172173	0.73634	NA	NA	NA	NA	-0.5809	-0.300855
SRB4	NA	-1.195852	0.950664	-0.771081	0.442138	0.112406	0.376496	0.617966	-0.535428	0.354346	0.333442	-0.01649	-0.06944	1.650231	0.342856	-0.191144	0.217348	-0.266556	0.055495	-0.211186	-1.052289	-0.11312	NA	0.036449	NA	0.019711	-1.946772	0.332484	0.263976	-0.190353	NA	-0.019337	-1.767354	0.120331	0.033281
SRB7	NA	-2.145583	NA	1.230924	-3.593355	0.504793	0.340976	1.166177	0.012941	NA	1.823987	-3.035243	NA	-4.295857	0.885161	0.058439	0.562853	-0.651697	0.828194	1.218451	-0.991391	NA	-1.205996	-4.873064	NA	0.397519	-4.171302	1.098478	0.954044	1.538802	1.673524	NA	1.939308	1.297651	0.142922
SRC1	NA	-4.492202	-0.027205	0.194567	-1.566799	0.595317	0.390591	-2.168066	0.821435	NA	-0.652789	-1.985484	-1.007069	-12.159772	-0.982138	0.298382	-0.014103	-0.891859	0.633027	-0.316421	NA	-0.343384	NA	-0.787769	NA	-1.194668	-4.393738	0.009538	-6.173818	0.353096	-3.934205	-12.577827	0.22723	0.130842	0.127048
SRL2	NA	0.415644	-0.119731	-0.09833	-0.644112	0.327179	0.085103	-0.286429	-0.326437	-1.699369	-0.460874	-0.355236	0.017234	NA	-0.005609	-0.065176	0.587514	0.252224	1.303322	NA	1.164848	-0.057274	NA	0.048169	NA	-0.362368	NA	-0.233998	-0.334985	-0.446708	0.45988	0.677443	0.090694	0.386688	-0.545541
SRN2	-6.651677	-3.594082	NA	0.796032	NA	0.522872	0.379529	NA	0.119428	-2.677077	-0.641745	-4.286568	-1.830868	0.577359	1.059648	0.719443	0.494147	-1.061799	0.837414	NA	NA	0.676806	NA	-1.109121	-5.85728	-0.657388	-3.039871	0.211304	0.349988	1.611463	0.375099	-1.407632	-1.175342	-0.611863	2.109844
SRP40	-0.660395	-1.239096	1.304085	0.47778	-1.445598	-1.318626	-1.158325	0.045256	-0.419147	-1.269028	NA	1.450446	-1.024064	NA	-0.664338	-0.193003	0.248724	0.63554	0.457553	0.43251	0.339858	-0.841864	0.169775	-0.049625	-3.866775	-0.287495	0.247176	-0.073403	-0.250427	-0.121671	0.501659	0.25682	0.232472	-0.446577	0.120729
SSA2	1.89516	0.776219	-0.610874	0.302427	0.293675	-0.21128	0.650659	-0.232351	0.799904	-0.137016	0.420123	1.058392	0.692688	0.886916	-0.49139	-0.446441	-0.405146	0.406333	0.464925	NA	0.747465	0.149496	NA	0.551007	NA	-0.455581	NA	0.850116	0.161396	0.109722	-0.398141	0.577919	-0.333862	0.507483	1.282604
SSA3	NA	-0.514041	-0.698495	0.30143	-0.208077	0.356568	-0.439789	-0.120458	0.325704	-0.426028	0.833215	0.260124	-0.294866	1.062953	0.041362	-0.198395	0.67357	0.01933	0.812414	-0.658023	-0.794269	0.160854	NA	-0.344811	NA	-0.665871	0.744009	-0.234598	-0.11945	-0.243205	0.859017	-0.376588	NA	-0.514034	0.251334
SSD1	NA	-4.055075	NA	0.927971	1.250347	-0.158405	0.410791	NA	-0.349462	-2.901306	-0.569567	0.243104	NA	NA	-0.759503	-1.886461	1.019463	NA	0.717318	-0.585317	-2.078118	NA	-2.016282	NA	NA	0.061657	NA	-0.716283	NA	0.770543	0.435494	NA	1.620807	1.573666	0.143939
SSE1	NA	-2.595658	-5.013693	-1.082602	NA	-0.596474	-0.897239	-4.831262	0.069261	NA	NA	-1.355522	-0.484526	-2.457475	-0.06318	-0.861573	-2.042258	-0.267929	-0.803152	0.015674	NA	-0.63059	NA	0.52564	NA	0.639245	-1.152393	-0.377203	0.378358	-0.568815	NA	-0.026614	-0.589808	0.469387	0.674117
SSF2	-0.11741	0.464682	1.070686	-0.040596	0.592243	-0.481971	-0.621683	0.671391	0.079747	-2.190479	0.162506	0.284603	-0.031938	-0.926553	-0.769351	0.203174	-0.524008	0.132834	0.156227	0.159701	0.824076	NA	0.819453	0.72035	-1.521281	0.44738	0.430279	-0.050486	0.8008	-0.208317	0.014177	NA	-1.768439	-0.636346	0.24214
SSH1	NA	1.140888	NA	-0.645674	-0.681755	-0.664813	-0.804883	1.233543	-0.742375	-1.226106	-0.443882	0.350189	NA	NA	-0.32835	-1.518959	-0.226545	0.617805	-0.608132	-0.133744	0.742227	-0.616216	NA	-0.175075	-1.0292	-0.514621	1.109999	-0.251108	-0.095548	0.198554	-1.049603	-0.128332	0.306412	0.043919	-1.2102
SSK1	0.923723	NA	0.744761	-0.505851	0.242858	0.537296	0.212969	-0.513158	-0.064772	-0.034439	0.183389	-0.513692	0.597062	-4.687796	0.068129	-0.435241	-0.092474	0.451228	0.303524	NA	0.848454	-0.13704	0.878472	0.464642	-1.378896	-0.190968	NA	-0.490647	0.874081	-0.056178	-1.039237	-0.119267	1.349114	-0.449958	1.016887
SSK2	NA	1.039322	-0.093407	0.083699	0.244102	0.243	0.324033	-1.360577	0.564092	-1.890044	1.290705	0.199433	0.741665	NA	0.202635	-0.010345	-0.075788	0.390492	-0.357079	5.40E-05	0.133657	-0.052864	0.430119	0.898272	NA	0.722715	-0.235012	0.100369	1.095745	-0.196746	-1.069259	-1.268555	1.300858	-0.55168	-0.499244
SSM4	NA	0.001224	-0.483651	-1.040183	0.577438	-0.812915	-0.741682	0.301172	-1.228179	0.44043	1.022983	0.593107	1.449989	NA	-0.337261	-0.573533	0.924956	0.422185	-0.411495	0.312557	2.134586	-0.142652	1.476082	0.426587	NA	0.223384	0.60298	0.482241	0.068498	-0.584464	0.431476	-0.202768	1.054066	-1.023479	-0.358695
SST2	NA	-0.092721	-0.287327	-0.111789	-2.76366	0.155484	-0.230582	-2.163482	-0.657527	1.524871	0.306646	-0.671796	NA	-4.138226	0.807439	0.214717	0.645268	-2.605088	0.51136	-0.230251	-0.729901	1.164087	-0.530243	-1.170212	NA	0.522126	-0.733754	0.573294	-0.911917	0.11558	-2.753917	0.510576	0.406079	-0.53012	1.554693
STB1	NA	NA	-0.497522	-0.719281	0.209764	0.814716	0.632453	0.554745	0.700339	NA	-1.799403	-1.245808	-1.419724	2.420871	0.547165	-0.227851	0.608806	-0.896251	-0.403431	0.255069	0.147025	0.308937	-1.64711	NA	NA	0.496776	0.272017	-0.535324	1.03469	-0.40735	1.479479	-0.327888	NA	0.144408	0.003006
STB5	2.856392	1.643336	2.181373	0.581377	-1.068218	-0.154496	-1.060806	-1.239792	-0.066995	-1.635371	0.860847	0.747757	0.765991	1.264816	0.393896	0.345848	0.05749	0.812576	0.281974	0.763942	0.758271	0.113726	-0.546446	3.570269	NA	-1.331464	0.454934	-2.194538	-0.67086	-0.490928	-0.957193	-0.285884	1.371002	-2.029505	-0.685235
STD1	NA	1.060408	-0.797155	-0.183849	0.6137	0.240023	NA	-2.016783	NA	NA	-0.064471	0.500269	0.659915	-1.133581	1.375743	-0.096169	-0.78046	-0.200053	-0.46012	-0.282747	NA	-0.187346	-0.282565	0.260949	NA	-0.069969	0.136685	0.225474	0.902674	0.302242	-1.388105	0.375178	0.496684	0.766852	0.264803
STE24	NA	0.482455	-2.779893	0.740924	-0.221688	1.1366	0.914309	-0.746132	0.283873	-1.120672	0.177353	-0.341866	-1.370904	1.953676	0.36176	0.68047	1.083898	-0.441695	1.295782	-0.66757	NA	1.112238	NA	-3.90E-05	NA	-0.430461	-0.882557	-0.100548	0.008493	0.107424	0.274694	-0.655141	-0.405851	0.329748	0.88554
STE50	NA	-1.662822	NA	NA	-2.822777	-0.116042	0.25214	NA	0.845083	-3.352676	0.754919	NA	-0.455285	NA	-0.493505	-0.219914	0.860555	NA	1.004071	0.762645	0.080556	0.030012	-0.424042	1.61146	NA	-0.229933	0.148018	-0.765028	0.672159	-0.2128	-4.550755	-1.782791	0.175544	-0.475345	-1.606809
STH1	-0.740518	NA	-0.845835	-0.025403	-0.036713	0.39337	0.484384	0.346734	-0.117504	-0.334681	0.296023	-0.005271	-0.254108	NA	0.281482	0.368183	0.019808	-0.061207	-0.589398	0.732283	NA	-0.560727	-0.413792	-1.049042	NA	-0.640831	-0.320205	NA	-0.258526	-0.005423	0.57596	0.613516	NA	-0.368699	0.288932
STI1	NA	-0.199461	-1.509109	-0.274544	-0.563481	0.749004	NA	NA	NA	NA	NA	-0.351564	NA	NA	0.290385	0.684098	-0.949473	1.049084	-1.683124	-0.210913	1.009737	0.440288	-0.304873	-1.456126	NA	-0.6495	-0.161692	0.804759	-0.390778	-0.10561	NA	0.715546	-0.230407	0.404305	-1.15066
STM1	-4.860816	-1.380108	-3.450628	0.668367	-2.13565	-0.162572	1.800739	-0.218195	1.625143	-6.586993	0.146275	-1.645376	-0.782373	0.315232	1.224024	0.637692	0.279379	0.109025	0.393784	-0.045628	-0.00728	0.446857	NA	0.379165	-5.213997	-0.20312	NA	0.897887	-0.169784	1.752942	-1.739899	-1.0358	0.809626	-0.371538	-0.126346
STP1	-2.406906	1.512962	0.413983	-1.473755	-0.102712	NA	0.650509	-0.23071	0.077019	-1.613709	0.113549	1.206681	0.757175	1.467655	0.146633	0.264596	-0.888951	1.260741	-1.28576	1.000998	0.954311	-0.548616	-2.321586	0.147994	0.712455	0.017281	1.317849	0.313708	3.093935	0.131543	-0.197416	0.088222	1.804564	0.671278	0.253806
STP2	NA	0.313202	-0.238871	-0.049543	NA	NA	0.361346	NA	-0.258728	NA	0.97052	2.118863	0.186249	NA	-0.98984	-0.471244	0.268116	1.102507	0.071415	0.471421	NA	-0.136002	0.980508	0.060225	0.43428	-0.243309	NA	-0.332299	1.540399	-0.66425	NA	-0.269681	-1.326727	0.046208	NA
STP4	-0.129684	0.425479	NA	-0.141953	0.536681	0.144861	0.038191	NA	-0.110975	0.308147	0.368548	-0.497937	0.278951	-0.552325	0.160453	-0.119394	0.209435	-0.476293	0.093856	0.252236	0.075197	0.276475	-0.49698	-0.756113	NA	0.267959	0.99542	0.468008	0.841875	0.540232	NA	0.05726	-0.946779	0.317606	0.383052
STV1	NA	-0.042426	0.207011	-0.660395	0.441136	-0.041098	-0.037216	1.596163	0.2015	-0.430787	-0.520787	1.089396	1.23086	NA	0.140952	0.257677	-0.200167	1.667524	0.093236	1.027916	NA	-0.274744	NA	0.409857	NA	-0.658259	0.542751	0.196381	0.696311	-0.846327	0.747917	-0.57303	-0.270552	-0.261823	-0.483167
SUA7	-2.217204	-1.271765	-0.4335	0.022836	-0.912347	0.108201	0.039896	-0.574867	-0.010606	-5.081285	0.609514	0.233578	-0.635124	-0.289271	0.389751	0.229908	0.350131	-0.482848	0.162278	0.013326	-0.609907	1.025421	NA	0.656137	-1.673385	-0.546948	-0.372631	-0.098826	NA	0.256066	0.12788	-0.347048	1.743035	-0.431847	0.680022
SUB1	NA	-0.998664	NA	-1.257504	-1.093183	0.028878	0.068661	-0.616751	1.180941	NA	-1.857617	-2.948874	-1.086338	-6.686733	0.905848	0.302517	-1.775019	-0.712378	-1.587971	-0.471204	NA	-1.12603	NA	2.152912	NA	0.872381	-0.654188	1.088498	-0.117077	1.055248	0.752635	-0.361064	-1.058121	-0.281199	1.016712
SUM1	-7.674814	-1.467546	1.547673	-0.269089	-1.260163	0.158283	-0.078076	1.22393	0.445704	NA	0.276332	-0.757657	-0.3542	-1.377153	1.333643	0.234035	-1.243547	-0.051936	-0.350831	-0.443688	0.503189	NA	NA	-1.228444	-4.389813	0.389338	0.323006	-0.951513	NA	0.050902	1.501199	NA	-0.596023	0.204647	0.365507
SUR1	NA	-1.292821	0.160665	0.817275	0.012351	0.057965	-0.382033	1.060357	-0.552129	-1.862287	0.575987	0.328852	0.691105	NA	0.461562	0.148923	0.442788	-0.666238	0.765728	-0.568858	-0.301489	1.095174	-0.214668	-0.410394	NA	0.34012	-1.510627	-0.400841	-0.096825	-0.016411	0.439131	0.356784	0.127171	-0.271389	-0.615577
SUR2	3.611601	-0.701553	NA	-1.14664	-1.024619	-0.609055	-0.284994	-0.596687	0.068699	0.660591	1.094305	0.959173	0.838584	NA	0.257295	0.168962	-1.04649	0.014256	-1.030701	0.606839	0.250854	NA	NA	-0.470545	NA	-0.560197	-0.009523	-1.290401	-0.067428	-0.425295	0.416955	NA	NA	0.085659	-0.825241
SUR4	NA	-2.455247	NA	-1.57842	NA	-0.364485	0.013235	NA	0.230562	-0.090053	-2.388055	-1.713375	-0.220795	-0.571662	0.774984	0.410236	-0.359998	-2.376601	-1.161896	-2.91385	NA	0.73868	-1.280417	-0.272323	NA	-3.504387	NA	-0.504616	-3.409863	-0.283238	-3.88246	0.458144	-0.80226	-0.525538	0.11531
SUT2	NA	0.714369	NA	0.059657	1.541375	0.79593	-0.123795	0.260408	1.059036	-0.703909	-1.827373	-0.255508	-0.169233	0.106737	0.165783	0.400877	-0.685124	0.471884	0.0295	-0.409189	0.615893	-0.412444	-0.267092	-0.816316	NA	-0.161873	-0.23728	-0.121678	-0.633769	-0.001955	0.11172	-0.149212	-2.185168	-0.119946	0.839511
SVP26	NA	0.930211	-0.534216	-0.185073	0.565026	0.519566	-0.836326	0.820892	-0.034702	NA	0.450588	0.589	0.393973	NA	-0.21591	-0.177004	-0.326451	NA	0.117136	0.35698	NA	-0.878793	-0.975354	1.444185	NA	0.00803	-0.339018	0.420303	NA	-1.264601	0.415422	0.103768	0.532051	-0.154077	-1.532021
SWD1	-1.247634	-5.034292	2.012918	1.300933	-2.470965	-0.321401	-0.115362	-5.779698	0.762275	-7.575792	1.355163	0.682631	-0.073064	NA	0.076687	0.07715	0.718932	-0.142242	0.773912	0.317579	-0.751222	1.174972	NA	2.817256	NA	-1.42949	-2.093906	-0.675564	0.463615	0.31211	-6.311798	-5.296545	-0.308322	-1.492454	0.093231
SWD3	-1.595085	-3.076662	NA	1.115529	-2.581032	0.07917	-0.187793	-3.698317	0.626068	-5.719341	NA	1.474505	0.593219	NA	0.672547	-0.125371	0.520937	0.738035	0.896366	0.741134	-0.994153	1.412237	-1.544234	2.151643	-2.890879	-1.416937	-2.817232	0.033898	0.963507	-0.24568	-4.065247	-5.895995	0.113318	-0.398873	-0.245851
SWE1	NA	NA	-2.157184	-0.12182	0.285375	-0.664704	-0.068035	NA	-1.635248	2.120348	NA	0.129514	NA	0.472634	-1.075551	0.981315	-0.984101	0.746786	0.202477	1.240183	0.064493	-0.180604	NA	-2.628554	NA	-0.370945	-0.822777	-0.586882	-0.544892	-0.564709	NA	-0.495969	0.579824	-0.706839	0.611153
SWF1	-0.310816	NA	NA	-0.709089	NA	0.517556	-0.26152	-0.64084	-0.065329	-0.033267	0.950591	-0.683244	NA	NA	NA	0.293057	0.372181	NA	-0.051262	0.696464	1.250955	NA	NA	-1.498276	NA	0.619731	NA	0.138791	NA	0.603827	0.510784	-0.012975	0.896522	NA	0.061865
SWI4	-0.961656	-3.992638	NA	-0.542144	-0.536061	0.048169	0.727987	0.424423	1.717256	-3.297044	0.108985	0.777096	1.527399	NA	-0.503086	0.269992	-0.378757	1.343361	NA	0.74332	0.276359	0.111267	0.271831	2.579709	-2.544371	-0.37099	-2.819114	1.331488	-0.213309	0.063088	NA	-1.140898	1.112796	-1.094056	-0.040579
SWM1	NA	-5.467794	-2.266441	2.056352	-5.132215	0.624972	0.536427	-6.524753	1.811194	-0.012136	0.051619	-1.730467	-3.15204	-9.318759	-0.309858	-0.096694	1.770221	-2.088275	1.695795	-0.664853	-1.384922	NA	-0.041774	0.433691	NA	-0.721722	-4.80018	-1.32687	2.412217	0.723943	NA	NA	0.191698	-1.464898	-0.652049



UBX3	NA	-1.845149	NA	0.441441	0.040712	0.043161	0.004426	NA	0.323532	-0.018911	-0.049778	0.024712	0.487994	0.855141	0.181717	0.203455	0.497783	-0.306067	-0.684971	0.238161	0.164245	-0.598874	0.199513	-0.688034	NA	0.427612	1.442847	0.302346	-0.57838	0.31782	1.368177	-0.109198	0.516616	0.089706	0.090236
UBX4	NA	NA	-13.078683	0.067992	-0.836499	0.142262	0.536263	0.25216	0.679216	-3.116374	-0.168617	-0.34149	-0.93032	-1.375424	-0.02872	0.048174	0.766605	-0.567198	0.064606	-0.563208	NA	0.535608	NA	1.031978	NA	-0.101424	-1.603916	0.742548	-2.391881	0.472166	-0.342369	-0.614221	-1.573318	0.533817	0.572171
UBX6	0.112741	NA	-0.318093	-0.36266	0.256251	-0.317106	-0.607251	0.73146	-0.15436	-0.461634	-0.06996	-0.147246	-0.170244	1.688543	0.378066	0.225892	0.446523	NA	0.10106	-0.134334	0.93635	-0.156931	0.794178	0.569757	NA	NA	0.429436	0.579626	0.237568	-0.13542	-0.053533	0.181806	-1.251998	0.129398	-0.382902
UBX7	NA	0.632822	0.960648	-0.867941	-0.026802	0.514907	0.284083	0.401421	-1.048388	0.222791	-0.980889	-0.858642	0.784785	NA	0.208815	-0.168619	-1.004239	1.233758	-0.885452	0.415168	NA	0.293066	-0.506132	-0.238071	NA	-0.600733	-0.175021	0.334653	-0.2932	-0.283321	1.513407	0.23959	-1.084361	0.117796	-0.25461
UFD2	NA	NA	-2.849116	0.535813	NA	-0.779332	-0.272359	-1.174989	NA	NA	NA	-0.286434	NA	NA	NA	0.146565	-0.193539	-2.173269	-0.275881	-0.137011	NA	-1.165301	NA	NA	1.077199	0.036703	NA	-0.746256	NA	0.833682	NA	NA	0.718553	-0.422838	NA
UGA1	4.104499	-0.087647	NA	0.706569	-1.377041	-0.574273	-0.312033	-0.479282	0.47057	0.565782	NA	-0.444963	-0.24123	NA	-0.516637	0.222043	-0.076225	NA	0.608926	-0.23446	-0.24333	0.103348	NA	0.659452	NA	-0.153231	-0.174541	-0.769452	NA	-0.214501	NA	0.793197	0.414187	0.138231	NA
UGA3	NA	-0.857889	NA	0.074386	-0.241156	0.356574	0.778564	-0.001545	0.316254	0.973386	0.111101	-0.775807	-0.265961	-1.987564	-0.045018	0.081373	0.254825	-0.463489	0.45105	0.326594	0.64179	0.284322	0.324413	-0.050418	NA	0.255191	0.37242	0.148391	0.606491	0.623734	-0.292137	0.178501	0.220135	-0.175913	0.753498
ULS1	NA	-1.631843	1.334905	0.190233	-0.424927	0.135043	-0.047401	-10.80445	-0.074109	-2.324311	0.223025	-0.040177	-0.974192	0.697836	0.102537	-0.036964	-0.331793	0.110371	0.316908	0.166246	-2.860862	-0.638383	NA	0.767768	0.79047	-0.216231	-0.895806	-0.251363	2.247818	-0.22725	NA	0.441983	-1.489305	-0.552308	-0.05447
UME1	NA	-0.975039	-3.109366	0.429002	NA	0.520164	-0.306271	0.559555	0.310461	-2.269496	1.361893	0.655698	-0.877662	-2.054549	0.21158	-0.045649	1.119862	-0.944077	0.961034	-0.563221	-0.619202	1.311623	NA	-1.187227	NA	-1.842713	-2.36975	-0.352668	-0.203303	0.351937	0.989	-0.639113	0.321134	0.354793	0.504581
UME6	-4.128475	-0.822566	NA	0.690252	-0.448838	-0.864886	NA	-8.300993	0.210957	NA	1.030098	0.82332	0.235952	NA	-0.209964	-0.353335	1.334842	-0.832458	0.778569	0.811359	-0.933132	NA	-1.448996	1.990733	NA	-1.962607	0.310629	-0.79852	0.4582	-1.033726	NA	NA	1.510843	0.34325	-1.270839
UPF3	0.968821	2.499913	0.179059	-0.836892	0.854431	-0.20968	-0.092668	0.904976	0.259431	-1.366684	-2.429327	-0.06147	0.533324	-0.529173	0.872722	-0.660173	-0.641863	2.012549	-1.181183	2.44561	0.206373	0.443798	NA	0.800007	NA	2.184248	1.367193	0.897382	-4.57431	-0.132638	-0.175164	0.358285	-0.799091	1.565174	-0.658472
URE2	NA	-0.376075	-0.815606	0.598229	-1.051582	-0.067779	0.344353	-1.081542	-0.132339	-2.371328	2.087625	1.801255	NA	NA	-0.509209	NA	0.865253	0.375175	1.302756	1.630657	1.291261	0.513757	2.076212	NA	NA	-0.210803	0.133521	0.38091	0.792654	0.069646	-0.752787	-1.60342	NA	-0.358519	-1.334867
URM1	NA	0.044053	-8.243774	-0.947253	0.386201	-0.875023	-0.430112	1.462225	0.040545	-2.232138	-0.722853	1.374273	0.953283	-6.949565	-0.656013	-0.010163	0.024098	1.382649	0.266683	1.972428	0.776011	0.96937	NA	-1.950156	NA	0.642299	0.156662	0.801312	-0.067778	-0.747206	1.207437	-1.066731	1.408161	0.473905	-0.141984
URN1	NA	-0.322848	0.763407	0.158236	0.160214	-0.664771	-0.306931	0.056619	0.166839	-1.999388	-0.127274	-0.598364	0.155899	-0.027001	0.475979	-0.178221	1.452514	0.099068	0.093171	-0.09079	0.668786	0.546543	NA	0.143233	NA	0.317911	-0.225603	-0.512941	0.695993	0.362972	0.702076	0.362815	-1.741021	0.004655	-0.540011
USA1	NA	0.014836	0.001708	0.129527	-0.068353	0.112648	0.863883	-0.132437	1.189407	0.365131	0.509245	0.141171	0.011517	-0.07229	-0.002924	0.69193	-0.549425	0.442588	0.722771	0.0484	NA	0.18276	0.046681	0.797656	NA	0.143807	-0.310939	0.807441	0.34674	-0.149168	-0.409831	-0.475682	-0.781171	-0.445438	0.37457
UTH1	NA	NA	NA	2.276993	NA	0.307743	NA	0.944009	NA	5.628042	NA	-1.335087	NA	NA	NA	0.834832	0.490766	1.066454	NA	1.931985	NA	-0.324482	NA	5.041765	NA	2.009674	NA	NA	0.890158	5.631757	NA	4.69589	NA	NA	0.214414
VAC14	NA	NA	-0.870962	1.04018	1.075776	-0.135987	-0.606816	-0.128201	-0.567679	2.612722	0.736332	-1.495403	-1.525442	0.445457	0.815292	-0.071376	0.729376	-0.269313	-0.195256	-1.10624	-0.03025	0.706617	NA	-1.906588	NA	0.858427	NA	0.146967	-0.723521	0.695705	NA	0.674277	NA	-0.284929	0.7186
VAC7	0.6821	-0.872645	0.464681	0.273179	-0.554018	0.345042	-0.271361	-0.289478	-0.440276	0.307627	0.513862	0.056129	0.215545	NA	-0.507546	-0.770302	-0.303127	0.209029	0.306808	0.840702	-0.034759	0.336354	NA	0.205415	NA	-0.029025	0.682605	-0.848665	NA	-0.361263	0.07489	-0.136353	0.326503	-0.087246	NA
VAC8	NA	1.05902	-3.29483	-0.055064	-0.38389	0.046445	-0.772025	-2.160255	-0.966651	NA	-4.938695	-0.603838	-1.055635	-4.386231	-0.894011	-0.180801	1.315526	-0.797917	0.071431	0.259283	0.289504	0.882348	-0.09801	-1.724339	NA	0.133647	-1.35679	0.019619	-0.508597	0.592377	NA	-0.193496	1.487993	-0.351738	-0.203325
VAM10	NA	-1.570406	-6.125456	0.833995	-0.380986	0.337226	NA	-1.177271	NA	NA	-0.164135	-2.517638	0.27231	-0.345841	0.734998	0.845069	0.79476	-0.40433	0.101586	-0.334149	NA	0.720948	NA	1.067604	NA	-0.014063	0.450372	-0.177885	-1.683641	1.37088	-4.662594	-0.041317	-2.020924	-3.443692	0.709313
VAM3	NA	-3.000389	-4.219958	0.65874	-2.278768	-0.689197	NA	-1.918344	NA	NA	NA	-1.752991	-1.77983	0.852264	0.087027	-0.176647	0.269255	0.270041	0.383659	0.697007	-0.943296	0.184187	NA	0.129506	1.444052	0.20244	-2.102556	0.229609	0.351547	1.08787	NA	0.964468	-0.136792	-1.365429	-0.461442
VAM7	NA	-4.568532	-4.538227	0.399324	-2.621029	0.236792	-0.339992	-3.45297	-0.194621	-0.609855	0.063492	-2.128106	0.311415	NA	0.513397	0.651602	0.662307	0.682481	0.20587	0.620533	NA	0.19867	NA	-0.172554	NA	-0.784914	-1.489739	NA	-0.274666	1.225989	-6.439623	0.649218	-0.662155	-0.808714	0.076331
VHR2	NA	-0.52236	0.701755	0.141148	-0.082782	0.290514	0.401444	-0.969949	0.908882	-2.853504	0.480048	0.828921	0.723322	NA	-0.046858	-0.562055	0.988102	0.263595	0.363339	0.301701	NA	-0.016892	NA	0.847525	NA	-0.007611	0.239711	0.035561	0.607032	-0.628008	NA	-0.209628	-1.028872	-0.181359	-0.544855
VID22	NA	-0.932349	0.080505	-0.00091	NA	0.635941	-0.221415	-3.198539	0.070001	-5.70481	1.596094	NA	-1.475566	-3.513323	-0.203526	0.242322	0.140988	NA	0.26234	-0.626888	-0.569853	0.730097	0.455097	0.031084	-0.235505	-1.454969	NA	0.072109	-2.348788	0.6366	-5.760461	-0.414845	1.052932	-0.626119	0.491885
VIK1	NA	NA	NA	0.286725	NA	0.471321	0.080583	-1.158799	0.381379	-3.662915	-0.667399	0.62979	0.233394	-1.849349	0.132492	-0.394326	0.22687	0.322968	0.178824	-0.622351	NA	0.825925	NA	-0.537252	NA	-0.493723	-0.218161	-0.232277	0.25853	-0.09272	0.219174	-1.524268	-0.08523	0.119066	-0.767774
VIP1	NA	-1.456271	-0.224006	-0.926603	-3.374518	0.280918	0.733562	1.678575	-0.234128	NA	-0.66263	-6.81672	-0.298747	-1.016276	0.085894	-0.347003	-0.402298	0.981575	-1.095391	-0.165182	0.098536	0.52902	NA	0.52147	-2.360312	1.100026	NA	-1.086346	-0.827007	1.266421	0.853925	-0.523776	NA	-0.793785	0.519732
VMS1	-3.8918	0.205936	-2.045014	0.757918	-1.170954	0.065799	0.174509	NA	0.079145	-3.033091	0.900048	-0.822229	0.572816	-0.301585	NA	1.989543	0.984889	-0.58883	0.978422	0.022511	0.397825	1.193778	-0.251664	-0.049808	NA	-2.397551	-1.275287	0.643633	-1.862473	0.738182	0.062355	-0.274592	0.299581	NA	0.347923
VPS1	-1.575156	-0.396776	NA	0.492443	-0.887769	0.180019	-0.936632	1.44864	-0.202061	-5.427506	-1.261545	-2.150754	0.729249	NA	0.667147	0.026786	0.148645	-0.07515	0.611739	0.142884	1.045802	-0.414445	NA	-1.921416	-7.513758	1.140952	-0.573175	0.019155	-1.484552	0.292603	NA	-4.63773	NA	-0.523124	-0.184872
VPS13	NA	0.292698	-5.170808	-0.130877	0.006065	-0.221266	0.1318	0.43456	-0.148923	NA	0.399758	-0.393518	0.126024	1.727794	0.366052	-0.647908	-0.069813	0.065741	-0.14262	NA	-0.555833	-0.001965	NA	0.250883	NA	0.237957	NA	0.564168	0.529522	-0.075039	0.01968	0.286755	-1.893185	-0.698298	0.949331
VPS17	NA	NA	NA	0.546443	NA	-0.161728	NA	NA	NA	NA	NA	-1.338144	-0.754818	NA	0.682088	0.878249	0.789399	NA	0.843597	0.760948	NA	0.269896	0.691466	0.13158	1.290219	-0.273819	-0.450787	0.486881	-0.605458	0.994184	NA	-0.203535	0.791602	-0.908761	0.614461
VPS21	NA	-0.103624	NA	0.791316	-2.467142	0.036171	NA	2.69178	NA	NA	-0.353799	-2.111414	-0.975947	NA	-0.130578	0.333129	0.433746	0.246041	0.204174	0.971099	0.364917	0.078014	0.44646	1.193902	NA	1.339467	NA	0.471894	0.316157	0.332177	2.73859	-1.378649	-1.953003	0.11742	1.227482
VPS24	-0.574869	NA	0.465851	0.278942	-2.212448	0.933737	NA	NA	0.379978	-5.525368	-0.199033	-1.814418	-0.442135	-4.953675	-0.164544	0.542909	0.315303	0.127861	0.731133	-0.402674	-0.975568	1.190834	NA	-0.261823	-2.153555	-1.526563	NA	-0.501614	-2.285479	1.73567	NA	-4.179723	0.984079	0.149475	-0.007815
VPS27	NA	-3.19361	NA	1.154492	-0.961118	-0.057515	-0.425183	-0.84165	0.715862	NA	0.535397	-2.098179	-0.452732	0.196981	0.265483	1.254547	1.76643	-0.099429	0.33111	0.076065	NA	1.208881	NA	-0.15204	NA	NA	-2.051746	0.46169	0.197923	1.887012	-0.998988	-0.930454	1.620685	0.639579	-0.469338
VPS29	-8.779335	-3.973043	-5.594486	0.759505	-3.806295	-0.047704	0.927469	-2.2167	0.514087	0.358522	-0.402795	-3.993886	-0.17635	1.490125	0.735452	0.364162	0.32716	-1.670379	-0.305778	-2.027635	NA	0.143163	NA	-0.838714	-3.459207	-2.627988	-2.413532	-0.351948	-1.368358	0.472496	NA	0.713894	-0.051652	-1.665398	0.25997
VPS30	NA	NA	-4.351451	0.365642	NA	0.008381	0.409049	0.244572	0.951161	-1.285306	-0.503016	-1.643725	-0.348978	1.144711	0.969296	0.505392	0.697322	-1.533679	0.424594	-0.374808	-0.399222	0.032385	-0.554819	0.466878	NA	0.695768	-0.065394	0.713051	-0.527001	0.235618	1.950507	0.398401	NA	-0.628379	0.975576
VPS35	-1.449144	NA	-5.639755	0.939034	-2.102666	0.183902	-0.349799	-0.550161	0.659552	0.463751	NA	-4.947418	-0.852767	NA	0.386667	0.554729	0.19389	-1.383097	0.454362	-0.264889	0.384502	0.991492	-1.739934	-0.355755	-12.587928	-1.585762	-2.223862	-0.6513	-2.686433	0.739513	-0.667575	-0.290142	0.043543	-1.484954	0.322083
VPS38	NA	-0.271868	-1.413321	1.266404	0.760633	0.651873	-0.696847	1.549067	-0.08693	NA	-1.010357	-2.87811	-2.537014	NA	0.593	0.522276	1.419296	-1.877283	0.705197	-1.297794	-0.636368	0.2889	-1.422558	0.390422	NA	-0.06531	NA	0.70663	-0.126983	1.171637	NA	1.295231	-0.702399	-2.592617	1.529783
VPS41	NA	NA	-2.533766	0.165671	-1.941187	-0.456835	-1.411219	NA	0.887919	3.687896	NA	-1.308773	0.563033	NA	NA	0.856282	0.152366	-0.621311	-0.180528	0.210968	NA	-1.044949	1.113206	NA	NA	0.570851	-1.280782	-0.516169	0.122685	1.614726	NA	NA	-1.620042	NA	-0.868789
VPS5	NA	-0.649399	NA	0.256063	-1.138893	0.848401	NA	0.717914	NA	NA	-0.344949	-1.169123	-0.094481	-1.798377	1.427277	0.861293	0.698662	-0.896178	-0.004337	-0.687118	NA	1.097576	NA	-0.359333	NA	-0.430692	-1.431233	0.174816	-0.002114	0.483594	0.015173	-0.437817	1.099685	-1.432143	0.303868
VPS51	NA	-0.107052	-4.421849	0.361056	NA	-1.325265	-0.317957	NA	0.079066	NA	0.748691	-1.331277	NA	NA	-1.21939	-0.446436	-0.283542	NA	-0.182966	1.604	0.546152	-1.290303	1.995138	-1.176767	NA	-0.20478	NA	-0.097632	0.714368	0.069674	-0.481897	-2.181558	0.022447	-2.049962	0.530516
VPS53	NA	NA	NA	0.110955	NA	-0.310085	-0.164254	NA	0.285306	-1.288094	-0.559856	-1.622078	NA	-3.061474	0.676145	-0.165797	0.609047	0.571292	0.023692	1.484473	NA	0.324648	0.898332	-0.812325	2.259913	NA	-1.271222	0.4045	0.050621	0.452772	0.040401	-0.430365	1.120257	-0.618713	0.660306
VPS70	-0.076784	0.025835	NA	0.314592	-1.830837	0.07291	0.081646	0.188028	0.497905	0.260808	0.206242	-1.531017	0.046468	0.113237	-0.569736	0.293511	0.307003	0.719385	0.54256	0.153109	-0.199812	0.267595	0.650546	-0.045708	NA	0.895486	0.193151	0.326931	-0.124127	-0.119057	0.191911	0.159461	-0.045432	-1.073852	0.499354
VPS71	NA	-4.632043	NA	-0.657074	-4.863548	-1.607613	0.191303	-7.911801	NA	3.180265	NA	-9.548761	NA	NA	-0.179788	0.536856	-1.14322	-1.15518	-1.753978	-0.981707	NA	-2.130987	-8.257604	NA	NA	-1.171406	-2.406228	-0.918765	1.089944	0.771222	NA	1.248656	NA	NA	0.93173
VPS74	0.338084	-0.283733	0.347401	0.205157	1.022721	NA	-0.835742	0.486094	-1.446311	0.808714	-0.808969	-0.280015	0.356013	-1.20479	-0.024668	0.302288	0.543011	-1.608719	0.022944	-0.400642	0.470234	0.685715	NA	-0.140278	NA	-0.836356	-0.045748	0.673939	-0.853361	-0.064026	-0.858659	NA	NA	-0.139769	-0.610959
VPS75	NA	NA	-0.393767	-0.108241	-1.242101	0.413903	-0.155212	1.118902	1.071625	-1.694088	-0.27698	-0.360513	-1.6564	NA	0.630491	NA	0.265718	0.384237	-0.731415	0.173469	NA	0.129287	-0.387622	NA	-3.663241	0.385956	NA	-0.316358	0.039676	0.759032	1.904202	-1.331392	NA	0.567532	0.357543
VPS8	NA	-2.20299	NA	0.763673	-0.517097	-0.64319	-0.026956	-0.543124	-0.174253	-3.396229	0.773	-1.210442	1.075053	NA	1.224935	0.517708	0.758663	0.352439	0.784083	0.219721	NA	0.747398	NA	0.924073	NA	0.429255	NA	-0.495632	-0.071497	0.722566	-0.329411	-1.793971	1.173124	-3.592315	0.04075
VPS9	0.298791	-5.154153	NA	1.629728	-1.612508	0.936625	0.463276	-1.870441	-0.4809	-1.281625	0.828859	-1.553362	0.664181	0.06262	1.607053	0.318065	0.784991	0.500397	0.228742	-0.10267	NA	0.221299	-0.889788	1.593223	NA	-1.0961	-2.742463	-0.43515	-0.727074	0.915612	-1.848268	0.919679	1.707459	-4.068834	1.030494
VRP1	NA	-3.838018	NA	0.788902	-2.046133	-0.081867	-1.23404	-2.068514	0.343518	1.275939	1.158885	-1.344425	-0.274026	NA	-4.297295	-0.597545	0.951347	-0.252176	1.112265	0.107936	0.715371	NA	-0.324528	-3.306752	NA	-1.145664	NA	-1.070669	-2.058079	0.195103	-2.330237	0.602027	-0.864697	-2.274896	NA
VTA1	-2.071924	0.028515	-0.123396	-0.007201	0.202309	0.244557	-0.863177	0.843221	0.432883	NA	NA	0.016652	-0.815552	1.667502	-0.437439	0.571334	-0.426317	0.195607	0.16386	-0.190997	-0.943802	0.820557	NA	0.392402	NA	1.137748	-1.696667	0.365876	-1.218238	1.119278	0.751504	-0.01338	-0.723575	0.355287	1.461425
VTC1	-1.285495	-0.991537	-1.39709	0.15774	-1.413561	0.090354	-0.284068	-0.754507	-0.405082	-2.394189	-1.481308	-1.634008	-0.58327	NA	1.09867	0.306696	0.203949	-1.443377	0.334496	-1.146088	-1.464662	0.859123	NA	-0.141862	NA	-0.095797	0.829111	NA	-0.343698	0.262658	NA	-0.277297	NA	-0.115354	0.335224
WHI2	NA	-0.35974	0.196455	0.357834	-0.345321	-0.270444	NA	-1.436916	NA	NA	-0.230334	-1.560403	-0.021044	-3.029447	0.071402	-0.156825	0.272438	-0.635032	0.40858	NA	0.321271	0.634549	1.226593	0.353475	NA	-0.120247	0.773931	0.330751	-0.260963	-0.031751	NA	-0.484689	-0.133399	-1.388578	-0.189887
WHI4	NA	NA	1.4775	0.355014	NA	0.326004	0.378812	NA	0.288765	1.078954	-1.977903	-1.669216	NA	-2.851953	0.597639	0.570815	-0.476527	0.683257	-0.71674	0.610464	NA	-0.027002	NA	0.197821	1.272156	1.009828	1.265135	0.464251	-0.588717	0.429068	-0.930502	-0.42863	-1.341652	-0.455373	0.80358
WHI5	NA	0.766921	-0.098376	-2.539577	-1.704344	-0.465699	NA	-1.454026	NA	NA	-1.101233	-3.040086	-0.328184	-4.334696	-0.277866	-0.253275	-1.39953	-0.461926	-0.758499	0.828328	0.394134	-1.037006	1.088931	-0.227362	NA	1.115398	1.426162	0.038001	1.408211	0.049658	NA	-1.470506	-3.170076	0.402093	-0.557914
WSS1	0.230698	-0.153053	-0.028646	0.047072	-0.552431	-0.293798	-0.014567	1.71106	0.020046	-1.072246	0.185235	0.695941	0.388136	-0.623659	0.149718	-0.242086	-0.618127	1.317877	-0.399135	0.535828	0.26752	-0.308731	-0.267285	-0.315617	-0.556467	0.223165	-0.21211	0.428997	NA	-4.936058	2.201916	-0.062116	1.538495	-0.112143	-0.252699
XRS2	0.240183	0.056703	NA	0.161151	-2.391426	NA	-1.331349	NA	0.284319	0.053756	-0.917378	-2.176013	3.07279	NA	0.018269	0.738676	0.011244	1.65237	-0.156859	2.095655	NA	1.730087	1.010977	0.061178	NA	-0.830204	0.102478	1.794632	-0.622754	-0.01072	NA	NA	NA	0.559167	1.001884
YAP1	NA	-0.501682	0.533617	0.253705	-0.348799	-0.005562	-0.385976	-2.168517	0.30576	-1.413802	0.483138	1.221473	-1.375008	NA	-0.137574	-0.480041	-0.215131	-0.303142	0.125385	0.261018	NA	0.428149	-0.566297	-0.287677	-2.564821	0.133222	-1.464522	0.345444	0.689092	0.616971	-2.159224	-0.258904	1.577647	0.1175	0.583211
YAP3	NA	-0.499794	0.762453	0.646112	-0.017965	0.279598	1.270335	-0.903997	-0.275539	NA	-0.697466	-1.207918	0.119573	-0.90627	0.510362	0.366717	0.572742	NA	-0.595495	-0.598765	0.077824	0.139255	NA	1.332138	NA	0.293852	0.045695	-0.381173	0.213089	0.546525	-1.939631	0.984127	-0.8013	0.672858	0.733543
YAP5	0.899534	-0.294617	-0.785448	0.594789	NA	0.63427	0.950374	-1.551422	0.639376	0.469183	-0.455647	-0.606558	-0.534842	0.209568	0.703908	0.388874	0.659753	-0.085676	0.266202	-0.90976	0.166357	0.801597	0.543105	0.567069	NA	0.110136	0.512181	1.000632	0.617654	0.478444	-0.017097	0.214222	-0.547283	-0.312499	-0.68585
YAR1	NA	0.883898	0.456819	-0.093075	NA	0.228153	0.005725	2.629973	-0.020844	NA	0.019358	-0.472167	0.105423	0.923502	0.4857	-0.297452	-0.954973	0.807397	-0.081575	-0.446492	-0.449597	0.104244	0.509202	-0.803568	NA	1.320879	0.969707	0.869313	NA	0.817167	1.959148	0.137457	-1.39819	0.192614	0.551609
YBL036C	NA	0.433614	NA	-0.607906	-0.455994	0.15443	-0.139422	-0.705917	-0.223495	0.515175	0.920372	0.022853	-1.106193	NA	0.443154	-0.21363	-0.133088	0.446506	-0.028419	-0.244324	-0.354693	-0.789006	-0.279945	1.338758	-2.172174	1.017818	0.29002	0.34054	-0.342982	-0.395319	-0.404608	-0.052514	-0.835778	-1.266929	-0.574129
YBL081W	NA	NA	NA	-0.056433	-2.54193	0.794741	1.365503	NA	2.296918	0.057697	-0.606378	-2.68916	-0.036865	-2.738899	1.800556	1.146886	-1.098181	-0.692282	-0.427569	-0.507939	-0.838284	-0.274938	NA	0.236654	NA	0.944419	NA	1.735117	0.67815	0.91047	NA	1.585381	0.554701	-0.112883	1.628487
YBL086C	0.919666	-0.281471	1.157319	0.343692	0.404987	-0.120809	-0.547853	-0.527927	0.211036	0.788871	0.713099	0.421927	0.173495	1.172015	0.086889	0.002343	0.148465	-1.373141	0.002795	-0.172383	0.12905	0.49178	-0.173909	0.225159	NA	0.358384	0.171335	0.242673	-0.212352	0.207698	-0.482439	-0.148866	0.642118	-0.793322	-0.203872
YBP2	NA	-1.115293	NA	-0.685686	-0.522493	-1.71003	-0.274587	NA	-0.604599	0.529096	-0.119131	-0.231508	0.455208	NA	-0.066955	-0.566426	0.097003	-0.659219	-0.814485	-0.168949	1.221031	-0.160968	0.104224	0.300193	-1.274198	-0.246472	1.070055	0.3918	-0.035417	-1.09317	1.40192	1.27061	-0.635165	-1.241127	-0.940537
YBR141C	-0.011799	-0.530087	0.04248	-0.094845	-0.401606	0.654478	-0.652654	0.309799	-0.157876	-0.687756	NA	-0.424804	-0.503694	NA	-0.208531	0.129393	0.549301	-0.017367	0.034838	-0.536263	0.108631	0.152963	NA	0.337095	NA	-0.667216	-0.796661	0.106508	0.516103	0.340808	0.304138	0.542153	-1.698272	0.081181	-0.02491
YBR238C	4.232747	-2.53565	0.635097	0.560906	NA	NA	-0.959922	-0.88624	0.166685	2.388025	NA	-0.165909	NA	NA	-0.120387	-0.862844	0.007872	-0.125243	NA	0.239062	NA	0.260088	-0.835312	-0.406232	NA	-0.274575	NA	-0.166149	0.571473	-0.130713	NA	0.694178	NA	-0.202104	-0.719565
YCH1	0.810019	0.787533	0.357763	0.112908	-0.046539	-0.518306	0.134626	0.347709	0.123	-2.239275	0.282012	-0.062098	1.392558	-0.274891	-0.178173	0.038115	-0.723692	0.708016	0.22396	0.201682	0.171835	0.454921	0.820479	0.215151	NA	-0.311863	0.784699	-0.453609	1.985239	0.088786	0.04909	-0.686077	-1.895508	-0.177422	-0.9041
YCK1	NA	0.231245	-0.200005	0.62466	0.416979	0.407117	0.998212	-0.26328	-0.103382	-1.397735	-0.322546	-0.057717	0.072185	-1.060667	0.104449	0.550041	0.082841	-0.049334	0.611857	0.08117	1.014763	-0.319346	0.696005	0.61965	-0.428236	0.492073	0.220236	0.515241	-0.144139	-0.007228	NA	0.845081	NA	-0.079976	0.056523
YCK2	-0.741956	-0.170147	0.856771	-0.268646	0.41909	0.415559	0.617887	-0.551434	-0.340919	0.436257	NA	-0.826155	0.310034	-0.947866	0.495671	NA	-0.247757	-0.070497	-0.238021	-0.484979	0.414355	0.123337	0.678978	0.381088	NA	0.367193	0.652008	0.906819	-0.696091	0.347152	-0.33376	0.584379	-0.070378	-0.245562	0.531229
YCK3	-0.858583	-0.03583	-0.237967	0.292941	0.337481	0.433761	-0.054286	-2.391435	-0.619303	-0.979203	-1.4758	0.467536	-0.425454	-4.969447	0.65101	-0.082729	-0.187879	0.503793	NA	-0.215353	0.432743	-1.1311	-1.102263	-2.018829	NA	0.145937	0.113551	NA	NA	-0.26428	NA	0.641467	NA	0.774298	0.201916
YCL001W-A	NA	NA	0.322656	NA	NA	-0.695168	-0.066411	0.728011	-0.279807	1.263724	NA	NA	-0.698062	2.477314	-0.219681	0.556852	-0.683506	NA	0.341675	-0.646828	0.203331	0.28796	0.093019	0.539101	NA	-0.52279	-0.800815	1.167156	0.562266	0.100793	0.970217	0.33498	-1.106621	0.214817	-0.043162
YCR050C	1.98579	0.94359	0.465329	NA	0.116459	0.052574	0.221673	0.751425	-0.199248	-0.045436	-0.521425	NA	0.472966	NA	0.448663	-0.176911	-0.35796	NA	-0.036396	-0.211664	0.260979	0.307946	2.186375	-0.097748	NA	0.389756	1.238545	0.0297	0.560484	0.072648	-0.048338	-0.028106	-0.96034	-0.507895	-1.1717
YCR061W	1.260454	0.286663	0.310968	NA	-0.083669	-0.17337	0.054878	-1.299062	0.042374	-0.274533	-0.103298	0.52889	-0.3437	NA	0.428973	-0.165357	0.237028	NA	0.135722	-0.117056	NA	-0.041	-0.345743	1.10336	NA	0.50491	0.336129	0.608668	0.314616	-0.39466	0.610561	0.028513	-2.2861	-0.151053	1.131374
YDJ1	NA	-1.69044	NA	-8.243745	-9.153503	0.738266	-0.765645	-4.982876	1.1607	-1.314606	-4.776149	-5.715633	0.801007	-0.754282	0.699624	0.205441	-8.138077	-1.200737	-6.435388	-0.568791	-0.130466	-0.612209	-3.102523	0.475993	-5.33846	-1.450823	-2.146559	0.450682	-0.918818	0.537184	-2.919992	-0.500075	-2.812572	-2.694757	NA
YDL176W	NA	NA	NA	-0.218819	1.302974	0.380307	0.318652	0.310574	-0.962731	0.377231	-0.14604	0.601564	-0.401942	2.802551	0.220401	0.242222	0.189606	0.315021	-0.370063	0.190773	0.765918	-0.002979	NA	-0.132377	NA	0.45969	0.003534	-0.290582	-1.131384	-0.023431	-0.656839	-0.658826	-0.09269	-0.008684	0.301523
YDR061W	NA	0.035747	-0.421422	0.414838	-0.125638	0.628891	0.179448	NA	0.561991	1.313285	-1.114632	-1.389306	-1.152786	-0.260516	NA	0.341375	0.163027	0.507467	0.27527	-1.164343	NA	0.242668	-0.261282	0.639145	-0.832116	0.796274	1.413757	0.654821	0.18797	0.509048	-0.095101	0.491415	-0.084254	NA	0.489665
YDR131C	NA	NA	0.677882	-1.449533	-1.395886	0.30499	-0.68928	-0.463023	-0.692068	2.515157	NA	-0.037623	NA	NA	NA	-0.165951	0.395728	NA	-0.074103	0.506936	0.320098	NA	NA	NA	NA	-0.833265	NA	-1.346994	NA	-0.013555	NA	1.227518	-0.189948	NA	-0.266794
YDR161W	NA	-2.33724	0.556067	-0.016924	-0.218618	-0.235812	0.542666	-1.470955	0.434258	NA	0.600294	-0.049789	NA	-2.011955	NA	0.09298	-0.01932	0.900495	0.269899	1.050726	NA	NA	NA	0.088683	NA	0.435544	1.12467	-0.057897	-2.07433	0.449372	NA	-0.337929	0.774201	NA	-0.093061
YDR306C	NA	NA	1.139355	-0.674922	0.101861	1.37466	-0.354061	-1.018284	0.030763	-0.365849	-1.605596	0.320518	-0.105969	-1.165861	0.247186	-0.34469	0.102996	0.466546	-0.420661	-0.471408	0.245079	NA	0.216011	-0.515398	NA	-0.109268	-0.406691	0.442049	-0.311746	0.556089	0.529787	NA	NA	0.392631	0.312262
YEF1	NA	-1.120743	NA	0.262426	0.630384	0.204522	1.076444	0.163218	-0.371164	0.236757	0.747512	0.350016	0.202482	NA	-0.213598	0.362709	0.151149	-0.104245	0.354621	-0.411798	0.097149	0.013707	0.052488	-0.855354	NA	0.338078	-0.189988	0.007957	-0.933489	-0.127855	NA	0.189754	0.743874	-0.616181	-0.027698
YEL043W	NA	-1.944002	-0.771822	0.224756	-0.794065	-0.746827	-0.909401	-0.638633	-0.076507	-5.808695	1.937425	-0.532304	0.357948	1.920062	0.078961	0.213899	0.533934	1.155503	0.848825	0.943436	NA	0.172934	0.825861	-1.352881	NA	-0.461117	-0.481804	-0.38078	-1.482803	-0.899247	-0.032341	-3.915068	0.586252	-0.434303	-0.733124
YER156C	NA	NA	0.32238	NA	NA	NA	-0.026753	NA	NA	NA	NA	1.914689	NA	NA	-0.261777	-0.359954	0.255781	-0.222665	NA	0.048053	NA	-0.403121	NA	-2.289385	NA	0.76052	NA	NA	NA	0.204946	NA	0.053655	0.441256	-0.351195	NA
YGL081W	-2.653853	1.413134	NA	-0.742557	-1.884312	0.405586	-0.280837	-0.576927	-0.297797	-2.642817	-0.83553	-1.601455	1.103858	NA	-0.435462	-0.382538	-2.675093	1.151838	-1.66773	1.433749	NA	-2.99828	NA	-0.705152	NA	-0.064716	-0.182817	NA	4.084805	0.014815	-4.63662	-1.228478	0.293332	1.113281	-0.710828
YGL242C	-0.765837	-0.446636	1.35195	-0.05073	NA	1.438198	0.650981	NA	-0.07566	-1.117565	-0.953237	-0.121757	0.022411	-1.076624	-0.06043	0.560673	-0.117083	0.6588	0.339321	-0.523663	-0.045665	-0.592499	1.800649	0.46127	-4.08401	0.544392	-0.044223	NA	-0.312787	0.03827	0.271551	-0.411979	NA	-0.02636	0.710693
YGR054W	NA	NA	NA	0.124385	-0.714247	-0.771599	-0.498058	-0.648868	0.189559	0.273297	0.327135	0.125711	NA	-1.128449	0.82073	0.542987	-0.305466	-0.356265	0.038295	0.04818	0.312467	NA	NA	0.444082	NA	-1.042563	0.631181	-0.498601	-0.336368	-0.48935	-1.305488	-0.541596	-0.768038	-0.139323	0.166241
YGR122W	NA	NA	NA	0.691408	-1.369278	-1.018727	-0.02486	1.175551	-2.106435	4.502875	1.245245	-2.91513	NA	NA	1.311547	0.248688	-0.191273	-0.58449	-0.15194	0.420338	NA	0.47504	NA	-2.494604	NA	0.363621	-1.149682	-0.058601	0.79688	-0.074842	NA	-3.875846	1.591624	0.688222	0.259307
YGR237C	NA	-2.03171	-3.984969	-0.084772	-0.543825	0.050744	-0.257064	0.644851	0.067691	0.210806	-0.261475	0.208285	-0.689018	0.878062	0.078988	-0.202183	0.276258	0.114379	0.050558	0.286152	-0.870356	0.348526	NA	1.105381	NA	0.366565	-0.633673	-0.073363	-0.078343	-0.139687	NA	0.097711	0.032313	0.284582	0.141768
YHP1	NA	-0.733635	0.495229	0.748351	-0.783114	NA	0.425662	-1.556583	0.822539	1.567561	-0.981726	-0.103557	-1.332027	-3.369743	0.174687	0.534614	0.073384	0.143143	-0.15027	-0.287986	-0.709173	-0.07289	NA	-1.46778	-2.30172	0.135387	0.368661	0.033793	0.507213	0.102121	-1.831367	-0.18426	0.445148	-0.302273	1.064004
YHR078W	NA	0.455082	-0.307351	-0.121354	0.939029	-0.352905	0.213841	-1.029615	-0.296909	1.414037	0.273956	0.490995	-0.602187	0.725582	0.943378	0.463354	0.173404	-0.235203	0.441295	-0.226298	0.670347	-0.525022	NA	-0.432364	-0.353953	-0.343643	NA	NA	-0.109174	0.300857	NA	0.285673	NA	0.47382	0.23854
YIL029C	4.291677	-0.902645	0.208786	0.124357	-0.265876	-0.200366	0.066187	-1.043249	-0.040937	NA	NA	0.209802	0.155523	-2.44516	-0.576568	-0.129633	0.933189	-0.252843	0.165137	-0.568418	0.306436	-0.261472	0.532506	-0.2203	NA	-0.20511	0.828844	-0.143189	-0.094887	-0.026762	4.796974	-0.294944	0.513369	-1.28729	0.594524
YIP3	NA	NA	-0.18593	-0.553468	-0.458469	-0.397147	-0.796715	1.149176	0.177677	1.085945	0.617043	-0.003851	0.363657	NA	0.095815	-0.304268	0.166406	-0.358524	-0.508668	0.001921	0.469061	-0.402597	0.271783	-0.525764	NA	0.156616	-0.542384	0.052726	-0.665362	-0.17633	-0.933943	0.626015	-0.54893	0.78379	-0.114634
YIP5	NA	-2.251743	-0.112497	-2.112718	-0.825293	-0.867523	-0.584658	-0.865888	-0.064207	NA	0.063023	-0.700375	NA	-2.001385	0.420913	0.156938	-0.947828	0.343687	-0.173132	0.808362	NA	-0.856146	0.312947	0.129491	NA	-0.276915	-0.780192	NA	-0.427894	0.372675	-1.242827	1.044726	-0.014623	-0.276632	-0.743939
YJL055W	NA	NA	0.229231	NA	NA	0.299168	1.228991	-1.608066	-0.772514	4.499071	NA	-0.586497	NA	NA	0.378396	0.346272	-0.470646	NA	-0.013205	NA	NA	0.257627	NA	NA	1.750351	NA	0.266584	0.470319	0.588309	0.355429	NA	0.453184	-0.531345	-0.464865	NA
YKE2	NA	0.28577	0.286656	-0.857938	-5.376754	0.099566	-1.094086	0.205975	0.196766	NA	-0.271075	1.099552	0.435969	-2.40856	-0.089957	-1.024532	0.563313	0.119335	-0.231082	0.434815	0.671743	0.063747	0.548681	-0.443152	-4.887289	-1.416428	NA	-2.075593	0.503608	-1.15451	0.481828	NA	0.764498	-1.682874	0.011077
YKL023W	NA	NA	-0.626598	-0.031876	NA	-0.783142	0.630404	NA	-0.024459	NA	NA	-1.326582	NA	NA	-0.204462	-0.707735	0.349671	NA	-0.667751	0.561743	-1.452306	-0.099194	NA	0.08413	NA	-0.343708	NA	-0.89905	-1.008447	0.223683	NA	-2.410552	NA	-0.099556	NA
YKU70	NA	NA	-0.65663	2.059788	NA	0.718193	0.713507	1.702318	NA	NA	1.376613	0.994643	NA	NA	-0.983822	NA	NA	0.661894	1.603444	0.241722	-1.102118	1.137271	-0.335	1.14929	-2.032464	0.302796	0.089887	1.6456	NA	NA	1.472536	0.868399	-1.372638	-0.135275	NA
YKU80	0.649972	-1.329042	-1.916391	1.345536	0.082185	0.097576	1.491017	-0.298454	0.876892	-0.26728	1.08436	0.065373	1.822429	-2.490144	-1.665337	-1.044228	1.832183	-1.082164	1.197308	-0.239031	NA	-0.038228	1.663406	0.092757	NA	-0.071865	-0.406783	1.278318	NA	NA	0.335037	-0.246447	NA	-1.090826	0.373288
YLR177W	0.044913	-1.12218	0.608661	-0.980463	-2.143152	-0.17688	-0.671056	-1.442683	-0.254194	0.947363	0.702171	-1.104735	-0.486933	-1.360748	0.116036	0.045245	0.31851	-1.538728	-0.039491	0.590405	-0.040127	-0.319687	NA	0.402053	-6.863957	0.504349	0.302423	-0.236653	-0.709692	0.0552	NA	0.182309	0.520806	-0.281696	-0.931097
YLR224W	NA	0.0504	-0.555548	-0.021343	1.169583	0.289229	-0.440174	0.169951	0.508543	-1.121075	0.759112	0.36405	0.169385	1.293434	-0.156295	-0.430504	0.627495	-0.025897	0.348804	0.058852	-0.20583	0.781107	NA	0.365436	NA	0.234012	0.354904	0.420489	1.335616	0.208951	-1.878552	-0.34043	0.605688	0.015402	-0.371734
YLR278C	4.546331	0.210427	0.887377	-0.98741	0.647327	0.031115	0.597992	-0.287274	-0.331314	1.870876	NA	0.103066	0.390395	0.019801	-0.024959	-0.336494	0.227968	-0.371961	-0.179239	-0.470387	-0.333818	0.208024	0.542365	-0.44498	NA	-0.318346	0.943188	0.346009	0.929373	-0.594202	NA	-1.242858	-0.126114	-0.193271	0.785882

YLR287C	0.423683	0.053025	0.045332	0.214308	-0.97266	0.068729	0.438836	-0.427703	0.327442	0.531213	-0.037021	-0.535072	-0.346605	-0.09885	0.037503	0.43913	-0.004582	-0.080413	0.379425	0.384317	NA	-0.283455	1.070352	-0.1135	NA	-0.136253	-0.379816	0.149606	-0.327875	0.097429	-0.77898	-0.142274	-2.099005	-0.550597	0.459299
YMD8	0.826623	0.915749	-0.942011	0.159514	0.002521	0.204392	-0.763306	0.09409	0.129285	-1.224344	-0.454196	-0.259471	-0.071651	-0.118398	0.185255	0.16125	0.45234	-0.130413	-0.412239	-0.676306	NA	0.151161	0.17402	1.339547	NA	0.086223	-0.992938	0.385051	-0.534249	0.869994	0.072315	-0.109668	-0.648802	0.137538	0.350344
YME1	NA	0.137275	0.97104	-0.467471	-0.657967	-0.613143	1.08369	-1.352823	-0.640047	-3.847351	1.410659	1.603514	1.752326	-0.610619	-0.215182	-0.021049	0.204696	1.890921	-0.18078	1.660316	1.4401	-0.326652	1.478999	0.172146	NA	-0.779224	-0.238758	-0.096047	1.388127	-1.56721	NA	-3.131646	1.745258	0.219291	-1.017644
YML108W	NA	0.354316	0.614491	-0.387786	-0.183889	-0.328559	0.457257	-0.333242	0.632292	-0.555823	0.144829	-0.664176	NA	1.963274	-0.31563	0.06722	0.558468	0.113193	0.455285	-0.125235	NA	0.310501	NA	0.100924	NA	-0.225672	0.557916	0.862576	-0.48046	-0.033396	0.242891	0.208728	-0.021946	-0.098114	-0.262558
YML119W	NA	NA	0.022468	-0.38228	0.710875	-0.96614	0.055318	-0.330576	1.162304	0.354578	0.820893	-0.173681	0.179943	0.560304	0.309679	0.56896	0.782536	-0.148347	0.088207	0.095808	NA	-0.558441	-0.053259	-0.112718	NA	0.187364	0.510242	-0.239614	-0.762991	-0.403471	-1.65441	-0.15743	0.037974	-0.533269	-1.019785
YMR010W	NA	0.122125	-0.392922	-0.090158	0.3301	0.186841	-0.951095	-1.497262	0.31217	-1.276739	-0.075355	0.323423	-1.006521	-0.787152	-0.526192	0.024663	-0.389503	0.089145	0.008045	0.460604	NA	0.342025	1.74194	0.676585	NA	-0.013982	0.338144	0.730677	-0.029166	0.434346	-0.320137	-0.379245	-0.846652	-0.707478	0.669401
YMR102C	NA	0.582998	0.906127	0.119401	-0.05921	-0.214738	-1.052892	0.894878	0.355694	-0.320868	0.188362	-0.436977	0.821474	0.942239	0.110226	-0.290906	-0.252217	0.883251	-0.218387	-0.404657	0.98639	-0.895899	-0.797508	0.558208	NA	0.158795	0.268758	-0.062295	NA	NA	0.661612	-0.110288	-1.140292	0.857525	0.62112
YMR111C	NA	-1.572195	-3.500785	0.361685	-1.060794	0.505289	0.78086	1.08492	0.660161	-8.917024	-1.21215	-1.002475	-0.359845	NA	0.154167	-0.112199	0.135239	-0.257316	0.141985	0.142982	NA	0.472369	-0.667425	-0.873469	NA	0.509579	-1.605267	0.042111	NA	NA	1.785793	-3.397188	0.452699	0.079207	1.284144
YMR209C	NA	0.317484	-0.218228	-0.131177	0.15344	0.181174	0.177504	-0.419716	-0.194136	NA	0.064472	-0.046085	NA	0.195985	0.554165	0.39608	0.007754	-0.365723	0.010197	0.039901	-0.429681	0.989042	0.772925	0.405119	NA	-0.504872	-0.024756	0.132609	NA	NA	NA	0.089797	0.679427	-0.090428	NA
YND1	NA	1.246757	NA	-0.139116	NA	-0.577607	0.006087	0.401267	0.091238	1.790071	NA	-2.466329	NA	NA	0.41578	0.811195	-0.166662	-0.431137	-0.221556	-0.587618	-0.05355	0.04802	0.526031	0.771826	NA	0.479669	-0.381066	0.437392	-0.703934	0.149921	NA	-0.286256	-0.791579	-1.076667	NA
YNG1	NA	-1.598053	0.047119	0.600517	-1.199423	0.408384	NA	0.382878	NA	NA	-1.330132	-0.967624	0.391566	-1.624925	0.650856	0.195097	0.795801	-0.026125	0.184712	-0.570076	-0.242551	0.903924	NA	0.528954	-7.677917	0.291509	-1.095618	0.124266	0.213246	0.261219	-0.874454	-0.536256	-2.086436	0.29326	0.43275
YOR342C	-2.698132	-0.312834	-0.319564	0.550212	1.1494	-1.332323	-0.618865	-0.370225	0.569928	0.235722	0.308404	0.440493	0.140004	NA	0.338042	-0.076571	NA	-0.32572	0.344927	0.205685	0.093282	0.910502	0.242843	-0.313584	-1.6697	0.131126	0.20539	-0.838863	0.51296	-0.377352	-0.615749	-0.110238	0.509902	0.195073	0.234378
YOS9	NA	1.462847	-0.172632	-0.203594	0.505835	-0.624495	-0.6009	NA	-0.537919	0.927636	0.917781	0.516468	0.449447	1.179322	NA	-0.448891	-0.192077	0.727784	0.171221	-0.24663	NA	-1.199588	0.633646	0.243263	NA	-0.408452	0.246553	0.178829	0.421973	-0.328067	0.472163	0.68092	-0.845505	NA	-0.192411
YPL041C	NA	-0.668525	-0.271047	-0.262226	1.151177	-0.293889	0.585379	-0.275337	0.22744	-0.556327	0.064797	-0.460788	0.257595	1.063455	-0.055336	0.01891	-0.051092	0.01923	0.105936	0.287807	0.575047	0.087952	-0.90271	-0.347176	NA	-1.055342	0.987551	0.391472	3.32576	0.685676	0.396285	0.102803	-0.8589	0.483516	0.449867
YPL068C	NA	-0.871406	0.608532	-0.619695	-0.877327	-0.165164	0.234553	0.810174	0.370005	-0.737464	0.67759	0.121914	0.835805	1.928153	-0.019552	0.067327	-0.209981	-0.04175	-0.14845	0.489898	0.368359	0.761551	NA	-0.233278	-2.352721	0.443939	0.285171	-0.005246	1.199096	0.43963	-0.48449	0.328612	-0.962382	-0.357072	0.169309
YPL113C	NA	NA	0.756433	-0.079433	NA	0.335549	0.753574	-0.332434	1.226591	-2.801934	-1.676288	-0.329303	-0.893606	NA	0.476031	0.369497	-0.535438	-1.205993	0.77732	0.49281	0.119215	-0.550124	NA	1.444688	NA	-0.329731	-0.452774	0.995129	0.760244	-0.271813	NA	-0.363901	-0.160637	0.000132	0.903871
YPL150W	-0.812803	0.332159	-0.056021	-0.618203	NA	-0.045015	-0.468719	1.014601	-0.770644	-2.493011	1.658132	0.743207	0.223329	-0.312397	0.169718	-0.02597	-0.222088	0.564996	0.63457	0.439885	NA	-0.124761	NA	0.497425	-4.608281	-0.417109	0.879327	-0.799191	-0.658094	-0.258776	1.267421	-0.375822	-1.557988	-0.455082	-0.59482
YPR022C	NA	-0.775601	-0.133654	0.237092	0.8934	0.117735	-0.661155	0.040233	-0.494165	0.273527	0.150636	-0.361996	-0.580182	NA	0.103925	-0.077916	-0.473953	-0.297422	0.024595	0.297304	1.179036	0.523241	0.450913	0.3165	NA	-0.417123	0.69635	-0.494798	0.350322	0.502181	1.170228	0.089805	-1.850911	0.213234	1.611548
YPR063C	NA	-0.936702	0.361363	-1.556101	1.012143	-0.561313	-0.33025	-0.485738	0.371171	NA	0.555139	1.086906	0.070851	-0.478136	-0.216633	-0.18766	-0.676805	0.641982	-0.396789	-0.216814	-0.246287	-0.790661	NA	1.047829	NA	-0.254671	-1.373758	-0.14934	NA	-0.070036	0.408982	0.422744	-1.624748	-0.125479	-0.052874
YPR174C	NA	0.512573	0.460092	0.143892	-0.368652	0.18521	0.673169	-1.55863	0.84648	0.866291	-0.663746	-2.100232	-0.196524	-1.454981	0.35199	-0.30664	0.322919	-0.737534	-0.116664	0.43701	NA	0.573212	NA	0.525593	NA	1.011891	NA	-0.297914	1.652309	0.259894	-1.529675	-0.100667	-3.04053	-0.35882	0.078819
YPT31	NA	-1.32883	-2.087254	-0.264131	-0.596651	-0.07566	0.525964	-0.002231	0.371125	-1.579864	0.245796	0.026757	0.644431	-0.263724	1.098064	0.253328	0.166248	NA	-0.455595	-0.074289	0.712329	0.083576	NA	-0.55866	NA	-0.334333	-0.276915	-0.166789	-1.164299	-0.061785	NA	-0.077495	-0.35261	0.036169	-0.491522
YPT6	NA	-0.951858	-13.923406	0.543664	-0.329314	0.766095	-0.180938	-0.33117	-0.127613	-0.108054	1.15791	-0.215044	0.729636	NA	-0.032584	-0.028124	1.099139	1.015051	-0.386884	0.446096	1.435165	-1.922774	NA	-1.586809	NA	-0.73711	0.290375	0.11671	0.150297	-0.09036	NA	-2.243679	0.004924	0.142068	0.696182
YPT7	-3.93071	-2.687165	-4.001849	-0.115076	-1.17759	1.344934	0.181057	-2.514805	1.088524	NA	-0.912643	-1.22243	0.013522	NA	1.489843	0.571358	-0.077771	0.368082	-0.146704	-0.337193	NA	0.645912	0.664697	0.739784	NA	0.569326	-2.468563	0.100189	-0.565367	1.620053	-2.625131	0.826057	-0.86448	-0.106663	0.18678
YSN1	NA	0.108744	NA	0.051055	-0.344174	-0.619959	-0.556749	0.075112	-1.446701	NA	0.093105	0.247748	-0.304497	-0.556079	0.085462	0.101084	0.536143	0.179542	-0.043509	0.56113	NA	-1.826371	-1.053164	-0.217294	NA	0.715859	0.259397	0.144331	1.090166	-0.053784	-0.229005	0.639542	-1.932388	0.263222	-1.398254
YSY6	-1.529364	-0.430477	0.383756	-0.577921	-1.711452	-0.166305	0.859723	-0.220286	-0.460775	-2.838974	NA	-0.428928	0.067768	-3.596878	-0.331355	-0.441841	-0.686191	0.616527	0.435543	1.19497	-0.393209	-0.120729	-0.634615	0.550394	NA	0.226147	-0.422296	0.071714	NA	0.316645	-0.900214	-1.051283	0.048521	0.458769	0.379208
YTA7	NA	-1.389583	NA	-0.789092	-2.16759	0.340274	0.821038	1.350186	-0.400387	4.527531	NA	-1.280633	0.228921	0.371121	1.704155	1.25634	-1.037244	0.924977	-2.066689	0.680106	-2.074183	-1.629274	0.607813	NA	NA	0.596336	-7.255049	-0.284431	-0.88498	-0.112832	NA	NA	NA	-0.195914	0.259384
YUR1	-1.008497	NA	0.875735	-0.218862	0.383034	-0.032265	0.621322	0.247638	1.532102	-0.022186	-1.251904	NA	-0.261837	-1.356455	0.680362	0.999841	-0.242535	-0.000923	0.087807	-1.060049	0.466346	0.647631	NA	0.267083	NA	NA	-0.112186	0.378883	-0.015667	-0.174031	-0.066469	-0.646939	-0.001029	-0.992032	0.629737
ZDS1	NA	-0.901944	-1.540129	0.707755	-0.1343	-0.179711	-0.3095	0.686361	-0.422024	-0.384471	0.577993	1.037444	NA	NA	0.156515	0.083887	0.484658	-0.373972	-0.299684	-1.34981	-0.505898	0.464019	0.202775	-1.516045	NA	-0.570911	2.679638	0.798976	NA	NA	1.080514	-0.808451	-1.721838	-0.852103	NA

Table 2.2: All quantified phosphopeptides

Protein				log2 Ratio				T-test				Normalized abundance														
				mutant vs WT				mutant vs WT				wt			rad53			mec1-100-tel1			mec1-100-tel1-pph3					
SwissProt	SGD	Sequence	Variable modifications ([position] description)	rad53 vs. WT	tel1 mec1-100 vs. WT	pph3 vs. WT	rad53 vs. tel1 mec1-100	rad53 vs. WT	tel1 mec1-100 vs. WT	pph3 vs. WT	rad53 vs. tel1 mec1-100	131114_1981-1_3uL	131114_1981-2_3uL	131114_1981-3_3uL	131115_7373-1_3uL	131115_7373-2_3uL	131115_7373-3_3uL	131116_6913-1_3uL	131116_6913-2_3uL	131116_6913-3_3uL	131115_7734-1_3uL	131115_7734-2_3uL	131115_7734-3_3uL	m/z	Charge	Best peptide match/ Score
DNM1	YLL001W	CGTRYLAK	[3] Phospho (ST)	0.25	-0.53	-0.28	0.78	0.331	0.239	0.378	0.03	1.09E+07	3.42E+06	4.35E+06	9.23E+06	6.01E+06	6.97E+06	3.76E+06	5.69E+06	3.46E+06	9.62E+06	3.38E+06	2.40E+06	524.73767	2	15.41
GLK1	YCL040W	SFDDLHK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.17	-0.06	0.08	0.23	0.227	0.371	0.316	0.15	1.94E+06	1.67E+06	2.30E+06	2.23E+06	1.80E+06	2.61E+06	1.80E+06	1.73E+06	2.14E+06	2.24E+06	1.87E+06	2.12E+06	492.19739	2	15.54
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALRK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.95	-0.63	-0.06	-0.31	0.067	0.117	0.437	0.22	3.52E+07	2.10E+07	1.64E+07	1.59E+07	1.44E+07	7.39E+06	1.69E+07	1.91E+07	1.09E+07	2.64E+07	2.40E+07	1.92E+07	1037.7628	3	68.66
ZEO1	YOL109W	NEATPEAEQVK	[4] Phospho (ST)	0.38	0.12	-0.04	0.26	0.097	0.357	0.443	0.12	2.55E+06	1.37E+06	2.31E+06	2.85E+06	2.34E+06	2.92E+06	2.24E+06	1.78E+06	2.74E+06	2.21E+06	1.64E+06	2.18E+06	648.27901	2	45.12
ZEO1	YOL109W	EQAEASIDNLK	[6] Phospho (ST)	0.09	0.30	0.45	-0.21	0.348	0.097	0.029	0.10	2.97E+06	1.95E+06	2.96E+06	3.03E+06	2.36E+06	2.99E+06	3.01E+06	3.06E+06	3.65E+06	3.78E+06	3.33E+06	3.62E+06	649.28746	2	46.67
RPS6A	YPL090C	RASSLKA	[3] Phospho (ST)|[4] Phospho (ST)	-0.70	-1.12	-0.74	0.41	0.233	0.157	0.237	0.14	3.90E+06	6.42E+05	1.65E+06	1.68E+06	8.60E+05	1.26E+06	8.11E+05	1.11E+06	9.40E+05	2.05E+06	8.92E+05	7.68E+05	446.68765	2	17.05
GLY1	YEL046C	SESTEVDVDGNAIR	[3] Phospho (ST)	-0.17	0.02	0.02	-0.20	0.142	0.394	0.434	0.11	3.57E+06	3.26E+06	3.83E+06	3.31E+06	2.61E+06	3.54E+06	3.54E+06	3.42E+06	3.88E+06	3.86E+06	3.41E+06	3.50E+06	786.3335	2	73.75
NEW1	YPL226W	GTPKPVDTDDEED	[8] Phospho (ST)	0.02	-0.19	0.21	0.21	0.481	0.298	0.264	0.22	2.20E+06	1.27E+06	2.49E+06	2.42E+06	1.61E+06	2.00E+06	1.59E+06	1.47E+06	2.16E+06	2.59E+06	1.76E+06	2.56E+06	749.28539	2	34.7
ZUO1	YGR285C	NHTWSEFER	[3] Phospho (ST)	-0.14	-0.06	-0.16	-0.08	0.222	0.360	0.277	0.11	2.45E+06	3.53E+06	2.96E+06	2.59E+06	2.68E+06	2.86E+06	2.99E+06	2.79E+06	2.80E+06	1.93E+06	3.04E+06	3.04E+06	643.25363	2	27.7
GPD1	YDL022W	RSSSSVSLK	[4] Phospho (ST)|[7] Phospho (ST)	-0.51	-0.83	-0.23	0.33	0.261	0.182	0.398	0.20	2.61E+06	5.05E+05	1.35E+06	1.33E+06	8.73E+05	9.38E+05	5.37E+05	1.15E+06	8.17E+05	2.30E+06	7.54E+05	7.52E+05	555.7332	2	23.55
FEN1	YCR034W	NVPTPSPSPKPQHR	[4] Phospho (ST)|[8] Phospho (ST)	-0.32	-0.42	-0.20	0.11	0.068	0.033	0.166	0.25	1.79E+06	1.33E+06	1.51E+06	1.38E+06	1.07E+06	1.27E+06	1.20E+06	1.00E+06	1.26E+06	1.52E+06	1.10E+06	1.40E+06	567.92226	3	21.67
SUR7	YML052W	SHERPDDVSV	[9] Phospho (ST)	0.06	-0.02	-0.20	0.08	0.225	0.425	0.024	0.22	1.20E+06	1.15E+06	1.29E+06	1.33E+06	1.18E+06	1.30E+06	1.19E+06	1.09E+06	1.32E+06	1.11E+06	9.87E+05	1.08E+06	610.75076	2	43.73
YLR419W	YLR419W	IPTVVKYPFVLFTTSQVTNKLYLR	[3] Phospho (ST)|[18] Phospho (ST)|[22] Phos	0.30	0.20	0.31	0.09	0.035	0.179	0.040	0.29	3.40E+06	2.98E+06	3.96E+06	4.49E+06	3.97E+06	4.24E+06	4.80E+06	3.43E+06	3.69E+06	4.60E+06	3.89E+06	4.30E+06	767.63119	4	20.27
LEU1	YGL009C	VEVTSEDEK	[5] Phospho (ST)	-0.15	-1.84	-0.23	1.70	0.421	0.086	0.391	0.01	1.61E+06	4.55E+05	5.47E+05	1.08E+06	6.06E+05	6.77E+05	3.81E+05	2.05E+05	1.42E+05	1.17E+06	4.61E+05	6.02E+05	558.229	2	29.28
ERB1	YMR049C	RAASEESDVEEDEDK	[7] Phospho (ST)	0.40	-0.05	0.36	0.45	0.051	0.431	0.100	0.02	1.22E+06	9.81E+05	1.57E+06	1.83E+06	1.55E+06	1.60E+06	1.13E+06	1.06E+06	1.47E+06	1.82E+06	1.31E+06	1.70E+06	894.84422	2	89.36
YDR365W-B	R365W-B	SPSIDASPPENNSSHNIVPIK	[3] Phospho (ST)	-0.99	-0.24	-0.27	-0.75	0.000	0.022	0.051	0.00	4.12E+06	4.62E+06	4.67E+06	2.28E+06	2.11E+06	2.36E+06	3.77E+06	4.07E+06	3.51E+06	3.08E+06	4.13E+06	3.90E+06	761.69452	3	47.66
YJR030C	YJR030C	YMDTPTLKNIR	[1] Phospho (Y)	0.08	-0.12	0.10	0.20	0.354	0.375	0.359	0.31	1.58E+06	1.53E+06	1.89E+06	1.65E+06	1.47E+06	2.15E+06	2.24E+06	1.05E+06	1.31E+06	1.25E+06	1.88E+06	2.22E+06	716.33434	2	26.09
SSK22	YCR073C	YLFFLLNLK	[1] Phospho (Y)	0.09	0.13	0.64	-0.04	0.432	0.432	0.175	0.47	2.49E+05	6.18E+05	9.71E+05	6.31E+05	6.20E+05	7.03E+05	1.05E+06	2.63E+05	6.91E+05	5.65E+05	8.86E+05	1.41E+06	625.8334	2	15.22
LYS20	YDL182W	NFHAEVSTPQVLSAK	[8] Phospho (ST)	0.32	0.32	0.08	0.00	0.062	0.102	0.386	0.50	8.45E+05	1.32E+06	1.16E+06	1.45E+06	1.34E+06	1.37E+06	1.60E+06	1.19E+06	1.36E+06	8.80E+05	1.32E+06	1.31E+06	569.94219	3	42.96
PFK2	YMR205C	VHSYTDLAYR	[3] Phospho (ST)	-0.31	0.04	-0.12	-0.35	0.196	0.460	0.372	0.17	7.28E+05	1.32E+06	7.87E+05	7.42E+05	7.42E+05	8.06E+05	1.36E+06	7.56E+05	8.10E+05	6.93E+05	9.82E+05	9.44E+05	652.78748	2	41.09
PFK2	YMR205C	NAVSTKPTPPPAPEASAESGLSSK	[23] Phospho (ST)	0.29	0.06	0.20	0.22	0.025	0.154	0.033	0.04	2.24E+06	2.10E+06	2.02E+06	2.86E+06	2.57E+06	2.32E+06	2.31E+06	2.14E+06	2.19E+06	2.22E+06	2.57E+06	2.50E+06	801.72062	3	28.73
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALR	[N-term] Acetyl (Protein N-term)|[6] Phospho	-0.16	0.12	-0.08	-0.28	0.373	0.351	0.437	0.26	3.80E+06	4.56E+06	6.76E+06	3.45E+06	7.02E+06	3.03E+06	4.78E+06	6.57E+06	5.06E+06	3.95E+06	7.18E+06	3.22E+06	995.06523	3	55.27
ZEO1	YOL109W	LEETKESLQNK	[7] Phospho (ST)	0.14	-0.34	0.06	0.48	0.192	0.054	0.376	0.02	6.16E+05	4.87E+05	6.12E+05	7.05E+05	5.67E+05	6.15E+05	4.26E+05	3.95E+05	5.30E+05	7.17E+05	5.59E+05	5.15E+05	699.82947	2	64.66
LHP1	YDL051W	SEKPQQEEQEKPQSR	[N-term] Acetyl (Protein N-term)|[14] Phosph	-0.25	-0.81	-0.33	0.56	0.324	0.126	0.286	0.04	1.72E+06	6.12E+05	8.76E+05	9.54E+05	7.26E+05	1.02E+06	5.37E+05	5.24E+05	7.67E+05	1.08E+06	6.38E+05	8.22E+05	650.62485	3	36.71
PMA1	YGL008C	SVEDFMAAMQRVSTQHEK	[13] Phospho (ST)|[14] Phospho (ST)	-0.89	-0.40	-0.13	-0.49	0.066	0.197	0.348	0.26	3.60E+06	3.79E+06	2.52E+06	1.78E+06	3.00E+06	5.76E+05	2.21E+06	3.91E+06	1.39E+06	2.54E+06	4.11E+06	2.41E+06	751.97523	3	17.94
YPR137C-B	R137C-B	HSDSYSENETNHTNVPISSTGGTNNK	[6] Phospho (ST)	-0.74	-0.38	0.11	-0.36	0.009	0.046	0.308	0.03	3.34E+06	2.40E+06	2.85E+06	1.95E+06	1.55E+06	1.64E+06	2.44E+06	2.16E+06	1.99E+06	3.48E+06	2.43E+06	3.38E+06	957.40067	3	56.53
ACC1	YNR016C	AVSVSDLSYVANSQSSPLR	[3] Phospho (ST)	-0.04	0.28	0.39	-0.32	0.445	0.159	0.080	0.09	2.83E+06	3.77E+06	2.29E+06	2.61E+06	3.43E+06	2.64E+06	3.90E+06	3.99E+06	2.91E+06	3.55E+06	4.51E+06	3.60E+06	1030.4893	2	122.67
SOD1	YJR104C	FEQASESEPTTVSYEIAGNSPNAER	[20] Phospho (ST)	0.44	0.44	0.35	0.00	0.014	0.014	0.027	0.50	2.16E+06	1.86E+06	1.77E+06	2.56E+06	2.93E+06	2.36E+06	2.46E+06	2.95E+06	2.44E+06	2.41E+06	2.73E+06	2.21E+06	931.73526	3	71.92
ACC1	YNR016C	AVSVSDLSYVANSQSSPLR	[9] Phospho (Y)	-0.02	0.32	0.30	-0.34	0.474	0.116	0.142	0.08	1.46E+06	2.08E+06	1.30E+06	1.34E+06	1.95E+06	1.48E+06	2.16E+06	2.20E+06	1.69E+06	1.69E+06	2.30E+06	1.94E+06	687.32926	3	53.31
LTE1	YAL024C	NIVNNTDSPTLK	[10] Phospho (ST)	0.60	0.50	0.43	0.10	0.002	0.009	0.009	0.19	7.43E+05	6.54E+05	8.08E+05	1.11E+06	1.05E+06	1.19E+06	9.24E+05	1.05E+06	1.15E+06	1.08E+06	9.28E+05	9.52E+05	698.33131	2	35.99
LEU1	YGL009C	DQDQSSPKVEVTSEDEK	[5] Phospho (ST)|[13] Phospho (ST)	0.28	0.00	-0.01	0.27	0.192	0.494	0.482	0.18	2.37E+06	1.33E+06	1.94E+06	2.82E+06	1.96E+06	2.05E+06	1.37E+06	2.18E+06	2.10E+06	2.30E+06	1.47E+06	1.81E+06	1040.9039	2	15.01
PWP1	YLR196W	ATLEEAEGESGVEDDAATGSSNK	[10] Phospho (ST)	0.44	0.00	0.39	0.44	0.011	0.495	0.022	0.01	2.31E+06	1.78E+06	2.09E+06	3.02E+06	2.78E+06	2.58E+06	1.85E+06	2.13E+06	2.19E+06	2.94E+06	2.40E+06	2.77E+06	1173.9769	2	79.14
PIL1	YGR086C	TYSLR	[3] Phospho (ST)	0.95	1.11	0.90	-0.16	0.046	0.025	0.068	0.05	2.50E+04	1.03E+05	1.63E+05	1.99E+05	1.71E+05	1.92E+05	1.99E+05	2.20E+05	2.09E+05	2.23E+05	1.63E+05	1.57E+05	360.15988	2	15.9
LYS21	YDL131W	DFHAELSTPLLKPVNK	[8] Phospho (ST)	-0.41	0.15	0.07	-0.56	0.112	0.356	0.423	0.10	8.33E+05	1.30E+06	8.20E+05	7.42E+05	8.47E+05	6.35E+05	1.54E+06	8.50E+05	8.90E+05	7.13E+05	1.37E+06	1.02E+06	630.324	3	29.8
GPD2	YOL059W	SDSAVSIVHLK	[6] Phospho (ST)	-0.31	-0.10	-0.32	-0.21	0.133	0.370	0.137	0.18	5.23E+05	8.76E+05	7.22E+05	5.73E+05	5.32E+05	6.10E+05	8.22E+05	6.13E+05	5.47E+05	4.94E+05	6.34E+05	5.75E+05	618.30589	2	60.67
MCK1	YNL307C	KLEHNQPSISYICSR	[11] Phospho (Y)	0.15	0.12	0.15	0.03	0.130	0.144	0.180	0.38	1.22E+06	1.23E+06	1.47E+06	1.49E+06	1.31E+06	1.53E+06	1.38E+06	1.38E+06	1.50E+06	1.38E+06	1.30E+06	1.65E+06	637.96466	3	64.2
SSK2	YNR031C	YKIEDHNYLLKQLK	[1] Phospho (Y)	-1.38	-1.62	-0.40	0.24	0.066	0.053	0.258	0.18	3.67E+06	1.32E+06	1.75E+06	9.83E+05	6.43E+05	9.63E+05	6.48E+05	6.92E+05	8.49E+05	1.71E+06	1.23E+06	2.15E+06	942.98703	2	15
YDR365W-B	R365W-B	MESQQLSQHSPISHGSACASVTSK	[N-term] Acetyl (Protein N-term)|[7] Phospho	-0.51	0.38	1.11	-0.89	0.100	0.091	0.001	0.04	1.23E+06	1.05E+06	1.02E+06	8.14E+05	1.10E+06	3.96E+05	1.76E+06	1.44E+06	1.09E+06	2.23E+06	2.16E+06	2.74E+06	893.72431	3	28.51
CDC37	YDR168W	IELSDDSDVEVHPNVDKK	[4] Phospho (ST)|[7] Phospho (ST)	-0.41	0.04	-0.19	-0.45	0.003	0.358	0.041	0.01	9.38E+05	8.69E+05	1.01E+06	7.05E+05	7.37E+05	6.87E+05	8.80E+05	1.09E+06	9.37E+05	8.78E+05	7.86E+05	8.12E+05	733.64717	3	24.16
LEU1	YGL009C	DQDQSSPKVEVTSEDEK	[6] Phospho (ST)|[13] Phospho (ST)	0.29	0.05	-0.01	0.24	0.211	0.446	0.488	0.24	9.25E+05	4.96E+05	7.83E+05	1.16E+06	7.58E+05	7.75E+05	5.28E+05	9.02E+05	8.49E+05	9.65E+05	5.60E+05	6.62E+05	694.27179	3	40.61
ZEO1	YOL109W	LEETKESLQNK	[7] Phospho (ST)	0.26	-0.23	0.09	0.49	0.087	0.129	0.329	0.02	1.95E+05	1.63E+05	2.15E+05	2.64E+05	2.10E+05	2.14E+05	1.61E+05	1.37E+05	1.90E+05	2.46E+05	1.91E+05	1.74E+05	466.88874	3	17.21
FEN1	YCR034W	NVPTPSPSPKPQHR	[4] Phospho (ST)|[6] Phospho (ST)	-0.68	-1.42	-0.95	0.74	0.009	0.001	0.003	0.02	1.40E+06	1.16E+06	1.16E+06	9.46E+05	7.13E+05	6.69E+05	5.04E+05	3.53E+05	5.39E+05	7.78E+05	5.40E+05	6.08E+05	851.37979	2	17.01
LYS20	YDL182W	NFHAEVSTPQVLSAK	[8] Phospho (ST)	0.17	0.18	-0.24	-0.01	0.301	0.315	0.305	0.48	6.89E+05	1.50E+06	1.08E+06	1.16E+06	1.28E+06	1.24E+06	1.48E+06	9.84E+05	1.24E+06	5.49E+05	1.10E+06	1.13E+06	854.40973	2	41.83
ESF2	YNR054C	KVEDIESENESDIEEEQKQEEK	[7] Phospho (ST)|[11] Phospho (ST)	-0.32	-0.27	-0.04	-0.05	0.171	0.249	0.450	0.43	1.38E+06	7.73E+05	9.72E+05	9.07E+05	9.04E+05	6.93E+05	6.01E+05	1.13E+06	8.62E+05	1.26E+06	8.10E+05	9.60E+05	942.05002	3	46.53
PAN1	YIR006C	TGFGNNEIYTK	[1] Phospho (ST)	-0.31	-0.07	-0.16	-0.24	0.023	0.314	0.098	0.10	4.76E+05	4.32E+05	4.92E+05	3.98E+05	3.25E+05	4.06E+05	3.83E+05	4.46E+05	5.07E+05	4.70E+05	3.84E+05	3.94E+05	662.2849	2	52.89
TDH3	YGR192C	TASGNIIPSSTGAAK	[1] Phospho (ST)	-0.32	0.23	0.05	-0.55	0.056	0.096	0.371	0.01	8.18E+05	1.08E+06	1.04E+06	7.35E+05	7.32E+05	8.85E+05	1.20E+06	1.23E+06	1.01E+06	1.10E+06	9.78E+05	9.50E+05	727.84852	2	66.35
YDR365W-B	R365W-B	AHNVSTSNNSPSTDNDSISK	[10] Phospho (ST)	-0.12	-0.49	-0.05	0.37	0.335	0.082	0.431	0.06	7.64E+05	4.70E+05	5.28E+05	6.32E+05	5.11E+05	4.79E+05	3.71E+05	3.76E+05	5.04E+05	7.17E+05	5.05E+05	4.75E+05	718.96953	3	41.88
BCY1	YIL033C	RTSVSGETLQPNNFDDWTPDHYK	[3] Phospho (ST)	-0.29	0.19	0.07	-0.48	0.140	0.231	0.388	0.02	1.51E+06	1.77E+06	1.08E+06	1.22E+06	1.26E+06	1.10E+06	1.93E+06	1.67E+06	1.39E+06	1.26E+06	1.78E+06	1.55E+06	929.74017	3	57.05
YOL103W-B	L103W-B	AVSPTDSTPPSTHTEDSK	[3] Phospho (ST)	-0.21	0.06	0.21	-0.27	0.140	0.401	0.116	0.14	5.71E+05	6.10E+05	7.64E+05	6.04E+05	4.87E+05	5.92E+05	7.52E+05	5.09E+05	7.66E+05	7.36E+05	6.85E+05	8.35E+05	646.27713	3	35.96
SPN1	YPR133C	HISTDFSDDDLEK	[7] Phospho (ST)	-0.13	-0.15	-0.07	0.02	0.079	0.043	0.185	0.31	8.81E+05	8.33E+05	9.62E+05	7.94E+05	7.93E+05	8.60E+05	8.24E+05	7.94E+05	7.90E+05	8.72E+05	8.36E+05	8.49E+05	801.32331	2	62.77
SAS10	YDL153C	DYGSEDEAVSR	[4] Phospho (ST)	0.23	-0.10	0.20	0.34	0.176	0.348	0.254	0.08	4.12E+05	2.79E+05	4.44E+05	5.14E+05	3.85E+05	4.35E+05	2.80E+05	3.70E+05	4.06E+05	5.50E+05	3.54E+05	4.01E+05	654.24311	2	56.38
VBA4	YDR119W	IDDSPQDEVNSIK	[11] Phospho (ST)	-0.17	-0.11	-0.03	-0.06	0.211	0.301	0.433	0.39	6.70E+05	5.79E+05	8.06E+05	6.15E+05	5.11E+05	6.99E+05	5.63E+05	5.76E+05	7.61E+05	6.86E+05	5.89E+05	7.37E+05	770.33318	2	54.74
SUR7	YML052W	SHERPDDVSV	[1] Phospho (ST)|[9] Phospho (ST)	0.20	0.16	0.16	0.04	0.217	0.330	0.298	0.44	5.05E+05	2.80E+05	4.51E+05	5.09E+05	4.61E+05	4.49E+05	3.20E+05	5.89E+05	4.73E+05	5.43E+05	3.91E+05	4.42E+05	650.73386	2	22.9
PWP2	YCR057C	RPSDDDDNESEDDDKQEEVDISK	[10] Phospho (ST)	0.14	-0.07	0.16	0.21	0.235	0.353	0.216	0.05	1.18E+06	7.95E+05	1.01E+06	1.20E+06	9.62E+05	1.13E+06	9.51E+05	9.41E+05	9.52E+05	1.24E+06	9.59E+05	1.14E+06	920.69375	3	68.81
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALRK	[N-term] Acetyl (Protein N-term)|[6] Phospho	-1.05	-0.80	-0.19	-0.25	0.075	0.101	0.337	0.30	2.77E+06	1.57E+06	1.17E+06	1.07E+06	1.16E+06	4.27E+05	1.15E+06	1.31E+06	6.93E+05	1.78E+06	1.60E+06	1.46E+06	778.57387	4	59.94
LSB3	R024C-A	FTAPTSPSTSSPK	[8] Phospho (ST)	-0.07	0.18	0.11	-0.24	0.393	0.178	0.320	0.18	3.85E+05	3.59E+05	4.58E+05	3.56E+05	3.08E+05	4.85E+05	5.11E+05	3.74E+05	4.75E+05	3.75E+05	3.75E+05	5.51E+05	694.31094	2	49.51
LHP1	YDL051W	SEKPQQEEQEKPQSR	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.24	-1.00	-0.47	0.76	0.334	0.102	0.230	0.01	1.54E+06	5.66E+05	7.06E+05	8.14E+05	6.77E+05	8.88E+05	4.04E+05	4.11E+05	5.88E+05	8.33E+05	5.25E+05	6.76E+05	975.43366	2	36.02
YDR365W-B	R365W-B	AVSPTDSTPPSTHTEDSK	[3] Phospho (ST)	-0.22	0.01	0.27	-0.23	0.162	0.484	0.121	0.20	7.36E+05	9.02E+05	1.11E+06	7.80E+05	7.30E+05	8.52E+05	1.10E+06	6.50E+05	1.02E+06	9.95E+05	1.04E+06	1.29E+06	968.91262	2	68.46
DCP2	YNL118C	NPISSTVSSNQQSPK	[13] Phospho (ST)	-0.02	-0.19	-0.13	0.17	0.423	0.134	0.222	0.09	6.46E+05	5.12E+05	6.11E+05	5.81E+05	5.79E+05	5.84E+05	4.34E+05	5.46E+05	5.67E+05	5.90E+05	4.44E+05	5.77E+05	827.37804	2	50.81
KRI1	YNL308C	EVSPESFGLTAR	[3] Phospho (ST)	0.17	0.11	0.12	0.06	0.248	0.335	0.330	0.34	4.48E+05	7.43E+05	5.48E+05	5.82E+05	7.39E+05	6.38E+05	7.15E+05	6.02E+05	5.58E+05	5.07E+05	7.13E+05	6.71E+05	686.81144	2	58.21
CDC3	YLR314C	EEQVSIKQDPEQEER	[5] Phospho (ST)	-0.03	-0.16	-0.21	0.13	0.444	0.262	0.243	0.26	4.21E+05	3.46E+05	5.31E+05	4.60E+05	3.48E+05	4.60E+05	3.50E+05	3.55E+05	4.58E+05	3.28E+05	3.10E+05	4.82E+05	641.94941	3	40.92
SEC31	YDL195W	VPSLVATSESPR	[3] Phospho (ST)	-0.09	0.07	-0.22	-0.15	0.319	0.359	0.169	0.16	6.02E+05	8.10E+05	8.32E+05	6.40E+05	6.80E+05	7.93E+05	7.88E+05	6.91E+05	8.69E+05	5.20E+05	6.50E+05	7.51E+05	661.82167	2	45.74
HTA2	YBL003C	TAKASQEL	[5] Phospho (ST)	3.34	-0.63	1.29	3.97	0.002	0.153	0.050	0.00	7.89E+04	2.49E+04	5.56E+04	6.85E+05	4.65E+05	4.61E+05	2.68E+04	3.95E+04	3.63E+04	1.95E+05	9.44E+04	1.00E+05	464.2128	2	28.54
NET1	YJL076W	IVSNNSDDEDEDIGER	[6] Phospho (ST)	0.37	0.02	0.14	0.35	0.111	0.466	0.295	0.11	8.40E+05	5.15E+05	8.25E+05	8.95E+05	7.89E+05	1.14E+06	6.32E+05	6.64E+05	9.21E+05	9.28E+05	6.97E+05	7.75E+05	943.86858	2	76.88
RCK2	YLR248W	DVSQITSSPKK	[8] Phospho (ST)	0.52	0.68	0.85	-0.16	0.059	0.052	0.010	0.26	1.07E+05	1.53E+05	2.13E+05	2.14E+05	2.07E+05	2.59E+05	2.83E+05	1.86E+05	2.89E+05	2.77E+05	2.66E+05	3.08E+05	635.30827	2	36.74
NOP8	YOL144W	LIEDSDNDIDHAK	[5] Phospho (ST)	0.34	-0.08	0.14	0.43	0.043	0.358	0.270	0.02	4.05E+05	3.69E+05	5.22E+05	5.70E+05	5.03E+05	5.70E+05	3.94E+05	3.44E+05	4.85E+05	4.50E+05	4.10E+05	5.68E+05	782.83057	2	59.54
RRP15	YPR143W	IIDNEQSDAEEDDDEEEEDDDFPRK	[7] Phospho (ST)	-0.15	-0.23	-0.02	0.08	0.033	0.006	0.448	0.07	1.83E+06	1.64E+06	1.74E+06	1.65E+06	1.53E+06	1.52E+06	1.43E+06	1.49E+06	1.50E+06	1.96E+06	1.55E+06	1.64E+06	1026.39	3	90.85
SAM3	YPL274W	IETESTTIPNDSDR	[5] Phospho (ST)	-0.39	-0.16	-0.22	-0.24	0.048	0.198	0.111	0.12	5.96E+05	5.94E+05	7.59E+05	4.96E+05	4.16E+05	5.74E+05	5.74E+05	5.13E+05	6.62E+05	5.88E+05	4.87E+05	5.93E+05	829.35235	2	63.58
TRP3	YKL211C	SVHAATNPINK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.76	1.05	1.22	-0.30	0.026	0.003	0.008	0.13	1.40E+05	1.75E+05	1.90E+05	3.01E+05	2.08E+05	3.43E+05	3.59E+05	2.93E+05	3.96E+05	3.30E+05	3.50E+05	5.00E+05	637.3007	2	33
ENP2	YGR145W	ALTAAEESDEER	[8] Phospho (ST)	0.62	0.02	0.12	0.60	0.027	0.473	0.308	0.03	3.45E+05	2.31E+05	3.84E+05	5.01E+05	4.12E+05	5.67E+05	2.42E+05	3.16E+05	4.17E+05	3.31E+05	3.23E+05	3.87E+05	700.78291	2	38.6
YRB1	YDR002W	KEGDDAPESPDIHFEPVVHLEK	[9] Phospho (ST)	1.34	0.63	0.92	0.70	0.000	0.092	0.003	0.02	2.27E+05	3.74E+05	3.55E+05	7.60E+05	8.36E+05	8.17E+05	6.91E+05	3.91E+05	4.00E+05	5.46E+05	6.43E+05	6.23E+05	642.79738	4	43.23
CAB3	YKL088W	SIHDESNFER	[1] Phospho (ST)	-0.14	-0.14	-0.05	0.00	0.135	0.153	0.280	0.49	2.94E+05	2.48E+05	2.87E+05	2.41E+05	2.35E+05	2.78E+05	2.59E+05	2.19E+05	2.74E+05	2.73E+05	2.61E+05	2.68E+05	657.26144	2	35.6
PSR1	YLL010C	GDAVKDTSR	[8] Phospho (ST)	-0.94	-0.02	-0.09	-0.93	0.113	0.489	0.440	0.02	1.41E+06	5.24E+05	6.23E+05	5.37E+05	3.40E+05	4.54E+05	8.10E+05	6.67E+05	1.06E+06	1.16E+06	6.63E+05	5.75E+05	514.72757	2	20.7
CRP1	YHR146W	RESTEGVLDGSK	[3] Phospho (ST)	0.09	0.03	0.29	0.06	0.239	0.439	0.050	0.37	2.74E+05	2.39E+05	3.05E+05	3.08E+05	2.70E+05	2.92E+05	2.74E+05	2.29E+05	3.33E+05	3.03E+05	3.23E+05	3.73E+05	679.30332	2	55.72
YPR137C-B	R137C-B	TVPQISDQETEK	[6] Phospho (ST)	-0.62	-0.02	0.38	-0.61	0.003	0.458	0.029	0.02	6.09E+05	5.23E+05	6.25E+05	3.86E+05	3.36E+05	4.17E+05	4.66E+05	6.21E+05	6.49E+05	8.60E+05	6.58E+05	7.61E+05	727.82472	2	56.28
ARG81	YML099C	SSIPEKYK	[7] Phospho (Y)	0.38	0.02	0.24	0.36	0.121	0.481	0.196	0.21	1.52E+05	1.53E+05	2.08E+05	1.89E+05	1.90E+05	2.88E+05	2.55E+05	1.06E+05	1.60E+05	1.61E+05	1.94E+05	2.49E+05	516.2415	2	26.2

BBC1	YJL020C	TAEVSHDIENSSQNTTGNVLPVSSPQTR	[24] Phospho (ST)	-0.09	0.07	-0.11	-0.16	0.351	0.337	0.276	0.23	1.11E+06	9.22E+05	8.27E+05	1.11E+06	8.07E+05	7.80E+05	9.64E+05	1.14E+06	9.07E+05	1.01E+06	7.99E+05	8.52E+05	1016.7995	3	48.31
GPD1	YDL022W	RSSSSVSLK	[4] Phospho (ST)	-0.11	-0.34	-0.13	0.23	0.414	0.266	0.412	0.08	3.58E+05	1.40E+05	1.75E+05	2.04E+05	1.85E+05	2.38E+05	1.93E+05	1.64E+05	1.77E+05	2.92E+05	1.67E+05	1.59E+05	515.74982	2	43.24
SPN1	YPR133C	VVEATPEDGTASSQKSTINAENENTK	[12] Phospho (ST)|[13] Phospho (ST)	0.25	-0.40	-0.07	0.64	0.168	0.087	0.394	0.01	1.43E+06	8.81E+05	1.34E+06	1.48E+06	1.22E+06	1.62E+06	9.13E+05	8.30E+05	1.02E+06	1.17E+06	9.47E+05	1.35E+06	960.74543	3	20.06
GPD2	YOL059W	SDSAVSIVHLK	[3] Phospho (ST)|[6] Phospho (ST)	-0.45	-0.92	-0.55	0.47	0.004	0.017	0.050	0.13	5.11E+05	5.43E+05	5.05E+05	3.80E+05	4.27E+05	3.37E+05	2.62E+05	4.12E+05	1.52E+05	4.31E+05	4.31E+05	2.00E+05	658.28926	2	36.57
NOP12	YOL041C	LFGTNPIAETEESGNEK	[13] Phospho (ST)	0.23	0.17	0.19	0.07	0.156	0.150	0.122	0.36	1.05E+06	1.30E+06	1.01E+06	1.21E+06	1.60E+06	1.14E+06	1.22E+06	1.39E+06	1.16E+06	1.17E+06	1.41E+06	1.26E+06	958.42068	2	68.49
MOB1	YIL106W	WNTANAANNAGSVSPTK	[14] Phospho (ST)	0.27	0.63	0.49	-0.36	0.046	0.008	0.001	0.05	3.20E+05	2.94E+05	3.26E+05	3.82E+05	3.28E+05	4.21E+05	4.12E+05	4.84E+05	5.57E+05	4.35E+05	4.20E+05	4.65E+05	891.89453	2	74.4
STU2	YLR045C	RSSESIGDLPHR	[3] Phospho (ST)	-0.10	-0.02	0.00	-0.09	0.172	0.469	0.493	0.35	1.91E+05	2.26E+05	2.24E+05	2.03E+05	1.83E+05	2.10E+05	2.56E+05	1.58E+05	2.19E+05	2.01E+05	1.89E+05	2.49E+05	478.55578	3	42.34
YNL054W-B	L054W-B	HSDSYSDNETNHTNVPISSTGGTNNK	[4] Phospho (ST)	-0.85	-0.06	0.31	-0.79	0.010	0.343	0.110	0.00	7.53E+05	5.44E+05	6.77E+05	4.58E+05	3.06E+05	3.27E+05	5.94E+05	6.14E+05	6.79E+05	9.25E+05	6.37E+05	8.86E+05	952.72851	3	58.32
SEC16	YPL085W	YAPVSPTVQQK	[5] Phospho (ST)	-0.35	-0.08	-0.14	-0.26	0.070	0.336	0.260	0.13	3.15E+05	3.70E+05	4.23E+05	2.77E+05	2.45E+05	3.47E+05	3.79E+05	2.82E+05	3.84E+05	2.88E+05	3.03E+05	4.11E+05	649.31286	2	38.13
CAF20	YOR276W	GSGEDDEEETETTPTSTVPVATIAQETLK	[13] Phospho (ST)	0.39	0.20	0.17	0.20	0.183	0.269	0.336	0.28	1.36E+06	1.72E+06	8.83E+05	1.68E+06	2.32E+06	1.20E+06	1.61E+06	1.71E+06	1.22E+06	1.30E+06	1.99E+06	1.16E+06	1039.1285	3	50.4
YEF3	YLR249W	ELGDAYVSSDEEF	[6] Phospho (Y)|[8] Phospho (ST)	0.43	1.11	-0.08	-0.68	0.403	0.182	0.463	0.31	5.10E+05	2.16E+06	4.65E+05	1.01E+05	3.91E+06	2.06E+05	4.82E+05	4.09E+06	2.19E+06	7.84E+05	8.44E+05	1.33E+06	810.77472	2	16.85
HXT1	YHR094C	NESFHDNLSESQVQPAVAPPNTGK	[9] Phospho (ST)	-0.93	-0.73	-0.51	-0.20	0.000	0.001	0.002	0.12	7.17E+05	6.98E+05	7.35E+05	4.15E+05	3.40E+05	3.75E+05	3.64E+05	4.86E+05	4.49E+05	4.33E+05	5.20E+05	5.53E+05	882.73338	3	27.29
LEM3	YNL323W	GAIVSGDNPEEEEDVDASEFEEDEVKPVR	[18] Phospho (ST)	-0.49	-0.03	-0.22	-0.45	0.065	0.441	0.220	0.01	1.00E+06	1.39E+06	8.83E+05	7.28E+05	8.99E+05	7.08E+05	1.18E+06	1.05E+06	9.65E+05	7.89E+05	1.11E+06	9.17E+05	1090.8001	3	82.59
YRO2	YBR054W	KAQEEEEDVATDSE	[11] Phospho (ST)|[13] Phospho (ST)	0.06	0.13	-0.15	-0.07	0.452	0.418	0.394	0.45	7.78E+05	2.41E+05	6.17E+05	7.14E+05	6.06E+05	3.88E+05	2.98E+05	8.93E+05	6.00E+05	6.92E+05	3.51E+05	4.29E+05	870.3007	2	47.1
AIM21	YIR003W	SNNEVTEHSDSEDLTEK	[9] Phospho (ST)	-0.15	0.06	-0.13	-0.21	0.248	0.386	0.269	0.12	2.90E+05	1.95E+05	2.48E+05	2.45E+05	1.83E+05	2.31E+05	2.25E+05	2.57E+05	2.80E+05	2.43E+05	1.93E+05	2.34E+05	671.93535	3	25.82
RPS3	YNL178W	EEEPILAPSVK	[9] Phospho (ST)	-0.25	-0.15	-0.56	-0.10	0.097	0.241	0.064	0.26	5.71E+05	7.85E+05	6.33E+05	5.08E+05	5.89E+05	5.73E+05	7.01E+05	5.15E+05	5.80E+05	2.77E+05	5.91E+05	4.77E+05	646.31324	2	31.66
VTC2	YFL004W	ITSQGDLEADGSSDEETEQEPHSK	[12] Phospho (ST)|[13] Phospho (ST)	-0.68	-0.31	-0.21	-0.37	0.042	0.203	0.263	0.12	1.50E+06	8.39E+05	1.19E+06	7.07E+05	7.01E+05	7.88E+05	6.49E+05	1.18E+06	1.01E+06	1.23E+06	7.92E+05	1.03E+06	917.01881	3	39.96
ERB1	YMR049C	RAASEESDVEEDEDK	[7] Phospho (ST)	0.51	0.08	0.39	0.43	0.059	0.404	0.121	0.04	1.42E+05	1.13E+05	2.09E+05	2.51E+05	2.13E+05	1.96E+05	1.57E+05	1.38E+05	1.96E+05	2.37E+05	1.64E+05	2.09E+05	596.89847	3	36.31
AKL1	YBR059C	ARQSLDLER	[4] Phospho (ST)	0.14	-0.21	0.16	0.35	0.275	0.248	0.258	0.10	1.31E+05	1.46E+05	1.98E+05	1.69E+05	1.52E+05	2.03E+05	1.52E+05	9.83E+04	1.62E+05	1.60E+05	1.60E+05	2.10E+05	584.27956	2	36.41
YDR365W-B	R365W-B	SPSIDASPPENNSSHNIVPIK	[1] Phospho (ST)	-1.31	-0.35	-0.59	-0.96	0.005	0.091	0.074	0.00	1.46E+06	2.31E+06	2.02E+06	7.07E+05	7.50E+05	8.80E+05	1.60E+06	1.55E+06	1.39E+06	7.68E+05	1.61E+06	1.47E+06	1142.0368	2	55.22
YGR054W	YGR054W	SSETSPDSTPAPSAPASTNAPTNNK	[5] Phospho (ST)	0.26	0.28	0.04	-0.02	0.122	0.088	0.442	0.45	4.94E+05	3.57E+05	5.10E+05	6.27E+05	4.84E+05	5.16E+05	4.90E+05	5.99E+05	5.59E+05	5.78E+05	3.36E+05	4.87E+05	837.0279	3	36.29
RPS3	YNL178W	ALPDAVTIIEPKEEEPILAPSVK	[21] Phospho (ST)	-0.14	-0.06	0.01	-0.08	0.367	0.443	0.488	0.42	1.01E+06	1.46E+06	7.78E+05	8.99E+05	1.33E+06	7.16E+05	1.41E+06	8.96E+05	8.16E+05	8.26E+05	1.51E+06	9.42E+05	847.11693	3	30.52
PUF6	YDR496C	ISIDSSDEESELSK	[5] Phospho (ST)|[6] Phospho (ST)	-0.61	-0.12	-0.24	-0.49	0.105	0.400	0.088	0.26	7.88E+05	8.03E+05	8.15E+05	1.79E+05	8.18E+05	5.77E+05	3.81E+05	1.19E+06	6.36E+05	7.57E+05	7.49E+05	5.27E+05	849.82424	2	36.73
BUD3	YCL014W	AADVENLSDDDEHRQNESR	[8] Phospho (ST)	0.37	0.29	0.43	0.08	0.097	0.202	0.098	0.37	2.41E+05	1.61E+05	2.91E+05	3.18E+05	2.56E+05	3.19E+05	2.73E+05	2.18E+05	3.57E+05	3.14E+05	2.49E+05	3.70E+05	760.64353	3	62.95
CDC39	YCR093W	RQTPLQSNA	[3] Phospho (ST)	0.22	-0.47	-0.15	0.69	0.322	0.191	0.377	0.06	2.95E+05	1.11E+05	2.01E+05	2.15E+05	1.79E+05	3.12E+05	1.33E+05	1.17E+05	1.88E+05	2.27E+05	1.46E+05	1.75E+05	547.75272	2	24.44
NOP8	YOL144W	LIEDSDNDIDHAK	[5] Phospho (ST)	0.42	0.04	0.16	0.38	0.049	0.437	0.271	0.02	1.41E+05	1.33E+05	2.06E+05	2.28E+05	1.95E+05	2.18E+05	1.64E+05	1.40E+05	1.89E+05	1.81E+05	1.52E+05	2.02E+05	522.22243	3	40.28
BUD21	YOR078W	HVTFDKLDESDENEEALAK	[10] Phospho (ST)	-0.04	-0.42	-0.12	0.39	0.272	0.024	0.189	0.04	5.94E+05	5.69E+05	6.05E+05	6.13E+05	5.50E+05	5.61E+05	4.96E+05	3.36E+05	4.87E+05	5.49E+05	4.61E+05	6.18E+05	757.33423	3	68.64
SSK22	YCR073C	SIGCDLVPK	[1] Phospho (ST)	-0.74	-0.71	-0.08	-0.04	0.047	0.056	0.384	0.47	1.04E+06	6.60E+05	8.38E+05	7.24E+05	4.21E+05	3.68E+05	7.53E+05	3.65E+05	4.35E+05	5.85E+05	9.04E+05	9.02E+05	534.74299	2	15.39
UBP1	YDL122W	FEQEFEDSEEEK	[8] Phospho (ST)	0.30	0.22	0.25	0.08	0.012	0.030	0.026	0.11	4.96E+05	4.68E+05	5.64E+05	6.06E+05	6.13E+05	6.62E+05	5.86E+05	5.72E+05	6.23E+05	6.47E+05	6.02E+05	5.73E+05	813.29892	2	49.25
SUI3	YPL237W	AGLDNVDAESK	[10] Phospho (ST)	0.42	0.44	0.02	-0.03	0.084	0.157	0.477	0.47	1.95E+05	1.08E+05	1.96E+05	2.35E+05	1.91E+05	2.41E+05	1.71E+05	1.96E+05	3.12E+05	2.08E+05	1.24E+05	1.74E+05	599.75316	2	58.82
MPP10	YJR002W	HSSPDPYGINDK	[3] Phospho (ST)	-0.40	-0.89	-0.38	0.49	0.006	0.000	0.014	0.02	4.04E+05	3.76E+05	3.90E+05	3.25E+05	2.57E+05	3.03E+05	2.27E+05	1.73E+05	2.32E+05	2.72E+05	2.77E+05	3.51E+05	705.292	2	38.76
CDC3	YLR314C	EEQVSIKQDPEQEER	[5] Phospho (ST)	-0.05	-0.25	-0.25	0.20	0.389	0.137	0.215	0.15	4.27E+05	3.99E+05	5.41E+05	4.41E+05	3.86E+05	4.92E+05	3.58E+05	3.30E+05	4.58E+05	3.00E+05	3.30E+05	5.22E+05	962.41978	2	63.74
UTP14	YML093W	NRELAAVSSDEDNEDHDIAR	[8] Phospho (ST)|[9] Phospho (ST)	-0.54	-0.47	-0.16	-0.07	0.017	0.063	0.228	0.39	5.96E+05	4.59E+05	4.60E+05	3.38E+05	3.86E+05	3.16E+05	2.87E+05	4.76E+05	3.30E+05	5.44E+05	4.06E+05	4.03E+05	805.98696	3	46.74
CDC37	YDR168W	IELSDDSDVEVHPNVDKK	[4] Phospho (ST)|[7] Phospho (ST)	-0.49	-0.11	-0.27	-0.38	0.001	0.264	0.005	0.05	6.98E+05	6.53E+05	7.11E+05	4.48E+05	5.23E+05	5.02E+05	5.11E+05	7.44E+05	6.61E+05	5.90E+05	5.35E+05	5.88E+05	1099.9669	2	22.86
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALR	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.42	-0.15	-0.07	-0.27	0.205	0.345	0.420	0.30	1.11E+06	1.22E+06	6.83E+05	6.40E+05	1.17E+06	4.38E+05	9.82E+05	1.13E+06	6.05E+05	7.46E+05	1.19E+06	9.34E+05	746.55033	4	59.1
AVT1	YJR001W	RLSVTLNNAGRPR	[3] Phospho (ST)	0.12	-0.05	-0.14	0.18	0.286	0.422	0.283	0.28	2.15E+05	2.55E+05	2.82E+05	2.54E+05	2.32E+05	3.34E+05	3.03E+05	1.74E+05	2.49E+05	1.85E+05	2.13E+05	2.87E+05	511.93851	3	30.85
YPR091C	YPR091C	RPSQPLNTLSPK	[3] Phospho (ST)	-0.28	-0.18	0.05	-0.11	0.028	0.150	0.325	0.26	3.06E+05	3.69E+05	3.23E+05	2.57E+05	2.66E+05	2.97E+05	3.44E+05	2.56E+05	2.83E+05	3.27E+05	3.32E+05	3.74E+05	709.36154	2	50.99
SSZ1	YHR064C	EENAEEDDESEWSDDEPEVVR	[10] Phospho (ST)|[13] Phospho (ST)	-0.71	0.03	0.00	-0.74	0.111	0.480	0.497	0.22	1.33E+06	1.41E+06	1.06E+06	2.55E+05	1.36E+06	7.11E+05	6.34E+05	2.26E+06	9.81E+05	1.30E+06	1.24E+06	1.25E+06	889.97612	3	34.07
ARO9	YHR137W	RIGSGIK	[4] Phospho (ST)	-0.07	-0.40	0.10	0.33	0.323	0.098	0.227	0.15	8.07E+04	6.59E+04	7.66E+04	7.49E+04	5.91E+04	7.82E+04	7.67E+04	5.23E+04	4.01E+04	8.69E+04	7.18E+04	7.97E+04	405.71523	2	28.05
YER138C	YER138C	HSDSYSENETNHTNVPISSTGGTNNK	[13] Phospho (ST)	-0.75	-0.30	0.17	-0.44	0.009	0.075	0.246	0.02	4.84E+05	3.50E+05	4.45E+05	2.92E+05	2.31E+05	2.37E+05	3.84E+05	3.45E+05	3.06E+05	5.71E+05	3.72E+05	4.95E+05	718.30195	4	17.62
MRH1	YDR033W	APVASPRPAATPNLSK	[11] Phospho (ST)	-0.37	-0.04	-0.32	-0.33	0.016	0.456	0.104	0.23	1.59E+05	1.91E+05	1.76E+05	1.39E+05	1.19E+05	1.47E+05	2.45E+05	1.02E+05	1.64E+05	1.14E+05	1.23E+05	1.83E+05	552.95417	3	19.77
ZEO1	YOL109W	NEATPEAEQVKK	[4] Phospho (ST)	-1.19	-0.42	-2.18	-0.78	0.230	0.373	0.154	0.20	6.08E+05	1.32E+05	4.69E+04	2.08E+05	5.62E+04	8.01E+04	1.01E+05	1.49E+05	3.41E+05	8.92E+04	4.52E+04	3.97E+04	712.3265	2	48.47
BFR2	YDR299W	DSVDDNENSDDGLDIPK	[9] Phospho (ST)	0.04	-0.25	0.01	0.29	0.334	0.102	0.472	0.08	9.44E+05	8.50E+05	8.54E+05	9.14E+05	9.85E+05	8.25E+05	6.20E+05	9.10E+05	7.02E+05	9.09E+05	1.03E+06	7.25E+05	964.37709	2	54.37
FLC3	YGL139W	NENASTDALRVEAPK	[6] Phospho (ST)	0.31	0.28	0.35	0.03	0.065	0.111	0.047	0.43	1.35E+05	1.29E+05	1.80E+05	1.81E+05	1.69E+05	2.00E+05	1.74E+05	1.58E+05	2.08E+05	1.94E+05	1.71E+05	2.03E+05	565.59655	3	28.19
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALRK	[N-term] Acetyl (Protein N-term)|[6] Phospho	-0.97	-0.70	-0.48	-0.26	0.031	0.031	0.117	0.23	1.49E+06	1.01E+06	1.71E+06	8.11E+05	9.57E+05	3.89E+05	7.89E+05	9.33E+05	8.69E+05	1.10E+06	1.29E+06	6.47E+05	1037.7616	3	54.63
YJR029W	YJR029W	HSDSYSENETNHTNVPISSTGGTNNK	[4] Phospho (ST)|[5] Phospho (Y)	-1.27	-0.99	-0.10	-0.28	0.002	0.008	0.365	0.17	9.34E+05	6.69E+05	7.86E+05	3.33E+05	2.88E+05	3.70E+05	2.91E+05	5.08E+05	4.07E+05	8.06E+05	5.16E+05	9.11E+05	984.05625	3	49.27
SPN1	YPR133C	VVEATPEDGTASSQK	[13] Phospho (ST)	0.87	-0.35	-0.96	1.22	0.012	0.124	0.019	0.00	2.69E+05	1.64E+05	2.62E+05	4.93E+05	3.50E+05	4.27E+05	1.68E+05	1.67E+05	2.11E+05	1.27E+05	8.92E+04	1.40E+05	799.85183	2	30.47
ZUO1	YGR285C	NHTWSEFER	[5] Phospho (ST)	0.02	0.20	0.17	-0.18	0.455	0.165	0.284	0.04	1.15E+05	1.85E+05	1.65E+05	1.47E+05	1.52E+05	1.73E+05	1.83E+05	1.82E+05	1.69E+05	1.29E+05	1.99E+05	1.94E+05	429.1714	3	28.55
PAF1	YBR279W	RLDDGDSDDENLDVNHIISR	[7] Phospho (ST)	-0.23	-0.10	-0.26	-0.13	0.234	0.286	0.197	0.32	3.67E+05	5.29E+05	4.73E+05	2.63E+05	5.00E+05	4.04E+05	4.16E+05	4.53E+05	4.08E+05	2.58E+05	4.58E+05	4.28E+05	793.3471	3	70.8
NUP60	YAR002W	RASATVPSAPYR	[3] Phospho (ST)	0.12	0.14	-0.07	-0.02	0.317	0.337	0.423	0.47	1.26E+05	1.95E+05	1.92E+05	1.52E+05	1.91E+05	2.14E+05	2.38E+05	1.30E+05	1.97E+05	1.17E+05	1.44E+05	2.26E+05	678.32698	2	56.36
ERB1	YMR049C	AASEESDVEEDEDK	[6] Phospho (ST)	-0.18	-0.47	0.10	0.28	0.286	0.120	0.360	0.13	2.68E+05	1.49E+05	2.77E+05	2.39E+05	1.84E+05	1.87E+05	1.26E+05	1.87E+05	1.89E+05	2.39E+05	2.44E+05	2.59E+05	816.79346	2	54.7
GPD1	YDL022W	RSSSSVSLK	[7] Phospho (ST)	0.20	-0.57	-0.28	0.77	0.344	0.198	0.325	0.00	3.53E+05	1.02E+05	1.88E+05	2.69E+05	2.14E+05	2.58E+05	1.40E+05	1.47E+05	1.47E+05	2.27E+05	1.46E+05	1.56E+05	515.74955	2	32.34
GIN4	YDR507C	RASVINVEK	[3] Phospho (ST)	-0.24	-0.26	-0.23	0.02	0.030	0.149	0.146	0.47	1.26E+05	1.35E+05	1.52E+05	1.13E+05	1.16E+05	1.21E+05	1.29E+05	8.06E+04	1.36E+05	9.07E+04	1.22E+05	1.40E+05	548.28145	2	47.64
GIN4	YDR507C	LSTIVNQSSPTPASR	[3] Phospho (ST)	-0.40	0.26	0.13	-0.67	0.012	0.030	0.112	0.00	5.13E+05	5.21E+05	4.33E+05	3.97E+05	3.79E+05	3.34E+05	6.34E+05	5.47E+05	5.80E+05	5.06E+05	5.58E+05	5.41E+05	819.39849	2	33.22
SHP1	YBL058W	LGSPIPGESSPAEVPK	[3] Phospho (ST)	0.15	0.52	-0.31	-0.36	0.300	0.082	0.209	0.11	3.29E+05	5.75E+05	3.98E+05	3.96E+05	5.07E+05	5.45E+05	7.16E+05	4.58E+05	6.90E+05	2.38E+05	4.01E+05	4.13E+05	822.89844	2	61.49
RNR2	YJL026W	AAADALSDLEIK	[7] Phospho (ST)	-0.39	-0.03	0.25	-0.36	0.129	0.456	0.207	0.08	2.72E+05	4.37E+05	2.92E+05	2.24E+05	3.15E+05	2.24E+05	3.73E+05	3.38E+05	2.69E+05	3.43E+05	4.86E+05	3.60E+05	648.8085	2	54.53
UBP1	YDL122W	IIEHSDVENENVK	[5] Phospho (ST)	0.11	0.23	0.15	-0.12	0.309	0.226	0.323	0.34	1.32E+05	1.62E+05	1.95E+05	1.56E+05	1.63E+05	2.09E+05	2.20E+05	1.33E+05	2.21E+05	1.34E+05	1.69E+05	2.40E+05	803.36193	2	55.13
MAK5	YBR142W	AADELGIDVDSDEDDISK	[11] Phospho (ST)	-0.50	-0.20	0.11	-0.29	0.084	0.156	0.205	0.21	6.23E+05	7.96E+05	6.67E+05	3.10E+05	6.88E+05	4.80E+05	5.34E+05	7.24E+05	5.53E+05	7.55E+05	7.87E+05	7.03E+05	993.90777	2	55
SPN1	YPR133C	HISTDFSDDDLEK	[7] Phospho (ST)	0.06	0.12	0.03	-0.06	0.354	0.212	0.424	0.19	1.47E+05	1.55E+05	1.97E+05	1.64E+05	1.70E+05	1.85E+05	1.89E+05	1.76E+05	1.76E+05	1.77E+05	1.63E+05	1.69E+05	534.55072	3	15.98
NUP2	YLR335W	ETYDSNESDDDVTPSTK	[8] Phospho (ST)	0.31	0.19	0.22	0.12	0.081	0.227	0.221	0.24	4.02E+05	2.58E+05	3.24E+05	4.48E+05	3.80E+05	3.94E+05	3.00E+05	4.12E+05	4.11E+05	4.73E+05	3.12E+05	3.61E+05	991.87338	2	44.3
YRB1	YDR002W	EGDDAPESPDIHFEPVVHLEK	[8] Phospho (ST)	0.69	0.52	0.56	0.17	0.006	0.022	0.053	0.11	2.07E+05	2.93E+05	2.17E+05	3.48E+05	4.18E+05	3.91E+05	3.73E+05	2.98E+05	3.56E+05	2.75E+05	4.39E+05	3.45E+05	814.02903	3	32.45
NAN1	YPL126W	MTQSLGIEQYKLSVVSGGK	[N-term] Acetyl (Protein N-term)|[10] Phosph	0.02	-0.63	0.15	0.66	0.482	0.090	0.390	0.17	8.71E+05	4.72E+05	7.44E+05	1.13E+06	4.18E+05	5.78E+05	2.60E+05	5.75E+05	5.10E+05	1.18E+06	6.89E+05	4.37E+05	716.35677	3	31.13
CAF20	YOR276W	DIVADKPILGFNAFAALESEDEDDEA	[19] Phospho (ST)	0.14	-0.06	-0.22	0.20	0.377	0.442	0.326	0.27	2.44E+06	3.17E+06	1.29E+06	2.01E+06	3.37E+06	2.21E+06	2.56E+06	2.35E+06	1.69E+06	2.01E+06	2.61E+06	1.30E+06	958.75925	3	53.17
AIM21	YIR003W	SNNEVTEHSDSEDLTEK	[9] Phospho (ST)	-0.16	0.02	-0.13	-0.18	0.194	0.437	0.201	0.13	3.30E+05	2.51E+05	2.91E+05	2.80E+05	2.19E+05	2.83E+05	2.82E+05	2.79E+05	3.26E+05	2.64E+05	2.39E+05	2.92E+05	1007.3997	2	58.68
GSY2	YLR258W	VARPLSVPGSPR	[6] Phospho (ST)|[10] Phospho (ST)	0.96	0.78	0.54	0.18	0.000	0.004	0.007	0.07	6.50E+04	7.00E+04	8.71E+04	1.45E+05	1.46E+05	1.39E+05	1.11E+05	1.30E+05	1.40E+05	1.17E+05	1.03E+05	1.04E+05	465.88977	3	17.28
YPR091C	YPR091C	KNDDSADERESDNPILTSNPK	[5] Phospho (ST)	-0.20	-0.25	0.06	0.04	0.051	0.063	0.354	0.38	4.04E+05	3.69E+05	3.51E+05	3.47E+05	2.92E+05	3.38E+05	3.16E+05	2.71E+05	3.61E+05	3.62E+05	3.47E+05	4.63E+05	809.02229	3	66.6
TRM2	YKR056W	RLSSPLTDSGNR	[4] Phospho (ST)	0.31	-0.43	-0.38	0.74	0.068	0.039	0.060	0.00	1.54E+05	1.28E+05	1.81E+05	1.91E+05	1.69E+05	2.14E+05	1.23E+05	1.00E+05	1.21E+05	1.14E+05	1.03E+05	1.38E+05	691.8247	2	31.83
PMA1	YGL008C	SVEDFMAAMQRVSTQHEK	[13] Phospho (ST)|[14] Phospho (ST)	-0.88	-0.33	-0.10	-0.54	0.085	0.245	0.381	0.25	4.56E+05	5.34E+05	3.40E+05	2.11E+05	4.40E+05	7.41E+04	3.06E+05	5.54E+05	1.94E+05	3.43E+05	5.54E+05	3.45E+05	564.2327	4	17.65
ABF1	YKL112W	ADDEEDLSDENIQPELR	[8] Phospho (ST)	0.01	-0.02	-0.17	0.03	0.482	0.451	0.146	0.45	6.72E+05	6.48E+05	5.85E+05	5.37E+05	7.72E+05	6.08E+05	5.44E+05	7.49E+05	5.86E+05	5.49E+05	6.62E+05	4.88E+05	1034.4246	2	55.88
BUD21	YOR078W	LDESDENEEALAK	[4] Phospho (ST)	0.33	0.18	0.20	0.15	0.087	0.250	0.195	0.23	1.62E+05	1.60E+05	2.34E+05	2.30E+05	2.08E+05	2.60E+05	2.00E+05	1.76E+05	2.55E+05	2.37E+05	1.86E+05	2.15E+05	771.81467	2	68.6
PLP2	YOR281C	GVIPERAPSPTAK	[9] Phospho (ST)	-0.07	-0.03	0.14	-0.04	0.267	0.470	0.294	0.45	1.70E+05	2.00E+05	1.79E+05	1.65E+05	1.65E+05	1.93E+05	2.47E+05	1.08E+05	1.84E+05	1.43E+05	2.13E+05	2.50E+05	701.85903	2	37.75
MCM1	YMR043W	SDIEEGTPTNNGQQK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.01	-0.13	0.03	0.14	0.488	0.391	0.469	0.33	5.69E+05	2.42E+05	4.58E+05	4.53E+05	3.44E+05	4.82E+05	2.53E+05	4.19E+05	4.92E+05	5.63E+05	3.42E+05	3.94E+05	870.36022	2	67.68
NRD1	YNL251C	SRSPPAPFSQPSTGR	[1] Phospho (ST)|[3] Phospho (ST)	0.08	-0.05	-0.27	0.12	0.312	0.442	0.072	0.35	2.33E+05	2.38E+05	2.82E+05	3.00E+05	2.26E+05	2.67E+05	1.67E+05	3.33E+05	2.28E+05	2.33E+05	1.73E+05	2.17E+05	577.91361	3	31.85
SCP160	YJL080C	LTYEPIDLSSILSDGEEK	[10] Phospho (ST)	-0.52	-0.17	-0.14	-0.35	0.125	0.318	0.380	0.12	8.95E+05	1.30E+06	6.57E+05	6.36E+05	8.51E+05	5.05E+05	9.01E+05	9.52E+05	6.85E+05	7.75E+05	1.21E+06	6.06E+05	1044.9856	2	91.26
YOR296W	YOR296W	LLDYKINLK	[4] Phospho (Y)	-2.67	-3.42	-0.42	0.75	0.096	0.083	0.347	0.15	7.80E+05	1.92E+05	1.59E+05	5.03E+04	3.89E+04	8.82E+04	2.91E+04	6.06E+04	1.56E+04	9.11E+04	3.27E+05	4.27E+05	600.32478	2	17.47
YMR221C	YMR221C	SVLETYVEDK	[1] Phospho (ST)	-0.50	-0.07	-0.28	-0.43	0.027	0.346	0.079	0.05	2.08E+05	2.58E+05	2.04E+05	1.68E+05	1.81E+05	1.26E+05	2.39E+05	2.22E+05	1.77E+05	1.81E+05	2.11E+05	1.63E+05	631.78181	2	45.47
BBC1	YJL020C	DLPEPISPETKK	[7] Phospho (ST)	0.53	0.60	0.65	-0.07	0.007	0.060	0.019	0.39	1.12E+05	1.56E+05	1.38E+05	1.84E+05	1.95E+05	2.06E+05	2.57E+05	1.43E+05	2.17E+05	1.74E+05	2.12E+05	2.50E+05	717.35031	2	32.14
NDI1	YML120C	ITEETIPYGTLIWATGNK	[5] Phospho (ST)|[8] Phospho (Y)|[10] Phosph	-0.14	-0.24	-0.51	0.10	0.347	0.124	0.161	0.39	8.12E+05	7.91E+05	1.04E+06	8.78E+05	4.76E+05	1.05E+06	6.36E+05	7.97E+05	8.12E+05	9.37E+05	2.00E+05	7.19E+05	582.48637	4	22.29
VMA2	YBR127C	ARDDADEDEEDPDTRSSGK	[16] Phospho (ST)	1.25	0.59	0.64	0.66	0.019	0.073	0.051	0.08	1.59E+05	1.82E+05	2.19E+05	4.30E+05	3.07E+05	5.92E+05	3.60E+05	1.90E+05	2.94E+05	3.84E+05	2.33E+05	2.58E+05	729.94866	3	50.52
NHA1	YLR138W	LPSLDK	[3] Phospho (ST)	0.22	0.32	0.45	-0.10	0.223	0.114	0.041	0.28	4.38E+04	4.40E+04	6.84E+04	6.51E+04	4.89E+04	6.78E+04	6.31E+04	5.92E+04	7.32E+04	7.21E+04	7.17E+04	6.96E+04	376.68336	2	25.59
VTC3	YPL019C	HVIADLEDHESSDEEGTALPK	[11] Phospho (ST)|[12] Phospho (ST)	-1.94	-0.70	-0.66	-1.24	0.002	0.039	0.014	0.03	1.18E+06	1.07E+06	8.17E+05	1.59E+05	3.86E+05	2.52E+05	4.72E+05	8.82E+05	5.27E+05	5.83E+05	6.75E+05	6.86E+05	818.00392	3	51.97
YNL054W-B	L054W-B	AHNVSTSNNSPSTDNDSISK	[10] Phospho (ST)	-0.05	-0.74	-0.12	0.69	0.430	0.045	0.361	0.01	5.05E+05	3.08E+05	3.17E+05	4.15E+05	3.71E+05	3.04E+05	2.01E+05	2.07E+05	2.69E+05	4.40E+05	3.10E+05	2.88E+05	1077.9512	2	76.8
YLR257W	YLR257W	SINSESFSSPSLR	[1] Phospho (ST)	-0.06	0.08	-0.14	-0.13	0.347	0.316	0.214	0.18	2.03E+05	2.57E+05	2.13E+05	1.98E+05	2.35E+05	2.14E+05	2.09E+05	2.68E+05	2.32E+05	1.96E+05	2.34E+05	1.82E+05	745.82936	2	84.07
MCM3	YEL032W	VRQPASNSGSPIK	[6] Phospho (ST)|[10] Phospho (ST)	-0.47	-0.72	-0.47	0.25	0.110	0.062	0.135	0.15	3.95E+05	2.04E+05	3.03E+05	2.49E+05	1.97E+05	2.06E+05	1.33E+05	1.99E+05	2.16E+05	2.87E+05	1.74E+05	1.88E+05	750.83461	2	19.49

DEF1	YKL054C	KEISDIK	[4] Phospho (ST)	-7.74	-2.27	-0.36	-5.47	0.003	0.007	0.180	0.00	2.12E+05	1.07E+05	1.87E+05	7.48E+02	7.44E+02	8.41E+02	3.81E+04	2.86E+04	3.79E+04	1.62E+05	1.04E+05	1.29E+05	456.72547	2	28.59
CHS2	YBR038W	YAANLQESPK	[8] Phospho (ST)	1.21	2.24	1.86	-1.03	0.013	0.001	0.001	0.00	1.87E+04	3.51E+04	4.59E+04	7.22E+04	6.29E+04	9.55E+04	1.59E+05	1.34E+05	1.80E+05	1.21E+05	1.05E+05	1.35E+05	600.76755	2	25.9
HXT2	YMR011W	LETDESPIQTK	[3] Phospho (ST)	0.00	-0.10	-0.18	0.10	0.500	0.286	0.210	0.29	2.36E+05	2.92E+05	3.18E+05	2.85E+05	2.35E+05	3.26E+05	2.77E+05	2.21E+05	2.89E+05	2.21E+05	2.24E+05	3.03E+05	670.80346	2	41.46
FLC3	YGL139W	NENASTDALRVEAPK	[5] Phospho (ST)	0.11	-0.11	0.17	0.22	0.251	0.251	0.119	0.12	2.06E+05	1.93E+05	2.40E+05	2.06E+05	2.19E+05	2.64E+05	1.93E+05	1.74E+05	2.26E+05	2.29E+05	2.24E+05	2.64E+05	847.89149	2	81.09
NOG2	YNR053C	AASFQDSTIPDAR	[3] Phospho (ST)	-0.85	-1.65	-0.59	0.80	0.002	0.000	0.005	0.00	2.74E+05	2.97E+05	3.44E+05	1.61E+05	1.61E+05	1.85E+05	9.05E+04	9.14E+04	1.09E+05	2.00E+05	1.88E+05	2.20E+05	729.81741	2	58.35
ENT5	YDR153C	NNNINSNSDDDDDEFGDFQSETSPDTTAPK	[8] Phospho (ST)	-0.45	-0.04	-0.05	-0.41	0.075	0.434	0.373	0.14	1.08E+06	9.39E+05	8.20E+05	5.69E+05	9.35E+05	5.80E+05	7.40E+05	1.18E+06	8.38E+05	1.02E+06	8.69E+05	8.52E+05	1123.7662	3	24.74
UBP1	YDL122W	IIEHSDVENENVK	[5] Phospho (ST)	0.14	0.26	-0.01	-0.11	0.265	0.206	0.488	0.34	6.25E+04	7.66E+04	9.50E+04	8.16E+04	7.63E+04	1.01E+05	1.07E+05	6.57E+04	1.07E+05	6.05E+04	6.78E+04	1.04E+05	535.91001	3	17.12
TMA17	YDL110C	LEGADDRLEADDSDDLENIDSGDLALYK	[13] Phospho (ST)	-0.30	0.48	-0.04	-0.78	0.192	0.059	0.459	0.00	8.73E+05	1.18E+06	6.43E+05	6.82E+05	8.67E+05	6.51E+05	1.35E+06	1.34E+06	1.08E+06	7.23E+05	1.18E+06	7.21E+05	1049.79	3	95.57
CDC19	YAL038W	RTSIIGTIGPK	[3] Phospho (ST)	-0.61	-0.13	-0.22	-0.48	0.018	0.387	0.201	0.19	1.01E+05	1.44E+05	1.19E+05	6.94E+04	8.29E+04	8.61E+04	1.72E+05	6.74E+04	9.36E+04	8.16E+04	1.05E+05	1.26E+05	611.83154	2	41.34
MSC3	YLR219W	RLSTSSAAPPTSR	[3] Phospho (ST)|[6] Phospho (ST)	0.21	-0.09	-0.05	0.30	0.222	0.384	0.449	0.05	2.07E+05	1.12E+05	1.95E+05	2.17E+05	1.80E+05	1.97E+05	1.34E+05	1.77E+05	1.71E+05	2.21E+05	1.32E+05	1.43E+05	745.82372	2	24.87
PBP2	YBR233W	DADSHSDNDHDSPDNVPSDVHLR	[6] Phospho (ST)	-0.10	-0.12	-0.02	0.02	0.219	0.170	0.443	0.45	1.96E+05	2.04E+05	2.26E+05	2.16E+05	1.98E+05	1.70E+05	2.16E+05	1.86E+05	1.75E+05	2.26E+05	1.75E+05	2.17E+05	656.76311	4	34.38
GPD2	YOL059W	RSDSAVSIVHLK	[4] Phospho (ST)|[7] Phospho (ST)	-0.51	-0.35	-0.26	-0.16	0.010	0.106	0.064	0.29	1.31E+05	1.24E+05	1.53E+05	8.32E+04	1.02E+05	1.01E+05	8.47E+04	1.42E+05	9.36E+04	1.29E+05	1.05E+05	1.08E+05	491.22873	3	29.23
TOD6	YBL054W	RSSFNSHAPTEPISR	[3] Phospho (ST)|[14] Phospho (ST)	0.13	-0.08	0.15	0.21	0.237	0.328	0.270	0.03	1.17E+05	1.16E+05	1.60E+05	1.55E+05	1.34E+05	1.41E+05	1.15E+05	1.33E+05	1.23E+05	1.70E+05	1.16E+05	1.51E+05	615.92733	3	23.27
BDF1	YLR399C	RSSAQEDAPIVIR	[3] Phospho (ST)	-0.32	-0.38	-0.30	0.05	0.024	0.018	0.072	0.30	1.69E+05	2.07E+05	2.07E+05	1.43E+05	1.58E+05	1.64E+05	1.52E+05	1.36E+05	1.61E+05	1.39E+05	1.45E+05	1.89E+05	761.37501	2	60.63
LHP1	YDL051W	RNSFAVIEFTPEVLDR	[3] Phospho (ST)	0.91	0.44	0.40	0.47	0.042	0.215	0.184	0.14	1.88E+05	3.79E+05	1.77E+05	3.60E+05	5.96E+05	4.41E+05	4.87E+05	2.61E+05	2.59E+05	3.24E+05	4.04E+05	2.54E+05	658.32353	3	39.09
PTP3	YER075C	PSSYPEQLTSTSSSTIMPPK	[2] Phospho (ST)|[15] Phospho (ST)	-0.30	0.10	0.22	-0.40	0.168	0.114	0.137	0.11	4.34E+05	4.42E+05	4.28E+05	4.99E+05	2.56E+05	3.05E+05	4.26E+05	5.01E+05	4.71E+05	6.15E+05	4.41E+05	4.58E+05	766.65531	3	15.34
SEC16	YPL085W	IGDSLQGSPQR	[8] Phospho (ST)	-0.04	0.44	0.38	-0.48	0.447	0.101	0.113	0.09	1.27E+05	1.02E+05	1.57E+05	1.13E+05	1.05E+05	1.57E+05	1.40E+05	1.59E+05	2.24E+05	2.05E+05	1.28E+05	1.70E+05	619.28227	2	52.86
PGA2	YNL149C	NQGLDPDSDADIEELLEE	[8] Phospho (ST)	-0.07	0.10	0.13	-0.17	0.421	0.400	0.371	0.34	1.46E+06	1.68E+06	9.71E+05	1.18E+06	1.73E+06	1.00E+06	1.27E+06	2.07E+06	1.07E+06	1.47E+06	2.04E+06	9.95E+05	1041.426	2	22.1
NNT1	YLR285W	SDIESLGEAAGLFEEPEDFLPPPPK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.38	0.46	0.21	-0.08	0.169	0.129	0.297	0.41	8.92E+05	8.29E+05	5.11E+05	9.20E+05	1.29E+06	7.02E+05	9.23E+05	1.38E+06	7.82E+05	8.81E+05	1.12E+06	5.73E+05	962.75264	3	64.32
CYC8	YBR112C	SPQENTLPR	[1] Phospho (ST)	-0.34	-0.11	-0.23	-0.23	0.160	0.363	0.239	0.12	1.22E+05	6.54E+04	1.11E+05	8.69E+04	6.67E+04	8.20E+04	7.87E+04	9.13E+04	1.06E+05	9.17E+04	7.08E+04	9.18E+04	561.25227	2	29
GAL11	YOL051W	DVEVIKQLSLDASKTNLR	[9] Phospho (ST)|[13] Phospho (ST)	0.21	-0.75	0.85	0.95	0.376	0.086	0.163	0.14	2.87E+05	1.59E+05	2.67E+05	4.69E+05	1.40E+05	2.14E+05	9.60E+04	2.26E+05	1.03E+05	7.59E+05	2.72E+05	2.53E+05	548.02213	4	16.32
NUP60	YAR002W	SNVVVAETSPEKK	[9] Phospho (ST)	-0.61	-0.03	-0.21	-0.58	0.016	0.456	0.147	0.05	1.90E+05	2.45E+05	1.81E+05	1.17E+05	1.40E+05	1.47E+05	2.53E+05	1.47E+05	2.04E+05	1.75E+05	1.57E+05	2.00E+05	734.35831	2	49.95
DIG2	YDR480W	EEDHSGKPPTITTSPAEK	[5] Phospho (ST)	-0.60	-0.34	0.08	-0.25	0.006	0.069	0.316	0.13	1.54E+05	1.50E+05	1.85E+05	1.19E+05	1.07E+05	9.81E+04	1.44E+05	9.87E+04	1.42E+05	1.54E+05	1.64E+05	1.99E+05	668.63688	3	25.43
VTC3	YPL019C	ISVPDGK	[2] Phospho (ST)	-0.35	0.09	0.14	-0.44	0.147	0.373	0.301	0.04	5.47E+04	4.08E+04	7.14E+04	4.18E+04	3.62E+04	5.25E+04	5.16E+04	5.84E+04	6.72E+04	6.42E+04	5.14E+04	6.86E+04	398.18608	2	26.25
NRD1	YNL251C	NRSRSPPAPFSQPSTGR	[3] Phospho (ST)|[5] Phospho (ST)	-0.02	-0.17	-0.19	0.15	0.447	0.247	0.172	0.27	3.64E+05	3.37E+05	4.41E+05	3.74E+05	3.23E+05	4.25E+05	2.57E+05	4.18E+05	3.40E+05	3.51E+05	2.70E+05	3.76E+05	667.96171	3	25.26
WHI3	YNL197C	RPSLLSQR	[3] Phospho (ST)	0.01	-0.33	-0.32	0.35	0.465	0.143	0.088	0.13	1.27E+05	1.61E+05	1.49E+05	1.42E+05	1.35E+05	1.64E+05	1.47E+05	7.24E+04	1.27E+05	9.84E+04	1.06E+05	1.45E+05	518.76853	2	36.44
ERB1	YMR049C	RAASEESDVEEDEDK	[4] Phospho (ST)|[7] Phospho (ST)	0.68	-0.03	0.11	0.71	0.056	0.475	0.412	0.03	2.63E+05	1.04E+05	1.94E+05	3.37E+05	3.25E+05	2.38E+05	1.16E+05	2.38E+05	1.96E+05	2.94E+05	1.44E+05	1.70E+05	934.82772	2	40.97
GFD1	YMR255W	ATEISPPPVSPSK	[10] Phospho (ST)	-0.23	0.34	0.17	-0.57	0.054	0.051	0.138	0.01	2.77E+05	3.52E+05	3.16E+05	2.56E+05	2.77E+05	2.71E+05	4.59E+05	3.51E+05	3.81E+05	3.14E+05	3.95E+05	3.56E+05	695.33735	2	20.24
HOM3	YER052C	KGESTPPHPPENLSSSFYEK	[4] Phospho (ST)	-0.46	-0.12	-0.32	-0.33	0.049	0.367	0.162	0.19	3.37E+05	5.05E+05	3.92E+05	2.87E+05	2.81E+05	3.33E+05	5.30E+05	2.84E+05	3.21E+05	2.24E+05	3.64E+05	4.00E+05	771.01424	3	43.72
MRD1	YPR112C	EENNKDEAPNLVIENESDDEYSALNR	[17] Phospho (ST)	0.01	0.00	0.05	0.01	0.478	0.494	0.352	0.49	6.51E+05	6.57E+05	5.08E+05	6.09E+05	6.91E+05	5.28E+05	5.80E+05	7.13E+05	5.26E+05	6.02E+05	6.69E+05	6.10E+05	1029.7731	3	53.02
LEO1	YOR123C	FYGEDANNFSDQDETTHTFK	[10] Phospho (ST)	0.14	0.23	-0.15	-0.09	0.147	0.022	0.159	0.24	2.30E+05	2.60E+05	2.33E+05	2.49E+05	3.03E+05	2.46E+05	2.61E+05	2.90E+05	2.96E+05	1.82E+05	2.38E+05	2.34E+05	815.98906	3	54.01
HOM2	YDR158W	NRDSGYGVSVGR	[4] Phospho (ST)	-0.05	-0.07	-0.03	0.02	0.402	0.312	0.435	0.43	9.87E+04	9.02E+04	1.22E+05	9.77E+04	8.67E+04	1.17E+05	9.90E+04	9.78E+04	9.93E+04	1.10E+05	8.59E+04	1.09E+05	673.79572	2	52.52
VAC8	YEL013W	DSSDEASVSPIADNER	[7] Phospho (ST)	0.97	0.76	0.42	0.20	0.000	0.007	0.013	0.10	2.28E+05	2.46E+05	2.33E+05	4.43E+05	4.77E+05	4.62E+05	3.29E+05	4.12E+05	4.60E+05	3.27E+05	3.46E+05	2.72E+05	886.35686	2	68.67
GIN4	YDR507C	FLGSSFNIDK	[4] Phospho (ST)	-0.47	-0.02	-0.12	-0.45	0.050	0.467	0.352	0.01	2.06E+05	2.68E+05	1.87E+05	1.55E+05	1.87E+05	1.36E+05	2.29E+05	2.24E+05	2.02E+05	1.60E+05	2.75E+05	1.73E+05	604.27446	2	59.82
SGV1	YPR161C	YTSVVVTR	[2] Phospho (ST)	0.35	0.37	0.16	-0.02	0.051	0.117	0.172	0.47	7.49E+04	8.63E+04	9.29E+04	1.02E+05	9.51E+04	1.27E+05	1.36E+05	7.81E+04	1.15E+05	8.15E+04	9.49E+04	1.07E+05	502.74442	2	51.61
KIN1	YDR122W	FEGSDDDENHPLPPLNVAK	[4] Phospho (ST)	-0.04	0.24	0.08	-0.28	0.387	0.026	0.272	0.03	2.41E+05	2.95E+05	2.74E+05	2.34E+05	2.98E+05	2.56E+05	3.15E+05	3.36E+05	3.07E+05	2.53E+05	3.17E+05	2.89E+05	725.32001	3	51.16
BDF1	YLR399C	RSSAQEDAPIVIR	[3] Phospho (ST)	-0.20	-0.14	-0.22	-0.06	0.090	0.173	0.107	0.20	8.37E+04	9.80E+04	1.10E+05	8.32E+04	8.53E+04	8.59E+04	8.83E+04	8.19E+04	9.45E+04	8.31E+04	7.38E+04	9.30E+04	507.91882	3	39.09
BDF1	YLR399C	DASSLSPTSAGSR	[4] Phospho (ST)	0.48	0.25	-0.15	0.23	0.074	0.191	0.282	0.19	9.84E+04	7.88E+04	1.32E+05	1.42E+05	1.16E+05	1.74E+05	1.03E+05	1.17E+05	1.48E+05	8.47E+04	8.93E+04	1.04E+05	658.27994	2	73.09
MAK21	YDR060W	LIQGLSDDDDAKSEQEFDAVADEDADDK	[6] Phospho (ST)|[13] Phospho (ST)	-0.50	-0.02	-0.10	-0.47	0.174	0.478	0.342	0.24	8.76E+05	1.20E+06	8.06E+05	3.07E+05	1.11E+06	6.23E+05	5.80E+05	1.40E+06	8.51E+05	9.05E+05	1.04E+06	7.40E+05	1072.0894	3	67.9
LYS21	YDL131W	DFHAELSTPLLK	[8] Phospho (ST)	0.08	0.60	0.17	-0.52	0.415	0.137	0.350	0.14	5.10E+04	1.12E+05	7.35E+04	6.70E+04	1.04E+05	8.06E+04	1.70E+05	7.84E+04	1.11E+05	5.59E+04	1.10E+05	1.02E+05	484.23753	3	29.32
TPS3	YMR261C	VCSPSQEASASSISASR	[5] Phospho (ST)	0.22	-0.03	0.25	0.24	0.071	0.417	0.120	0.10	2.02E+05	1.89E+05	2.04E+05	2.27E+05	2.03E+05	2.61E+05	1.84E+05	1.72E+05	2.28E+05	2.23E+05	1.97E+05	2.85E+05	902.38327	2	105.96
UBP1	YDL122W	RIIEHSDVENENVK	[6] Phospho (ST)	-0.03	-0.29	-0.12	0.26	0.230	0.115	0.075	0.14	1.29E+05	1.24E+05	1.33E+05	1.28E+05	1.22E+05	1.27E+05	1.13E+05	7.32E+04	1.28E+05	1.21E+05	1.09E+05	1.25E+05	587.94383	3	51.82
VIP1	YLR410W	FTPVNITSPNLSFQK	[8] Phospho (ST)	0.41	0.18	0.08	0.22	0.088	0.238	0.399	0.09	2.65E+05	3.76E+05	2.16E+05	3.66E+05	4.37E+05	3.33E+05	3.53E+05	3.04E+05	3.18E+05	2.61E+05	3.65E+05	2.78E+05	886.93601	2	40.21
BOI1	YBL085W	SLEPSSESVR	[1] Phospho (ST)	-0.32	-0.10	-0.02	-0.21	0.073	0.335	0.453	0.15	9.19E+04	7.66E+04	1.10E+05	7.52E+04	6.93E+04	7.94E+04	7.51E+04	7.92E+04	1.06E+05	1.03E+05	7.72E+04	9.36E+04	585.75615	2	32.22
MAK11	YKL021C	KRDAETADIGDQSEVESDTEELK	[13] Phospho (ST)|[17] Phospho (ST)	-0.03	-0.15	-0.06	0.12	0.415	0.293	0.422	0.33	3.97E+05	3.09E+05	3.41E+05	3.34E+05	3.78E+05	3.13E+05	2.62E+05	4.19E+05	2.64E+05	4.51E+05	2.70E+05	2.86E+05	909.04216	3	45.35
MDG1	YNL173C	SIFSQEVVELPDSEDETQQVNK	[13] Phospho (ST)	-0.28	-0.08	-0.39	-0.20	0.208	0.403	0.113	0.27	4.93E+05	5.26E+05	3.16E+05	2.98E+05	4.77E+05	3.26E+05	3.77E+05	5.38E+05	3.51E+05	3.10E+05	4.07E+05	3.02E+05	867.72641	3	30.67
LSB3	R024C-A	LAPTNSGGSGGKLDDPSGASSYYASHR	[6] Phospho (ST)|[9] Phospho (ST)	-0.79	-0.58	-0.48	-0.21	0.002	0.037	0.007	0.26	4.47E+05	3.90E+05	3.73E+05	2.69E+05	2.09E+05	2.21E+05	2.22E+05	3.71E+05	2.18E+05	2.78E+05	2.69E+05	3.21E+05	938.05878	3	41.18
YDR333C	YDR333C	DKGSDDDDDEEFDK	[4] Phospho (ST)	0.20	-0.21	-0.14	0.41	0.267	0.286	0.324	0.13	2.95E+05	1.68E+05	2.32E+05	3.24E+05	2.65E+05	2.07E+05	1.32E+05	2.48E+05	2.21E+05	2.53E+05	1.93E+05	1.87E+05	912.80229	2	76.55
FPR4	YLR449W	GEYYNQDNNDGLEEDESESEQEADVPK	[17] Phospho (ST)|[19] Phospho (ST)	-0.37	-0.34	0.05	-0.03	0.236	0.286	0.431	0.49	1.39E+06	9.24E+05	8.62E+05	4.13E+05	1.28E+06	7.70E+05	4.01E+05	1.47E+06	6.36E+05	1.24E+06	1.06E+06	9.90E+05	1088.3967	3	38.28
PMA1	YGL008C	SVEDFMAAMQRVSTQHEK	[13] Phospho (ST)|[14] Phospho (ST)	-1.02	-0.36	-0.10	-0.66	0.052	0.234	0.404	0.20	8.75E+05	1.08E+06	6.47E+05	4.13E+05	7.25E+05	1.42E+05	6.33E+05	1.05E+06	3.41E+05	5.98E+05	1.20E+06	6.19E+05	1127.458	2	21.34
EDE1	YBL047C	YPAPGTSPSHNEGNSK	[6] Phospho (ST)	0.19	0.22	0.24	-0.03	0.042	0.172	0.045	0.45	1.04E+05	8.75E+04	9.46E+04	1.16E+05	1.04E+05	1.07E+05	1.20E+05	8.36E+04	1.30E+05	1.12E+05	1.02E+05	1.24E+05	574.90891	3	28.36
NHA1	YLR138W	KRTLTPAPPR	[3] Phospho (ST)|[5] Phospho (ST)	-0.14	0.09	-0.09	-0.23	0.135	0.166	0.262	0.04	5.83E+04	6.10E+04	6.71E+04	5.83E+04	4.99E+04	6.16E+04	6.25E+04	6.51E+04	7.10E+04	6.70E+04	4.99E+04	5.79E+04	432.87897	3	16.28
IST2	YBR086C	VPTVGSYGVAGATLPETIPTSK	[6] Phospho (ST)|[7] Phospho (Y)	-0.49	0.03	-0.29	-0.52	0.145	0.468	0.226	0.14	7.98E+05	1.06E+06	5.32E+05	5.34E+05	7.72E+05	4.02E+05	7.56E+05	1.13E+06	5.61E+05	6.30E+05	8.10E+05	5.12E+05	769.03142	3	20.76
PRS5	YOL061W	TLSFSR	[3] Phospho (ST)	-0.07	0.22	0.05	-0.29	0.369	0.171	0.408	0.06	4.30E+04	6.50E+04	5.12E+04	5.29E+04	4.63E+04	5.28E+04	6.15E+04	7.13E+04	5.32E+04	5.61E+04	6.05E+04	4.81E+04	395.67849	2	22.17
DNF2	YDR093W	LRTSLDR	[3] Phospho (ST)	-0.11	0.49	0.73	-0.61	0.454	0.257	0.149	0.11	2.35E+04	8.71E+03	6.93E+04	2.20E+04	2.13E+04	5.06E+04	4.89E+04	3.61E+04	5.79E+04	5.70E+04	4.92E+04	6.21E+04	470.7343	2	18.7
NET1	YJL076W	KSSLETIVEK	[3] Phospho (ST)	0.16	-0.06	0.19	0.22	0.155	0.395	0.215	0.17	8.80E+04	9.25E+04	1.07E+05	1.01E+05	9.77E+04	1.23E+05	1.12E+05	7.16E+04	9.31E+04	8.14E+04	1.18E+05	1.30E+05	607.30763	2	50.21
TSL1	YML100W	IASPIQHEHDSGSR	[3] Phospho (ST)	0.28	-0.42	0.14	0.71	0.002	0.122	0.289	0.03	6.74E+04	6.74E+04	6.24E+04	8.28E+04	7.78E+04	7.96E+04	6.90E+04	2.73E+04	5.10E+04	5.62E+04	6.77E+04	9.37E+04	538.57397	3	27.53
RRP5	YMR229C	SKVEDAEYESSDDEDEK	[8] Phospho (Y)|[11] Phospho (ST)	-0.18	-0.31	-0.30	0.13	0.303	0.304	0.208	0.40	5.69E+05	2.78E+05	4.27E+05	4.02E+05	3.99E+05	3.26E+05	1.23E+05	5.33E+05	3.75E+05	3.89E+05	2.99E+05	3.46E+05	1067.8671	2	44.95
CHD1	YER164W	AAAHQQNYFNDSDDEDDEDNIK	[12] Phospho (ST)	-0.40	-0.09	-0.14	-0.31	0.057	0.343	0.295	0.06	3.17E+05	2.25E+05	3.14E+05	2.40E+05	1.86E+05	2.22E+05	2.42E+05	3.14E+05	2.51E+05	3.21E+05	2.09E+05	2.48E+05	878.66868	3	75.87
TPK3	YKL166C	KLSITAK	[3] Phospho (ST)	0.25	-0.80	-0.32	1.05	0.083	0.066	0.274	0.03	3.93E+04	3.63E+04	3.80E+04	5.15E+04	3.72E+04	4.65E+04	2.32E+04	6.39E+03	3.57E+04	1.40E+04	2.47E+04	5.24E+04	420.73304	2	47.65
AIM38	YNR018W	IITGAWAASLYGSWVIVNK	[11] Phospho (Y)	-1.36	-1.75	0.29	0.39	0.162	0.131	0.372	0.26	4.82E+05	1.33E+05	8.68E+04	8.03E+04	1.36E+05	5.69E+04	5.30E+04	1.09E+05	4.64E+04	1.30E+05	3.75E+05	3.52E+05	710.36507	3	19.77
MRH1	YDR033W	PAATPNLSK	[8] Phospho (ST)	-0.21	0.25	0.21	-0.46	0.140	0.148	0.131	0.03	6.91E+04	6.56E+04	9.12E+04	6.28E+04	6.69E+04	6.60E+04	9.32E+04	7.27E+04	1.04E+05	8.20E+04	8.37E+04	9.59E+04	489.73616	2	33.64
SSD1	YDR293C	NQSQQPQQQLSPFR	[11] Phospho (ST)	-0.20	0.08	0.12	-0.28	0.013	0.349	0.223	0.12	2.36E+05	2.20E+05	2.44E+05	1.94E+05	2.07E+05	2.10E+05	1.87E+05	2.61E+05	2.92E+05	2.60E+05	2.11E+05	2.89E+05	883.40531	2	49.6
NUP2	YLR335W	ETYDSNESDDDVTPSTK	[3] Phospho (Y)|[8] Phospho (ST)	-0.01	-0.22	-0.13	0.20	0.486	0.346	0.388	0.30	6.74E+05	2.79E+05	4.83E+05	4.94E+05	4.13E+05	5.16E+05	2.31E+05	5.99E+05	4.07E+05	5.74E+05	3.36E+05	4.04E+05	1031.8567	2	29.63
SLA2	YNL243W	TPTPTPPVVAEPAISPRPVSQR	[1] Phospho (ST)|[15] Phospho (ST)	-0.58	-0.02	-0.12	-0.56	0.056	0.472	0.359	0.03	3.15E+05	4.87E+05	3.04E+05	2.58E+05	2.55E+05	2.25E+05	3.57E+05	4.38E+05	2.95E+05	3.27E+05	4.25E+05	2.67E+05	819.73657	3	27.29
PAN1	YIR006C	GLDEDEDDGWSDEDESNNR	[11] Phospho (ST)	-0.25	0.04	-0.02	-0.29	0.080	0.442	0.452	0.14	5.46E+05	4.16E+05	4.51E+05	3.56E+05	4.25E+05	4.04E+05	3.77E+05	6.06E+05	4.66E+05	4.46E+05	4.56E+05	4.95E+05	1138.8911	2	64.92
CDC14	YFR028C	SSAVPQTSPGQPR	[8] Phospho (ST)	0.07	1.34	0.81	-1.27	0.343	0.001	0.009	0.00	8.33E+04	6.55E+04	8.81E+04	8.45E+04	7.24E+04	9.14E+04	1.86E+05	1.87E+05	2.26E+05	1.62E+05	1.14E+05	1.41E+05	696.31916	2	30.73
LAC1	YKL008C	STIKPSPSNNNLK	[N-term] Acetyl (Protein N-term)|[8] Phospho	-0.07	0.27	0.41	-0.34	0.402	0.207	0.083	0.17	1.51E+05	1.02E+05	1.46E+05	1.14E+05	1.04E+05	1.62E+05	1.16E+05	1.62E+05	2.02E+05	1.70E+05	1.45E+05	2.16E+05	761.36936	2	30.4
CBF5	YLR175W	EYVPLDNAEQSTSSSQETK	[18] Phospho (ST)	2.19	0.04	-0.62	2.16	0.001	0.413	0.003	0.00	2.68E+05	2.18E+05	2.52E+05	1.36E+06	1.11E+06	9.00E+05	2.14E+05	2.91E+05	2.52E+05	1.68E+05	1.45E+05	1.67E+05	1096.9653	2	38.96
BUD22	YMR014W	TANANQTHSNIDYDTDDGNEK	[13] Phospho (Y)	-0.06	0.11	0.03	-0.17	0.389	0.341	0.458	0.26	1.79E+05	1.26E+05	1.40E+05	1.65E+05	1.37E+05	1.26E+05	1.30E+05	2.02E+05	1.49E+05	1.94E+05	1.14E+05	1.47E+05	801.65083	3	57.41
LYS21	YDL131W	DFHAELSTPLLK	[8] Phospho (ST)	-0.09	0.55	0.02	-0.65	0.404	0.170	0.484	0.12	1.09E+05	2.16E+05	1.23E+05	1.17E+05	1.67E+05	1.36E+05	3.24E+05	1.41E+05	1.92E+05	1.06E+05	1.83E+05	1.64E+05	725.85286	2	47.93
MCK1	YNL307C	KLEHNQPSISYICSR	[11] Phospho (Y)	0.09	-0.21	-0.09	0.31	0.168	0.041	0.344	0.01	4.55E+05	5.36E+05	5.28E+05	5.13E+05	5.35E+05	5.74E+05	4.30E+05	4.14E+05	4.66E+05	3.94E+05	4.25E+05	6.07E+05	956.44281	2	46.14
DCP2	YNL118C	NPISSTVSSNQQSPK	[13] Phospho (ST)	0.12	-0.02	-0.08	0.14	0.201	0.459	0.365	0.16	7.71E+04	7.12E+04	9.64E+04	8.60E+04	9.19E+04	8.88E+04	6.55E+04	8.81E+04	8.76E+04	9.27E+04	6.33E+04	7.61E+04	551.92109	3	34.1
YAK1	YJL141C	TVYTYIQSR	[5] Phospho (Y)	0.41	0.72	-0.09	-0.31	0.091	0.140	0.400	0.27	4.39E+04	8.69E+04	5.80E+04	8.86E+04	8.09E+04	8.17E+04	7.57E+04	1.64E+05	7.16E+04	7.19E+04	5.18E+04	5.36E+04	605.77907	2	49.55
TOD6	YBL054W	RNSFIPSTQIPHSTTK	[3] Phospho (ST)	-0.10	-0.14	0.11	0.04	0.210	0.307	0.293	0.44	1.17E+05	1.29E+05	1.01E+05	1.03E+05	1.14E+05	1.07E+05	1.39E+05	7.97E+04	9.69E+04	9.94E+04	1.41E+05	1.34E+05	631.97903	3	37.38
SMI1	YGR229C	GEDSGSADVQSVQDHESVK	[11] Phospho (ST)	0.12	-0.07	0.06	0.19	0.256	0.377	0.375	0.21	1.45E+05	1.20E+05	1.59E+05	1.79E+05	1.38E+05	1.44E+05	1.27E+05	1.09E+05	1.67E+05	1.72E+05	1.24E+05	1.46E+05	685.28374	3	20.39
TGL1	YKL140W	RLSAYLESSK	[3] Phospho (ST)	0.03	0.22	0.01	-0.19	0.446	0.316	0.490	0.32	9.02E+04	1.52E+05	1.39E+05	1.27E+05	1.21E+05	1.41E+05	2.16E+05	9.80E+04	1.29E+05	1.06E+05	1.36E+05	1.41E+05	617.29761	2	44.75
PHO84	YML123C	ASTAVESLDNHPPK	[3] Phospho (ST)|[7] Phospho (ST)	-2.74	-1.20	-0.87	-1.54	0.000	0.003	0.006	0.00	3.79E+05	2.78E+05	3.77E+05	5.92E+04	4.30E+04	5.28E+04	1.30E+05	1.84E+05	1.36E+05	2.07E+05	1.60E+05	1.99E+05	813.33475	2	42.04
MRH1	YDR033W	APVASPRPAATPNLSK	[5] Phospho (ST)	-0.16	0.49	0.25	-0.65	0.037	0.096	0.056	0.06	8.37E+04	9.25E+04	8.32E+04	7.63E+04	7.34E+04	8.17E+04	1.58E+05	8.25E+04	1.23E+05	1.02E+05	9.05E+04	1.17E+05	552.95398	3	20.24
UTP14	YML093W	EINGEFDNSSDNDK	[10] Phospho (ST)	-0.05	-0.47	0.14	0.42	0.454	0.172	0.353	0.10	2.67E+05	1.14E+05	2.50E+05	1.99E+05	1.67E+05	2.46E+05	1.08E+05	1.58E+05	1.91E+05	2.42E+05	2.00E+05	2.51E+05	832.31059	2	31.51
LYS21	YDL131W	DFHAELSTPLLKPVNK	[8] Phospho (ST)	-0.59	0.13	0.06	-0.72	0.121	0.406	0.456	0.10	1.99E+05	3.96E+05	2.12E+05	1.74E+05	2.10E+05	1.52E+05	4.42E+05	2.10E+05	2.31E+05	1.63E+05	3.98E+05	2.79E+05	944.9828	2	35.36
RPL17A	YKL180W	RFNSSIGR	[4] Phospho (ST)	-1.19	-0.62	0.75	-0.57	0.075	0.179	0.071	0.10	2.10E+04	4.10E+04	6.73E+04	1.77E+04	1.51E+04	2.37E+04	2.98E+04	1.78E+04	3.65E+04	6.78E+04	5.99E+04	9.02E+04	508.73728	2	36.82
YAK1	YJL141C	RKSSLVVPPAR	[3] Phospho (ST)|[4] Phospho (ST)	0.31	0.19	-0.15	0.12	0.110	0.297	0.317	0.34	1.07E+05	1.22E+05	1.63E+05	1.74E+05	1.35E+05	1.76E+05	1.05E+05	1.96E+05	1.44E+05	1.51E+05	9.11E+04	1.12E+05	457.23	3	29.27
VNX1	YNL321W	SHSVPDLNTATPSSPK	[14] Phospho (ST)	0.34	0.36	0.09	-0.02	0.045	0.045	0.264	0.46	1.48E+05	1.98E+05	1.79E+05	2.18E+05	1.98E+05	2.51E+05	2.55E+05	1.97E+05	2.21E+05	1.74E+05	1.90E+05	1.94E+05	859.39362	2	78.3

CHO1	YER026C	RASSIFSINTTPLAPPNATDIQK	[10] Phospho (ST)	-0.43	-0.06	-0.05	-0.36	0.080	0.400	0.441	0.05	5.06E+05	4.73E+05	3.16E+05	3.11E+05	3.70E+05	2.82E+05	4.74E+05	4.15E+05	3.49E+05	3.28E+05	5.54E+05	3.70E+05	841.42779	3	16.85
IGO2	R132W-A	SEDLSPTSSR	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.01	0.10	0.10	-0.09	0.489	0.382	0.369	0.37	1.33E+05	7.73E+04	1.29E+05	1.23E+05	9.26E+04	1.26E+05	8.87E+04	1.32E+05	1.43E+05	1.47E+05	1.00E+05	1.18E+05	600.74308	2	20.74
HSP12	YFL014W	ASEALKPDSQK	[9] Phospho (ST)	4.92	-0.36	-1.40	5.29	0.002	0.224	0.031	0.00	1.10E+04	5.62E+03	5.96E+03	2.41E+05	1.60E+05	2.85E+05	7.01E+03	3.90E+03	6.65E+03	3.85E+03	2.53E+03	2.19E+03	627.29214	2	42.09
PIL1	YGR086C	ALLELLDDSPVTPGETRPAYDGYEASK	[12] Phospho (ST)	0.70	0.35	-0.13	0.36	0.022	0.242	0.402	0.14	2.64E+05	3.78E+05	1.82E+05	4.72E+05	4.62E+05	4.08E+05	5.03E+05	2.98E+05	2.46E+05	1.79E+05	3.92E+05	1.81E+05	996.46971	3	49.3
EDC3	YEL015W	SNSTSLPAANK	[3] Phospho (ST)	0.05	0.42	0.57	-0.38	0.465	0.232	0.171	0.15	4.23E+04	3.24E+04	9.42E+04	6.55E+04	5.51E+04	5.36E+04	5.00E+04	9.75E+04	7.88E+04	1.16E+05	6.18E+04	7.28E+04	585.26435	2	62.22
SVL3	YPL032C	KPSFPQLQQSANVR	[3] Phospho (ST)	-0.28	-0.36	-0.41	0.08	0.053	0.048	0.031	0.24	3.29E+05	4.25E+05	4.35E+05	3.25E+05	3.20E+05	3.32E+05	3.03E+05	3.49E+05	2.70E+05	2.61E+05	3.22E+05	3.09E+05	560.61418	3	47.97
UTP14	YML093W	ELAAVSSDEDNEDHDIAR	[6] Phospho (ST)|[7] Phospho (ST)	-0.26	-0.09	-0.32	-0.17	0.136	0.386	0.060	0.29	2.23E+05	1.73E+05	2.43E+05	1.43E+05	1.95E+05	1.97E+05	1.43E+05	2.59E+05	2.01E+05	1.64E+05	1.80E+05	1.70E+05	715.93913	3	22.77
MYO4	YAL029C	IYSTWLVK	[2] Phospho (Y)	0.14	0.05	0.22	0.08	0.270	0.454	0.324	0.43	6.58E+04	4.94E+04	5.64E+04	5.91E+04	5.30E+04	7.67E+04	8.34E+04	2.62E+04	6.86E+04	4.16E+04	5.55E+04	1.03E+05	545.27003	2	16.29
BUD22	YMR014W	ETTSDNEDLLIK	[4] Phospho (ST)	-0.02	-0.02	0.03	0.00	0.432	0.413	0.437	0.49	2.35E+05	2.40E+05	2.21E+05	2.30E+05	2.61E+05	1.93E+05	2.23E+05	2.51E+05	2.12E+05	2.31E+05	2.80E+05	1.97E+05	729.32512	2	31.59
IST2	YBR086C	VPTVGSYGVAGATLPETIPTSK	[3] Phospho (ST)|[6] Phospho (ST)	-0.53	-0.15	-0.27	-0.39	0.110	0.365	0.240	0.19	1.44E+06	1.79E+06	9.17E+05	9.85E+05	1.19E+06	6.86E+05	1.18E+06	1.72E+06	8.45E+05	1.18E+06	1.42E+06	8.25E+05	1153.0426	2	57.26
BEM1	YBR200W	KLSDLSLSGSK	[3] Phospho (ST)|[6] Phospho (ST)	-0.60	-0.14	-0.15	-0.46	0.007	0.285	0.244	0.09	1.35E+05	1.11E+05	1.22E+05	9.51E+04	7.32E+04	7.46E+04	8.68E+04	1.44E+05	1.04E+05	1.39E+05	9.74E+04	9.57E+04	647.78867	2	31.96
PBP1	YGR178C	TVSPTTQISAGK	[3] Phospho (ST)	0.33	0.07	-0.05	0.27	0.067	0.371	0.411	0.02	9.67E+04	1.31E+05	1.53E+05	1.66E+05	1.46E+05	1.68E+05	1.46E+05	1.24E+05	1.28E+05	1.31E+05	1.09E+05	1.27E+05	635.3069	2	79.95
NOC2	YOR206W	DLLDFAGTNPLDGIDSQDEGEDAER	[16] Phospho (ST)	-0.03	0.13	-0.10	-0.16	0.478	0.370	0.416	0.31	5.89E+05	9.73E+05	4.08E+05	5.27E+05	8.91E+05	5.15E+05	7.65E+05	8.04E+05	5.92E+05	4.92E+05	8.42E+05	4.98E+05	924.72334	3	81.66
NOP12	YOL041C	LFGTNPIAETEESGNEKEEESSK	[13] Phospho (ST)	-0.11	-0.09	0.18	-0.02	0.246	0.274	0.156	0.40	3.24E+05	3.58E+05	2.69E+05	3.07E+05	3.13E+05	2.61E+05	3.18E+05	2.83E+05	2.95E+05	3.17E+05	4.05E+05	3.55E+05	869.04534	3	47.31
ZEO1	YOL109W	NEATPEAEQVKKEEQNIADGVEQK	[4] Phospho (ST)	-0.85	-0.59	-0.46	-0.26	0.002	0.007	0.061	0.12	4.12E+05	3.90E+05	3.45E+05	2.47E+05	1.81E+05	2.10E+05	2.96E+05	2.48E+05	2.17E+05	1.96E+05	2.75E+05	3.66E+05	922.09458	3	39.72
MAK21	YDR060W	NLLTNTPVDYEYESDAEEEQGDK	[12] Phospho (Y)	-0.06	-0.04	-0.17	-0.02	0.396	0.444	0.253	0.46	4.62E+05	6.05E+05	3.70E+05	4.46E+05	5.08E+05	4.21E+05	4.65E+05	5.64E+05	3.68E+05	4.33E+05	4.68E+05	3.74E+05	913.71225	3	63.07
LYS21	YDL131W	DFHAELSTPLLKPVNK	[8] Phospho (ST)	-0.31	0.27	0.16	-0.58	0.218	0.298	0.370	0.14	5.88E+04	1.08E+05	6.60E+04	5.80E+04	7.78E+04	5.28E+04	1.40E+05	7.00E+04	7.13E+04	4.94E+04	1.19E+05	9.22E+04	472.99467	4	16.14
IST2	YBR086C	SSAESSNATNNNTLGTESK	[2] Phospho (ST)	-0.47	-0.51	-0.26	0.04	0.151	0.145	0.288	0.44	3.43E+05	1.52E+05	2.58E+05	2.13E+05	1.84E+05	1.48E+05	1.25E+05	1.96E+05	2.09E+05	2.86E+05	1.51E+05	1.92E+05	996.41292	2	72.77
SKG3	YLR187W	NEDLGSLK	[6] Phospho (ST)	0.27	0.25	0.34	0.02	0.185	0.204	0.124	0.45	4.32E+04	3.10E+04	5.72E+04	6.16E+04	4.47E+04	5.25E+04	4.27E+04	5.61E+04	5.73E+04	6.36E+04	4.93E+04	5.37E+04	478.21051	2	22.46
PFK2	YMR205C	VHSYTDLAYR	[4] Phospho (Y)	-0.36	0.21	-0.19	-0.57	0.230	0.345	0.347	0.10	2.82E+04	6.88E+04	3.82E+04	3.56E+04	3.52E+04	3.44E+04	7.49E+04	3.82E+04	4.35E+04	2.98E+04	4.46E+04	4.41E+04	435.52733	3	34.91
SLA1	YBL007C	AAASTPEPNLK	[5] Phospho (ST)	0.43	-0.08	0.00	0.51	0.074	0.376	0.493	0.06	8.99E+04	8.31E+04	1.19E+05	1.28E+05	1.06E+05	1.58E+05	1.07E+05	6.80E+04	1.00E+05	8.04E+04	8.98E+04	1.22E+05	589.77621	2	26.32
TAF4	YMR005W	NVSPTTNLR	[3] Phospho (ST)	0.75	0.26	-0.09	0.49	0.014	0.167	0.356	0.05	3.81E+04	3.38E+04	4.86E+04	6.44E+04	5.76E+04	8.06E+04	3.99E+04	4.54E+04	5.88E+04	3.34E+04	3.41E+04	4.59E+04	541.2556	2	31.6
RCK2	YLR248W	DVSQITSSPKK	[3] Phospho (ST)	0.07	-0.12	-0.04	0.19	0.405	0.381	0.439	0.24	2.15E+04	3.00E+04	4.13E+04	3.59E+04	3.03E+04	3.12E+04	3.28E+04	1.90E+04	3.37E+04	3.09E+04	2.93E+04	2.97E+04	423.87432	3	21.48
EDE1	YBL047C	YPAPGTSPSHNEGNSK	[6] Phospho (ST)	-0.15	-0.46	-0.42	0.31	0.194	0.034	0.008	0.12	2.22E+05	1.83E+05	1.89E+05	2.12E+05	1.63E+05	1.60E+05	1.45E+05	1.11E+05	1.75E+05	1.52E+05	1.42E+05	1.50E+05	861.86042	2	49.01
YLR257W	YLR257W	GESYQSAEQEIDHTAPEK	[3] Phospho (ST)	1.04	0.68	0.76	0.36	0.003	0.004	0.000	0.06	7.04E+04	7.99E+04	7.79E+04	1.86E+05	1.49E+05	1.35E+05	1.32E+05	1.30E+05	1.04E+05	1.25E+05	1.23E+05	1.39E+05	700.29205	3	53.61
RCN2	YOR220W	SRSTDDAVSLQDNNLALLEDHR	[3] Phospho (ST)	0.54	0.63	0.29	-0.08	0.034	0.089	0.174	0.39	1.60E+05	2.46E+05	1.42E+05	2.62E+05	2.81E+05	2.54E+05	3.80E+05	2.59E+05	2.06E+05	1.99E+05	2.64E+05	2.07E+05	850.393	3	63.57
RPL1B	YGL135W	ITSSQVR	[4] Phospho (ST)	2.55	0.05	-0.20	2.50	0.003	0.461	0.388	0.00	1.92E+04	5.54E+03	1.15E+04	8.78E+04	5.40E+04	7.05E+04	1.04E+04	1.18E+04	1.53E+04	1.68E+04	7.98E+03	6.75E+03	435.70754	2	29.38
PAR32	YDL173W	GGAGNIISPK	[8] Phospho (ST)	0.35	0.03	-0.04	0.32	0.182	0.453	0.445	0.18	5.89E+04	7.21E+04	9.58E+04	7.98E+04	7.85E+04	1.31E+05	7.52E+04	6.67E+04	8.97E+04	6.33E+04	7.47E+04	8.33E+04	497.24214	2	34.38
NET1	YJL076W	IEAPSPSVNK	[5] Phospho (ST)	0.24	0.90	0.85	-0.65	0.142	0.006	0.005	0.02	4.98E+04	4.03E+04	5.53E+04	6.54E+04	4.62E+04	6.07E+04	8.27E+04	8.10E+04	1.07E+05	8.58E+04	7.56E+04	1.01E+05	561.26533	2	17.86
UTP14	YML093W	ELAAVSSDEDNEDHDIAR	[6] Phospho (ST)|[7] Phospho (ST)	-0.40	-0.35	-0.44	-0.05	0.053	0.113	0.015	0.43	4.21E+05	3.27E+05	4.13E+05	2.28E+05	3.16E+05	3.36E+05	2.10E+05	3.79E+05	3.23E+05	2.87E+05	2.76E+05	2.92E+05	1073.4052	2	36.01
RFA1	YAR007C	FANENPNSQK	[8] Phospho (ST)	2.79	-0.08	1.41	2.87	0.010	0.468	0.049	0.01	4.03E+04	1.12E+04	9.94E+03	1.99E+05	9.25E+04	1.33E+05	3.49E+04	1.20E+04	1.13E+04	7.20E+04	3.10E+04	6.03E+04	614.75322	2	25.38
ENT1	YDL161W	GTGRSDENDDDLQR	[2] Phospho (ST)	0.18	-0.49	0.00	0.68	0.270	0.116	0.498	0.01	1.37E+05	7.22E+04	9.00E+04	1.25E+05	1.12E+05	1.02E+05	6.09E+04	6.65E+04	8.49E+04	1.22E+05	8.25E+04	9.43E+04	829.32737	2	33.65
NRD1	YNL251C	SRSPPAPFSQPSTGR	[1] Phospho (ST)|[3] Phospho (ST)	-0.02	-0.28	-0.34	0.26	0.429	0.156	0.023	0.19	2.76E+05	2.70E+05	3.01E+05	2.97E+05	2.42E+05	2.95E+05	1.70E+05	3.12E+05	2.16E+05	2.44E+05	1.86E+05	2.38E+05	866.36682	2	20.97
MTC1	YJL123C	EADATPDDDRSSISSNSNK	[15] Phospho (ST)	0.11	-0.76	-0.26	0.87	0.362	0.040	0.209	0.01	2.09E+05	1.18E+05	1.63E+05	2.11E+05	1.77E+05	1.40E+05	8.17E+04	8.74E+04	1.19E+05	1.57E+05	1.11E+05	1.41E+05	1044.9222	2	49.63
TOD6	YBL054W	SFSHSITTNTPNVK	[3] Phospho (ST)	0.21	0.08	0.44	0.13	0.231	0.392	0.058	0.22	5.56E+04	1.04E+05	8.27E+04	9.50E+04	8.09E+04	1.04E+05	9.86E+04	7.87E+04	7.86E+04	1.05E+05	1.13E+05	1.10E+05	806.87226	2	47.21
AIM21	YIR003W	SIPEEQREQSPNK	[10] Phospho (ST)	0.29	0.15	0.03	0.14	0.165	0.348	0.474	0.31	1.31E+05	6.85E+04	9.95E+04	1.29E+05	1.04E+05	1.34E+05	8.24E+04	1.02E+05	1.48E+05	1.33E+05	6.75E+04	1.04E+05	811.36484	2	45.24
FRA1	YLL029W	RASLFLR	[3] Phospho (ST)	-0.02	0.13	-0.27	-0.14	0.474	0.404	0.263	0.38	3.51E+04	6.27E+04	4.76E+04	4.16E+04	4.97E+04	5.23E+04	7.98E+04	2.70E+04	5.20E+04	2.44E+04	4.22E+04	5.43E+04	471.74977	2	27.98
VPS27	YNR006W	ANSSPTTNIDHLK	[4] Phospho (ST)	0.34	0.36	0.32	-0.02	0.048	0.050	0.042	0.47	7.45E+04	7.11E+04	8.71E+04	8.69E+04	9.41E+04	1.15E+05	1.02E+05	8.29E+04	1.14E+05	8.81E+04	9.23E+04	1.11E+05	739.33815	2	40.37
YEF3	YLR249W	KLSSAELR	[3] Phospho (ST)	0.94	0.37	0.32	0.58	0.025	0.240	0.257	0.03	1.16E+04	3.53E+04	4.16E+04	4.96E+04	6.01E+04	6.08E+04	4.51E+04	2.61E+04	4.29E+04	2.77E+04	3.99E+04	4.30E+04	492.24988	2	30.84
GLY1	YEL046C	SESTEVDVDGNAIR	[4] Phospho (ST)	-0.09	0.25	0.00	-0.34	0.296	0.068	0.492	0.01	5.90E+04	6.64E+04	8.04E+04	6.56E+04	5.84E+04	6.94E+04	8.26E+04	7.57E+04	8.66E+04	7.57E+04	6.53E+04	6.51E+04	524.55778	3	26.56
TAF4	YMR005W	PAFNLSPGK	[6] Phospho (ST)	-0.12	0.57	0.04	-0.68	0.222	0.004	0.438	0.00	3.72E+04	4.87E+04	4.27E+04	3.56E+04	4.30E+04	3.98E+04	6.58E+04	5.86E+04	6.60E+04	3.21E+04	5.43E+04	4.58E+04	505.73911	2	38.1
SLN1	YIL147C	APGSDDEEGGNLGRPIENPK	[4] Phospho (ST)	-0.03	-0.07	0.12	0.04	0.332	0.255	0.123	0.35	1.28E+05	1.41E+05	1.44E+05	1.40E+05	1.26E+05	1.38E+05	1.46E+05	1.22E+05	1.24E+05	1.61E+05	1.37E+05	1.49E+05	711.31578	3	61.44
MSB1	YOR188W	RDSAPDNQGIYHTVISK	[3] Phospho (ST)	-0.32	-0.23	0.07	-0.08	0.008	0.025	0.305	0.19	1.60E+05	1.64E+05	1.80E+05	1.45E+05	1.27E+05	1.33E+05	1.55E+05	1.35E+05	1.38E+05	1.84E+05	1.48E+05	1.98E+05	660.9771	3	47.27
HRP1	YOL123W	SSDEEDFNDIYGDDKPTTTEEVKK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.13	0.08	0.04	-0.21	0.390	0.436	0.403	0.38	6.35E+05	5.72E+05	5.09E+05	2.60E+05	8.10E+05	5.00E+05	4.00E+05	9.75E+05	4.40E+05	6.41E+05	6.31E+05	4.92E+05	988.7267	3	60.46
NHA1	YLR138W	IHSLVDK	[3] Phospho (ST)	-0.88	0.72	-0.37	-1.61	0.082	0.107	0.233	0.03	5.07E+04	3.91E+04	2.24E+04	3.14E+04	1.20E+04	1.75E+04	6.40E+04	3.60E+04	8.54E+04	4.15E+04	2.56E+04	1.99E+04	446.22044	2	21.17
EDE1	YBL047C	RANSNEDGESVSSIQESPK	[17] Phospho (ST)	-0.15	0.07	0.29	-0.22	0.247	0.379	0.136	0.15	1.46E+05	1.22E+05	1.76E+05	1.41E+05	1.10E+05	1.49E+05	1.59E+05	1.30E+05	1.76E+05	1.73E+05	1.50E+05	2.21E+05	705.30594	3	40.05
RPL17A	YKL180W	FNSSIGR	[4] Phospho (ST)	-1.32	-0.73	0.70	-0.59	0.055	0.138	0.061	0.08	2.73E+04	3.79E+04	7.15E+04	1.98E+04	1.55E+04	1.94E+04	1.99E+04	2.51E+04	3.75E+04	8.36E+04	6.45E+04	7.34E+04	430.68663	2	32.66
MKT1	YNL085W	SNLSSPSSASSSASPATTVTK	[4] Phospho (ST)|[5] Phospho (ST)	-0.17	0.09	0.12	-0.26	0.153	0.393	0.322	0.23	5.18E+05	4.08E+05	5.35E+05	4.76E+05	3.99E+05	4.26E+05	3.92E+05	7.20E+05	4.44E+05	6.81E+05	4.63E+05	4.45E+05	1063.9488	2	81.36
PHO91	YNR013C	RPSNTFNLDADR	[3] Phospho (ST)	0.44	0.06	0.03	0.38	0.027	0.349	0.441	0.02	1.14E+05	1.41E+05	1.51E+05	1.68E+05	1.71E+05	2.10E+05	1.44E+05	1.29E+05	1.49E+05	1.07E+05	1.47E+05	1.62E+05	743.32817	2	44.96
VHS2	YIL135C	RPSTIGLDR	[3] Phospho (ST)	0.08	-0.17	-0.13	0.26	0.357	0.293	0.322	0.22	5.81E+04	7.99E+04	7.95E+04	7.06E+04	6.72E+04	9.23E+04	7.96E+04	4.07E+04	7.25E+04	5.23E+04	6.16E+04	8.54E+04	547.77151	2	48.62
YOR343W-A	R343W-A	VNNDHINESTVSSQYLSDDNELSLRPATER	[17] Phospho (ST)	-0.62	-0.16	-0.19	-0.46	0.002	0.189	0.070	0.04	5.78E+05	6.68E+05	6.73E+05	3.77E+05	4.12E+05	4.61E+05	6.28E+05	6.38E+05	4.52E+05	5.15E+05	6.19E+05	5.45E+05	871.65013	4	62.84
SEC16	YPL085W	SSEEQPENISK	[10] Phospho (ST)	0.35	0.03	-0.14	0.32	0.116	0.467	0.313	0.10	8.21E+04	4.78E+04	7.87E+04	1.01E+05	7.43E+04	8.98E+04	6.82E+04	5.78E+04	8.63E+04	7.29E+04	5.15E+04	6.44E+04	664.27355	2	15.82
MRH1	YDR033W	PAATPNLSK	[4] Phospho (ST)	-1.57	-0.58	-2.13	-0.99	0.164	0.319	0.128	0.18	1.51E+05	3.13E+04	2.71E+04	4.15E+04	1.03E+04	1.85E+04	2.58E+04	2.70E+04	8.73E+04	1.43E+04	1.44E+04	1.90E+04	489.73643	2	37.88
YLR413W	YLR413W	AVQESDSTTSRIIEEHESPIDAEK	[7] Phospho (ST)|[10] Phospho (ST)	-0.94	-0.55	-0.66	-0.39	0.012	0.057	0.025	0.09	5.95E+05	3.95E+05	4.30E+05	2.47E+05	2.76E+05	2.17E+05	2.46E+05	3.93E+05	3.28E+05	2.97E+05	3.18E+05	2.86E+05	944.40653	3	24.48
ENT1	YDL161W	RNQLVAASSPQQLQQQK	[9] Phospho (ST)	0.03	0.18	0.21	-0.16	0.445	0.252	0.251	0.26	1.21E+05	9.66E+04	1.39E+05	1.34E+05	1.05E+05	1.24E+05	9.85E+04	1.50E+05	1.57E+05	1.69E+05	9.59E+04	1.46E+05	668.67261	3	33.62
EIS1	YMR031C	NNSITSATSK	[3] Phospho (ST)	0.36	-0.43	0.12	0.78	0.258	0.273	0.441	0.00	1.48E+05	3.41E+04	7.78E+04	1.28E+05	1.01E+05	1.05E+05	5.40E+04	7.25E+04	6.72E+04	1.63E+05	6.35E+04	5.60E+04	551.74257	2	43.92
GIP3	YPL137C	STSISNAVVSSK	[3] Phospho (ST)	-0.04	0.08	0.16	-0.11	0.410	0.279	0.160	0.16	1.04E+05	7.88E+04	9.76E+04	9.58E+04	8.01E+04	9.74E+04	1.03E+05	9.18E+04	1.01E+05	9.30E+04	1.06E+05	1.14E+05	630.2994	2	60.36
SKG6	YHR149C	SATPPAIGR	[3] Phospho (ST)	0.20	0.05	-0.23	0.15	0.114	0.410	0.109	0.18	3.66E+04	4.96E+04	4.89E+04	5.23E+04	4.78E+04	5.51E+04	4.90E+04	3.78E+04	5.27E+04	3.98E+04	3.49E+04	4.04E+04	475.22879	2	43.55
SEC31	YDL195W	NSRVPSLVATSESPR	[2] Phospho (ST)|[6] Phospho (ST)	-0.59	-0.32	-0.38	-0.26	0.007	0.084	0.025	0.15	1.35E+05	1.15E+05	1.41E+05	8.40E+04	7.76E+04	9.91E+04	8.48E+04	1.29E+05	9.88E+04	1.12E+05	1.02E+05	8.70E+04	587.26392	3	26.28
YPL247C	YPL247C	RSSISFGSSQR	[3] Phospho (ST)	-0.08	-0.11	-0.01	0.03	0.214	0.147	0.451	0.41	8.18E+04	8.63E+04	8.57E+04	8.25E+04	7.03E+04	8.72E+04	8.27E+04	6.82E+04	8.39E+04	9.17E+04	7.15E+04	8.80E+04	646.29335	2	57.36
MCK1	YNL307C	LEHNQPSISYICSR	[10] Phospho (Y)	0.33	0.30	0.10	0.02	0.024	0.053	0.197	0.42	6.96E+04	8.31E+04	9.07E+04	9.78E+04	1.10E+05	9.81E+04	9.21E+04	9.50E+04	1.13E+05	8.46E+04	8.77E+04	8.92E+04	595.26639	3	54.26
GNP1	YDR508C	KSSYITVDGIK	[4] Phospho (Y)|[6] Phospho (ST)	-0.72	-0.19	-0.68	-0.53	0.007	0.299	0.016	0.12	1.17E+05	1.61E+05	1.46E+05	9.04E+04	8.26E+04	8.45E+04	9.53E+04	1.79E+05	9.71E+04	9.24E+04	1.04E+05	6.84E+04	685.80435	2	42.24
SPT6	YGR116W	RVGDEGNAAESESDNVAASR	[11] Phospho (ST)	0.01	-0.14	-0.10	0.14	0.476	0.202	0.300	0.13	1.31E+05	1.12E+05	1.46E+05	1.38E+05	1.19E+05	1.35E+05	1.30E+05	1.04E+05	1.21E+05	1.43E+05	1.03E+05	1.17E+05	705.29681	3	45.94
NAB2	YGL122C	SQEQYTENLK	[N-term] Acetyl (Protein N-term)|[5] Phospho	2.02	0.59	-0.41	1.43	0.001	0.023	0.056	0.00	4.87E+04	4.26E+04	6.06E+04	2.41E+05	1.96E+05	1.78E+05	6.19E+04	8.55E+04	8.08E+04	4.38E+04	3.76E+04	3.32E+04	681.28522	2	28.88
GPD2	YOL059W	RSDSAVSIVHLK	[4] Phospho (ST)	0.07	-0.11	-0.02	0.18	0.402	0.418	0.476	0.33	3.74E+04	7.56E+04	6.19E+04	5.83E+04	6.10E+04	6.46E+04	8.40E+04	4.20E+04	3.64E+04	5.50E+04	5.13E+04	6.63E+04	464.573	3	26.09
URB2	YJR041C	SNLSYSVVSK	[6] Phospho (ST)	0.02	-1.50	-0.61	1.52	0.482	0.072	0.198	0.00	1.13E+05	3.35E+04	5.96E+04	7.00E+04	5.86E+04	8.09E+04	2.94E+04	3.33E+04	1.03E+04	6.15E+04	3.54E+04	3.84E+04	582.26968	2	25.81
STF2	YGR008C	DRRGSNLQSHEQK	[5] Phospho (ST)	0.17	-0.22	-0.82	0.39	0.288	0.353	0.093	0.21	1.19E+05	7.93E+04	6.27E+04	9.46E+04	1.11E+05	8.89E+04	4.56E+04	5.43E+04	1.25E+05	8.01E+04	2.26E+04	4.56E+04	545.58448	3	26.23
MSC3	YLR219W	RLSTSSAAPPTSR	[3] Phospho (ST)	0.23	0.03	0.21	0.20	0.097	0.465	0.234	0.28	6.43E+04	4.59E+04	6.23E+04	6.56E+04	6.39E+04	7.28E+04	8.03E+04	3.50E+04	6.12E+04	6.11E+04	5.33E+04	8.46E+04	705.83977	2	33.74
SPA2	YLL021W	GPEQLKSPEVQR	[7] Phospho (ST)	-0.03	0.18	0.22	-0.21	0.339	0.082	0.046	0.07	4.17E+04	3.94E+04	4.28E+04	4.12E+04	3.69E+04	4.30E+04	4.84E+04	4.08E+04	5.07E+04	4.97E+04	4.25E+04	5.24E+04	483.23595	3	37.75
BDP1	YNL039W	RLSTISNK	[3] Phospho (ST)	0.21	-1.12	-0.10	1.33	0.221	0.055	0.356	0.02	4.48E+04	2.60E+04	3.25E+04	4.15E+04	3.35E+04	4.48E+04	3.03E+04	8.70E+03	8.70E+03	3.34E+04	2.72E+04	3.55E+04	499.75513	2	35.13
ACC1	YNR016C	SEESLFESSPQK	[N-term] Acetyl (Protein N-term)|[9] Phospho	-0.09	0.36	0.28	-0.45	0.348	0.118	0.071	0.08	2.30E+05	3.02E+05	2.16E+05	2.04E+05	2.85E+05	2.12E+05	2.61E+05	4.05E+05	2.94E+05	3.13E+05	3.19E+05	2.78E+05	745.30903	2	38.65
GIP3	YPL137C	SSSVSNAALCNTEKPDLK	[2] Phospho (ST)	0.16	0.20	0.06	-0.04	0.222	0.188	0.332	0.43	9.06E+04	9.00E+04	6.91E+04	1.00E+05	1.04E+05	7.51E+04	9.23E+04	1.15E+05	7.98E+04	8.95E+04	9.09E+04	8.04E+04	667.63815	3	28.66
SFP1	YLR403W	RPSVSNPPYHR	[3] Phospho (ST)	0.09	-0.16	-0.17	0.25	0.353	0.309	0.271	0.15	4.77E+04	7.25E+04	7.93E+04	7.22E+04	6.40E+04	7.59E+04	7.55E+04	4.42E+04	5.84E+04	5.35E+04	5.41E+04	7.00E+04	463.88552	3	32.99
YDR348C	YDR348C	NLSLSR	[3] Phospho (ST)	-0.22	-0.38	-0.13	0.16	0.189	0.102	0.313	0.09	3.88E+04	2.51E+04	4.08E+04	2.98E+04	3.05E+04	2.98E+04	2.32E+04	2.77E+04	2.98E+04	3.64E+04	2.65E+04	3.28E+04	385.18404	2	19.8
ENT2	YLR206W	TRSNPHDSSPSYQDDLEK	[1] Phospho (ST)|[3] Phospho (ST)	0.00	-0.48	-0.26	0.48	0.496	0.075	0.162	0.04	2.03E+05	1.38E+05	1.78E+05	1.86E+05	1.70E+05	1.62E+05	9.70E+04	1.63E+05	1.11E+05	1.72E+05	1.12E+05	1.49E+05	745.95825	3	31.31
MFT1	YML062C	RDGLLNEAEGDNIDEDYESDEDEERK	[19] Phospho (ST)	-0.29	-0.10	-0.51	-0.18	0.032	0.241	0.010	0.13	2.96E+05	3.50E+05	3.00E+05	2.70E+05	2.31E+05	2.76E+05	2.73E+05	3.38E+05	2.71E+05	1.94E+05	2.16E+05	2.56E+05	1045.7573	3	82.61
PSP1	YDR505C	GSFTTELSCR	[2] Phospho (ST)	-0.25	0.22	-0.21	-0.46	0.016	0.051	0.029	0.01	6.20E+04	6.65E+04	7.02E+04	5.30E+04	6.00E+04	5.43E+04	7.06E+04	7.46E+04	8.56E+04	6.09E+04	5.82E+04	5.25E+04	619.2501	2	62.26
HXT2	YMR011W	LETDESPIQTK	[6] Phospho (ST)	0.40	0.28	0.21	0.13	0.052	0.090	0.223	0.25	6.99E+04	6.89E+04	9.16E+04	1.07E+05	8.36E+04	1.14E+05	8.93E+04	8.36E+04	1.06E+05	7.95E+04	7.40E+04	1.13E+05	670.80523	2	34.12
ILV3	YJR016C	YVMADLINVGGTQSVIK	[12] Phospho (ST)|[14] Phospho (ST)	-0.10	-0.43	0.36	0.33	0.404	0.209	0.235	0.22	1.24E+05	6.36E+04	7.11E+04	9.62E+04	5.91E+04	8.65E+04	8.95E+04	3.65E+04	6.65E+04	6.92E+04	1.10E+05	1.53E+05	656.64012	3	16.04
RPL12A	YEL054C	IGPLGLSPKK	[7] Phospho (ST)	2.36	2.22	0.61	0.14	0.000	0.011	0.055	0.34	1.22E+04	1.65E+04	1.42E+04	6.39E+04	7.39E+04	8.25E+04	8.86E+04	4.00E+04	7.11E+04	1.57E+04	2.21E+04	2.76E+04	545.30729	2	30.91
PRP19	YLL036C	SSQQAVAITR	[2] Phospho (ST)	0.95	-0.15	-0.34	1.09	0.001	0.280	0.086	0.00	8.58E+04	7.19E+04	9.84E+04	1.78E+05	1.52E+05	1.63E+05	9.77E+04	7.02E+04	6.35E+04	7.31E+04	5.28E+04	7.70E+04	570.77413	2	49.98
REG1	YDR028C	DSEGNAQSEEEHDLERGYGSDDENSK	[20] Phospho (ST)	-0.24	-0.02	0.31	-0.22	0.245	0.480	0.175	0.21	4.64E+05	2.83E+05	3.06E+05	3.79E+05	2.50E+05	2.64E+05	3.28E+05	4.21E+05	2.93E+05	5.33E+05	3.34E+05	4.43E+05	993.04701	3	66.46
FAS1	YKL182W	IPAVEYFGGESPVDVQSQVDSSSVSEDSAVFK	[25] Phospho (ST)	0.12	0.17	-0.14	-0.05	0.351	0.291	0.332	0.43	1.07E+06	1.26E+06	6.97E+05	1.13E+06	1.31E+06	8.50E+05	1.15E+06	1.33E+06	9.10E+05	9.45E+05	1.10E+06	6.90E+05	1147.1877	3	49.82
DPB3	YBR278W	SALDVGEHSDSSDIEVDHTK	[11] Phospho (ST)|[12] Phospho (ST)	-0.56	-0.43	-0.25	-0.13	0.003	0.055	0.086	0.32	1.63E+05	1.43E+05	1.47E+05	1.14E+05	1.01E+05	9.13E+04	8.33E+04	1.45E+05	1.08E+05	1.48E+05	1.03E+05	1.30E+05	767.63918	3	33.73

FLC2	YAL053W	NKNDSELFELRK	[5] Phospho (ST)	0.60	0.16	0.73	0.44	0.007	0.322	0.012	0.06	5.02E+04	6.53E+04	7.71E+04	9.76E+04	9.61E+04	9.78E+04	9.62E+04	6.43E+04	5.43E+04	1.14E+05	8.87E+04	1.18E+05	524.91891	3	30.05
TSL1	YML100W	SATRSPSAFNR	[5] Phospho (ST)	0.43	-0.66	-0.07	1.10	0.156	0.106	0.433	0.01	2.32E+04	5.00E+04	5.91E+04	7.33E+04	4.59E+04	5.95E+04	2.86E+04	2.36E+04	3.12E+04	4.47E+04	3.58E+04	4.57E+04	637.2877	2	27.26
CAF20	YOR276W	KKGSGEDDEEETETTPTSTVPVATIAQETLK	[14] Phospho (ST)|[15] Phospho (ST)	0.28	0.31	-0.05	-0.03	0.192	0.170	0.434	0.46	4.97E+05	5.08E+05	3.07E+05	5.03E+05	6.68E+05	4.24E+05	4.82E+05	6.86E+05	4.59E+05	4.48E+05	4.87E+05	3.35E+05	1151.1825	3	39.64
YMR295C	YMR295C	SSISNTSDHDGANRASDVK	[16] Phospho (ST)	-0.18	-0.09	-0.08	-0.08	0.184	0.367	0.362	0.37	1.02E+05	8.59E+04	7.02E+04	8.16E+04	6.93E+04	7.72E+04	1.04E+05	6.73E+04	7.06E+04	9.57E+04	6.68E+04	8.14E+04	680.95847	3	31.24
NSG2	YNL156C	RSVSIDSTK	[4] Phospho (ST)|[7] Phospho (ST)	-0.11	-2.63	-0.60	2.52	0.451	0.057	0.255	0.05	1.30E+05	3.87E+04	4.48E+04	1.18E+05	4.12E+04	3.83E+04	1.47E+04	1.21E+04	7.63E+03	7.92E+04	3.06E+04	3.07E+04	576.7385	2	30.32
PSH1	YOL054W	NSALAVADDSDDGITR	[10] Phospho (ST)	0.15	0.09	-0.02	0.07	0.093	0.284	0.427	0.31	2.74E+05	2.59E+05	3.07E+05	2.88E+05	3.11E+05	3.35E+05	2.53E+05	3.35E+05	3.02E+05	2.64E+05	2.88E+05	2.78E+05	850.36305	2	62.91
YLR257W	YLR257W	SNSLITSTDPVEDHISK	[1] Phospho (ST)	0.13	0.12	-0.04	0.01	0.305	0.282	0.414	0.49	1.17E+05	1.50E+05	1.04E+05	1.22E+05	1.67E+05	1.16E+05	1.46E+05	1.44E+05	1.13E+05	1.17E+05	1.34E+05	1.08E+05	641.63039	3	32.96
MMS21	YEL019C	YRTGELTAPK	[1] Phospho (Y)	0.21	0.50	1.37	-0.30	0.377	0.123	0.016	0.26	2.69E+04	1.20E+04	3.73E+04	1.93E+04	2.14E+04	4.72E+04	3.96E+04	3.11E+04	3.72E+04	5.14E+04	6.04E+04	8.51E+04	608.29627	2	44.1
PHO84	YML123C	ASTAVESLDNHPPK	[3] Phospho (ST)|[7] Phospho (ST)	-2.57	-0.94	-0.74	-1.63	0.001	0.008	0.014	0.00	1.28E+05	1.02E+05	1.48E+05	2.59E+04	1.78E+04	2.00E+04	5.98E+04	7.96E+04	5.81E+04	8.57E+04	6.28E+04	7.83E+04	542.55876	3	25.46
LEU1	YGL009C	DQDQSSPKVEVTSEDEK	[6] Phospho (ST)	0.10	-0.06	0.32	0.16	0.356	0.411	0.158	0.17	2.98E+05	1.71E+05	2.19E+05	2.74E+05	2.19E+05	2.43E+05	2.08E+05	1.94E+05	2.56E+05	3.40E+05	2.26E+05	2.92E+05	1000.9161	2	33.18
CHS3	YBR023C	ISDEGVAEDEFDKDGDVDNFEESSTQPINK	[24] Phospho (ST)	0.11	0.17	0.26	-0.06	0.273	0.198	0.123	0.40	3.79E+05	4.34E+05	4.87E+05	3.99E+05	4.56E+05	5.53E+05	5.84E+05	4.45E+05	4.35E+05	4.65E+05	4.63E+05	6.26E+05	1137.1431	3	33.2
LEU1	YGL009C	DQDQSSPKVEVTSEDEK	[6] Phospho (ST)	0.16	-0.02	0.35	0.18	0.291	0.472	0.190	0.24	1.56E+05	9.32E+04	1.28E+05	1.72E+05	1.19E+05	1.30E+05	1.03E+05	1.19E+05	1.50E+05	2.19E+05	1.23E+05	1.38E+05	667.61422	3	36.73
BCY1	YIL033C	RTSVSGETLQPNNFDDWTPDHYK	[3] Phospho (ST)	-0.28	0.22	0.05	-0.51	0.167	0.233	0.426	0.04	1.42E+05	1.75E+05	1.02E+05	1.11E+05	1.31E+05	1.01E+05	1.96E+05	1.63E+05	1.29E+05	1.15E+05	1.64E+05	1.55E+05	697.557	4	22.46
PBP1	YGR178C	VADSGVSDSVDDLAK	[9] Phospho (ST)	-0.16	0.08	0.23	-0.24	0.155	0.239	0.020	0.07	1.17E+05	1.27E+05	1.41E+05	1.02E+05	1.11E+05	1.33E+05	1.41E+05	1.22E+05	1.45E+05	1.47E+05	1.48E+05	1.56E+05	779.33835	2	61.46
SLU7	YDR088C	YEYLKKK	[1] Phospho (Y)	-0.40	-0.30	-0.31	-0.10	0.043	0.286	0.211	0.43	6.11E+04	7.48E+04	5.42E+04	5.42E+04	4.54E+04	4.45E+04	8.73E+04	2.77E+04	3.99E+04	2.68E+04	6.80E+04	5.84E+04	526.26227	2	20.55
ABF1	YKL112W	ADDEEDLSDENIQPELR	[8] Phospho (ST)	0.18	0.20	-0.27	-0.02	0.253	0.240	0.111	0.47	1.13E+05	1.55E+05	1.39E+05	1.18E+05	1.91E+05	1.52E+05	1.26E+05	2.01E+05	1.41E+05	1.02E+05	1.33E+05	1.03E+05	689.95162	3	30.56
VTC2	YFL004W	SNFNTASEPLASASK	[12] Phospho (ST)	-0.56	-0.03	-0.16	-0.53	0.005	0.370	0.134	0.00	1.51E+05	1.75E+05	1.67E+05	1.06E+05	9.88E+04	1.29E+05	1.52E+05	1.69E+05	1.62E+05	1.68E+05	1.32E+05	1.42E+05	802.3543	2	48.29
DBP2	YNL112W	DRSDSEIAQFR	[5] Phospho (ST)	0.33	-0.18	0.39	0.51	0.055	0.128	0.090	0.03	1.05E+05	8.89E+04	1.02E+05	1.39E+05	1.02E+05	1.33E+05	7.31E+04	9.31E+04	9.57E+04	1.64E+05	1.02E+05	1.22E+05	702.30153	2	43.05
NBP2	YDR162C	RQSITLPDDYIVNQR	[3] Phospho (ST)	-0.24	0.27	0.15	-0.51	0.165	0.098	0.228	0.01	7.91E+04	1.21E+05	1.01E+05	7.94E+04	9.83E+04	7.71E+04	1.32E+05	1.17E+05	1.14E+05	1.01E+05	1.20E+05	1.13E+05	633.31098	3	27.98
TPO1	YLL028W	ILTGSVNEPDRVEVDYTNCAPMGGDRPYPPSLPSR	[3] Phospho (ST)|[5] Phospho (ST)	-0.56	-0.03	0.06	-0.53	0.098	0.461	0.432	0.12	9.69E+05	8.72E+05	6.53E+05	5.34E+05	8.30E+05	3.33E+05	7.50E+05	1.04E+06	6.60E+05	7.01E+05	1.24E+06	6.66E+05	1005.7011	4	53.99
BUD6	YLR319C	RLSSVVTTSPDK	[3] Phospho (ST)	0.42	0.03	-0.03	0.38	0.055	0.449	0.448	0.12	6.47E+04	7.71E+04	6.64E+04	7.58E+04	8.98E+04	1.13E+05	9.38E+04	5.40E+04	6.55E+04	5.12E+04	7.01E+04	8.28E+04	685.33888	2	53.26
UGP1	YKL035W	THSTYAFESNTNSVAASQMR	[5] Phospho (Y)	-0.49	-0.15	0.40	-0.34	0.129	0.361	0.072	0.26	2.53E+05	1.63E+05	1.65E+05	1.82E+05	1.52E+05	7.99E+04	1.59E+05	2.52E+05	1.13E+05	2.86E+05	2.48E+05	2.31E+05	761.32291	3	53.79
RPL12A	YEL054C	IGPLGLSPK	[7] Phospho (ST)	2.39	2.45	0.75	-0.06	0.001	0.001	0.040	0.40	1.29E+04	2.83E+04	2.01E+04	8.95E+04	1.30E+05	1.02E+05	1.30E+05	9.65E+04	1.08E+05	2.77E+04	4.14E+04	3.39E+04	481.25953	2	27.86
YDR365W-B	R365W-B	AHNVSTSNNSPSTDNDSISK	[5] Phospho (ST)	-0.28	-0.45	-0.12	0.17	0.180	0.109	0.340	0.22	1.53E+05	8.60E+04	1.31E+05	1.16E+05	9.31E+04	9.64E+04	7.93E+04	7.86E+04	1.13E+05	1.34E+05	9.86E+04	1.08E+05	718.9695	3	25.36
PHO8	YDR481C	SSDSLVTDSAAGATAFACALK	[9] Phospho (ST)	-0.41	0.14	-0.06	-0.55	0.141	0.346	0.422	0.06	3.57E+05	4.69E+05	2.44E+05	2.81E+05	3.10E+05	2.16E+05	3.63E+05	5.00E+05	3.16E+05	3.47E+05	3.79E+05	3.01E+05	1061.973	2	86.95
ABP1	YCR088W	KEPVKTPSPAPAAK	[6] Phospho (ST)|[8] Phospho (ST)	1.50	1.92	0.78	-0.42	0.000	0.001	0.018	0.02	2.60E+04	1.78E+04	2.29E+04	6.62E+04	5.79E+04	6.45E+04	8.92E+04	7.02E+04	9.32E+04	4.70E+04	3.15E+04	3.63E+04	527.58785	3	20.01
YRB1	YDR002W	EGDDAPESPDIHFEPVVHLEK	[8] Phospho (ST)	0.85	0.62	0.54	0.24	0.012	0.028	0.078	0.11	4.65E+04	7.92E+04	5.33E+04	8.99E+04	1.22E+05	1.11E+05	9.84E+04	7.82E+04	9.75E+04	6.37E+04	1.04E+05	9.30E+04	610.77338	4	17.85
GIP3	YPL137C	SSSVSNAALCNTEKPDLK	[5] Phospho (ST)	0.04	-0.10	-0.14	0.14	0.429	0.352	0.234	0.28	1.85E+05	1.77E+05	1.25E+05	1.80E+05	1.88E+05	1.34E+05	1.54E+05	1.81E+05	1.22E+05	1.54E+05	1.48E+05	1.40E+05	1000.954	2	55.93
BMS1	YPL217C	IYGKPVQEEDADIDNLPSDEEPYTNDDDVQDSEPR	[18] Phospho (ST)	-0.77	-0.71	-0.41	-0.05	0.048	0.063	0.132	0.41	4.98E+05	3.89E+05	2.55E+05	1.89E+05	2.28E+05	2.54E+05	2.25E+05	2.91E+05	1.81E+05	2.63E+05	3.25E+05	2.70E+05	1022.6854	4	39.58
YRB2	YIL063C	VHSGSEQLANASEDTK	[3] Phospho (ST)	-0.29	-0.04	0.03	-0.25	0.164	0.455	0.466	0.18	6.72E+04	6.03E+04	9.64E+04	6.07E+04	5.23E+04	7.01E+04	7.73E+04	5.31E+04	8.80E+04	6.89E+04	6.39E+04	9.51E+04	876.87532	2	86.88
STV1	YMR054W	NQSVEDLSFLEQGYQHR	[3] Phospho (ST)	-0.48	-0.05	-0.27	-0.43	0.043	0.407	0.108	0.03	2.27E+05	3.17E+05	2.42E+05	1.80E+05	2.20E+05	1.63E+05	2.38E+05	2.91E+05	2.31E+05	1.96E+05	2.39E+05	2.16E+05	710.64839	3	44.58
YLR257W	YLR257W	GESYQSAEQEIDHTAPEK	[3] Phospho (ST)	0.87	0.34	0.54	0.54	0.003	0.025	0.007	0.01	1.35E+05	1.51E+05	1.25E+05	2.92E+05	2.37E+05	2.23E+05	1.79E+05	1.87E+05	1.52E+05	1.82E+05	1.90E+05	2.23E+05	1049.9345	2	74.15
GAL11	YOL051W	KLSISNAASQQPTPR	[9] Phospho (ST)	-0.14	0.04	-0.14	-0.17	0.278	0.443	0.313	0.19	3.82E+04	5.86E+04	5.98E+04	4.36E+04	4.84E+04	5.05E+04	6.26E+04	4.32E+04	5.49E+04	3.98E+04	4.34E+04	5.89E+04	559.94914	3	21.03
NUP159	YIL115C	LPETPSDEDGEVVEEEAQKSPIGK	[4] Phospho (ST)|[20] Phospho (ST)	-0.57	0.23	-0.04	-0.80	0.018	0.120	0.383	0.02	2.37E+05	2.63E+05	2.44E+05	1.20E+05	2.04E+05	1.77E+05	2.43E+05	3.46E+05	2.82E+05	2.04E+05	2.76E+05	2.42E+05	915.05961	3	24.71
CAF20	YOR276W	KGSGEDDEEETETTPTSTVPVATIAQETLK	[14] Phospho (ST)	0.92	0.63	0.89	0.29	0.002	0.090	0.031	0.17	1.90E+05	1.64E+05	1.17E+05	3.14E+05	3.07E+05	2.72E+05	3.24E+05	2.48E+05	1.57E+05	3.04E+05	3.67E+05	2.03E+05	1081.8287	3	43.6
PHO8	YDR481C	SSDSLVTDSAAGATAFACALK	[9] Phospho (ST)	-0.44	0.24	-0.10	-0.68	0.138	0.228	0.374	0.03	1.65E+05	2.31E+05	1.26E+05	1.22E+05	1.64E+05	9.98E+04	1.95E+05	2.49E+05	1.73E+05	1.51E+05	1.90E+05	1.46E+05	708.31763	3	46.2
SER33	YIL074C	RVSITK	[5] Phospho (ST)	0.38	0.17	-0.43	0.21	0.201	0.370	0.153	0.32	5.59E+04	2.88E+04	3.32E+04	4.07E+04	4.28E+04	6.98E+04	6.09E+04	2.45E+04	4.69E+04	3.29E+04	2.66E+04	2.80E+04	392.20983	2	32.34
SUM1	YDR310C	SASISGISDHQQEGYQPLEQEK	[3] Phospho (ST)	-0.38	-0.13	-0.45	-0.25	0.125	0.327	0.088	0.11	1.11E+05	1.79E+05	1.16E+05	1.19E+05	1.04E+05	8.97E+04	1.08E+05	1.45E+05	1.19E+05	1.02E+05	9.94E+04	9.72E+04	837.70691	3	66.63
NUP60	YAR002W	RASATVPSAPYRK	[3] Phospho (ST)	-1.05	-0.97	-0.62	-0.08	0.056	0.066	0.127	0.34	1.20E+05	7.03E+04	5.14E+04	3.61E+04	3.72E+04	4.34E+04	5.02E+04	3.49E+04	3.83E+04	5.67E+04	4.12E+04	5.93E+04	495.25154	3	18.87
MAK11	YKL021C	DAETADIGDQSEVESDTEELKK	[15] Phospho (ST)|[17] Phospho (ST)	-0.38	-0.12	-0.43	-0.26	0.175	0.376	0.054	0.32	2.51E+05	2.13E+05	1.73E+05	1.07E+05	2.43E+05	1.40E+05	1.35E+05	2.87E+05	1.63E+05	1.39E+05	1.85E+05	1.49E+05	857.00965	3	17.09
YRB2	YIL063C	VHSGSEQLANASEDTK	[3] Phospho (ST)	-0.25	-0.09	-0.10	-0.16	0.214	0.400	0.362	0.28	3.98E+04	2.92E+04	5.20E+04	3.69E+04	2.78E+04	3.70E+04	3.41E+04	3.06E+04	4.91E+04	3.76E+04	3.14E+04	4.34E+04	584.91908	3	28.6
DIG1	YPL049C	NSPGGNSVGQESELEHVPEEDDSGDK	[2] Phospho (ST)	0.01	0.01	-0.41	0.00	0.468	0.476	0.045	0.50	1.96E+05	1.48E+05	2.06E+05	2.05E+05	1.80E+05	1.71E+05	1.49E+05	1.82E+05	2.25E+05	1.56E+05	1.34E+05	1.24E+05	931.37754	3	67
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALR	[9] Phospho (ST)	-0.47	0.54	0.71	-1.01	0.089	0.079	0.074	0.03	2.32E+05	2.51E+05	1.97E+05	1.40E+05	2.33E+05	1.17E+05	3.67E+05	4.05E+05	2.17E+05	3.19E+05	5.29E+05	2.69E+05	981.05667	3	48.08
RCN2	YOR220W	SPSITVNEFFH	[1] Phospho (ST)	0.29	0.45	0.27	-0.16	0.250	0.067	0.255	0.30	1.05E+05	1.51E+05	8.58E+04	1.19E+05	1.94E+05	1.04E+05	1.63E+05	1.70E+05	1.34E+05	1.12E+05	1.91E+05	1.11E+05	679.29571	2	53.84
YRB1	YDR002W	KEGDDAPESPDIHFEPVVHLEK	[9] Phospho (ST)	1.08	0.47	0.62	0.61	0.002	0.109	0.023	0.02	9.81E+04	1.68E+05	1.41E+05	2.57E+05	2.90E+05	3.12E+05	2.46E+05	1.60E+05	1.57E+05	1.82E+05	2.35E+05	2.08E+05	856.72705	3	55.77
GDH2	YDL215C	TLSFQR	[3] Phospho (ST)	0.97	1.28	0.78	-0.31	0.008	0.002	0.011	0.07	8.32E+03	1.38E+04	1.57E+04	2.56E+04	2.07E+04	2.79E+04	2.63E+04	3.42E+04	3.15E+04	2.38E+04	1.99E+04	2.13E+04	416.19173	2	27.54
NSG2	YNL156C	NTVSSNNLER	[4] Phospho (ST)	0.33	-0.24	0.10	0.57	0.240	0.314	0.409	0.07	4.92E+04	1.83E+04	5.07E+04	6.42E+04	3.98E+04	4.45E+04	2.49E+04	3.31E+04	4.20E+04	5.11E+04	3.28E+04	4.32E+04	607.26236	2	38.18
SMI1	YGR229C	GEDSGSADVQSVQDHESVK	[11] Phospho (ST)|[17] Phospho (ST)	0.11	-0.24	-0.07	0.35	0.365	0.270	0.420	0.09	2.42E+05	1.19E+05	1.97E+05	2.22E+05	1.80E+05	1.98E+05	1.12E+05	1.85E+05	1.75E+05	2.03E+05	1.33E+05	1.94E+05	1067.4042	2	26.21
NPL6	YMR091C	SDSEGGLASEVEHEK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.14	-0.41	-1.14	0.27	0.134	0.045	0.000	0.15	1.28E+05	1.38E+05	1.33E+05	1.27E+05	1.32E+05	1.02E+05	8.58E+04	1.29E+05	8.48E+04	5.28E+04	7.04E+04	5.72E+04	848.34179	2	76.85
GPA1	YHR005C	SDTDRDAETVTQNEDADRNNSSR	[21] Phospho (ST)	-0.11	-0.25	0.10	0.14	0.313	0.204	0.385	0.24	1.48E+05	1.07E+05	1.75E+05	1.42E+05	1.29E+05	1.28E+05	1.18E+05	9.46E+04	1.48E+05	1.36E+05	1.20E+05	2.05E+05	892.69738	3	25.91
CRP1	YHR146W	EVAHNVQELTPQVEAVTPLINEPEPLPTPEAQISIPESSKVEPV	[28] Phospho (ST)|[34] Phospho (ST)	-0.28	-0.03	-0.27	-0.24	0.246	0.461	0.266	0.15	5.97E+05	7.79E+05	3.58E+05	4.40E+05	5.86E+05	4.06E+05	5.36E+05	6.55E+05	5.03E+05	4.59E+05	6.18E+05	3.65E+05	1129.7579	5	23.41
ASK10	YGR097W	TNSTGNVPCLTAEK	[3] Phospho (ST)	-0.17	0.18	0.20	-0.35	0.152	0.246	0.209	0.12	9.33E+04	8.28E+04	1.02E+05	8.69E+04	6.95E+04	9.12E+04	7.76E+04	1.30E+05	1.08E+05	1.35E+05	8.87E+04	9.63E+04	786.3416	2	56.09
SUB1	YMR039C	LLSDDEYEDDNNNDSTNNDK	[7] Phospho (Y)	-0.33	0.26	0.23	-0.59	0.106	0.147	0.133	0.03	2.00E+05	1.46E+05	2.02E+05	1.80E+05	1.31E+05	1.26E+05	1.73E+05	2.56E+05	2.30E+05	2.47E+05	2.06E+05	1.91E+05	803.96624	3	52.41
PSY4	YBL046W	ENISSPLGK	[4] Phospho (ST)	0.13	0.06	-0.30	0.08	0.205	0.385	0.064	0.33	5.03E+04	5.41E+04	6.55E+04	6.39E+04	5.46E+04	6.80E+04	5.83E+04	4.93E+04	6.92E+04	4.08E+04	4.61E+04	5.15E+04	512.73906	2	15.27
NSG2	YNL156C	ILSASSIHENFPSR	[3] Phospho (ST)|[6] Phospho (ST)	-0.16	-0.43	-0.44	0.27	0.236	0.073	0.007	0.22	1.22E+05	1.47E+05	1.26E+05	9.22E+04	1.47E+05	1.14E+05	8.33E+04	1.32E+05	7.75E+04	1.01E+05	9.49E+04	9.54E+04	573.25014	3	23.26
AMD1	YML035C	TLSASAQHILPETLK	[3] Phospho (ST)	-0.04	0.32	0.12	-0.36	0.469	0.231	0.405	0.10	3.59E+04	8.64E+04	4.59E+04	4.97E+04	6.75E+04	4.69E+04	8.39E+04	6.69E+04	5.91E+04	4.40E+04	7.94E+04	5.91E+04	563.62563	3	37.72
SSZ1	YHR064C	TLEPIPKEENAEEDDESEWSDDEPEVVR	[17] Phospho (ST)|[20] Phospho (ST)	-1.56	-0.83	-0.42	-0.73	0.023	0.116	0.147	0.21	7.30E+05	9.08E+05	4.22E+05	1.04E+05	3.58E+05	2.36E+05	1.83E+05	6.99E+05	2.79E+05	4.93E+05	5.63E+05	4.83E+05	1149.4634	3	30.5
HXT1	YHR094C	MNSTPDLISPQK	[N-term] Acetyl (Protein N-term)|[4] Phospho	-1.20	-0.86	-0.21	-0.34	0.014	0.017	0.205	0.28	3.04E+05	3.39E+05	2.53E+05	1.21E+05	2.08E+05	6.02E+04	1.77E+05	2.17E+05	9.96E+04	2.28E+05	3.31E+05	2.14E+05	726.82659	2	27.54
PAN1	YIR006C	QIEDAQNESDEEETNGK	[9] Phospho (ST)	-0.33	-0.48	0.03	0.15	0.235	0.173	0.477	0.29	3.52E+05	1.39E+05	2.56E+05	2.37E+05	1.76E+05	1.80E+05	1.36E+05	1.79E+05	2.21E+05	3.15E+05	1.83E+05	2.63E+05	1008.3897	2	28.19
KRI1	YNL308C	YREVSPESFGLTAR	[1] Phospho (Y)	0.13	0.25	0.09	-0.12	0.347	0.270	0.402	0.35	5.35E+04	1.01E+05	7.31E+04	7.42E+04	1.00E+05	7.44E+04	1.23E+05	7.05E+04	7.79E+04	5.73E+04	1.04E+05	8.21E+04	564.59828	3	44.4
KRE6	YPR159W	AIASSPSLNSNLSK	[5] Phospho (ST)	0.03	0.02	0.29	0.02	0.415	0.451	0.068	0.46	1.00E+05	9.84E+04	1.20E+05	1.20E+05	9.14E+04	1.16E+05	1.06E+05	9.56E+04	1.21E+05	1.41E+05	1.09E+05	1.41E+05	734.85608	2	45.42
GSY2	YLR258W	VARPLSVPGSPR	[10] Phospho (ST)	0.35	0.54	0.63	-0.20	0.044	0.068	0.034	0.24	3.28E+04	4.50E+04	4.15E+04	4.65E+04	4.84E+04	5.68E+04	6.56E+04	4.00E+04	6.85E+04	5.00E+04	5.77E+04	7.68E+04	658.3484	2	23.29
SSD1	YDR293C	RHSLGLNEAK	[3] Phospho (ST)	0.19	-0.31	-0.14	0.50	0.156	0.230	0.347	0.11	3.88E+04	4.54E+04	5.44E+04	5.52E+04	4.62E+04	5.65E+04	5.42E+04	1.97E+04	3.79E+04	3.07E+04	3.54E+04	5.97E+04	402.19932	3	47.44
XRN1	YGL173C	GEIKPSSGTNSTECQSPK	[16] Phospho (ST)	0.06	-0.27	0.11	0.34	0.422	0.259	0.401	0.06	9.09E+04	4.55E+04	5.49E+04	6.92E+04	6.64E+04	6.45E+04	4.08E+04	5.34E+04	6.44E+04	9.39E+04	5.30E+04	5.94E+04	662.95392	3	44.38
MET4	YNL103W	QEQSHEGDSYSTEFINLFGK	[4] Phospho (ST)|[10] Phospho (Y)|[11] Phosp	0.01	0.51	0.41	-0.50	0.489	0.098	0.060	0.19	4.82E+05	5.13E+05	4.12E+05	4.54E+05	7.44E+05	2.22E+05	6.10E+05	9.06E+05	4.86E+05	5.79E+05	7.60E+05	5.25E+05	852.64658	3	15.88
TPS3	YMR261C	ISKKLEQDFSSFPVVTDDITFK	[11] Phospho (ST)|[16] Phospho (ST)	-0.19	-0.37	0.20	0.18	0.355	0.247	0.312	0.37	7.43E+05	3.40E+05	4.97E+05	6.82E+05	3.32E+05	3.73E+05	2.48E+05	6.13E+05	3.59E+05	7.80E+05	5.52E+05	4.83E+05	902.09478	3	16.76
SYP1	YCR030C	SAFGNIGHR	[1] Phospho (ST)	-0.01	0.06	-0.13	-0.07	0.479	0.377	0.282	0.38	3.16E+04	4.00E+04	4.34E+04	4.19E+04	2.83E+04	4.38E+04	3.99E+04	3.49E+04	4.48E+04	3.01E+04	3.27E+04	4.25E+04	519.72959	2	32.19
PRB1	YEL060C	KVEFTKDDDEEPSDSEDK	[13] Phospho (ST)	-0.36	-0.07	-0.07	-0.30	0.048	0.364	0.344	0.08	1.33E+05	1.07E+05	1.45E+05	1.02E+05	8.59E+04	1.10E+05	1.04E+05	1.19E+05	1.43E+05	1.21E+05	1.09E+05	1.36E+05	731.62995	3	32.31
CUE5	YOR042W	EQHHEDSEEEDSWSQFVEK	[7] Phospho (ST)	0.15	0.10	0.31	0.06	0.146	0.360	0.049	0.41	2.40E+05	2.03E+05	2.07E+05	2.66E+05	2.43E+05	2.12E+05	2.38E+05	2.91E+05	1.65E+05	2.90E+05	2.26E+05	2.91E+05	818.9834	3	50.04
SPC29	YPL124W	KFQDDTLNR	[6] Phospho (ST)	-0.19	-0.37	-0.12	0.18	0.203	0.101	0.335	0.23	4.18E+04	3.25E+04	4.80E+04	3.88E+04	2.95E+04	3.88E+04	2.98E+04	2.57E+04	3.93E+04	3.54E+04	2.90E+04	4.81E+04	608.77164	2	49.27
CLA4	YNL298W	YAQNSSPTAAHFQPQR	[6] Phospho (ST)	0.08	0.43	0.39	-0.35	0.307	0.015	0.121	0.00	5.84E+04	6.15E+04	7.97E+04	7.54E+04	6.74E+04	6.85E+04	9.06E+04	8.52E+04	9.35E+04	8.75E+04	6.37E+04	1.10E+05	628.27929	3	16.79
FIP1	YJR093C	FLYGSDSELALPSSK	[3] Phospho (Y)	-0.19	-0.05	-0.12	-0.14	0.207	0.396	0.325	0.17	2.57E+05	3.24E+05	2.14E+05	2.47E+05	2.51E+05	1.98E+05	2.74E+05	2.60E+05	2.31E+05	2.58E+05	2.86E+05	1.87E+05	847.39003	2	48.94
OSH2	YDL019C	HAPPPVPNETDNDSQYVQDEK	[16] Phospho (Y)	-0.50	-0.27	-0.15	-0.22	0.011	0.071	0.137	0.09	2.15E+05	1.78E+05	2.25E+05	1.55E+05	1.29E+05	1.54E+05	1.46E+05	1.77E+05	1.89E+05	1.91E+05	1.69E+05	1.95E+05	820.68346	3	60.11
ZUO1	YGR285C	NHTWSEFERIEAEK	[5] Phospho (ST)	0.58	0.05	0.58	0.52	0.018	0.455	0.008	0.12	2.31E+05	2.45E+05	1.77E+05	3.80E+05	3.07E+05	2.88E+05	3.59E+05	1.64E+05	1.56E+05	3.13E+05	3.06E+05	3.59E+05	619.27243	3	23.94
EBP2	YKL172W	EEQEEEQDVPLSDVEFDSDADVVPHHK	[12] Phospho (ST)|[18] Phospho (ST)	-0.84	-0.23	-0.26	-0.61	0.108	0.332	0.165	0.24	3.19E+05	5.23E+05	3.75E+05	1.94E+04	3.68E+05	2.92E+05	1.32E+05	5.09E+05	3.97E+05	3.48E+05	3.25E+05	3.40E+05	1094.7731	3	29.64
ENT1	YDL161W	GTGRSDENDDDLQR	[5] Phospho (ST)	0.22	-0.53	-0.13	0.75	0.239	0.106	0.364	0.01	4.78E+04	2.49E+04	3.48E+04	4.81E+04	4.13E+04	3.57E+04	2.16E+04	2.18E+04	3.13E+04	4.15E+04	2.64E+04	3.05E+04	553.2201	3	41.95
TCB3	YML072C	RSPSNLNSTSVTPR	[12] Phospho (ST)	-0.45	-0.20	-0.16	-0.26	0.042	0.287	0.277	0.26	5.65E+04	7.81E+04	6.87E+04	4.00E+04	5.13E+04	5.70E+04	8.15E+04	3.75E+04	5.82E+04	4.87E+04	5.55E+04	7.80E+04	798.38076	2	26.63
HBT1	YDL223C	SISGGTFGFR	[1] Phospho (ST)	2.46	1.82	1.02	0.63	0.002	0.000	0.023	0.02	1.98E+04	2.75E+04	1.28E+04	8.65E+04	1.34E+05	1.09E+05	7.53E+04	7.03E+04	6.69E+04	3.38E+04	5.21E+04	3.56E+04	554.74514	2	59.38
HAL5	YJL165C	RNSLGVR	[3] Phospho (ST)	0.46	-0.23	-0.14	0.69	0.103	0.291	0.337	0.03	3.82E+04	1.90E+04	2.61E+04	3.35E+04	3.50E+04	4.63E+04	2.94E+04	1.60E+04	2.55E+04	2.56E+04	2.38E+04	2.63E+04	441.22127	2	42.99
RPL7A	YGL076C	ILTPESQLK	[3] Phospho (ST)	-0.04	0.39	-0.08	-0.43	0.447	0.235	0.421	0.20	8.30E+04	1.35E+05	8.45E+04	9.47E+04	1.12E+05	8.85E+04	2.01E+05	8.44E+04	1.11E+05	5.53E+04	1.27E+05	1.03E+05	554.78658	2	30.49
EDE1	YBL047C	RANSNEDGESVSSIQESPK	[17] Phospho (ST)	-0.14	-0.02	0.28	-0.12	0.190	0.452	0.197	0.32	1.98E+05	1.84E+05	2.08E+05	1.60E+05	1.63E+05	2.13E+05	2.19E+05	1.47E+05	2.15E+05	1.90E+05	2.00E+05	3.25E+05	1057.4553	2	80.14
PDR5	YOR153W	NANDPENVGERSDLSSDRK	[16] Phospho (ST)	-0.55	-0.54	0.32	-0.01	0.092	0.077	0.246	0.49	8.71E+04	5.40E+04	7.18E+04	6.77E+04	3.32E+04	4.48E+04	3.94E+04	4.16E+04	6.53E+04	1.29E+05	5.55E+04	8.17E+04	728.3174	3	18.64
YNL054W-B	L054W-B	HSDSYSDNETNHTNVPISSTGGTNNK	[5] Phospho (Y)	-0.87	-0.03	0.38	-0.85	0.010	0.428	0.103	0.00	1.01E+05	7.28E+04	9.43E+04	6.19E+04	4.15E+04	4.29E+04	8.62E+04	8.70E+04	9.02E+04	1.43E+05	8.81E+04	1.19E+05	714.79801	4	20.88
RRP5	YMR229C	SKVEDAEYESSDDEDEKLDK	[10] Phospho (ST)|[11] Phospho (ST)	-0.75	-0.78	-0.38	0.03	0.034	0.076	0.147	0.48	2.45E+05	1.45E+05	1.67E+05	1.10E+05	1.12E+05	1.08E+05	6.07E+04	1.67E+05	9.63E+04	1.54E+05	1.06E+05	1.67E+05	830.98251	3	69.13

YMR124W	YMR124W	TLSLTNGPR	[1] Phospho (ST)	-0.11	0.14	0.02	-0.25	0.313	0.236	0.470	0.03	2.90E+04	4.48E+04	4.16E+04	3.40E+04	3.27E+04	4.02E+04	3.97E+04	4.29E+04	4.50E+04	4.40E+04	3.74E+04	3.54E+04	519.75288	2	44.85
CYC8	YBR112C	LNSPNSNINK	[3] Phospho (ST)	-1.09	-1.68	-2.11	0.59	0.255	0.197	0.170	0.28	2.43E+05	3.58E+04	2.32E+04	8.53E+04	1.87E+04	3.75E+04	1.01E+04	2.35E+04	6.03E+04	2.77E+04	1.28E+04	2.95E+04	590.77131	2	35.91
WHI3	YNL197C	SRFSFSDPFSNDSPLSQQQSQQQQQQPQQPQQHSTQK	[4] Phospho (ST)	-0.23	-0.01	-0.52	-0.22	0.200	0.483	0.067	0.17	5.78E+05	7.78E+05	4.71E+05	5.71E+05	5.20E+05	4.68E+05	5.50E+05	7.47E+05	5.14E+05	4.03E+05	5.03E+05	3.66E+05	1099.9962	4	50.46
USA1	YML029W	SQSPVSFAPTQGR	[3] Phospho (ST)	-0.21	-0.08	-0.26	-0.13	0.072	0.310	0.069	0.16	6.13E+04	7.54E+04	7.70E+04	6.48E+04	5.84E+04	6.17E+04	6.61E+04	7.65E+04	6.00E+04	6.62E+04	5.25E+04	5.98E+04	721.32736	2	73.19
NUP2	YLR335W	KDESDSENDIEIK	[4] Phospho (ST)|[6] Phospho (ST)	0.62	0.21	-0.07	0.41	0.025	0.353	0.405	0.19	1.41E+05	8.22E+04	1.27E+05	1.73E+05	2.06E+05	1.60E+05	5.97E+04	2.05E+05	1.41E+05	1.36E+05	9.80E+04	1.00E+05	841.31643	2	35.09
NTH1	YDR001C	RLSSLSEFNDPFSNAEVYYGPPTDPR	[4] Phospho (ST)	0.34	0.39	0.46	-0.05	0.199	0.228	0.183	0.44	2.53E+05	4.11E+05	1.76E+05	2.97E+05	4.23E+05	3.43E+05	5.13E+05	3.50E+05	2.39E+05	3.09E+05	5.39E+05	3.08E+05	1013.4572	3	44.93
CDC48	YDL126C	RSVSDAELR	[4] Phospho (ST)	0.01	0.08	0.10	-0.07	0.473	0.396	0.337	0.40	2.60E+04	2.38E+04	3.20E+04	2.78E+04	2.50E+04	2.97E+04	3.52E+04	1.88E+04	3.27E+04	2.46E+04	2.72E+04	3.57E+04	556.75802	2	30.76
SKT5	YBL061C	ASSPQVHPYK	[N-term] Acetyl (Protein N-term)|[3] Phospho	0.53	0.62	0.45	-0.08	0.023	0.006	0.041	0.31	2.32E+04	2.85E+04	3.09E+04	3.32E+04	4.05E+04	4.59E+04	3.81E+04	4.17E+04	4.69E+04	4.45E+04	3.18E+04	3.66E+04	618.27669	2	22.15
AVT1	YJR001W	RQSILDHPVGSFK	[3] Phospho (ST)	0.24	0.12	-0.21	0.12	0.095	0.388	0.248	0.38	4.27E+04	6.06E+04	5.25E+04	5.61E+04	6.58E+04	6.18E+04	8.31E+04	3.48E+04	5.16E+04	3.10E+04	4.63E+04	5.76E+04	521.92794	3	23.26
MRH1	YDR033W	APVASPRPAATPNLSK	[11] Phospho (ST)	-0.55	-0.30	-0.53	-0.26	0.038	0.239	0.085	0.29	7.69E+04	1.12E+05	8.62E+04	5.63E+04	5.57E+04	7.55E+04	1.09E+05	4.35E+04	7.11E+04	4.29E+04	5.92E+04	8.82E+04	828.92782	2	36.48
SSB1	YDL229W	LSSEEIEK	[3] Phospho (ST)	0.73	0.38	0.22	0.35	0.036	0.175	0.220	0.15	1.87E+04	1.31E+04	2.52E+04	3.34E+04	2.42E+04	3.70E+04	1.93E+04	2.19E+04	3.31E+04	2.45E+04	2.00E+04	2.21E+04	507.72313	2	28.28
MSN4	YKL062W	SITTIDPNNYDK	[1] Phospho (ST)	-0.30	0.20	-0.31	-0.50	0.018	0.112	0.041	0.01	8.52E+04	9.54E+04	1.03E+05	8.08E+04	7.74E+04	7.15E+04	9.72E+04	1.24E+05	1.04E+05	7.21E+04	8.80E+04	6.85E+04	730.81965	2	41.26
SMI1	YGR229C	GEDSGSADVQSVQDHESVK	[11] Phospho (ST)	0.13	-0.18	0.20	0.31	0.249	0.181	0.167	0.09	1.69E+05	1.32E+05	1.67E+05	2.01E+05	1.54E+05	1.57E+05	1.28E+05	1.20E+05	1.64E+05	2.01E+05	1.45E+05	1.92E+05	1027.419	2	65.72
GPH1	YPR160W	RLTGFLPQEIK	[3] Phospho (ST)	0.88	1.32	0.48	-0.44	0.048	0.051	0.236	0.19	3.20E+04	8.32E+04	3.93E+04	7.75E+04	1.17E+05	8.96E+04	1.89E+05	7.69E+04	1.20E+05	4.07E+04	1.08E+05	6.59E+04	691.3661	2	38.49
MYO5	YMR109W	RPVSIAAAQHVPTAPASR	[4] Phospho (ST)	-0.38	0.03	-0.30	-0.41	0.104	0.476	0.195	0.20	7.54E+04	1.06E+05	6.63E+04	5.63E+04	7.22E+04	6.15E+04	1.22E+05	4.80E+04	8.25E+04	4.56E+04	8.10E+04	7.44E+04	636.99873	3	39.6
SVL3	YPL032C	ATGTPNLR	[4] Phospho (ST)	0.72	0.42	0.26	0.29	0.007	0.062	0.036	0.11	1.86E+04	1.56E+04	2.04E+04	2.50E+04	3.26E+04	3.22E+04	2.89E+04	1.91E+04	2.54E+04	2.11E+04	2.15E+04	2.30E+04	455.21323	2	18.9
AMD1	YML035C	TLSASAQHILPETLK	[3] Phospho (ST)	-0.21	0.18	0.02	-0.39	0.337	0.340	0.481	0.07	6.17E+04	1.55E+05	8.38E+04	7.57E+04	1.05E+05	7.96E+04	1.37E+05	1.03E+05	1.01E+05	7.44E+04	1.39E+05	9.15E+04	844.93529	2	69.58
CRN1	YLR429W	IETPVTPTETKK	[6] Phospho (ST)	0.63	0.42	0.02	0.21	0.009	0.261	0.473	0.34	2.48E+04	3.48E+04	3.25E+04	4.45E+04	4.44E+04	5.40E+04	6.82E+04	1.88E+04	3.62E+04	2.07E+04	3.24E+04	4.04E+04	475.24077	3	20.68
GPD2	YOL059W	RSDSAVSIVHLK	[4] Phospho (ST)|[7] Phospho (ST)	-0.51	-0.38	-0.22	-0.13	0.014	0.076	0.051	0.32	1.05E+05	1.05E+05	1.25E+05	6.38E+04	8.45E+04	8.66E+04	6.99E+04	1.11E+05	7.64E+04	9.71E+04	1.01E+05	8.83E+04	736.33902	2	22.67
SUR1	YPL057C	KDSNTNIVLLK	[3] Phospho (ST)	-0.65	-0.35	-0.27	-0.29	0.000	0.005	0.053	0.02	5.79E+04	5.50E+04	5.88E+04	3.43E+04	3.66E+04	3.88E+04	4.82E+04	4.00E+04	4.61E+04	3.82E+04	5.10E+04	5.29E+04	662.84723	2	46.38
HBT1	YDL223C	SFSTTKPTEYNLPK	[1] Phospho (ST)	2.09	1.25	0.61	0.84	0.000	0.002	0.001	0.00	3.50E+04	4.36E+04	3.77E+04	1.59E+05	1.59E+05	1.77E+05	1.09E+05	8.15E+04	8.54E+04	5.57E+04	6.22E+04	5.94E+04	846.89836	2	61.3
MRS6	YOR370C	LGQSFK	[4] Phospho (ST)	0.81	1.12	0.69	-0.31	0.134	0.091	0.158	0.26	1.64E+03	8.68E+03	1.81E+04	1.35E+04	1.41E+04	2.22E+04	1.33E+04	1.84E+04	3.00E+04	1.81E+04	1.23E+04	1.53E+04	380.17552	2	23.69
TCB3	YML072C	RSPSNLNSTSVTPR	[10] Phospho (ST)	-0.42	-0.40	-0.44	-0.02	0.044	0.108	0.061	0.47	3.22E+04	4.52E+04	4.12E+04	2.54E+04	2.97E+04	3.33E+04	3.93E+04	2.08E+04	2.97E+04	2.43E+04	2.66E+04	3.64E+04	532.58945	3	38.27
TIF4631	YGR162W	EEPAAPTSTATNMFSALMGESDDEE	[21] Phospho (ST)	-0.54	0.03	0.40	-0.57	0.203	0.478	0.256	0.23	5.03E+05	5.30E+05	3.15E+05	2.80E+05	5.57E+05	8.66E+04	4.00E+05	6.82E+05	2.90E+05	4.35E+05	9.73E+05	3.75E+05	904.02006	3	55.45
PWP2	YCR057C	RPSDDDDNESEDDDKQEEVDISK	[10] Phospho (ST)	0.30	-0.07	0.20	0.37	0.085	0.349	0.191	0.01	8.58E+04	5.84E+04	8.21E+04	1.03E+05	8.36E+04	9.11E+04	7.31E+04	7.06E+04	7.19E+04	9.81E+04	7.35E+04	8.75E+04	690.77136	4	37.44
SHS1	YDL225W	FLNSPDLPER	[4] Phospho (ST)	-0.13	0.36	0.22	-0.49	0.273	0.045	0.224	0.00	5.69E+04	8.58E+04	7.60E+04	5.94E+04	7.47E+04	6.57E+04	9.57E+04	8.62E+04	9.90E+04	6.55E+04	1.04E+05	8.44E+04	634.28966	2	30.25
YCR023C	YCR023C	RQSVGLIR	[3] Phospho (ST)	-0.23	-0.15	-0.19	-0.08	0.175	0.314	0.274	0.38	2.45E+04	3.81E+04	3.39E+04	2.34E+04	2.97E+04	2.92E+04	3.49E+04	2.00E+04	3.21E+04	2.09E+04	2.73E+04	3.65E+04	504.77079	2	26.98
YIL166C	YIL166C	QPVTFK	[4] Phospho (ST)	0.24	0.21	-0.08	0.03	0.201	0.246	0.403	0.45	2.62E+04	3.76E+04	4.76E+04	3.97E+04	4.09E+04	5.07E+04	4.72E+04	3.36E+04	4.81E+04	2.69E+04	3.81E+04	4.05E+04	400.19118	2	38.14
RTF1	YGL244W	SDLDEDLLALAGADESEEEDQVLTTTSAK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.35	0.20	-0.07	-0.55	0.212	0.309	0.434	0.08	1.03E+06	8.32E+05	4.71E+05	6.06E+05	7.73E+05	4.52E+05	8.96E+05	1.12E+06	6.55E+05	7.70E+05	9.20E+05	5.36E+05	1089.7917	3	61
MSL5	YLR116W	NRSPSPPPVYDAQGK	[5] Phospho (ST)	0.10	-0.13	0.18	0.23	0.272	0.245	0.238	0.05	6.83E+04	7.30E+04	9.32E+04	8.63E+04	7.79E+04	8.65E+04	7.67E+04	6.10E+04	7.59E+04	9.37E+04	6.74E+04	1.05E+05	564.9296	3	28.19
TOD6	YBL054W	SFSHSITTNTPNVK	[5] Phospho (ST)	0.28	0.26	0.50	0.02	0.139	0.158	0.027	0.46	1.98E+04	3.39E+04	2.80E+04	3.35E+04	2.91E+04	3.67E+04	3.75E+04	3.08E+04	2.98E+04	3.91E+04	3.71E+04	3.89E+04	538.25087	3	24.53
KRE6	YPR159W	AVSTANDNSFLQPPHR	[3] Phospho (ST)	-0.42	-0.22	-0.16	-0.20	0.003	0.031	0.203	0.01	1.36E+05	1.57E+05	1.56E+05	1.14E+05	1.13E+05	1.08E+05	1.28E+05	1.37E+05	1.21E+05	1.05E+05	1.43E+05	1.55E+05	611.9479	3	46.64
HXT1	YHR094C	SNSSNSYELESGR	[3] Phospho (ST)|[4] Phospho (ST)	-1.17	-0.97	-0.38	-0.19	0.030	0.062	0.217	0.36	2.07E+05	9.88E+04	1.57E+05	8.83E+04	6.37E+04	5.42E+04	4.40E+04	1.23E+05	6.84E+04	1.71E+05	9.54E+04	8.99E+04	795.28047	2	37.51
PTK2	YJR059W	RPTSPSISGSGSGGNSPSSSAGAR	[3] Phospho (ST)	0.45	-0.46	0.11	0.91	0.066	0.108	0.363	0.01	5.79E+04	3.93E+04	6.87E+04	8.28E+04	6.27E+04	8.13E+04	4.24E+04	2.93E+04	4.88E+04	6.18E+04	4.46E+04	7.30E+04	747.66842	3	78.73
VHS2	YIL135C	NFHNLSQR	[6] Phospho (ST)	0.01	-0.28	-0.21	0.30	0.486	0.264	0.280	0.21	2.52E+04	2.09E+04	3.76E+04	2.60E+04	2.50E+04	3.34E+04	1.70E+04	1.84E+04	3.33E+04	2.12E+04	2.06E+04	3.05E+04	548.24027	2	21.66
DAM1	YGR113W	SILHTIR	[1] Phospho (ST)	-0.04	0.30	-0.20	-0.34	0.458	0.249	0.332	0.15	1.57E+04	3.52E+04	2.22E+04	2.06E+04	2.58E+04	2.47E+04	3.99E+04	2.22E+04	2.82E+04	1.46E+04	2.63E+04	2.28E+04	460.24169	2	29.05
ASK10	YGR097W	RGNNSAQNLTTSSSTASR	[5] Phospho (ST)	-0.05	-0.10	0.26	0.05	0.395	0.372	0.288	0.44	6.17E+04	4.56E+04	6.11E+04	5.47E+04	4.60E+04	6.17E+04	3.41E+04	5.56E+04	6.71E+04	1.00E+05	3.90E+04	6.31E+04	644.62331	3	34.56
SYG1	YIL047C	RRSSVFENISR	[3] Phospho (ST)|[4] Phospho (ST)	-0.20	-0.01	-0.49	-0.19	0.130	0.494	0.046	0.33	5.78E+04	8.01E+04	7.65E+04	6.37E+04	5.91E+04	6.38E+04	4.97E+04	1.09E+05	5.43E+04	6.28E+04	4.80E+04	4.22E+04	504.22392	3	38.98
MDG1	YNL173C	VPVSSITSHAK	[5] Phospho (ST)|[8] Phospho (ST)	0.03	-0.11	-0.11	0.14	0.462	0.348	0.343	0.26	6.73E+04	4.24E+04	7.08E+04	6.31E+04	5.10E+04	6.96E+04	4.40E+04	6.29E+04	6.00E+04	6.38E+04	4.70E+04	5.63E+04	643.28308	2	18.43
MDS3	YGL197W	TSVSEAQNTQPQVANADAK	[2] Phospho (ST)	-0.42	-0.40	-0.37	-0.02	0.076	0.076	0.100	0.46	1.57E+05	1.06E+05	1.38E+05	1.16E+05	7.64E+04	1.07E+05	8.05E+04	1.10E+05	1.13E+05	1.01E+05	8.24E+04	1.27E+05	1019.9582	2	91.35
RPC82	YPR190C	RSGSNAAASLPSK	[4] Phospho (ST)	0.59	-0.20	0.17	0.79	0.000	0.129	0.115	0.00	3.55E+04	3.44E+04	3.73E+04	5.33E+04	5.31E+04	5.51E+04	3.38E+04	2.45E+04	3.53E+04	4.62E+04	3.79E+04	3.65E+04	663.31252	2	47.68
RPC19	YNL113W	HIQEEEEQDVDMTGDEEQEEEPDREK	[13] Phospho (ST)	0.07	-0.10	0.58	0.17	0.437	0.313	0.002	0.36	3.01E+05	2.53E+05	2.41E+05	3.55E+05	3.47E+05	1.30E+05	2.96E+05	2.46E+05	2.00E+05	4.18E+05	3.80E+05	3.93E+05	1085.0935	3	62.24
NRD1	YNL251C	SRSPPAPFSQPSTGRK	[1] Phospho (ST)|[3] Phospho (ST)	-0.65	-0.68	-0.41	0.03	0.005	0.059	0.104	0.48	1.34E+05	1.14E+05	1.41E+05	9.26E+04	7.09E+04	8.34E+04	5.09E+04	1.26E+05	6.53E+04	1.36E+05	6.98E+04	8.64E+04	620.6119	3	15.76
HYP2	YEL034W	MSDEEHTFETADAGSSATYPMQCSALR	[10] Phospho (ST)	-2.33	-0.72	-0.23	-1.60	0.002	0.043	0.256	0.02	5.44E+05	4.16E+05	3.70E+05	9.14E+04	1.35E+05	3.87E+04	3.07E+05	3.42E+05	1.57E+05	2.52E+05	5.12E+05	3.69E+05	1024.7406	3	63.02
DED1	YOR204W	SRDNSFR	[1] Phospho (ST)	0.27	-0.43	-0.02	0.69	0.322	0.257	0.490	0.04	7.83E+04	2.26E+04	3.85E+04	5.87E+04	3.92E+04	6.98E+04	3.44E+04	3.33E+04	3.61E+04	7.16E+04	3.22E+04	3.39E+04	481.1979	2	25.22
ALY2	YJL084C	NLSPINLLK	[3] Phospho (ST)	-0.05	0.08	0.53	-0.13	0.436	0.400	0.069	0.30	5.21E+04	8.05E+04	4.66E+04	5.11E+04	7.23E+04	4.91E+04	6.44E+04	7.44E+04	5.06E+04	7.94E+04	1.06E+05	7.38E+04	546.29714	2	30.77
SEC16	YPL085W	GHTSSISSYTPNQNEHASR	[5] Phospho (ST)	-0.27	-0.09	-0.08	-0.18	0.086	0.257	0.382	0.14	1.04E+05	1.16E+05	9.10E+04	1.01E+05	7.45E+04	8.34E+04	1.06E+05	8.92E+04	9.67E+04	8.09E+04	8.19E+04	1.31E+05	718.30861	3	28.3
ACF4	YJR083C	RLAIPISSPQR	[8] Phospho (ST)	-0.04	0.11	-0.37	-0.15	0.426	0.288	0.079	0.10	4.84E+04	7.49E+04	6.17E+04	5.64E+04	5.56E+04	6.79E+04	6.66E+04	6.39E+04	6.89E+04	4.29E+04	4.97E+04	5.08E+04	659.35552	2	41.6
AVT3	YKL146W	KSSGTTGGLLK	[3] Phospho (ST)	-0.72	0.52	0.37	-1.24	0.164	0.102	0.190	0.02	4.51E+04	1.72E+04	4.52E+04	1.49E+04	1.19E+04	3.86E+04	4.74E+04	4.69E+04	5.99E+04	5.29E+04	4.94E+04	3.65E+04	564.78665	2	44.44
PAF1	YBR279W	ESEGDSKTEGSEQEGENEKDEEIK	[2] Phospho (ST)	-0.12	-0.73	-0.58	0.62	0.328	0.006	0.016	0.05	1.03E+05	7.91E+04	8.55E+04	1.07E+05	7.32E+04	6.66E+04	5.24E+04	4.68E+04	6.15E+04	6.79E+04	4.79E+04	6.26E+04	921.70573	3	17.07
ENT2	YLR206W	TRSNPHDSSPSYQDDLEK	[3] Phospho (ST)	0.13	0.02	-0.40	0.10	0.223	0.466	0.054	0.33	6.79E+04	9.27E+04	6.85E+04	8.51E+04	8.26E+04	8.21E+04	1.00E+05	7.37E+04	5.93E+04	5.84E+04	5.12E+04	6.39E+04	719.30207	3	37.72
YPR036W-A	R036W-A	KNSLSLL	[3] Phospho (ST)	-0.95	-0.33	-0.34	-0.61	0.046	0.208	0.212	0.04	2.82E+04	5.84E+04	4.00E+04	1.69E+04	2.62E+04	2.25E+04	4.09E+04	3.22E+04	2.74E+04	2.46E+04	4.02E+04	3.53E+04	427.72276	2	27.99
ZIP1	YDR285W	EVSEGVAKETKESHGDPNDSETTLK	[3] Phospho (ST)|[23] Phospho (ST)	-0.86	-1.07	0.17	0.21	0.158	0.123	0.396	0.35	2.95E+05	8.28E+04	1.41E+05	1.43E+05	6.58E+04	7.69E+04	4.13E+04	1.08E+05	9.82E+04	2.40E+05	1.15E+05	2.28E+05	949.73786	3	15.38
ALY2	YJL084C	EVLSSPVLSPNVQPLDILIPHLPSTSLTR	[5] Phospho (ST)|[9] Phospho (ST)	-0.54	-0.05	0.02	-0.49	0.134	0.455	0.483	0.05	3.08E+05	4.73E+05	2.06E+05	2.09E+05	2.62E+05	2.10E+05	3.92E+05	3.06E+05	2.57E+05	3.18E+05	4.77E+05	2.08E+05	1094.897	3	49.7
BSC6	YOL137W	NLLSSSDSRRNSQDEDSLPNNTNLIK	[8] Phospho (ST)|[12] Phospho (ST)	-0.71	-0.34	-0.40	-0.37	0.005	0.109	0.023	0.13	2.29E+05	2.20E+05	1.84E+05	1.25E+05	1.49E+05	1.13E+05	1.41E+05	2.21E+05	1.38E+05	1.75E+05	1.67E+05	1.37E+05	1026.4567	3	31.58
SSD1	YDR293C	NQSQQPQQQLSPFR	[11] Phospho (ST)	-0.15	0.18	0.18	-0.33	0.112	0.256	0.196	0.13	5.37E+04	4.62E+04	5.71E+04	5.00E+04	4.60E+04	4.57E+04	4.13E+04	6.50E+04	7.19E+04	6.83E+04	4.69E+04	6.22E+04	589.2729	3	28.17
POG1	YIL122W	INASELASPR	[8] Phospho (ST)	0.16	0.58	0.19	-0.42	0.266	0.031	0.188	0.05	2.74E+04	4.11E+04	4.22E+04	3.61E+04	3.82E+04	4.93E+04	4.90E+04	5.08E+04	6.58E+04	3.77E+04	4.33E+04	4.56E+04	569.26884	2	36.49
APL5	YPL195W	AKNSPEPNEFLR	[4] Phospho (ST)	-0.17	-0.12	-0.21	-0.05	0.138	0.272	0.201	0.40	4.97E+04	6.25E+04	6.27E+04	4.65E+04	5.22E+04	5.66E+04	5.68E+04	4.21E+04	6.16E+04	3.69E+04	5.13E+04	6.26E+04	741.34351	2	43.85
STB1	YNL309W	TLLEAISPAK	[7] Phospho (ST)	-0.26	0.36	-0.05	-0.62	0.277	0.209	0.455	0.04	3.81E+04	9.16E+04	5.70E+04	4.53E+04	5.76E+04	5.27E+04	1.00E+05	7.99E+04	5.97E+04	4.76E+04	7.81E+04	5.44E+04	561.79422	2	33.73
NAB3	YPL190C	GEENGEVINTEEEEEEEHQQK	[10] Phospho (ST)	0.30	0.12	0.02	0.18	0.077	0.078	0.441	0.17	1.34E+05	1.20E+05	1.21E+05	1.79E+05	1.25E+05	1.57E+05	1.36E+05	1.28E+05	1.43E+05	1.22E+05	1.10E+05	1.48E+05	856.00842	3	32.29
GLN3	YER040W	SLQQNSLSR	[1] Phospho (ST)	-0.06	-0.36	-0.11	0.30	0.418	0.168	0.349	0.14	6.95E+04	3.87E+04	5.86E+04	6.28E+04	4.97E+04	4.75E+04	3.09E+04	4.61E+04	5.31E+04	5.79E+04	4.80E+04	4.89E+04	556.7587	2	40.22
INP52	YNL106C	SSTAPDEISTSTK	[2] Phospho (ST)	0.09	0.15	0.28	-0.06	0.357	0.271	0.139	0.41	4.98E+04	3.48E+04	4.84E+04	5.83E+04	3.90E+04	4.45E+04	4.00E+04	4.87E+04	5.87E+04	6.55E+04	4.94E+04	4.65E+04	702.30034	2	44.16
CYC8	YBR112C	AASVSPSTKPLNTEPESSSVQPTVSSESSTTK	[3] Phospho (ST)|[5] Phospho (ST)	-0.54	-0.27	-0.39	-0.27	0.041	0.157	0.083	0.11	4.51E+05	2.92E+05	4.15E+05	3.07E+05	2.40E+05	2.48E+05	2.76E+05	3.81E+05	3.01E+05	3.43E+05	2.62E+05	2.79E+05	1127.5067	3	45.43
GIP4	YAL031C	AHLASNSSRSPSVSPVR	[10] Phospho (ST)|[14] Phospho (ST)	-0.03	-0.29	-0.12	0.26	0.430	0.160	0.316	0.17	4.37E+04	3.59E+04	5.00E+04	4.70E+04	3.62E+04	4.36E+04	2.40E+04	4.19E+04	4.01E+04	5.00E+04	3.32E+04	3.62E+04	637.95394	3	23.95
RPS5	YJR123W	SDTEAPVEVQEDFEVVEEFTPVVLATPIPEEVQQAQTEIK	[N-term] Acetyl (Protein N-term)|[3] Phospho	-0.34	0.11	-0.77	-0.45	0.291	0.425	0.128	0.23	8.83E+05	5.56E+05	3.36E+05	3.79E+05	7.30E+05	2.94E+05	4.84E+05	9.60E+05	4.68E+05	1.74E+05	4.98E+05	3.71E+05	919.24199	5	36.58
NUM1	YDR150W	SFGNLR	[1] Phospho (ST)	0.18	0.11	0.08	0.07	0.251	0.346	0.341	0.39	1.30E+04	1.14E+04	1.78E+04	1.66E+04	1.29E+04	1.81E+04	1.22E+04	1.51E+04	1.81E+04	1.48E+04	1.46E+04	1.52E+04	387.17084	2	23.42
ECM21	YBL101C	RISNTLFSK	[3] Phospho (ST)	0.01	0.25	0.13	-0.24	0.473	0.201	0.298	0.21	2.63E+04	3.24E+04	2.67E+04	2.51E+04	2.92E+04	3.16E+04	4.37E+04	2.50E+04	3.29E+04	2.29E+04	3.34E+04	3.71E+04	573.28969	2	28.25
DUN1	YDL101C	REHSGDVTDSSFK	[4] Phospho (ST)	-5.70	-0.92	-0.04	-4.77	0.000	0.005	0.380	0.00	7.75E+04	6.60E+04	7.27E+04	1.20E+03	5.85E+02	2.36E+03	4.89E+04	2.56E+04	3.96E+04	6.62E+04	6.31E+04	8.07E+04	515.55091	3	37.83
GAT1	YFL021W	NPSPSIVKPGSR	[11] Phospho (ST)	-0.92	-0.60	-0.75	-0.31	0.001	0.001	0.001	0.02	5.58E+04	5.42E+04	6.27E+04	2.96E+04	2.68E+04	3.50E+04	3.71E+04	3.81E+04	3.84E+04	3.13E+04	3.33E+04	3.78E+04	659.82932	2	29.93
SIS1	YNL007C	SASSSPTYPEEETVQVNLPVSLEDLFVGK	[7] Phospho (ST)|[8] Phospho (Y)	0.16	0.11	-0.26	0.05	0.337	0.393	0.309	0.45	4.02E+05	4.27E+05	2.23E+05	3.30E+05	5.11E+05	3.31E+05	3.70E+05	4.97E+05	2.65E+05	2.45E+05	4.58E+05	1.77E+05	1094.8296	3	33.88
SAC7	YDR389W	IENVSPSK	[5] Phospho (ST)	0.19	0.11	0.36	0.08	0.327	0.390	0.255	0.34	3.33E+04	1.18E+04	2.52E+04	2.69E+04	2.19E+04	3.15E+04	2.31E+04	2.52E+04	2.77E+04	4.34E+04	2.12E+04	2.58E+04	477.22058	2	28.55
HSP42	YDR171W	KSSSFAHLQAPSPIPDPLQVSKPETR	[3] Phospho (ST)|[4] Phospho (ST)	0.87	1.23	0.75	-0.36	0.014	0.008	0.032	0.07	1.00E+05	1.69E+05	9.00E+04	2.03E+05	2.48E+05	2.05E+05	2.76E+05	3.35E+05	2.30E+05	2.03E+05	2.38E+05	1.66E+05	745.11164	4	29.43
BUD6	YLR319C	TPLPIENVRASPR	[11] Phospho (ST)	0.06	0.50	0.02	-0.44	0.420	0.087	0.480	0.04	2.21E+04	3.77E+04	2.25E+04	2.80E+04	2.90E+04	2.86E+04	4.66E+04	3.90E+04	3.07E+04	2.37E+04	3.01E+04	2.93E+04	510.59959	3	16.16
KIN2	YLR096W	SASPVVGEHQEK	[3] Phospho (ST)	0.72	-0.82	-0.05	1.54	0.087	0.131	0.440	0.03	5.33E+04	2.68E+04	3.26E+04	5.16E+04	4.75E+04	8.65E+04	4.00E+04	1.52E+04	8.85E+03	3.89E+04	3.48E+04	3.49E+04	674.30008	2	40.16
STE2	YFL026W	FYPGTLSSFQTDSINNDAK	[13] Phospho (ST)	-0.01	-0.25	-0.28	0.24	0.478	0.119	0.136	0.10	2.88E+05	3.72E+05	2.71E+05	2.92E+05	3.58E+05	2.74E+05	2.32E+05	2.94E+05	2.55E+05	2.43E+05	3.12E+05	2.15E+05	1092.9782	2	28.1
ALY2	YJL084C	RESVQDNLPSTIR	[3] Phospho (ST)	0.00	-0.02	0.15	0.03	0.488	0.446	0.156	0.45	5.18E+04	5.43E+04	5.87E+04	4.64E+04	5.70E+04	6.18E+04	4.83E+04	4.90E+04	6.49E+04	5.23E+04	6.17E+04	6.93E+04	797.88309	2	44.95
MYO5	YMR109W	RGSVYHVPLNIVQADAVR	[5] Phospho (Y)	-0.60	-0.25	-0.61	-0.35	0.093	0.272	0.096	0.13	1.49E+05	2.64E+05	1.49E+05	1.04E+05	1.37E+05	1.30E+05	2.03E+05	1.26E+05	1.43E+05	9.73E+04	1.47E+05	1.24E+05	692.0248	3	71.15
ZRT2	YLR130C	NEEIVATPIK	[7] Phospho (ST)	-0.10	0.27	0.64	-0.38	0.347	0.253	0.007	0.19	5.81E+04	7.42E+04	8.82E+04	7.18E+04	5.27E+04	8.07E+04	1.23E+05	5.67E+04	8.67E+04	1.19E+05	1.06E+05	1.19E+05	597.29507	2	36.8
AVT1	YJR001W	PEQEPLSPNGR	[7] Phospho (ST)	0.01	0.32	0.21	-0.31	0.460	0.088	0.062	0.08	5.72E+04	4.88E+04	6.41E+04	6.30E+04	5.68E+04	5.20E+04	6.37E+04	6.32E+04	8.57E+04	6.34E+04	6.63E+04	6.69E+04	652.28757	2	25.21
PAM1	YDR251W	LNSLSNQSTFR	[3] Phospho (ST)	-0.25	-0.23	-0.24	-0.03	0.033	0.058	0.049	0.43	5.20E+04	4.75E+04	5.35E+04	4.22E+04	3.85E+04	4.78E+04	4.36E+04	3.81E+04	4.92E+04	4.16E+04	3.88E+04	4.93E+04	673.80899	2	48.44
SCP160	YJL080C	LTYEPIDLSSILSDGEEK	[13] Phospho (ST)	-0.44	0.02	-0.08	-0.46	0.201	0.478	0.435	0.09	1.08E+05	1.83E+05	8.11E+04	7.76E+04	1.26E+05	7.04E+04	1.42E+05	1.35E+05	1.01E+05	9.57E+04	1.66E+05	8.94E+04	696.99297	3	61.28
XRN1	YGL173C	GEIKPSSGTNSTECQSPK	[16] Phospho (ST)	0.03	-0.42	-0.06	0.45	0.464	0.168	0.442	0.02	1.35E+05	7.06E+04	7.84E+04	9.45E+04	9.90E+04	9.68E+04	5.80E+04	6.79E+04	8.63E+04	1.16E+05	7.45E+04	8.28E+04	993.92744	2	65.57
MPP10	YJR002W	HSSPDPYGINDK	[3] Phospho (ST)	-0.28	-0.73	-0.41	0.45	0.109	0.016	0.051	0.02	2.83E+04	3.74E+04	4.19E+04	3.25E+04	2.64E+04	2.96E+04	2.33E+04	1.78E+04	2.37E+04	2.85E+04	2.45E+04	2.80E+04	470.52968	3	22.76
HSP42	YDR171W	SSSFAHLQAPSPIPDPLQVSKPETR	[3] Phospho (ST)	-0.46	-0.06	-0.26	-0.39	0.196	0.451	0.308	0.13	1.57E+05	3.03E+05	1.25E+05	1.48E+05	1.49E+05	1.30E+05	2.52E+05	1.68E+05	1.39E+05	1.37E+05	2.09E+05	1.42E+05	923.79246	3	60.89

MUK1	YPL070W	ILIVGTSVSSPNK	[7] Phospho (ST)	0.14	1.34	1.06	-1.20	0.181	0.001	0.002	0.00	4.74E+04	6.05E+04	6.32E+04	5.85E+04	6.91E+04	6.14E+04	1.36E+05	1.65E+05	1.33E+05	1.11E+05	1.36E+05	1.09E+05	697.86857	2	58.07
SWH1	YAR042W	SQSLSEITPGPHSR	[3] Phospho (ST)	-0.12	0.00	0.10	-0.12	0.245	0.500	0.303	0.17	5.51E+04	7.27E+04	6.25E+04	5.57E+04	5.29E+04	6.66E+04	6.30E+04	6.68E+04	6.05E+04	5.70E+04	6.74E+04	7.98E+04	788.36209	2	82.1
DOT6	YER088C	SNSHSFTNSLNQDPIVR	[7] Phospho (ST)	-0.75	-0.58	-0.36	-0.17	0.012	0.027	0.069	0.19	1.47E+05	1.87E+05	1.33E+05	1.01E+05	9.87E+04	7.85E+04	9.77E+04	1.24E+05	9.16E+04	1.35E+05	1.25E+05	1.04E+05	665.96891	3	36.79
MAF1	YDR005C	RDSNSFWEQK	[3] Phospho (ST)	-0.42	-0.27	-0.07	-0.16	0.030	0.094	0.341	0.08	5.16E+04	6.97E+04	7.05E+04	4.55E+04	4.95E+04	4.80E+04	4.83E+04	5.28E+04	5.83E+04	6.01E+04	5.46E+04	6.75E+04	688.7859	2	36.62
VPS54	YDR027C	IVVPEGSPSR	[7] Phospho (ST)	-0.70	-0.06	-0.22	-0.65	0.008	0.381	0.140	0.01	3.26E+04	3.37E+04	4.18E+04	2.29E+04	1.85E+04	2.49E+04	3.52E+04	2.89E+04	3.97E+04	2.51E+04	3.45E+04	3.31E+04	560.77355	2	22.4
MAK21	YDR060W	SLPVFASADDYAQYLDQDSD	[19] Phospho (ST)	-0.42	-0.26	-0.86	-0.16	0.269	0.371	0.127	0.42	1.09E+06	1.45E+06	3.59E+05	7.05E+05	1.02E+06	4.43E+05	5.17E+05	1.45E+06	4.54E+05	5.52E+05	6.06E+05	4.40E+05	1150.4686	2	65.97
HRP1	YOL123W	SSDEEDFNDIYGDDKPTTTEEVK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.18	0.23	0.13	-0.04	0.395	0.358	0.291	0.48	2.06E+05	2.66E+05	1.80E+05	8.61E+04	4.32E+05	2.23E+05	1.13E+05	4.26E+05	2.25E+05	2.79E+05	2.25E+05	2.08E+05	946.02768	3	34.91
GNP1	YDR508C	DSSSQLDNELNRK	[3] Phospho (ST)	0.07	-0.29	-0.04	0.36	0.356	0.042	0.446	0.04	7.56E+04	7.33E+04	9.36E+04	7.86E+04	7.55E+04	1.01E+05	6.38E+04	6.78E+04	6.63E+04	1.03E+05	6.42E+04	6.99E+04	793.34142	2	39.77
WHI4	YDL224C	KESVPFLR	[3] Phospho (ST)	-0.76	-0.50	-0.57	-0.26	0.012	0.057	0.090	0.19	6.74E+04	6.67E+04	4.86E+04	3.01E+04	3.63E+04	4.15E+04	5.54E+04	3.43E+04	3.94E+04	2.00E+04	5.49E+04	4.79E+04	528.26831	2	42.47
APL5	YPL195W	AKNSPEPNEFLR	[4] Phospho (ST)	0.25	0.79	0.21	-0.53	0.166	0.017	0.277	0.03	1.33E+04	1.88E+04	2.18E+04	1.87E+04	2.05E+04	2.51E+04	3.49E+04	2.45E+04	3.37E+04	1.37E+04	2.38E+04	2.49E+04	494.56448	3	30.73
CFD1	YIL003W	HEQPQIESPK	[8] Phospho (ST)	1.35	0.92	0.94	0.43	0.022	0.078	0.072	0.04	7.04E+03	2.35E+04	5.40E+04	6.29E+04	6.85E+04	8.41E+04	5.35E+04	4.59E+04	6.06E+04	5.50E+04	4.70E+04	6.02E+04	636.78488	2	35.15
RSN1	YMR266W	YKEEESRSAV	[8] Phospho (ST)	-0.21	-0.24	0.23	0.04	0.126	0.151	0.210	0.41	4.20E+04	3.19E+04	4.43E+04	3.41E+04	3.57E+04	3.27E+04	3.10E+04	2.86E+04	4.01E+04	5.56E+04	3.35E+04	4.95E+04	639.27402	2	34.69
STB1	YNL309W	FVEKPNTPPSSR	[7] Phospho (ST)	-0.03	0.05	0.00	-0.08	0.460	0.459	0.500	0.42	1.82E+04	2.78E+04	3.45E+04	2.23E+04	2.30E+04	3.33E+04	3.58E+04	1.51E+04	3.22E+04	1.88E+04	2.25E+04	3.91E+04	480.2289	3	20.07
RIM11	YMR139W	QLKPTEPNVSYICSR	[11] Phospho (Y)	-0.24	-0.10	-0.14	-0.13	0.085	0.297	0.279	0.23	5.89E+04	5.12E+04	4.54E+04	4.91E+04	4.07E+04	4.22E+04	4.20E+04	4.54E+04	5.74E+04	4.58E+04	3.66E+04	5.87E+04	624.62935	3	49.89
BUD21	YOR078W	HVTFDKLDESDENEEALAK	[10] Phospho (ST)	-0.04	-0.62	-0.28	0.58	0.405	0.012	0.141	0.04	2.54E+05	2.21E+05	2.40E+05	2.13E+05	2.04E+05	2.79E+05	1.92E+05	1.17E+05	1.56E+05	1.81E+05	1.48E+05	2.59E+05	1135.4972	2	72.64
SPA2	YLL021W	GPEQLKSPEVQR	[7] Phospho (ST)	-0.01	0.14	0.33	-0.15	0.464	0.215	0.020	0.21	4.08E+04	4.00E+04	4.44E+04	3.93E+04	3.96E+04	4.55E+04	5.26E+04	3.72E+04	4.79E+04	5.15E+04	4.74E+04	5.88E+04	724.35067	2	36.19
PAT1	YCR077C	RRSSYAFNNGNGATNLNK	[3] Phospho (ST)|[4] Phospho (ST)	-0.63	-0.67	-0.55	0.04	0.055	0.069	0.085	0.45	1.31E+05	7.94E+04	1.37E+05	7.28E+04	6.20E+04	8.99E+04	4.89E+04	9.94E+04	6.94E+04	9.79E+04	5.69E+04	8.30E+04	715.30788	3	42.7
GAL11	YOL051W	KLSISNAASQQPTPR	[3] Phospho (ST)	-0.19	-0.15	-0.18	-0.04	0.202	0.286	0.260	0.43	6.02E+04	8.46E+04	9.04E+04	6.24E+04	6.57E+04	7.80E+04	8.03E+04	5.32E+04	7.82E+04	5.51E+04	6.48E+04	8.72E+04	839.41925	2	66.57
EFR3	YMR212C	DANEDLHSLSSRGK	[8] Phospho (ST)|[11] Phospho (ST)	-0.20	-0.35	-0.18	0.15	0.142	0.156	0.211	0.30	9.86E+04	6.84E+04	9.12E+04	7.51E+04	7.57E+04	7.37E+04	4.68E+04	9.21E+04	6.36E+04	8.53E+04	6.29E+04	7.98E+04	844.83763	2	29.98
CTR9	YOL145C	TLSDSDEDDDDVVK	[3] Phospho (ST)|[5] Phospho (ST)	-0.35	-0.13	-0.44	-0.22	0.175	0.404	0.104	0.36	2.35E+05	1.37E+05	2.23E+05	1.03E+05	1.86E+05	1.77E+05	7.22E+04	2.76E+05	1.95E+05	1.76E+05	1.40E+05	1.23E+05	856.79532	2	41.02
HEK2	YBL032W	SDSASFLEEK	[3] Phospho (ST)	-0.05	0.02	-0.45	-0.06	0.394	0.464	0.046	0.05	7.74E+04	9.04E+04	1.14E+05	9.09E+04	8.93E+04	9.25E+04	9.32E+04	9.35E+04	9.85E+04	6.89E+04	7.56E+04	6.20E+04	596.74267	2	62.03
CDC24	YAL041W	RVSDVLPK	[3] Phospho (ST)	-0.11	0.02	-0.19	-0.13	0.348	0.482	0.298	0.36	2.54E+04	4.30E+04	4.30E+04	3.24E+04	3.14E+04	3.95E+04	4.94E+04	2.27E+04	4.08E+04	2.15E+04	3.86E+04	3.75E+04	497.26009	2	31.43
VHS2	YIL135C	SPSNQQYLLK	[3] Phospho (ST)	-0.24	0.17	-0.22	-0.41	0.135	0.234	0.151	0.03	4.45E+04	6.54E+04	6.41E+04	5.14E+04	4.74E+04	4.90E+04	5.44E+04	7.55E+04	6.61E+04	4.60E+04	5.13E+04	5.18E+04	629.29779	2	55.28
SWI6	YLR182W	IRSQLLK	[3] Phospho (ST)	-11.26	-4.80	-2.00	-6.46	0.001	0.001	0.002	0.01	5.10E+04	7.32E+04	7.55E+04	0.00E+00	5.14E+01	0.00E+00	3.42E+03	1.58E+03	2.15E+03	1.56E+04	1.53E+04	1.90E+04	469.26512	2	21.18
KEL1	YHR158C	SQELTISK	[7] Phospho (ST)	0.04	-0.37	-0.07	0.41	0.445	0.102	0.413	0.11	2.74E+04	1.91E+04	2.79E+04	3.29E+04	2.22E+04	2.14E+04	1.46E+04	2.29E+04	1.98E+04	3.05E+04	1.69E+04	2.36E+04	493.23376	2	33.91
ALR1	YOL130W	SSLVSPVLEIPHESK	[2] Phospho (ST)	-0.21	0.17	-0.16	-0.38	0.336	0.348	0.370	0.12	3.54E+04	8.78E+04	5.08E+04	4.61E+04	6.39E+04	4.07E+04	8.07E+04	6.42E+04	5.14E+04	4.14E+04	6.75E+04	4.65E+04	567.95391	3	54.74
UTP25	YIL091C	DIDSEDEQDPFESHFNQVPEK	[4] Phospho (ST)	0.09	0.12	0.14	-0.02	0.370	0.265	0.295	0.46	1.08E+05	1.42E+05	1.02E+05	1.03E+05	1.60E+05	1.13E+05	1.20E+05	1.41E+05	1.22E+05	9.86E+04	1.56E+05	1.35E+05	862.35138	3	66.55
MLF3	YNL074C	SSSILFQR	[3] Phospho (ST)	-0.46	0.33	-0.40	-0.79	0.130	0.221	0.160	0.04	2.41E+04	5.17E+04	4.30E+04	2.73E+04	2.87E+04	3.06E+04	3.73E+04	6.73E+04	4.52E+04	3.02E+04	3.33E+04	2.67E+04	509.24214	2	48.23
HSP42	YDR171W	SSSFAHLQAPSPIPDPLQVSKPETR	[3] Phospho (ST)	-0.46	-0.07	-0.16	-0.39	0.164	0.439	0.353	0.10	1.07E+05	1.65E+05	7.11E+04	8.46E+04	9.30E+04	7.20E+04	1.37E+05	1.07E+05	8.31E+04	8.77E+04	1.27E+05	9.21E+04	693.09623	4	17.83
DBP2	YNL112W	DRSDSEIAQFRK	[3] Phospho (ST)	0.26	-0.30	-0.09	0.56	0.079	0.037	0.223	0.02	3.80E+04	4.05E+04	4.35E+04	4.83E+04	4.13E+04	5.64E+04	3.83E+04	2.92E+04	3.16E+04	4.12E+04	3.34E+04	4.00E+04	511.235	3	17.43
YMR086W	YMR086W	NLENDTTSSPTQDLDEK	[9] Phospho (ST)	0.17	0.29	0.22	-0.12	0.201	0.105	0.180	0.31	1.02E+05	8.58E+04	1.04E+05	1.29E+05	8.85E+04	1.12E+05	9.69E+04	1.18E+05	1.44E+05	1.38E+05	8.77E+04	1.15E+05	993.91312	2	38.36
NSG2	YNL156C	RSVSIDSTK	[4] Phospho (ST)	0.43	-0.89	0.01	1.33	0.044	0.102	0.488	0.02	4.10E+04	2.37E+04	3.26E+04	4.26E+04	4.39E+04	4.50E+04	3.38E+04	1.35E+04	5.03E+03	3.97E+04	2.82E+04	2.99E+04	536.75508	2	27.8
PSH1	YOL054W	HVIITDDEEEEQRR	[5] Phospho (ST)	0.88	0.08	0.25	0.80	0.002	0.389	0.314	0.01	4.39E+04	5.00E+04	5.95E+04	1.06E+05	8.78E+04	8.90E+04	7.12E+04	4.04E+04	5.10E+04	4.32E+04	4.26E+04	9.66E+04	616.94401	3	39.9
BCY1	YIL033C	TSTPPLPMHFNAQR	[3] Phospho (ST)	0.10	0.37	0.37	-0.27	0.441	0.208	0.190	0.34	3.49E+04	5.55E+04	3.41E+04	4.43E+04	7.39E+04	1.50E+04	6.82E+04	6.09E+04	3.15E+04	3.60E+04	7.16E+04	5.37E+04	559.59236	3	20.3
YLL032C	YLL032C	TTIDNTSQSGASPQR	[9] Phospho (ST)	-0.03	0.54	0.34	-0.57	0.464	0.078	0.174	0.07	5.19E+04	3.11E+04	3.83E+04	5.05E+04	3.24E+04	3.61E+04	4.19E+04	6.95E+04	6.54E+04	6.74E+04	4.01E+04	4.66E+04	821.85778	2	34.24
SST2	YLR452C	NLSNENCSFKK	[3] Phospho (ST)	-0.15	-0.81	0.00	0.66	0.291	0.033	0.498	0.00	4.33E+04	2.48E+04	4.15E+04	3.56E+04	3.17E+04	3.15E+04	1.77E+04	1.97E+04	2.50E+04	4.39E+04	2.88E+04	3.70E+04	710.80019	2	40.69
MSC3	YLR219W	STAGNNNDSRANSITVK	[9] Phospho (ST)|[13] Phospho (ST)	0.23	-0.02	0.17	0.25	0.275	0.487	0.368	0.25	9.03E+04	4.05E+04	9.19E+04	1.07E+05	8.31E+04	7.15E+04	4.78E+04	9.95E+04	7.31E+04	1.18E+05	5.65E+04	7.49E+04	954.89606	2	20.88
YDR186C	YDR186C	NNSNSNLLFEK	[3] Phospho (ST)	-0.37	-0.29	-0.36	-0.08	0.013	0.115	0.027	0.38	7.34E+04	6.59E+04	6.80E+04	6.00E+04	5.38E+04	4.64E+04	4.27E+04	7.26E+04	5.40E+04	5.40E+04	6.28E+04	4.49E+04	680.30134	2	55.73
SMY2	YBR172C	TSSLIDSIGIQR	[3] Phospho (ST)	-2.02	-0.61	-0.52	-1.41	0.029	0.154	0.196	0.00	6.62E+04	1.55E+05	7.52E+04	1.99E+04	2.66E+04	2.67E+04	7.08E+04	7.31E+04	5.02E+04	5.35E+04	9.49E+04	5.84E+04	685.34058	2	54.25
SNF1	YDR477W	TSCGSPNYAAPEVISGK	[2] Phospho (ST)	-0.92	-0.32	-0.72	-0.60	0.000	0.076	0.001	0.03	1.40E+05	1.61E+05	1.43E+05	7.97E+04	7.65E+04	7.90E+04	1.08E+05	1.49E+05	9.96E+04	8.00E+04	9.82E+04	9.21E+04	909.39252	2	78.53
SEC16	YPL085W	KGSNNSNRPPVIPLGTQEPR	[3] Phospho (ST)	-0.35	-0.45	-0.32	0.10	0.059	0.028	0.093	0.30	1.19E+05	9.65E+04	1.29E+05	8.11E+04	8.31E+04	1.06E+05	7.15E+04	8.86E+04	9.23E+04	1.12E+05	7.46E+04	8.91E+04	747.71017	3	60.39
RPL36B	L249C-A	RLGSFTR	[4] Phospho (ST)	1.50	-1.01	-0.33	2.50	0.002	0.016	0.132	0.00	9.30E+03	1.44E+04	1.12E+04	3.77E+04	2.70E+04	3.37E+04	7.27E+03	3.84E+03	6.26E+03	7.26E+03	9.65E+03	1.09E+04	458.72361	2	23.79
ABP1	YCR088W	SFTPSKSPAPVSK	[3] Phospho (ST)	-0.17	0.76	0.01	-0.93	0.224	0.006	0.481	0.00	2.88E+04	3.77E+04	2.99E+04	2.85E+04	2.27E+04	3.43E+04	6.29E+04	4.96E+04	5.07E+04	2.86E+04	2.96E+04	3.88E+04	706.8447	2	23.3
UTP14	YML093W	DVNPWLANESDEEHTVK	[10] Phospho (ST)	-0.03	0.10	0.06	-0.13	0.465	0.355	0.407	0.32	5.28E+04	8.42E+04	6.06E+04	6.48E+04	8.17E+04	4.73E+04	6.42E+04	8.41E+04	6.34E+04	5.90E+04	7.70E+04	6.98E+04	688.29688	3	15.88
TPS3	YMR261C	NPNLSFDSHPPR	[5] Phospho (ST)	0.11	-0.03	0.35	0.14	0.332	0.454	0.116	0.14	1.78E+04	2.89E+04	3.22E+04	3.09E+04	2.74E+04	2.70E+04	2.91E+04	2.33E+04	2.48E+04	3.29E+04	2.91E+04	3.89E+04	487.54945	3	25.6
NSG2	YNL156C	ILSASSIHENFPSR	[3] Phospho (ST)|[5] Phospho (ST)	-0.27	-0.47	-0.46	0.20	0.053	0.050	0.005	0.25	1.61E+05	1.81E+05	1.68E+05	1.20E+05	1.63E+05	1.40E+05	9.82E+04	1.65E+05	1.05E+05	1.39E+05	1.19E+05	1.12E+05	859.37136	2	23.25
MTL1	YGR023W	GIDDQYSPTK	[7] Phospho (ST)	0.29	0.59	0.47	-0.30	0.050	0.024	0.063	0.07	2.02E+04	2.07E+04	2.76E+04	2.78E+04	2.72E+04	2.90E+04	2.89E+04	3.38E+04	4.07E+04	3.96E+04	2.69E+04	2.87E+04	602.25036	2	39.17
YAK1	YJL141C	RKSSLVVPPAR	[3] Phospho (ST)|[4] Phospho (ST)	0.30	0.23	-0.07	0.07	0.080	0.225	0.383	0.39	8.78E+04	1.02E+05	1.25E+05	1.31E+05	1.12E+05	1.45E+05	9.34E+04	1.58E+05	1.17E+05	1.18E+05	8.36E+04	9.85E+04	685.3413	2	15.67
GNP1	YDR508C	DSSSQLDNELNR	[4] Phospho (ST)	-0.36	-0.39	-0.27	0.03	0.159	0.173	0.219	0.46	5.69E+04	3.19E+04	6.15E+04	4.21E+04	3.27E+04	4.21E+04	2.65E+04	4.79E+04	4.01E+04	4.94E+04	3.69E+04	3.80E+04	729.29928	2	58.18
KIN28	YDL108W	AIPAPHEILTSNVVTR	[10] Phospho (ST)	0.01	0.22	0.06	-0.21	0.484	0.324	0.453	0.29	5.19E+04	1.10E+05	6.61E+04	7.36E+04	8.66E+04	7.04E+04	1.26E+05	6.47E+04	7.61E+04	4.43E+04	1.13E+05	8.12E+04	899.46707	2	50.23
CDC3	YLR314C	SLKEEQVSIKQDPEQEER	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.39	-0.40	-0.32	0.01	0.017	0.035	0.040	0.46	2.11E+05	1.67E+05	2.11E+05	1.55E+05	1.50E+05	1.44E+05	1.22E+05	1.58E+05	1.64E+05	1.55E+05	1.43E+05	1.73E+05	1187.514	2	20.63
SRP40	YKR092C	AEETPASSNESTPSASSSSSANK	[7] Phospho (ST)	-0.06	-0.41	0.18	0.35	0.447	0.229	0.348	0.09	2.07E+05	8.20E+04	1.11E+05	1.41E+05	1.10E+05	1.33E+05	7.54E+04	1.04E+05	1.22E+05	1.89E+05	1.18E+05	1.48E+05	1153.4622	2	79.05
SVL3	YPL032C	KPSFPQLQQSANVR	[3] Phospho (ST)	-0.46	-0.62	-0.69	0.16	0.044	0.023	0.031	0.10	2.56E+05	3.83E+05	3.59E+05	2.24E+05	2.41E+05	2.61E+05	2.14E+05	2.39E+05	1.96E+05	1.46E+05	2.33E+05	2.40E+05	840.4171	2	60.41
CRN1	YLR429W	IETPVTPTETK	[6] Phospho (ST)	0.88	0.65	0.15	0.23	0.005	0.082	0.305	0.24	3.23E+04	4.72E+04	4.73E+04	7.46E+04	6.92E+04	8.93E+04	8.63E+04	4.14E+04	7.12E+04	3.40E+04	4.97E+04	5.70E+04	648.31012	2	18.36
MRH1	YDR033W	APVASPRPAATPNLSK	[5] Phospho (ST)	-0.30	0.40	0.17	-0.69	0.102	0.153	0.232	0.07	6.09E+04	7.59E+04	5.72E+04	4.57E+04	4.86E+04	6.35E+04	1.13E+05	5.65E+04	8.54E+04	6.11E+04	6.85E+04	8.91E+04	828.92751	2	36.2
SPC110	YDR356W	RNTTQTQVVSPTK	[10] Phospho (ST)	0.89	0.56	0.68	0.33	0.085	0.182	0.114	0.19	1.37E+04	2.14E+04	5.22E+04	4.73E+04	4.25E+04	7.17E+04	5.08E+04	3.00E+04	4.77E+04	5.46E+04	4.05E+04	4.53E+04	770.3804	2	40.91
TPS2	YDR074W	RSASYTGAKV	[4] Phospho (ST)	-0.03	0.69	1.00	-0.72	0.485	0.152	0.071	0.03	1.21E+04	4.09E+03	2.93E+04	1.42E+04	1.03E+04	2.01E+04	2.75E+04	1.94E+04	2.63E+04	3.67E+04	2.40E+04	3.05E+04	560.2634	2	35.97
CHS2	YBR038W	TQFYRDSAHNSPVAPNR	[7] Phospho (ST)|[11] Phospho (ST)	0.90	2.35	1.65	-1.45	0.004	0.008	0.003	0.02	2.78E+04	2.56E+04	2.35E+04	4.88E+04	4.02E+04	5.52E+04	1.03E+05	1.83E+05	1.07E+05	9.89E+04	6.53E+04	7.77E+04	707.29737	3	26.16
AVT1	YJR001W	PEQEPLSPNGRK	[7] Phospho (ST)	-0.39	-0.15	0.04	-0.24	0.005	0.319	0.420	0.25	2.26E+04	1.97E+04	2.29E+04	1.75E+04	1.62E+04	1.60E+04	2.29E+04	1.15E+04	2.45E+04	1.71E+04	2.29E+04	2.73E+04	477.89267	3	17.32
VHS2	YIL135C	TVSNNAANSLSR	[11] Phospho (ST)	-0.33	-0.42	-0.47	0.09	0.098	0.066	0.059	0.37	3.89E+04	2.97E+04	3.78E+04	3.12E+04	2.10E+04	3.26E+04	1.91E+04	3.19E+04	2.83E+04	3.32E+04	1.95E+04	2.40E+04	657.29596	2	45.07
RPP2B	YDR382W	EEEAKEESDDDMGFGLFD	[8] Phospho (ST)	-0.90	-0.14	0.17	-0.76	0.061	0.356	0.331	0.12	1.13E+06	1.16E+06	7.69E+05	4.99E+05	9.27E+05	2.19E+05	9.04E+05	1.27E+06	6.09E+05	1.01E+06	1.60E+06	8.21E+05	1071.8917	2	42.12
NCB2	YDR397C	LHHNSVSDPVKSEDSS	[12] Phospho (ST)|[15] Phospho (ST)	0.13	-0.26	-0.30	0.39	0.312	0.243	0.194	0.10	7.45E+04	4.77E+04	8.48E+04	8.85E+04	6.91E+04	6.97E+04	3.84E+04	6.95E+04	6.52E+04	6.78E+04	4.29E+04	5.79E+04	633.2509	3	16.89
SRF1	YDL133W	SGSLEALQNAK	[1] Phospho (ST)	0.30	0.37	0.02	-0.06	0.105	0.095	0.466	0.38	2.01E+04	2.91E+04	3.12E+04	3.10E+04	3.02E+04	3.81E+04	2.74E+04	3.86E+04	3.78E+04	3.22E+04	2.41E+04	2.53E+04	599.27968	2	62.77
NCB2	YDR397C	LHHNSVSDPVK	[5] Phospho (ST)	-0.35	-0.12	-0.32	-0.23	0.090	0.395	0.137	0.31	2.46E+04	3.84E+04	3.54E+04	2.37E+04	2.74E+04	2.62E+04	4.49E+04	1.65E+04	2.90E+04	2.12E+04	2.56E+04	3.18E+04	438.20622	3	33.06
NUP2	YLR335W	KKDESDSENDIEIK	[5] Phospho (ST)|[7] Phospho (ST)	-0.13	-0.43	-0.45	0.30	0.304	0.168	0.095	0.22	1.05E+05	6.40E+04	8.62E+04	8.58E+04	8.07E+04	6.71E+04	4.01E+04	9.47E+04	5.45E+04	7.77E+04	4.95E+04	5.94E+04	603.91126	3	15.63
ROD1	YOR018W	SSTNLAALPK	[2] Phospho (ST)	-0.50	0.02	-0.24	-0.51	0.023	0.460	0.098	0.00	4.27E+04	5.03E+04	5.87E+04	3.24E+04	3.51E+04	4.01E+04	4.71E+04	5.35E+04	5.28E+04	4.62E+04	4.28E+04	3.93E+04	541.2685	2	38.84
SNG1	YGR197C	IQTGLFSPR	[3] Phospho (ST)	0.23	0.62	-0.07	-0.39	0.227	0.035	0.427	0.02	2.18E+04	4.41E+04	3.17E+04	3.50E+04	4.28E+04	3.69E+04	5.47E+04	4.43E+04	5.10E+04	2.07E+04	3.82E+04	3.39E+04	549.77107	2	42.91
NUP145	YGL092W	AYEPDLSDADFEGIEASPK	[7] Phospho (ST)	-0.08	0.20	0.03	-0.28	0.382	0.199	0.467	0.07	2.23E+05	3.21E+05	2.05E+05	2.23E+05	2.78E+05	2.08E+05	3.16E+05	2.87E+05	2.59E+05	2.09E+05	3.21E+05	2.33E+05	1067.4526	2	73.1
YOR343W-A	R343W-A	EVPSNQDPLAVSASNLPEFDRDSTK	[12] Phospho (ST)	-1.79	0.07	0.34	-1.85	0.004	0.396	0.104	0.00	1.69E+05	2.48E+05	1.63E+05	5.08E+04	6.68E+04	5.07E+04	2.43E+05	1.79E+05	1.86E+05	2.15E+05	2.86E+05	2.35E+05	932.76399	3	25.64
WHI4	YDL224C	TSSSPLGPSAAK	[4] Phospho (ST)	0.20	0.28	-0.01	-0.08	0.020	0.004	0.480	0.08	3.43E+04	3.92E+04	3.73E+04	4.05E+04	4.23E+04	4.45E+04	4.34E+04	4.55E+04	4.56E+04	4.51E+04	2.94E+04	3.56E+04	591.77362	2	60.57
NBA1	YOL070C	LLSSPLRQEK	[4] Phospho (ST)	0.06	0.93	0.58	-0.87	0.402	0.051	0.098	0.05	1.72E+04	2.65E+04	2.34E+04	2.15E+04	2.08E+04	2.75E+04	5.88E+04	2.68E+04	4.25E+04	2.13E+04	3.48E+04	4.41E+04	625.82926	2	31.78
ELF1	YKL160W	GALVDSDDE	[6] Phospho (ST)	0.02	0.14	0.35	-0.13	0.481	0.372	0.255	0.35	7.22E+04	3.19E+04	7.40E+04	7.20E+04	6.02E+04	4.82E+04	4.38E+04	8.11E+04	7.19E+04	1.10E+05	6.56E+04	5.11E+04	500.67938	2	24.69
PIN2	YOR104W	VAPLVYEEENFEGSSPQPQYDAR	[15] Phospho (ST)	-0.02	0.11	-0.26	-0.13	0.451	0.312	0.052	0.28	2.13E+05	2.55E+05	2.05E+05	1.96E+05	2.38E+05	2.31E+05	2.04E+05	3.04E+05	2.20E+05	1.98E+05	1.95E+05	1.70E+05	902.39442	3	44.67
STB3	YDR169C	LTATSEPTSR	[9] Phospho (ST)	-0.26	-0.45	-0.34	0.19	0.138	0.057	0.097	0.12	4.15E+04	3.08E+04	4.71E+04	3.50E+04	2.95E+04	3.54E+04	2.79E+04	2.59E+04	3.35E+04	3.58E+04	2.80E+04	3.08E+04	571.75804	2	25.17
YER138C	YER138C	TPTTVSEQNTEESIIADLPLPDLPPESPTEFPDPFK	[27] Phospho (ST)	-1.14	-0.10	-0.33	-1.03	0.085	0.430	0.298	0.04	5.14E+05	8.65E+05	2.59E+05	2.26E+05	3.04E+05	2.14E+05	6.97E+05	4.87E+05	3.40E+05	3.93E+05	6.02E+05	3.04E+05	1008.729	4	33.87
ACE2	YLR131C	TQLSPIHK	[4] Phospho (ST)	0.16	1.00	0.70	-0.85	0.373	0.030	0.094	0.04	1.12E+04	7.21E+03	1.66E+04	1.13E+04	9.25E+03	1.86E+04	2.83E+04	1.63E+04	2.56E+04	1.50E+04	1.55E+04	2.64E+04	502.25272	2	22.93
CDC48	YDL126C	FGLSPSK	[4] Phospho (ST)	0.37	1.45	0.73	-1.08	0.107	0.009	0.009	0.01	9.26E+03	1.60E+04	1.44E+04	1.41E+04	1.73E+04	1.98E+04	3.64E+04	2.65E+04	4.56E+04	2.11E+04	2.38E+04	2.10E+04	408.18864	2	33.45
MYO5	YMR109W	SMSLLGYR	[3] Phospho (ST)	-0.77	-0.03	-0.11	-0.74	0.160	0.482	0.427	0.13	2.23E+04	5.69E+04	2.51E+04	2.06E+04	3.09E+04	9.87E+03	3.79E+04	4.70E+04	1.74E+04	2.16E+04	4.53E+04	2.97E+04	503.72517	2	41.94
GAT1	YFL021W	SSTSVQSSATPPSNTSSNPDIK	[4] Phospho (ST)	-0.98	-0.59	-0.71	-0.39	0.006	0.022	0.017	0.00	2.59E+05	1.83E+05	1.92E+05	1.09E+05	9.92E+04	1.14E+05	1.31E+05	1.48E+05	1.42E+05	1.40E+05	1.09E+05	1.39E+05	1136.5031	2	62.63
TAF2	YCR042C	DAQDNDEEEEEGESDEEEEEGEEERR	[14] Phospho (ST)	0.16	0.00	0.07	0.16	0.258	0.494	0.405	0.24	2.30E+05	1.67E+05	1.57E+05	2.43E+05	1.91E+05	1.82E+05	1.63E+05	2.26E+05	1.63E+05	2.43E+05	1.41E+05	1.99E+05	1064.7065	3	63.37
NOP12	YOL041C	LFGTNPIAETEESGNEK	[13] Phospho (ST)	0.24	0.28	0.21	-0.04	0.243	0.154	0.142	0.45	7.30E+04	1.05E+05	8.42E+04	8.42E+04	1.41E+05	8.54E+04	9.70E+04	1.33E+05	8.98E+04	9.05E+04	1.03E+05	1.11E+05	639.28283	3	45.19
AVT1	YJR001W	PEQEPLSPNGRK	[7] Phospho (ST)	-0.30	-0.47	-0.10	0.17	0.063	0.097	0.346	0.30	4.83E+04	3.59E+04	4.17E+04	3.80E+04	3.23E+04	3.18E+04	3.53E+04	1.71E+04	3.82E+04	2.95E+04	3.94E+04	4.85E+04	716.33546	2	22.85
TRS85	YDR108W	SNSLFQR	[3] Phospho (ST)	-0.11	0.20	-0.07	-0.31	0.283	0.297	0.380	0.21	1.82E+04	2.08E+04	2.52E+04	1.92E+04	1.76E+04	2.27E+04	1.50E+04	3.27E+04	2.61E+04	2.49E+04	1.95E+04	1.67E+04	466.20534	2	35.58
YEH2	YLR020C	HSRPLSISSTTPLDLQR	[8] Phospho (ST)|[9] Phospho (ST)	-0.07	-0.03	-0.33	-0.04	0.368	0.460	0.073	0.45	1.00E+05	1.21E+05	8.74E+04	8.20E+04	1.13E+05	9.89E+04	9.34E+04	1.32E+05	7.69E+04	9.00E+04	8.64E+04	6.93E+04	689.99273	3	34.48

YDR348C	YDR348C	NPFLDDVSSATDFRRSPPPVSR	[11] Phospho (ST)|[16] Phospho (ST)	-0.37	0.22	-0.22	-0.59	0.057	0.115	0.134	0.01	7.74E+04	9.57E+04	7.29E+04	5.49E+04	7.51E+04	6.04E+04	8.88E+04	1.08E+05	8.91E+04	6.75E+04	8.14E+04	6.27E+04	655.79619	4	15.66
SEC7	YDR170C	VANPRVSYESSR	[8] Phospho (Y)	-0.30	-0.39	0.06	0.08	0.118	0.042	0.403	0.37	1.44E+04	1.86E+04	1.81E+04	1.75E+04	1.11E+04	1.29E+04	1.49E+04	1.09E+04	1.33E+04	2.28E+04	1.49E+04	1.57E+04	482.22418	3	18.82
RTT107	YHR154W	FSHLFEGLSDNDDHINDEK	[9] Phospho (ST)	-0.74	-0.40	-0.06	-0.34	0.009	0.035	0.406	0.01	1.23E+05	1.22E+05	9.05E+04	6.32E+04	7.52E+04	6.28E+04	8.70E+04	8.83E+04	7.87E+04	9.15E+04	1.36E+05	9.42E+04	771.32249	3	46.62
SPA2	YLL021W	YVSPIK	[3] Phospho (ST)	0.33	1.41	0.83	-1.08	0.292	0.029	0.087	0.02	2.20E+03	1.16E+04	1.65E+04	1.06E+04	1.23E+04	1.52E+04	3.32E+04	1.75E+04	2.98E+04	1.39E+04	1.84E+04	2.14E+04	393.69336	2	20.14
PIN4	YBL051C	SSSNLSLDSLSK	[3] Phospho (ST)	-0.38	-0.26	-0.59	-0.12	0.053	0.203	0.032	0.33	9.35E+04	1.17E+05	7.98E+04	7.69E+04	7.28E+04	7.30E+04	7.54E+04	1.06E+05	6.01E+04	6.67E+04	7.50E+04	5.08E+04	659.30233	2	44.15
BDF1	YLR399C	DASSLSPTSAGSRK	[6] Phospho (ST)	0.09	-0.29	-0.24	0.38	0.358	0.178	0.193	0.12	4.43E+04	2.99E+04	3.46E+04	4.33E+04	2.96E+04	4.32E+04	3.69E+04	2.08E+04	3.13E+04	3.80E+04	2.50E+04	2.92E+04	722.32775	2	32.36
MDS3	YGL197W	NNDEEDDEDPVSPKPVSK	[12] Phospho (ST)	0.00	0.20	0.28	-0.19	0.493	0.197	0.154	0.14	5.01E+04	4.39E+04	6.92E+04	6.36E+04	4.59E+04	5.41E+04	6.81E+04	5.61E+04	6.29E+04	7.26E+04	5.36E+04	7.13E+04	698.62292	3	15.93
GPR1	YDL035C	NDNSDITSNIK	[8] Phospho (ST)	-0.14	-0.09	0.08	-0.04	0.367	0.419	0.425	0.45	4.89E+04	2.16E+04	5.05E+04	4.14E+04	2.93E+04	3.92E+04	2.43E+04	4.78E+04	4.12E+04	5.21E+04	3.32E+04	4.22E+04	650.7746	2	18.34
CKI1	YLR133W	SYSVGYQAR	[3] Phospho (ST)	0.71	0.63	0.18	0.08	0.064	0.125	0.252	0.44	1.77E+04	2.18E+04	1.98E+04	3.82E+04	1.94E+04	3.92E+04	1.96E+04	4.60E+04	2.60E+04	2.90E+04	1.94E+04	1.87E+04	555.73489	2	42.15
CDC37	YDR168W	IELSDDSDVEVHPNVDK	[4] Phospho (ST)|[7] Phospho (ST)	-0.21	0.37	-0.05	-0.58	0.298	0.120	0.358	0.12	7.45E+04	7.83E+04	9.27E+04	4.05E+04	1.05E+05	6.69E+04	7.98E+04	1.36E+05	1.01E+05	7.89E+04	8.56E+04	7.32E+04	690.94866	3	36.37
YRA1	YDR381W	SLDEIIGSNK	[1] Phospho (ST)	1.59	2.75	2.42	-1.16	0.000	0.001	0.002	0.00	8.63E+03	9.66E+03	8.20E+03	2.53E+04	2.93E+04	2.50E+04	4.94E+04	7.04E+04	5.85E+04	4.84E+04	5.75E+04	3.58E+04	578.26922	2	53.66
SEC3	YER008C	NVSQGAVPSSAPPVSGGNYSHK	[3] Phospho (ST)	-0.28	-0.18	-0.21	-0.10	0.038	0.097	0.079	0.21	5.99E+04	5.45E+04	6.70E+04	5.11E+04	4.44E+04	5.36E+04	4.87E+04	5.86E+04	5.23E+04	5.32E+04	4.65E+04	5.70E+04	740.67467	3	63.84
RPC82	YPR190C	SGSNAAASLPSK	[3] Phospho (ST)	0.09	0.02	0.09	0.07	0.276	0.443	0.217	0.32	4.79E+04	4.04E+04	4.91E+04	5.56E+04	4.30E+04	4.76E+04	4.05E+04	4.86E+04	5.02E+04	5.21E+04	4.46E+04	4.99E+04	585.26096	2	58.14
PIN4	YBL051C	NSQISPPNSQIPINSQTLSQAQPPAQSQTQQR	[5] Phospho (ST)	-0.15	-0.27	-0.17	0.12	0.185	0.110	0.152	0.26	6.05E+05	5.12E+05	4.55E+05	4.82E+05	5.14E+05	4.19E+05	3.65E+05	5.13E+05	4.28E+05	5.07E+05	4.64E+05	4.24E+05	1185.2402	3	36.04
ALE1	YOR175C	DISASSPNLGGILK	[6] Phospho (ST)	-0.06	0.97	0.78	-1.02	0.426	0.010	0.029	0.01	4.98E+04	7.95E+04	4.87E+04	5.21E+04	6.99E+04	4.89E+04	1.33E+05	1.20E+05	9.45E+04	8.45E+04	1.27E+05	9.49E+04	726.3617	2	50.51
YCK1	YHR135C	TPEQHPNDDNSSLAASHK	[11] Phospho (ST)|[12] Phospho (ST)|[16] Ph	0.13	0.04	-0.32	0.09	0.214	0.463	0.099	0.42	7.09E+04	5.52E+04	5.77E+04	6.03E+04	7.49E+04	6.56E+04	2.78E+04	7.86E+04	8.27E+04	6.08E+04	3.90E+04	4.68E+04	729.9312	3	17.7
SEC9	YGR009C	NSLNHSNSTLNVGPSR	[8] Phospho (ST)	0.20	0.29	0.18	-0.09	0.127	0.036	0.274	0.28	3.04E+04	3.30E+04	3.67E+04	3.83E+04	3.27E+04	4.37E+04	4.33E+04	3.59E+04	4.31E+04	3.32E+04	2.94E+04	5.12E+04	592.93937	3	24.93
LHP1	YDL051W	RNSFAVIEFTPEVLDR	[3] Phospho (ST)	1.10	0.36	0.49	0.74	0.014	0.289	0.161	0.05	6.94E+04	1.57E+05	7.37E+04	1.83E+05	2.48E+05	2.14E+05	2.04E+05	9.00E+04	9.16E+04	1.46E+05	1.77E+05	9.97E+04	986.98165	2	84.5
RAD9	YDR217C	VNSTNIIEGSPK	[10] Phospho (ST)	-0.17	0.22	0.24	-0.38	0.189	0.162	0.074	0.05	3.19E+04	3.72E+04	4.39E+04	3.57E+04	2.87E+04	3.61E+04	4.50E+04	3.60E+04	5.02E+04	4.18E+04	4.45E+04	4.73E+04	669.81863	2	16.44
SPT6	YGR116W	RVGDEGNAAESESDNVAASR	[13] Phospho (ST)	-0.01	-0.30	-0.20	0.29	0.462	0.058	0.064	0.04	1.08E+05	9.10E+04	1.08E+05	1.04E+05	9.74E+04	1.05E+05	9.26E+04	6.79E+04	8.93E+04	8.98E+04	8.15E+04	9.57E+04	1057.4422	2	52.88
SAC7	YDR389W	SFGSTPVPPDVIASNK	[1] Phospho (ST)	-0.46	-0.15	-0.03	-0.32	0.024	0.218	0.413	0.08	1.70E+05	2.01E+05	1.57E+05	1.25E+05	1.49E+05	1.11E+05	1.48E+05	1.88E+05	1.42E+05	1.72E+05	1.89E+05	1.56E+05	848.40501	2	44.7
AKR1	YDR264C	AIRSGNEEESGNEQVNHNDEAEEDPLLTR	[4] Phospho (ST)	-0.01	-0.09	-0.03	0.08	0.460	0.265	0.445	0.27	2.61E+05	2.03E+05	2.33E+05	2.53E+05	2.30E+05	2.08E+05	2.37E+05	1.92E+05	2.25E+05	2.20E+05	1.96E+05	2.70E+05	1111.4822	3	43.88
PHO91	YNR013C	RPSNTFNLDADR	[5] Phospho (ST)	0.42	0.29	-0.05	0.13	0.064	0.138	0.446	0.07	1.77E+04	3.13E+04	3.16E+04	3.38E+04	3.64E+04	3.73E+04	3.39E+04	3.04E+04	3.42E+04	1.92E+04	2.77E+04	3.11E+04	495.88781	3	18.88
YLR257W	YLR257W	DDDIRDRSYTSVAELNR	[8] Phospho (ST)	0.13	0.25	0.06	-0.13	0.268	0.075	0.332	0.27	5.27E+04	6.40E+04	5.80E+04	7.73E+04	5.38E+04	5.95E+04	7.66E+04	5.90E+04	7.25E+04	6.01E+04	5.45E+04	6.69E+04	702.3178	3	16.79
RPP1B	YDL130W	EEEAAEESDDDMGFGLFD	[8] Phospho (ST)	-0.47	0.03	0.35	-0.50	0.207	0.472	0.226	0.22	9.68E+05	9.63E+05	5.74E+05	5.89E+05	9.89E+05	2.29E+05	7.95E+05	1.22E+06	5.43E+05	9.81E+05	1.53E+06	6.89E+05	1043.3623	2	27.92
KIN1	YDR122W	FEGSDDDENHPLPPLNVAK	[4] Phospho (ST)	-0.24	0.09	-0.05	-0.33	0.059	0.166	0.390	0.02	1.56E+05	1.81E+05	1.59E+05	1.23E+05	1.57E+05	1.41E+05	1.87E+05	1.70E+05	1.71E+05	1.31E+05	1.83E+05	1.67E+05	1087.4763	2	34.22
AGE2	YIL044C	STSVPVKK	[3] Phospho (ST)	-1.45	-1.81	-0.19	0.35	0.073	0.054	0.402	0.18	6.29E+04	2.54E+04	2.34E+04	1.16E+04	9.96E+03	1.92E+04	9.64E+03	1.11E+04	1.11E+04	1.84E+04	2.47E+04	5.50E+04	463.23892	2	15.14
SUI3	YPL237W	EGTPSANSSIQQEVGLPYSELLSR	[5] Phospho (ST)	-0.01	0.56	-0.26	-0.56	0.495	0.056	0.238	0.05	1.34E+05	2.07E+05	1.13E+05	1.19E+05	2.03E+05	1.31E+05	2.61E+05	2.15E+05	1.92E+05	1.17E+05	1.53E+05	1.09E+05	881.41791	3	58.13
PSP1	YDR505C	RNTQPVASFNPSLPTFQQQQQQPQQPQQPR	[3] Phospho (ST)	-0.56	-0.06	-0.48	-0.50	0.010	0.356	0.012	0.01	4.14E+05	5.16E+05	4.07E+05	2.78E+05	3.24E+05	3.06E+05	3.76E+05	4.65E+05	4.43E+05	3.07E+05	3.31E+05	3.18E+05	1195.2442	3	32.64
BUD3	YCL014W	AADVENLSDDDEHRQNESR	[18] Phospho (ST)	0.76	0.49	0.63	0.27	0.023	0.147	0.086	0.16	1.54E+04	1.04E+04	2.31E+04	2.97E+04	2.51E+04	2.78E+04	2.09E+04	1.72E+04	3.04E+04	3.00E+04	1.76E+04	2.78E+04	570.73421	4	16.12
SLG1	YOR008C	RISNGTFINGGPGGK	[3] Phospho (ST)|[6] Phospho (ST)	-0.55	-0.99	-0.72	0.44	0.071	0.027	0.049	0.02	9.23E+04	4.93E+04	8.29E+04	5.22E+04	4.90E+04	5.16E+04	2.95E+04	4.32E+04	4.03E+04	5.11E+04	3.70E+04	4.79E+04	817.85814	2	28.09
UBP1	YDL122W	DNEELQEIDNVSLDEPK	[12] Phospho (ST)	0.32	0.31	0.17	0.00	0.140	0.101	0.245	0.49	1.90E+05	2.42E+05	1.71E+05	2.60E+05	3.04E+05	1.88E+05	2.57E+05	2.87E+05	2.05E+05	2.25E+05	2.68E+05	1.84E+05	1033.9447	2	73.74
PRR1	YKL116C	VVSELIAPANLSPQR	[12] Phospho (ST)	-0.02	0.11	-0.05	-0.13	0.468	0.313	0.426	0.28	5.67E+04	8.92E+04	6.47E+04	5.31E+04	8.74E+04	6.66E+04	7.22E+04	8.13E+04	7.32E+04	5.63E+04	7.35E+04	7.39E+04	837.43535	2	26.73
DBF20	YPR111W	ISLNHSPK	[6] Phospho (ST)	-2.06	0.65	-0.56	-2.71	0.025	0.119	0.187	0.01	3.00E+04	1.74E+04	1.20E+04	5.94E+03	2.84E+03	5.44E+03	2.81E+04	2.23E+04	4.29E+04	1.97E+04	1.31E+04	7.39E+03	488.23622	2	26.14
CRN1	YLR429W	SASSSSTINHVLK	[4] Phospho (ST)	0.20	-0.17	-0.18	0.37	0.221	0.264	0.246	0.05	2.70E+04	4.50E+04	3.58E+04	4.40E+04	3.46E+04	4.50E+04	3.39E+04	3.54E+04	2.63E+04	2.87E+04	3.12E+04	3.53E+04	705.83532	2	45.83
RHO1	YPR165W	SQQVGNSIR	[N-term] Acetyl (Protein N-term)|[1] Phospho	1.28	-0.33	-0.47	1.61	0.001	0.237	0.060	0.00	2.20E+04	2.22E+04	2.72E+04	6.22E+04	5.00E+04	6.14E+04	7.99E+03	2.11E+04	2.78E+04	2.29E+04	1.42E+04	1.44E+04	555.75029	2	15.71
HXT7	YDR342C	SQDAAIAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIK	[N-term] Acetyl (Protein N-term)|[22] Phosph	-0.43	3.45	2.94	-3.88	0.168	0.015	0.000	0.01	1.12E+05	8.64E+04	6.17E+04	7.02E+04	8.58E+04	3.70E+04	4.62E+05	1.35E+06	1.03E+06	7.30E+05	6.49E+05	6.08E+05	1120.7324	4	25.76
GIP3	YPL137C	RSTSISNAVVSSK	[4] Phospho (ST)	0.90	0.63	0.26	0.27	0.006	0.019	0.125	0.09	1.69E+04	2.55E+04	1.85E+04	3.92E+04	4.22E+04	3.21E+04	3.64E+04	2.89E+04	2.89E+04	2.70E+04	2.34E+04	2.25E+04	708.34875	2	42.1
UGP1	YKL035W	THSTYAFESNTNSVAASQMR	[3] Phospho (ST)	-0.64	-0.27	0.34	-0.37	0.072	0.235	0.074	0.20	3.08E+05	2.16E+05	1.94E+05	1.91E+05	1.80E+05	8.92E+04	1.90E+05	2.67E+05	1.40E+05	3.21E+05	2.97E+05	2.93E+05	1141.481	2	117.9
FBA1	YKL060C	DYIMSPVGNPEGPEK	[5] Phospho (ST)	0.07	0.21	0.42	-0.14	0.450	0.189	0.170	0.40	9.60E+04	1.27E+05	9.83E+04	1.17E+05	1.79E+05	4.19E+04	1.49E+05	1.20E+05	1.02E+05	1.04E+05	2.06E+05	1.20E+05	856.86631	2	66.75
NPL6	YMR091C	SDSEGGLASEVEHEK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.64	-0.33	-0.95	-0.31	0.103	0.222	0.005	0.33	1.39E+05	1.49E+05	1.22E+05	3.59E+04	1.45E+05	8.19E+04	6.64E+04	1.71E+05	8.93E+04	8.58E+04	7.79E+04	4.85E+04	888.32491	2	18.62
HSP12	YFL014W	GVFQGVHDSAEK	[9] Phospho (ST)	2.06	1.49	0.73	0.58	0.000	0.002	0.008	0.01	1.17E+04	1.28E+04	1.56E+04	5.74E+04	5.62E+04	5.41E+04	4.31E+04	2.99E+04	3.95E+04	2.00E+04	2.08E+04	2.59E+04	677.2953	2	64.31
REB1	YBR049C	SPSHDNEAGSVDNSEISQLLQSAATK	[10] Phospho (ST)	-0.06	-0.26	-0.13	0.20	0.425	0.179	0.293	0.31	2.15E+05	1.92E+05	1.50E+05	1.74E+05	2.40E+05	1.19E+05	1.42E+05	1.99E+05	1.23E+05	1.60E+05	2.09E+05	1.40E+05	922.41817	3	68.05
MYO3	YKL129C	DYGTKLLAGKK	[2] Phospho (Y)	-0.96	-0.92	0.22	-0.04	0.075	0.082	0.331	0.40	1.17E+05	6.70E+04	4.67E+04	3.83E+04	4.16E+04	3.89E+04	3.81E+04	4.86E+04	3.55E+04	5.69E+04	1.08E+05	1.04E+05	637.33506	2	28.48
RMT2	YDR465C	EESVGSDDDATAANQQVYLK	[6] Phospho (ST)	-0.08	-0.04	-0.25	-0.05	0.070	0.312	0.018	0.26	1.66E+05	1.79E+05	1.84E+05	1.64E+05	1.69E+05	1.66E+05	1.60E+05	1.85E+05	1.71E+05	1.33E+05	1.52E+05	1.59E+05	1110.4716	2	99.38
BNI5	YNL166C	LADQTPHDDNSENCPNRSGGSTPLDSQTK	[21] Phospho (ST)|[22] Phospho (ST)	-0.48	-0.69	-0.20	0.21	0.071	0.037	0.290	0.08	1.88E+05	1.09E+05	1.53E+05	1.17E+05	1.00E+05	1.04E+05	7.96E+04	9.57E+04	1.02E+05	1.44E+05	8.51E+04	1.61E+05	1101.1085	3	17.81
NAP1	YKR048C	AQNDSEEEQVK	[5] Phospho (ST)	0.27	-0.45	0.18	0.72	0.364	0.321	0.440	0.03	6.96E+04	1.07E+04	2.17E+04	5.21E+04	3.28E+04	3.83E+04	2.08E+04	2.97E+04	2.41E+04	8.16E+04	1.94E+04	1.45E+04	678.76904	2	45.56
ADR1	YDR216W	LPESANNYTYSSGSPTR	[14] Phospho (ST)	1.08	0.53	0.47	0.55	0.000	0.001	0.003	0.00	6.75E+04	6.15E+04	7.33E+04	1.49E+05	1.27E+05	1.51E+05	9.97E+04	9.23E+04	1.00E+05	9.31E+04	8.82E+04	9.92E+04	962.40956	2	51.42
GDH3	YAL062W	STATNAKDAVWFGPPK	[2] Phospho (ST)	-1.25	-1.72	-0.24	0.47	0.078	0.047	0.341	0.24	1.13E+05	4.78E+04	4.93E+04	4.69E+04	1.75E+04	2.39E+04	1.03E+04	3.10E+04	2.25E+04	5.40E+04	8.01E+04	4.41E+04	590.61066	3	22.61
SST2	YLR452C	NLSNENCSFK	[3] Phospho (ST)	0.32	-0.25	0.00	0.57	0.145	0.273	0.497	0.04	3.55E+04	1.88E+04	3.42E+04	3.78E+04	3.17E+04	4.10E+04	1.59E+04	2.72E+04	3.14E+04	2.95E+04	2.34E+04	3.59E+04	646.7527	2	36.46
AVL9	YLR114C	SVSQISVNPGK	[1] Phospho (ST)	0.18	0.00	0.03	0.18	0.215	0.494	0.453	0.08	3.69E+04	2.33E+04	3.65E+04	3.68E+04	3.32E+04	3.92E+04	2.87E+04	3.37E+04	3.40E+04	3.42E+04	3.19E+04	3.23E+04	598.29009	2	42.76
MDS3	YGL197W	TSVSEAQNTQPQVANADAK	[2] Phospho (ST)	-0.29	-0.14	-0.27	-0.15	0.132	0.311	0.157	0.33	4.14E+04	3.30E+04	4.45E+04	3.98E+04	2.48E+04	3.27E+04	2.39E+04	4.14E+04	4.25E+04	3.53E+04	2.39E+04	3.97E+04	680.30712	3	27.12
SUR7	YML052W	EQATDPILTATGPEDMQQSASIVGPSSNANPVTATAATENQ	[19] Phospho (ST)	-0.23	0.07	0.25	-0.30	0.302	0.374	0.215	0.23	2.78E+05	3.00E+05	1.90E+05	2.12E+05	3.22E+05	1.22E+05	2.79E+05	2.99E+05	2.31E+05	2.50E+05	3.93E+05	2.72E+05	1105.2647	4	51.37
PAN1	YIR006C	SSSPSYSQFK	[3] Phospho (ST)	0.49	0.43	0.02	0.05	0.063	0.230	0.470	0.45	1.79E+04	2.92E+04	2.29E+04	3.76E+04	2.57E+04	3.46E+04	2.01E+04	5.01E+04	2.41E+04	3.00E+04	2.03E+04	2.07E+04	599.24536	2	43.42
MPP6	YNR024W	EFTGSQDDGEDEYDLDK	[5] Phospho (ST)	-0.16	-0.38	-0.73	0.22	0.083	0.040	0.003	0.10	1.80E+05	2.20E+05	2.00E+05	1.88E+05	1.78E+05	1.72E+05	1.26E+05	1.82E+05	1.54E+05	1.14E+05	1.40E+05	1.09E+05	1021.8738	2	77.64
BUD3	YCL014W	DLSSLYSEKK	[4] Phospho (ST)|[6] Phospho (Y)	-0.07	0.42	-0.06	-0.50	0.279	0.211	0.370	0.18	4.15E+04	3.94E+04	4.51E+04	3.85E+04	3.57E+04	4.54E+04	3.48E+04	8.75E+04	4.67E+04	4.66E+04	4.27E+04	3.16E+04	665.27254	2	27.29
RPL24B	YGR148C	SLKPEVR	[1] Phospho (ST)	-0.77	-0.27	-1.68	-0.49	0.162	0.374	0.052	0.31	3.02E+04	2.25E+04	8.25E+03	1.92E+04	6.62E+03	1.00E+04	6.61E+03	1.12E+04	3.25E+04	6.36E+03	3.32E+03	9.38E+03	454.73384	2	20.84
SWH1	YAR042W	SQSLSEITPGPHSR	[3] Phospho (ST)	-0.04	0.09	0.11	-0.14	0.330	0.088	0.275	0.07	2.50E+04	2.73E+04	2.85E+04	2.68E+04	2.34E+04	2.81E+04	2.91E+04	2.91E+04	2.80E+04	2.58E+04	2.60E+04	3.55E+04	525.91037	3	53.23
MOB2	L034C-B	RHSQTSFPAQK	[3] Phospho (ST)|[6] Phospho (ST)	-0.44	-0.09	0.01	-0.34	0.294	0.448	0.496	0.23	5.86E+04	7.41E+03	4.70E+04	2.31E+04	1.99E+04	4.04E+04	2.24E+04	4.27E+04	4.08E+04	5.61E+04	2.49E+04	3.26E+04	482.8691	3	26.77
YMR295C	YMR295C	TASVADPILDAVQEAQPFEQAADTFHDNMNR	[3] Phospho (ST)	-1.06	-0.04	-0.07	-1.02	0.115	0.472	0.458	0.07	3.05E+05	6.47E+05	2.56E+05	1.43E+05	3.56E+05	8.10E+04	4.39E+05	4.77E+05	2.61E+05	2.69E+05	6.36E+05	2.44E+05	1161.1849	3	94.14
SEC16	YPL085W	TSPSPTGPNPNNSPSPSSPISR	[18] Phospho (ST)	-0.78	-0.36	-0.21	-0.42	0.002	0.166	0.193	0.19	7.00E+04	8.12E+04	7.55E+04	4.98E+04	3.69E+04	4.54E+04	4.19E+04	8.83E+04	4.64E+04	8.50E+04	5.25E+04	5.86E+04	753.34161	3	27.93
RPS7B	YNL096C	SRTLTAVHDK	[1] Phospho (ST)	2.18	0.00	-1.20	2.17	0.001	0.500	0.089	0.00	1.03E+04	8.64E+03	2.46E+03	3.61E+04	3.07E+04	3.01E+04	9.38E+03	4.01E+03	8.04E+03	3.94E+03	1.88E+03	3.50E+03	403.19917	3	16.86
AKR1	YDR264C	AIRSGNEEESGNEQVNHNDEAEEDPLLTR	[4] Phospho (ST)|[10] Phospho (ST)	-0.67	-0.43	-0.45	-0.24	0.010	0.050	0.027	0.09	3.47E+05	2.54E+05	2.73E+05	1.81E+05	1.87E+05	1.83E+05	1.88E+05	2.56E+05	2.05E+05	2.21E+05	2.01E+05	2.16E+05	1138.1376	3	18.52
ABP1	YCR088W	EEPEQEEIAPSLPSRNSIPAPK	[11] Phospho (ST)	0.02	0.71	0.28	-0.69	0.469	0.012	0.180	0.01	5.86E+04	9.74E+04	6.82E+04	6.11E+04	8.88E+04	7.78E+04	1.35E+05	1.17E+05	1.14E+05	7.25E+04	1.09E+05	9.14E+04	833.39882	3	18.74
BLM10	YFL007W	SPGRPSSSQGEIK	[1] Phospho (ST)	0.15	1.22	1.19	-1.07	0.431	0.042	0.033	0.03	1.68E+04	7.12E+03	4.34E+04	1.61E+04	1.75E+04	4.13E+04	5.25E+04	3.96E+04	6.46E+04	5.78E+04	5.07E+04	4.51E+04	705.3245	2	26.25
TPS3	YMR261C	NPNLSFDSHPPR	[5] Phospho (ST)	-0.22	-0.20	0.20	-0.02	0.080	0.089	0.186	0.44	7.93E+04	6.44E+04	7.32E+04	6.02E+04	5.56E+04	6.99E+04	6.44E+04	5.53E+04	6.87E+04	7.63E+04	7.05E+04	1.02E+05	730.8213	2	29.55
GEA2	YEL022W	VNNEEAISEDDGIEEEHIHSEK	[8] Phospho (ST)	-0.12	0.40	0.32	-0.52	0.219	0.136	0.043	0.09	5.51E+04	7.09E+04	6.94E+04	6.58E+04	5.99E+04	5.41E+04	1.16E+05	6.43E+04	7.75E+04	7.13E+04	8.50E+04	8.76E+04	868.36487	3	45.11
MTR4	YJL050W	TVVAEYAIAQSLKNK	[6] Phospho (Y)	-0.55	-1.00	0.48	0.45	0.238	0.117	0.248	0.32	2.76E+05	1.13E+05	1.50E+05	2.24E+05	4.63E+04	9.88E+04	5.97E+04	1.71E+05	3.85E+04	3.96E+05	2.38E+05	1.18E+05	572.29353	3	17.1
RFA2	YNL312W	WSEDANDLAAGNDDSSGK	[16] Phospho (ST)	3.09	0.25	-0.33	2.84	0.000	0.178	0.079	0.00	3.61E+04	2.67E+04	3.56E+04	2.92E+05	2.74E+05	2.70E+05	3.02E+04	4.77E+04	3.90E+04	2.90E+04	2.15E+04	2.80E+04	966.36882	2	87.43
HXT2	YMR011W	LETDESPIQTK	[3] Phospho (ST)|[6] Phospho (ST)	-0.05	0.03	-0.21	-0.08	0.430	0.467	0.282	0.39	1.05E+05	5.82E+04	1.02E+05	8.37E+04	7.08E+04	1.01E+05	6.28E+04	1.08E+05	9.94E+04	9.85E+04	6.05E+04	7.06E+04	710.78644	2	19.88
KRI1	YNL308C	YREVSPESFGLTAR	[5] Phospho (ST)	0.06	0.23	0.11	-0.18	0.416	0.243	0.375	0.26	7.15E+04	1.15E+05	8.00E+04	8.32E+04	1.08E+05	8.56E+04	1.28E+05	7.56E+04	1.09E+05	7.03E+04	1.26E+05	9.13E+04	846.39436	2	43.46
MLF3	YNL074C	SNSNNSNPSFIFER	[6] Phospho (ST)	-0.69	-0.08	-0.24	-0.61	0.006	0.428	0.087	0.14	7.85E+04	9.83E+04	7.56E+04	5.45E+04	5.39E+04	4.83E+04	5.59E+04	1.23E+05	6.03E+04	7.62E+04	7.18E+04	6.61E+04	846.85556	2	40.29
SYP1	YCR030C	SNNWTPGEASDTPPLPPHATPK	[1] Phospho (ST)	-0.34	-0.15	-0.01	-0.19	0.013	0.179	0.456	0.17	3.04E+05	2.91E+05	2.67E+05	2.45E+05	2.36E+05	1.99E+05	2.14E+05	3.03E+05	2.59E+05	2.61E+05	3.01E+05	2.94E+05	798.69677	3	37.01
BDF1	YLR399C	SSAQEDAPIVIR	[1] Phospho (ST)	-0.59	0.03	-0.89	-0.62	0.047	0.450	0.024	0.01	5.33E+04	8.88E+04	8.08E+04	4.33E+04	4.90E+04	5.61E+04	7.11E+04	8.48E+04	7.17E+04	3.13E+04	5.03E+04	3.91E+04	683.32456	2	56.3
TIF1	YKR059W	SEGITDIEESQIQTNYDK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.01	-0.05	-0.16	0.06	0.486	0.415	0.197	0.42	4.84E+05	5.32E+05	3.69E+05	4.52E+05	6.11E+05	3.31E+05	4.15E+05	5.47E+05	3.73E+05	4.20E+05	4.32E+05	3.89E+05	1096.4688	2	84.44
ZEO1	YOL109W	LEETKESLQNK	[4] Phospho (ST)|[7] Phospho (ST)	0.32	0.10	0.40	0.22	0.218	0.396	0.185	0.19	2.85E+04	1.49E+04	3.80E+04	4.20E+04	3.17E+04	2.81E+04	2.38E+04	3.16E+04	3.21E+04	4.54E+04	2.62E+04	3.62E+04	739.81288	2	27.49
PMA1	YGL008C	TDTSSSSSSSASSVSAHQPTQEK	[4] Phospho (ST)	-0.90	-0.44	0.02	-0.46	0.077	0.202	0.488	0.11	1.25E+05	5.82E+04	6.59E+04	5.32E+04	3.36E+04	4.70E+04	4.52E+04	7.93E+04	5.95E+04	1.36E+05	4.27E+04	7.42E+04	821.67725	3	17.09
TRA1	YHR099W	AEQGDLDSPKEPQADELLDEFSK	[8] Phospho (ST)	-0.27	0.11	0.01	-0.38	0.217	0.324	0.483	0.07	1.03E+05	1.48E+05	9.07E+04	6.98E+04	1.21E+05	9.17E+04	1.20E+05	1.27E+05	1.20E+05	7.95E+04	1.43E+05	1.22E+05	881.05803	3	53.52
YCF1	YDR135C	NFSSEELSQK	[3] Phospho (ST)	0.09	0.23	0.30	-0.14	0.358	0.176	0.045	0.30	2.84E+04	2.18E+04	3.11E+04	3.07E+04	2.16E+04	3.45E+04	2.50E+04	3.34E+04	3.72E+04	3.35E+04	3.23E+04	3.41E+04	624.76141	2	30.03
MPP10	YJR002W	RISSGQDERHSSPDPYGINDK	[11] Phospho (ST)|[12] Phospho (ST)	0.23	0.51	0.16	-0.28	0.123	0.042	0.274	0.12	1.41E+05	1.12E+05	1.03E+05	1.58E+05	1.34E+05	1.25E+05	1.45E+05	2.06E+05	1.56E+05	1.58E+05	9.96E+04	1.39E+05	840.01832	3	16.83
CWC24	YLR323C	LVASDEEK	[4] Phospho (ST)	0.03	0.00	0.01	0.03	0.442	0.495	0.476	0.45	6.35E+04	4.06E+04	5.35E+04	5.71E+04	4.93E+04	5.45E+04	4.28E+04	4.41E+04	7.03E+04	5.87E+04	4.49E+04	5.56E+04	485.71	2	29.1
MSN4	YKL062W	SISSSLNR	[1] Phospho (ST)	-0.20	-0.15	-0.12	-0.05	0.254	0.336	0.373	0.43	2.02E+04	1.09E+04	1.85E+04	1.56E+04	1.34E+04	1.42E+04	1.04E+04	1.66E+04	1.77E+04	2.03E+04	1.21E+04	1.32E+04	472.2158	2	18.74
PAH1	YMR165C	SRRASSAAATSIDK	[1] Phospho (ST)|[5] Phospho (ST)	0.18	0.07	-0.05	0.11	0.222	0.399	0.447	0.34	1.78E+04	1.76E+04	2.47E+04	2.50E+04	1.84E+04	2.49E+04	1.52E+04	2.27E+04	2.55E+04	2.77E+04	1.19E+04	1.84E+04	527.56591	3	39.05
PWP2	YCR057C	LPLSNENDSSDEEENEK	[9] Phospho (ST)|[10] Phospho (ST)	0.16	0.17	0.10	-0.01	0.291	0.375	0.373	0.49	2.76E+05	1.70E+05	2.87E+05	2.14E+05	3.14E+05	2.90E+05	1.21E+05	4.03E+05	3.01E+05	3.33E+05	2.23E+05	2.31E+05	1054.8833	2	32.57

GTT3	YEL017W	AYIKEDDDEKPQSGDETSATK	[13] Phospho (ST)	0.45	-0.19	-0.28	0.64	0.050	0.236	0.177	0.02	3.30E+04	2.83E+04	4.22E+04	5.28E+04	3.88E+04	4.96E+04	2.79E+04	2.54E+04	3.73E+04	3.17E+04	2.04E+04	3.33E+04	803.01126	3	47.46
VTC2	YFL004W	SNFNTASEPLASASK	[5] Phospho (ST)	-0.09	0.29	0.24	-0.37	0.328	0.151	0.106	0.08	4.80E+04	6.70E+04	6.78E+04	6.15E+04	5.03E+04	6.05E+04	8.97E+04	7.53E+04	5.79E+04	7.86E+04	6.63E+04	7.10E+04	802.35266	2	43.62
SRP40	YKR092C	AEETPASSNESTPSASSSSSANK	[8] Phospho (ST)	-0.54	-1.56	-1.05	1.02	0.119	0.015	0.032	0.02	8.91E+04	4.45E+04	6.37E+04	5.99E+04	3.83E+04	3.73E+04	2.04E+04	1.83E+04	2.82E+04	3.91E+04	2.76E+04	2.86E+04	769.31478	3	22.17
PDA1	YER178W	YGGHSMSDPGTTYR	[5] Phospho (ST)	0.20	-0.66	0.23	0.86	0.429	0.042	0.242	0.27	4.81E+04	5.82E+04	3.49E+04	2.42E+04	1.24E+05	1.35E+04	2.83E+04	3.64E+04	2.46E+04	3.93E+04	6.74E+04	5.94E+04	804.81155	2	41.11
GNP1	YDR508C	DSSSQLDNELNRK	[3] Phospho (ST)	0.01	-0.10	0.06	0.11	0.471	0.310	0.420	0.19	1.73E+04	2.03E+04	2.46E+04	2.19E+04	2.08E+04	1.99E+04	1.71E+04	2.22E+04	1.87E+04	2.78E+04	1.96E+04	1.72E+04	529.23362	3	17.69
NAN1	YPL126W	MTQSLGIEQYKLSVVSGGK	[N-term] Acetyl (Protein N-term)|[10] Phosph	-0.27	-0.86	-0.11	0.59	0.266	0.031	0.389	0.15	2.45E+05	1.56E+05	2.33E+05	2.59E+05	1.06E+05	1.62E+05	6.87E+04	1.34E+05	1.46E+05	2.67E+05	1.96E+05	1.26E+05	1074.0307	2	16.94
BLM10	YFL007W	SATPTLQDQK	[1] Phospho (ST)|[3] Phospho (ST)	-0.34	-0.58	0.08	0.23	0.283	0.206	0.449	0.33	4.13E+04	1.28E+04	4.14E+04	3.50E+04	2.18E+04	1.84E+04	9.51E+03	3.15E+04	2.30E+04	5.31E+04	2.39E+04	2.40E+04	624.74924	2	17.79
MOB1	YIL106W	SFLQNFHISPGQTIR	[N-term] Acetyl (Protein N-term)|[9] Phospho	0.28	1.48	0.83	-1.20	0.255	0.002	0.041	0.00	5.20E+04	9.40E+04	4.28E+04	6.82E+04	9.47E+04	6.54E+04	1.97E+05	1.72E+05	1.57E+05	1.02E+05	1.39E+05	9.35E+04	933.94981	2	65.81
ATG13	YPR185W	YSSSFGNIR	[4] Phospho (ST)	0.10	0.24	0.09	-0.14	0.330	0.169	0.301	0.25	1.34E+04	2.02E+04	1.62E+04	1.63E+04	1.63E+04	2.08E+04	2.18E+04	1.57E+04	2.13E+04	1.76E+04	1.79E+04	1.78E+04	555.73568	2	32.74
FUI1	YBL042C	PVSDSGFDNSSK	[11] Phospho (ST)	-0.44	-0.43	0.09	-0.01	0.149	0.161	0.377	0.48	4.78E+04	2.37E+04	4.47E+04	3.58E+04	2.77E+04	2.19E+04	1.95E+04	3.24E+04	3.43E+04	4.17E+04	4.06E+04	4.15E+04	660.26126	2	42.16
MCK1	YNL307C	LEHNQPSISYICSR	[10] Phospho (Y)	-0.12	-0.27	0.05	0.16	0.314	0.171	0.403	0.17	1.23E+05	7.95E+04	8.69E+04	8.73E+04	9.75E+04	8.26E+04	7.17E+04	7.36E+04	9.46E+04	1.04E+05	9.72E+04	9.94E+04	892.39584	2	47.14
SPA2	YLL021W	NYWDVNDSPIIK	[8] Phospho (ST)	0.49	0.53	0.58	-0.04	0.075	0.066	0.061	0.41	4.51E+04	7.90E+04	4.69E+04	7.38E+04	9.35E+04	7.28E+04	8.90E+04	9.13E+04	6.69E+04	7.15E+04	1.02E+05	8.11E+04	772.34608	2	36.53
SIP1	YDR422C	DRQGSITSQLFNNRK	[5] Phospho (ST)	-0.33	-0.37	-0.09	0.04	0.103	0.054	0.331	0.43	8.12E+04	6.01E+04	8.12E+04	7.30E+04	4.92E+04	5.50E+04	4.94E+04	6.19E+04	6.11E+04	7.92E+04	5.88E+04	7.15E+04	615.29919	3	24.94
SEC16	YPL085W	TSPSPTGPNPNNSPSPSSPISR	[18] Phospho (ST)	-0.89	-0.83	-0.39	-0.06	0.002	0.014	0.036	0.43	1.75E+05	1.97E+05	1.54E+05	1.06E+05	8.34E+04	9.38E+04	7.49E+04	1.36E+05	8.40E+04	1.56E+05	1.16E+05	1.28E+05	1129.5087	2	28.65
TIF5	YPR041W	PFITWLETAESDDDEEDDE	[11] Phospho (ST)	-0.28	0.13	-0.28	-0.41	0.303	0.399	0.275	0.22	4.95E+05	4.72E+05	2.01E+05	3.21E+05	4.54E+05	1.88E+05	4.20E+05	5.97E+05	2.61E+05	2.43E+05	4.07E+05	3.11E+05	779.29413	3	51.68
CDC28	YBR160W	VGEGTYGVVYK	[6] Phospho (Y)	0.43	0.54	-0.07	-0.11	0.124	0.062	0.352	0.37	2.66E+04	3.84E+04	3.69E+04	3.70E+04	3.87E+04	6.15E+04	4.92E+04	3.73E+04	6.17E+04	3.22E+04	2.94E+04	3.54E+04	626.28744	2	50.95
YBL005W-B	L005W-B	VSTQANSQQPTTPPSSAVPENHHHASPQAAQVPLPQNGPYI	[26] Phospho (ST)	-0.66	-0.51	0.12	-0.15	0.011	0.043	0.300	0.33	4.12E+05	3.46E+05	3.49E+05	2.95E+05	1.97E+05	2.09E+05	2.12E+05	2.20E+05	3.45E+05	3.73E+05	3.26E+05	5.08E+05	1190.5643	4	16.02
YOX1	YML027W	LINSIDHSPSK	[8] Phospho (ST)	0.39	-0.13	-0.42	0.53	0.036	0.323	0.052	0.04	1.72E+04	2.14E+04	2.45E+04	2.55E+04	2.64E+04	3.09E+04	1.56E+04	1.66E+04	2.54E+04	1.36E+04	1.52E+04	1.83E+04	645.80803	2	29.89
PKH1	YDR490C	GNRSLTEADHALLSK	[4] Phospho (ST)	0.15	-0.03	0.05	0.18	0.201	0.472	0.425	0.31	2.80E+04	3.71E+04	2.84E+04	3.78E+04	3.60E+04	3.02E+04	4.43E+04	2.11E+04	2.64E+04	2.41E+04	3.24E+04	4.03E+04	564.60848	3	42.25
TPS3	YMR261C	VCSPSQEASASSISASR	[5] Phospho (ST)	0.28	0.30	0.34	-0.02	0.065	0.062	0.052	0.46	2.48E+04	2.41E+04	3.02E+04	3.08E+04	2.88E+04	3.64E+04	3.03E+04	2.95E+04	3.72E+04	3.37E+04	2.85E+04	3.81E+04	601.92457	3	15.96
NUP2	YLR335W	KDESDSENDIEIKGPEFK	[4] Phospho (ST)|[6] Phospho (ST)	-0.60	-0.24	-0.58	-0.37	0.051	0.255	0.001	0.25	1.30E+05	1.28E+05	1.15E+05	4.45E+04	1.11E+05	9.06E+04	6.97E+04	1.55E+05	9.21E+04	8.12E+04	8.86E+04	7.98E+04	747.30732	3	24.9
TCO89	YPL180W	NSAAPASPLSNEHITSSTNSGSDANR	[7] Phospho (ST)	-0.11	0.05	0.21	-0.16	0.348	0.409	0.167	0.20	9.03E+04	5.78E+04	8.70E+04	8.78E+04	5.78E+04	7.25E+04	7.65E+04	8.24E+04	8.41E+04	9.21E+04	8.18E+04	9.89E+04	889.05444	3	37.88
HOS4	YIL112W	TQSPILASR	[3] Phospho (ST)	-0.04	-0.20	-0.24	0.16	0.367	0.087	0.072	0.08	3.78E+04	3.97E+04	4.70E+04	4.23E+04	3.69E+04	4.17E+04	3.59E+04	3.36E+04	3.91E+04	3.77E+04	3.10E+04	3.68E+04	526.75728	2	28.42
ABP1	YCR088W	KSEPTIISPK	[8] Phospho (ST)	0.42	0.26	0.12	0.16	0.112	0.275	0.367	0.31	1.35E+04	2.00E+04	2.66E+04	2.11E+04	2.95E+04	3.00E+04	2.48E+04	1.54E+04	3.16E+04	1.65E+04	2.53E+04	2.33E+04	590.30463	2	29.28
HXT5	YHR096C	PVSSYISHEGPPKDELEELQK	[4] Phospho (ST)|[7] Phospho (ST)	-0.09	0.17	0.20	-0.26	0.316	0.246	0.113	0.16	9.86E+04	1.32E+05	1.12E+05	1.02E+05	1.26E+05	9.39E+04	1.09E+05	1.61E+05	1.16E+05	1.31E+05	1.43E+05	1.19E+05	848.04392	3	26.1
YRO2	YBR054W	AQEEEEDVATDSE	[10] Phospho (ST)|[12] Phospho (ST)	0.54	0.83	0.08	-0.29	0.204	0.194	0.458	0.35	1.18E+05	2.37E+04	1.19E+05	1.59E+05	1.53E+05	6.85E+04	5.32E+04	2.68E+05	1.42E+05	1.59E+05	6.89E+04	4.89E+04	806.25319	2	36.54
YDR089W	YDR089W	SIPLLSNKK	[1] Phospho (ST)	0.03	0.03	-0.31	0.00	0.437	0.425	0.128	0.48	1.89E+04	2.78E+04	2.64E+04	2.33E+04	2.39E+04	2.74E+04	2.61E+04	2.33E+04	2.54E+04	1.52E+04	2.21E+04	2.17E+04	540.29696	2	17.3
LCB2	YDR062W	PTTGVPGRFIR	[3] Phospho (ST)	0.35	-0.14	-0.37	0.48	0.039	0.300	0.061	0.05	2.36E+04	2.70E+04	3.06E+04	3.27E+04	3.14E+04	3.93E+04	3.04E+04	1.76E+04	2.58E+04	1.64E+04	2.41E+04	2.26E+04	640.82684	2	25.67
SKG1	YKR100C	SAAQSQLPNTFDK	[1] Phospho (ST)	0.10	0.18	0.03	-0.08	0.093	0.084	0.357	0.22	5.02E+04	4.64E+04	5.39E+04	5.42E+04	5.56E+04	5.21E+04	5.03E+04	5.92E+04	6.12E+04	5.37E+04	4.89E+04	5.10E+04	743.83294	2	63.66
PDA1	YER178W	YGGHSMSDPGTTYR	[1] Phospho (Y)	0.35	-0.50	0.37	0.86	0.385	0.082	0.139	0.28	2.14E+04	2.67E+04	1.67E+04	1.21E+04	6.53E+04	5.43E+03	1.49E+04	1.95E+04	1.13E+04	2.09E+04	3.53E+04	2.78E+04	536.87661	3	19.93
RAS2	YNL098C	NVNSSTTVVNAR	[5] Phospho (ST)	0.21	0.16	0.18	0.05	0.264	0.324	0.314	0.41	3.06E+04	1.42E+04	2.52E+04	2.92E+04	2.25E+04	2.94E+04	2.12E+04	2.60E+04	3.11E+04	2.75E+04	2.05E+04	3.11E+04	671.31168	2	44.36
NUP159	YIL115C	DGYVSGSEISVR	[5] Phospho (ST)	-0.36	0.33	-0.26	-0.69	0.110	0.097	0.161	0.01	5.31E+04	8.46E+04	8.29E+04	5.16E+04	5.46E+04	6.59E+04	7.95E+04	9.76E+04	1.00E+05	6.35E+04	6.60E+04	5.40E+04	674.79323	2	53.02
YBR085C-A	R085C-A	QSTNFTHSTGSFLQSAPVELTTVSGYQEFLK	[11] Phospho (ST)|[15] Phospho (ST)	-0.85	-0.02	-0.29	-0.83	0.098	0.484	0.284	0.10	4.88E+05	5.80E+05	2.03E+05	2.72E+05	2.86E+05	1.47E+05	3.79E+05	6.24E+05	2.48E+05	3.70E+05	4.27E+05	2.39E+05	1188.871	3	66.78
PIN4	YBL051C	SLSGLDLQNQNK	[3] Phospho (ST)	-0.61	-0.25	-0.36	-0.36	0.001	0.190	0.051	0.15	6.39E+04	7.23E+04	6.91E+04	4.52E+04	4.21E+04	4.74E+04	4.14E+04	7.79E+04	5.33E+04	5.12E+04	6.58E+04	4.26E+04	698.82763	2	61.26
MYO3	YKL129C	RGSVYHVPLNPVQATAVR	[5] Phospho (Y)	-0.29	0.40	-0.26	-0.70	0.196	0.139	0.251	0.02	4.82E+04	8.69E+04	5.36E+04	4.91E+04	5.30E+04	5.17E+04	1.01E+05	6.51E+04	8.24E+04	3.87E+04	6.47E+04	5.38E+04	682.02132	3	55.46
SPT6	YGR116W	GGILDELDDFIEDDEFSDEDDETR	[17] Phospho (ST)	-0.31	0.03	-0.46	-0.34	0.264	0.469	0.185	0.16	2.29E+05	3.13E+05	1.34E+05	1.50E+05	2.53E+05	1.42E+05	2.57E+05	2.51E+05	1.82E+05	1.27E+05	2.28E+05	1.37E+05	957.04059	3	76.61
SEC31	YDL195W	NSRVPSLVATSESPR	[2] Phospho (ST)|[6] Phospho (ST)	-0.68	-0.87	-0.55	0.20	0.010	0.005	0.030	0.02	2.04E+05	1.56E+05	1.51E+05	1.04E+05	1.03E+05	1.13E+05	9.81E+04	9.23E+04	8.84E+04	9.42E+04	1.19E+05	1.37E+05	880.39392	2	19.22
RPN13	YLR421C	MIGVLNNSSESDEEESNDEK	[11] Phospho (ST)	-0.46	-0.04	0.01	-0.42	0.181	0.449	0.487	0.23	2.96E+05	2.43E+05	2.86E+05	1.98E+05	3.24E+05	7.76E+04	2.48E+05	3.59E+05	1.98E+05	1.84E+05	3.60E+05	2.87E+05	1153.4565	2	72.18
SEC16	YPL085W	IGDSLQGSPQR	[4] Phospho (ST)|[8] Phospho (ST)	-0.32	-0.23	-0.21	-0.09	0.214	0.320	0.321	0.40	6.12E+04	2.85E+04	6.21E+04	4.53E+04	3.58E+04	4.07E+04	2.45E+04	5.41E+04	5.13E+04	5.92E+04	3.06E+04	4.11E+04	659.26574	2	17.73
IOC4	YMR044W	DREQSEEEEDIEDFGESEANPEK	[5] Phospho (ST)	-0.23	-0.01	-0.48	-0.21	0.067	0.461	0.006	0.14	1.61E+05	1.76E+05	1.56E+05	1.18E+05	1.56E+05	1.47E+05	1.67E+05	1.84E+05	1.37E+05	1.00E+05	1.21E+05	1.31E+05	931.0301	3	33.12
STF2	YGR008C	DRRGSNLQSHEQK	[5] Phospho (ST)	0.31	-0.09	-0.81	0.39	0.186	0.447	0.124	0.22	3.10E+04	1.95E+04	1.42E+04	2.63E+04	2.86E+04	2.50E+04	1.27E+04	1.32E+04	3.50E+04	2.12E+04	5.21E+03	1.05E+04	409.44033	4	26.57
POL1	YNL102W	LRENLNSSPTSEFK	[10] Phospho (ST)	-1.46	-1.84	-0.71	0.38	0.000	0.000	0.003	0.09	1.09E+05	1.09E+05	1.20E+05	4.18E+04	3.50E+04	4.63E+04	3.63E+04	2.21E+04	3.61E+04	5.99E+04	6.29E+04	8.43E+04	851.39451	2	38.85
SAK1	YER129W	LSELSNSPQK	[5] Phospho (ST)	-0.43	-0.30	-0.18	-0.13	0.034	0.171	0.192	0.33	4.25E+04	3.11E+04	4.16E+04	3.17E+04	2.69E+04	2.68E+04	2.12E+04	3.21E+04	4.03E+04	3.87E+04	2.95E+04	3.37E+04	591.77393	2	23.27
HAL5	YJL165C	SLSESIK	[3] Phospho (ST)	0.51	0.33	0.17	0.18	0.029	0.067	0.270	0.11	1.29E+04	9.61E+03	1.50E+04	2.03E+04	1.73E+04	1.60E+04	1.64E+04	1.65E+04	1.44E+04	1.78E+04	1.25E+04	1.21E+04	422.19663	2	24.65
YTA7	YGR270W	NNNALSFHNPSPAR	[11] Phospho (ST)	1.05	1.21	0.98	-0.16	0.000	0.001	0.001	0.10	2.34E+04	3.18E+04	2.99E+04	5.48E+04	6.11E+04	6.02E+04	6.50E+04	5.91E+04	7.28E+04	4.97E+04	5.74E+04	6.11E+04	809.86126	2	30.13
AVT4	YNL101W	RAQSTVLNSNPFYSR	[4] Phospho (ST)	-0.27	0.09	-0.26	-0.35	0.192	0.375	0.210	0.02	3.64E+04	6.47E+04	4.65E+04	3.72E+04	4.46E+04	4.08E+04	5.72E+04	5.32E+04	4.63E+04	3.63E+04	4.86E+04	3.82E+04	607.28842	3	30.77
MSN2	YMR037C	RSSVVIESTK	[3] Phospho (ST)	-0.84	0.26	-0.95	-1.10	0.116	0.317	0.091	0.04	3.65E+04	3.01E+04	1.10E+04	1.93E+04	9.86E+03	1.41E+04	2.94E+04	2.11E+04	4.23E+04	1.59E+04	1.26E+04	1.16E+04	593.29757	2	56.47
MSC3	YLR219W	RLSTSSAAPPTSR	[6] Phospho (ST)	0.27	0.09	0.05	0.18	0.022	0.395	0.416	0.29	1.16E+04	1.01E+04	1.23E+04	1.31E+04	1.32E+04	1.46E+04	1.64E+04	7.74E+03	1.21E+04	1.05E+04	9.73E+03	1.49E+04	470.89626	3	16.27
PAR32	YDL173W	SHQSLHATTSSPNNNAPIVVGR	[1] Phospho (ST)|[4] Phospho (ST)	0.08	0.13	-0.05	-0.05	0.282	0.275	0.391	0.41	6.96E+04	6.98E+04	8.42E+04	8.72E+04	7.15E+04	7.75E+04	6.62E+04	9.79E+04	7.99E+04	8.32E+04	5.63E+04	7.57E+04	816.36676	3	26.02
YMR086W	YMR086W	KFSGLSLR	[3] Phospho (ST)|[6] Phospho (ST)	-0.97	-0.35	-0.69	-0.62	0.006	0.227	0.031	0.16	3.49E+04	4.58E+04	3.32E+04	1.70E+04	2.23E+04	1.90E+04	1.84E+04	4.77E+04	2.32E+04	2.51E+04	2.95E+04	1.59E+04	534.2382	2	18.82
YTA7	YGR270W	RGSDVEDASNAK	[3] Phospho (ST)	0.98	-0.15	-0.35	1.13	0.051	0.352	0.165	0.04	2.92E+04	2.30E+04	1.54E+04	4.03E+04	3.04E+04	6.26E+04	2.66E+04	1.38E+04	2.04E+04	2.14E+04	1.61E+04	1.54E+04	664.77819	2	55.21
GRH1	YDR517W	ESDDLDDVSLNHDER	[9] Phospho (ST)	-0.14	-0.39	-0.02	0.26	0.091	0.029	0.455	0.07	5.44E+04	6.00E+04	6.48E+04	5.48E+04	5.16E+04	5.66E+04	5.03E+04	3.66E+04	4.97E+04	4.71E+04	6.00E+04	6.95E+04	919.85814	2	46.01
PUF4	YGL014W	TRTQSISFDNTPSSTSFIPPTNSVSEK	[3] Phospho (ST)	-0.50	-0.27	0.02	-0.23	0.071	0.218	0.473	0.27	3.54E+05	3.21E+05	2.35E+05	2.73E+05	1.58E+05	2.14E+05	2.34E+05	3.42E+05	1.82E+05	4.16E+05	2.70E+05	2.39E+05	1003.4642	3	18.83
BEM1	YBR200W	KLSDLSLSGSK	[3] Phospho (ST)	-0.50	-0.34	-0.01	-0.16	0.016	0.063	0.476	0.27	2.97E+04	2.52E+04	2.69E+04	1.89E+04	1.59E+04	2.31E+04	2.67E+04	1.78E+04	2.01E+04	2.41E+04	2.60E+04	3.13E+04	607.80538	2	38.08
BNI5	YNL166C	LADQTPHDDNSENCPNRSGGSTPLDSQTK	[18] Phospho (ST)	-0.12	-0.44	0.02	0.33	0.150	0.015	0.468	0.07	1.17E+05	1.13E+05	1.20E+05	1.22E+05	9.70E+04	1.04E+05	8.56E+04	7.00E+04	1.02E+05	1.16E+05	8.29E+04	1.57E+05	1074.4529	3	26.25
HRK1	YOR267C	SFLNFIGR	[1] Phospho (ST)	-1.23	-0.42	-0.44	-0.81	0.062	0.224	0.243	0.02	3.61E+04	7.91E+04	3.52E+04	1.58E+04	2.62E+04	2.23E+04	3.87E+04	4.38E+04	3.02E+04	3.12E+04	5.45E+04	2.55E+04	517.24731	2	38.03
STB1	YNL309W	PSASSPQSTFK	[5] Phospho (ST)	0.25	0.44	0.37	-0.20	0.129	0.070	0.057	0.17	1.71E+04	2.45E+04	2.66E+04	2.98E+04	2.59E+04	2.52E+04	2.94E+04	2.59E+04	3.74E+04	3.20E+04	2.64E+04	2.99E+04	608.76608	2	27.94
PWP2	YCR057C	DNKLPLSNENDSSDEEENEK	[12] Phospho (ST)|[13] Phospho (ST)	-0.87	-0.67	-0.47	-0.20	0.043	0.133	0.113	0.38	2.71E+05	1.49E+05	1.98E+05	7.71E+04	1.47E+05	1.14E+05	5.62E+04	2.18E+05	1.13E+05	1.85E+05	1.30E+05	1.31E+05	822.64611	3	24.63
SPA2	YLL021W	LASSGEVDKIESPR	[12] Phospho (ST)	-0.15	0.63	0.40	-0.78	0.255	0.075	0.148	0.06	4.15E+04	4.31E+04	4.09E+04	3.01E+04	3.37E+04	4.90E+04	8.15E+04	3.95E+04	7.27E+04	4.17E+04	4.66E+04	7.70E+04	784.37178	2	49.39
CRN1	YLR429W	IETPVTPTETKK	[6] Phospho (ST)	0.48	0.20	-0.10	0.28	0.029	0.360	0.376	0.29	3.01E+04	4.17E+04	3.55E+04	4.51E+04	4.64E+04	5.81E+04	6.63E+04	1.94E+04	3.78E+04	2.18E+04	3.40E+04	4.41E+04	712.35776	2	29.74
PKH1	YDR490C	SLTEADHALLSK	[1] Phospho (ST)	0.17	0.13	-0.27	0.03	0.267	0.335	0.244	0.45	2.10E+04	3.31E+04	3.55E+04	3.13E+04	2.99E+04	3.93E+04	3.91E+04	2.40E+04	3.53E+04	1.50E+04	2.83E+04	3.10E+04	682.82724	2	57.1
SRD1	YCR018C	KTTSRPK	[3] Phospho (ST)	0.43	0.23	0.22	0.20	0.028	0.223	0.136	0.18	1.64E+04	1.19E+04	1.80E+04	2.01E+04	1.99E+04	2.22E+04	1.81E+04	1.37E+04	2.23E+04	1.91E+04	1.63E+04	1.87E+04	449.23096	2	28.97
MET4	YNL103W	KYSDNEDDEYDDADLHGFEK	[3] Phospho (ST)	-0.43	-0.28	-0.56	-0.15	0.030	0.202	0.015	0.33	7.81E+04	8.78E+04	6.41E+04	6.27E+04	5.61E+04	5.17E+04	7.66E+04	7.52E+04	3.73E+04	5.38E+04	4.64E+04	5.57E+04	828.98371	3	74.14
DPP1	YDR284C	IPDEELHPLSDEGM	[10] Phospho (ST)	-0.86	0.13	0.29	-0.99	0.078	0.304	0.299	0.04	1.07E+05	1.63E+05	1.07E+05	6.09E+04	1.19E+05	2.88E+04	1.38E+05	1.57E+05	1.18E+05	9.19E+04	2.40E+05	1.28E+05	831.343	2	49.45
YOL103W-B	L103W-B	EVDPNISESNILPSK	[7] Phospho (ST)	-0.58	0.94	0.95	-1.52	0.031	0.004	0.002	0.00	7.40E+04	9.64E+04	6.69E+04	4.89E+04	6.26E+04	4.70E+04	1.55E+05	1.69E+05	1.30E+05	1.44E+05	1.68E+05	1.45E+05	861.40382	2	30.6
NUP2	YLR335W	KKDESDSENDIEIK	[5] Phospho (ST)|[7] Phospho (ST)	-0.29	-0.65	-0.61	0.36	0.188	0.098	0.056	0.19	1.46E+05	8.53E+04	9.97E+04	9.58E+04	1.01E+05	7.38E+04	4.39E+04	1.05E+05	6.22E+04	7.90E+04	6.35E+04	7.41E+04	905.36387	2	29.43
MED2	YDL005C	VVQNSPVSSVHTANFSER	[5] Phospho (ST)	0.09	-0.03	-0.04	0.12	0.301	0.460	0.440	0.31	3.32E+04	3.85E+04	4.85E+04	4.48E+04	4.24E+04	4.09E+04	4.97E+04	2.74E+04	4.06E+04	3.46E+04	3.48E+04	4.78E+04	679.98505	3	30.64
YMR111C	YMR111C	TITTSPTGVSR	[5] Phospho (ST)	-0.17	0.27	-0.07	-0.44	0.138	0.081	0.348	0.01	2.68E+04	2.47E+04	2.02E+04	2.12E+04	1.98E+04	2.26E+04	2.96E+04	2.49E+04	3.18E+04	2.58E+04	2.02E+04	2.25E+04	600.28659	2	19.12
VIP1	YLR410W	FTPVNITSPNLSFQK	[8] Phospho (ST)	0.30	0.09	0.15	0.21	0.170	0.365	0.334	0.14	3.87E+04	5.66E+04	3.15E+04	4.87E+04	6.21E+04	4.54E+04	4.80E+04	4.10E+04	4.64E+04	4.20E+04	6.10E+04	3.81E+04	591.62633	3	25.97
SMY2	YBR172C	VSTPVQQHPLLQR	[3] Phospho (ST)	-0.22	-0.15	-0.26	-0.07	0.281	0.376	0.293	0.41	1.42E+04	3.24E+04	2.51E+04	2.06E+04	2.16E+04	1.93E+04	2.95E+04	1.44E+04	2.09E+04	1.27E+04	2.13E+04	2.60E+04	528.27527	3	22.88
KEL1	YHR158C	NVSGPSTTLHK	[3] Phospho (ST)	-0.82	-0.94	-0.35	0.12	0.004	0.001	0.079	0.31	2.81E+04	2.50E+04	2.90E+04	1.61E+04	1.18E+04	1.88E+04	1.56E+04	1.17E+04	1.55E+04	2.07E+04	1.64E+04	2.73E+04	610.78731	2	33.07
TAT1	YBR069C	NSELESQEK	[6] Phospho (ST)	0.18	-1.19	-0.59	1.37	0.407	0.160	0.287	0.01	6.63E+04	9.50E+03	2.66E+04	4.75E+04	3.06E+04	3.74E+04	1.18E+04	1.58E+04	1.72E+04	3.93E+04	1.61E+04	1.25E+04	572.2333	2	22.34
KEL3	YPL263C	SLNGEEDDESDQDLDEILSSFSK	[10] Phospho (ST)	-0.32	0.20	0.03	-0.51	0.245	0.329	0.476	0.11	1.70E+05	2.41E+05	1.03E+05	1.28E+05	1.76E+05	1.10E+05	1.86E+05	2.61E+05	1.42E+05	1.39E+05	2.42E+05	1.43E+05	884.6971	3	31.21
VHS2	YIL135C	TRSLSSQSFDNETSPAHPR	[1] Phospho (ST)	-0.23	-0.48	-0.16	0.24	0.184	0.222	0.285	0.35	4.02E+04	6.22E+04	5.17E+04	4.06E+04	3.88E+04	5.18E+04	6.43E+04	3.68E+04	9.57E+03	4.16E+04	3.89E+04	5.76E+04	732.99427	3	49.73
SOL1	YNR034W	FYDDENLTE	[8] Phospho (ST)	-0.37	-0.27	-0.35	-0.10	0.022	0.072	0.076	0.24	7.42E+04	6.49E+04	5.85E+04	5.30E+04	5.37E+04	4.65E+04	4.64E+04	5.84E+04	5.93E+04	5.14E+04	6.33E+04	4.00E+04	613.21903	2	30.71
CRN1	YLR429W	SATPPSSITAAK	[3] Phospho (ST)	0.81	0.64	-0.08	0.17	0.009	0.016	0.376	0.13	1.95E+04	3.21E+04	3.21E+04	5.41E+04	4.20E+04	5.08E+04	4.53E+04	3.89E+04	4.62E+04	2.83E+04	2.44E+04	2.66E+04	605.78998	2	52.63
TFG1	YGR186W	AVDSSNNASNTVPSPIK	[14] Phospho (ST)	0.23	0.71	0.54	-0.48	0.055	0.008	0.004	0.01	6.67E+04	7.39E+04	8.79E+04	9.16E+04	8.58E+04	9.10E+04	1.20E+05	1.10E+05	1.45E+05	1.18E+05	1.07E+05	1.08E+05	890.91002	2	34.58
ENT1	YDL161W	RGTGRSDENDDDLQR	[3] Phospho (ST)|[6] Phospho (ST)	-0.18	-0.80	-0.53	0.63	0.347	0.108	0.185	0.03	6.79E+04	2.66E+04	4.18E+04	3.72E+04	4.45E+04	3.91E+04	1.56E+04	3.31E+04	2.94E+04	4.49E+04	2.33E+04	2.61E+04	631.90899	3	23.46
SAC7	YDR389W	LDHTTLSPISTSIPENSSDLQTSK	[11] Phospho (ST)	-0.14	0.11	0.14	-0.25	0.242	0.281	0.201	0.08	7.20E+04	9.49E+04	7.10E+04	6.61E+04	8.24E+04	6.77E+04	9.31E+04	9.01E+04	7.35E+04	8.23E+04	9.51E+04	8.50E+04	884.42071	3	43.74
TPO3	YPR156C	QIDGASSPSSNEDALESDNNEK	[17] Phospho (ST)	-0.30	-0.55	0.14	0.25	0.136	0.047	0.327	0.03	1.48E+05	1.01E+05	9.79E+04	1.02E+05	8.59E+04	9.37E+04	7.17E+04	8.09E+04	8.44E+04	1.47E+05	9.08E+04	1.45E+05	1193.9808	2	47.47
HNM1	YGL077C	EFSVAASDVELENEHVPWGK	[7] Phospho (ST)	-0.39	-0.05	-0.34	-0.34	0.177	0.447	0.233	0.06	8.44E+04	1.54E+05	8.34E+04	7.77E+04	9.54E+04	7.23E+04	1.19E+05	8.81E+04	1.04E+05	5.48E+04	1.08E+05	9.05E+04	775.01498	3	57.07
NUP159	YIL115C	LPETPSDEDGEVVEEEAQKSPIGK	[20] Phospho (ST)	0.07	0.45	0.35	-0.38	0.266	0.004	0.173	0.00	4.90E+04	6.13E+04	5.19E+04	5.58E+04	5.89E+04	5.54E+04	7.63E+04	7.45E+04	7.03E+04	4.49E+04	9.18E+04	7.07E+04	888.40473	3	28.69
RCN2	YOR220W	SSSSTSNLSLNR	[3] Phospho (ST)	0.43	0.72	0.68	-0.29	0.101	0.114	0.132	0.27	2.19E+04	1.34E+04	2.38E+04	3.02E+04	2.03E+04	2.92E+04	1.89E+04	4.79E+04	3.07E+04	4.87E+04	2.35E+04	2.26E+04	666.79357	2	52.42
CTR9	YOL145C	KTLSDSDEDDDDVVK	[4] Phospho (ST)|[6] Phospho (ST)	-0.24	-0.43	-0.54	0.18	0.234	0.178	0.081	0.31	1.67E+05	8.81E+04	1.32E+05	9.38E+04	1.05E+05	1.28E+05	5.33E+04	1.25E+05	1.10E+05	9.87E+04	8.27E+04	8.58E+04	920.84279	2	42.35

MSB1	YOR188W	RDSAPDNQGIYHTVISK	[3] Phospho (ST)	-0.52	-1.14	0.10	0.62	0.147	0.040	0.401	0.04	1.87E+05	8.62E+04	1.15E+05	1.14E+05	7.29E+04	8.32E+04	4.86E+04	6.47E+04	6.24E+04	1.69E+05	1.06E+05	1.42E+05	990.95684	2	23.18
SIP1	YDR422C	RSSFASLHSLQSR	[3] Phospho (ST)	-0.06	0.19	0.09	-0.25	0.432	0.359	0.416	0.27	2.33E+04	5.19E+04	3.34E+04	3.27E+04	3.61E+04	3.52E+04	6.16E+04	2.93E+04	3.32E+04	2.82E+04	4.22E+04	4.50E+04	519.25111	3	40.62
YPK1	YKL126W	DDDKTDTFCGTPEYLAPELLLGLGYTK	[14] Phospho (Y)	0.11	0.32	-0.11	-0.21	0.426	0.315	0.436	0.31	1.16E+05	2.56E+05	7.35E+04	1.42E+05	1.92E+05	1.46E+05	2.55E+05	1.96E+05	1.05E+05	1.46E+05	1.82E+05	8.50E+04	1038.1414	3	45.58
SGT1	YOR057W	GDNNSSHSPISPLK	[11] Phospho (ST)	0.15	0.36	0.45	-0.20	0.217	0.077	0.029	0.14	3.00E+04	3.59E+04	4.39E+04	4.37E+04	3.57E+04	4.29E+04	5.41E+04	3.92E+04	4.76E+04	4.58E+04	4.80E+04	5.58E+04	766.84095	2	33.24
MSB1	YOR188W	NAPGDCVSPVQQK	[8] Phospho (ST)	0.04	0.24	0.45	-0.20	0.418	0.292	0.032	0.31	4.85E+04	3.43E+04	5.08E+04	4.50E+04	4.31E+04	4.91E+04	2.92E+04	5.59E+04	7.31E+04	6.68E+04	5.35E+04	6.27E+04	740.31834	2	26.48
VPS74	YDR372C	ADSGDTSSIHSSANNTK	[3] Phospho (ST)	0.19	-1.73	-0.96	1.92	0.415	0.144	0.220	0.02	1.27E+05	3.56E+04	1.78E+04	9.90E+04	4.62E+04	6.11E+04	1.72E+04	9.82E+03	2.75E+04	3.67E+04	2.03E+04	3.55E+04	886.36011	2	83.88
NBP2	YDR162C	RQSITLPDDYIVNQR	[3] Phospho (ST)	-0.29	0.11	-0.04	-0.40	0.148	0.327	0.443	0.02	6.62E+04	1.10E+05	8.86E+04	6.45E+04	7.92E+04	7.29E+04	1.08E+05	8.97E+04	8.81E+04	6.79E+04	9.38E+04	9.62E+04	949.46049	2	52.23
SUM1	YDR310C	FHQIPSSPSNPVSQPAPVR	[6] Phospho (ST)	-0.36	0.42	-0.07	-0.78	0.035	0.069	0.329	0.02	6.06E+04	7.39E+04	7.59E+04	4.80E+04	5.30E+04	6.24E+04	8.77E+04	7.70E+04	1.16E+05	6.48E+04	6.08E+04	7.56E+04	709.0126	3	30.32
ENT1	YDL161W	NQLVAASSPQQLQQQK	[8] Phospho (ST)	-0.02	0.16	0.07	-0.18	0.463	0.316	0.376	0.28	6.57E+04	5.67E+04	8.17E+04	6.39E+04	6.89E+04	6.91E+04	4.98E+04	8.20E+04	9.66E+04	7.33E+04	5.84E+04	8.28E+04	924.45474	2	34.41
ASK10	YGR097W	VNTPAIDDYGNLITVER	[3] Phospho (ST)	-0.16	0.22	0.40	-0.38	0.337	0.269	0.158	0.13	1.15E+05	1.93E+05	1.13E+05	9.93E+04	1.62E+05	1.15E+05	2.00E+05	1.63E+05	1.26E+05	1.46E+05	2.41E+05	1.67E+05	985.4683	2	93.19
UFD1	YGR048W	APKSPEVIEID	[4] Phospho (ST)	-0.08	0.26	-0.09	-0.33	0.391	0.189	0.393	0.08	4.26E+04	7.37E+04	5.68E+04	5.00E+04	6.33E+04	5.10E+04	8.34E+04	6.23E+04	6.16E+04	3.95E+04	6.78E+04	5.52E+04	639.30558	2	17.06
EFR3	YMR212C	DNQISTSDLLSDSQVR	[5] Phospho (ST)	-0.65	-0.28	-0.10	-0.37	0.047	0.159	0.358	0.08	9.93E+04	1.61E+05	1.19E+05	7.66E+04	1.00E+05	6.45E+04	9.62E+04	1.20E+05	9.56E+04	1.12E+05	1.40E+05	1.02E+05	929.4152	2	79.86
HRK1	YOR267C	STSTVNLNNHYR	[3] Phospho (ST)	-0.75	-0.69	-0.41	-0.06	0.008	0.003	0.045	0.40	2.52E+04	3.06E+04	2.69E+04	1.75E+04	1.18E+04	1.97E+04	1.48E+04	1.90E+04	1.74E+04	2.58E+04	1.70E+04	1.97E+04	495.8877	3	27.97
VPS13	YLL040C	SPSPDPASLSSESER	[3] Phospho (ST)	0.95	0.89	0.50	0.05	0.000	0.007	0.025	0.37	4.08E+04	4.90E+04	4.58E+04	8.68E+04	8.30E+04	9.19E+04	9.79E+04	6.71E+04	8.71E+04	5.36E+04	7.51E+04	6.27E+04	813.3399	2	37.51
NUP100	YKL068W	AHSPQTDLKDDHDESTPDPQSK	[3] Phospho (ST)	0.21	-0.20	0.02	0.41	0.216	0.235	0.467	0.09	2.48E+04	2.57E+04	3.51E+04	4.08E+04	2.74E+04	3.10E+04	2.70E+04	1.84E+04	2.91E+04	2.63E+04	2.40E+04	3.66E+04	632.7695	4	17.74
CBF5	YLR175W	EYVPLDNAEQSTSSSQETKETEEEPKK	[11] Phospho (ST)	1.46	-0.89	-1.48	2.35	0.002	0.000	0.000	0.00	8.26E+04	7.74E+04	7.92E+04	2.64E+05	1.91E+05	2.03E+05	4.39E+04	4.32E+04	4.19E+04	2.34E+04	2.54E+04	3.68E+04	1055.1337	3	29.23
CHS3	YBR023C	KEESDSFVA	[6] Phospho (ST)	0.26	0.01	0.18	0.25	0.123	0.482	0.236	0.07	2.52E+04	2.21E+04	3.45E+04	3.54E+04	3.16E+04	3.09E+04	2.49E+04	2.51E+04	3.25E+04	2.84E+04	2.82E+04	3.57E+04	546.21849	2	16.52
RRP36	YOR287C	NLKPDLNSDVEEDDGNLLESIMANK	[8] Phospho (ST)	-0.26	-0.55	0.13	0.30	0.254	0.081	0.405	0.23	2.24E+05	2.74E+05	1.58E+05	1.99E+05	2.36E+05	1.14E+05	1.44E+05	1.91E+05	1.11E+05	2.09E+05	3.78E+05	1.31E+05	951.76781	3	53.62
SPT7	YBR081C	SDDVSSQTIK	[6] Phospho (ST)	1.52	-0.23	-0.52	1.75	0.027	0.305	0.176	0.02	1.81E+04	8.52E+03	1.59E+04	5.73E+04	3.98E+04	2.49E+04	7.60E+03	1.55E+04	1.32E+04	1.56E+04	7.73E+03	6.34E+03	580.24798	2	25.72
YKR023W	YKR023W	SLENLHLQSK	[1] Phospho (ST)	0.14	0.44	0.42	-0.31	0.271	0.034	0.070	0.01	1.22E+04	1.70E+04	2.03E+04	1.62E+04	1.92E+04	1.91E+04	2.29E+04	2.12E+04	2.33E+04	1.84E+04	2.30E+04	2.48E+04	624.80326	2	32.93
SPT5	YML010W	DENTSDKDTVDSGNVTTTESTER	[9] Phospho (ST)	0.59	0.09	0.20	0.50	0.014	0.339	0.221	0.03	4.69E+04	4.13E+04	5.52E+04	8.15E+04	6.12E+04	7.26E+04	4.68E+04	4.40E+04	6.16E+04	6.60E+04	4.14E+04	5.70E+04	861.0189	3	40.21
LYP1	YNL268W	LQVVSHETDINEDEEEAHYEDK	[5] Phospho (ST)|[8] Phospho (ST)	-1.41	-0.77	-0.93	-0.64	0.005	0.045	0.015	0.09	1.80E+05	1.14E+05	1.42E+05	6.10E+04	5.55E+04	4.77E+04	6.14E+04	1.23E+05	7.16E+04	7.76E+04	6.08E+04	9.04E+04	930.36717	3	47.62
SFL1	YOR140W	SSSTTNIPSR	[3] Phospho (ST)	0.04	0.18	0.04	-0.14	0.469	0.385	0.478	0.37	1.11E+04	9.70E+03	2.44E+04	1.78E+04	1.44E+04	1.42E+04	9.78E+03	2.46E+04	1.68E+04	2.53E+04	9.50E+03	1.16E+04	565.24935	2	55.9
SMY2	YBR172C	APIGTVVSPYSK	[8] Phospho (ST)	-0.66	-1.00	-0.37	0.34	0.149	0.089	0.258	0.03	8.06E+04	3.89E+04	3.14E+04	3.33E+04	2.73E+04	3.47E+04	2.74E+04	2.54E+04	2.26E+04	2.95E+04	4.08E+04	4.62E+04	649.82329	2	35.47
RAD5	YLR032W	DVAKIYK	[6] Phospho (Y)	-2.47	-3.11	-0.73	0.64	0.082	0.070	0.242	0.14	9.04E+04	2.86E+04	1.98E+04	6.05E+03	6.49E+03	1.25E+04	4.49E+03	7.82E+03	3.76E+03	1.32E+04	2.71E+04	4.34E+04	458.72959	2	15.13
ENT1	YDL161W	RNQLVAASSPQQLQQQK	[9] Phospho (ST)	0.04	-0.02	0.04	0.06	0.328	0.450	0.434	0.36	8.19E+04	7.63E+04	8.92E+04	8.36E+04	8.06E+04	8.97E+04	6.38E+04	8.80E+04	9.17E+04	9.33E+04	5.92E+04	1.02E+05	1002.5047	2	35.63
PAH1	YMR165C	RASSAAATSIDK	[3] Phospho (ST)	-0.10	-1.26	-0.66	1.17	0.382	0.038	0.105	0.02	3.91E+04	2.69E+04	2.08E+04	2.72E+04	2.33E+04	3.07E+04	1.53E+04	2.96E+03	1.79E+04	1.33E+04	1.42E+04	2.75E+04	629.29513	2	51.99
HER1	YOR227W	SSSISTSLNER	[3] Phospho (ST)	0.06	0.29	0.11	-0.23	0.309	0.058	0.320	0.10	2.41E+04	2.10E+04	2.22E+04	2.58E+04	2.10E+04	2.31E+04	2.43E+04	3.20E+04	2.60E+04	3.04E+04	1.90E+04	2.31E+04	630.77761	2	37.28
FPK1	YNR047W	NLSNLSLNEIK	[3] Phospho (ST)|[6] Phospho (ST)	-0.25	-0.09	-0.14	-0.16	0.236	0.392	0.288	0.36	7.01E+04	7.41E+04	5.18E+04	4.84E+04	7.68E+04	3.94E+04	4.47E+04	8.49E+04	5.41E+04	6.60E+04	6.70E+04	4.46E+04	702.81312	2	19.61
ERG6	YML008C	KPENAETPSQTSQEATQ	[12] Phospho (ST)	0.23	0.12	-0.10	0.11	0.237	0.383	0.397	0.34	1.40E+05	6.82E+04	9.04E+04	1.25E+05	1.07E+05	1.18E+05	7.33E+04	1.19E+05	1.33E+05	1.05E+05	7.02E+04	1.03E+05	963.41062	2	35.05
YKR018C	YKR018C	DSSNSEDSEDEEMDGPTLLHPGK	[8] Phospho (ST)	-0.39	0.36	0.61	-0.75	0.239	0.193	0.030	0.13	1.04E+05	1.03E+05	8.04E+04	6.66E+04	1.25E+05	2.76E+04	1.18E+05	1.72E+05	7.95E+04	1.31E+05	1.81E+05	1.26E+05	857.00273	3	44.32
UBP2	YOR124C	KNESNDAEVSENEDTTGLTSPTR	[10] Phospho (ST)	0.10	0.66	0.71	-0.55	0.287	0.119	0.003	0.15	7.92E+04	6.40E+04	8.16E+04	8.54E+04	6.64E+04	8.95E+04	1.74E+05	6.76E+04	1.13E+05	1.34E+05	1.24E+05	1.09E+05	858.69693	3	31.18
SOK1	YDR006C	SHSVPTILHSSLR	[3] Phospho (ST)	-0.21	0.12	-0.50	-0.33	0.286	0.385	0.147	0.14	2.67E+04	5.06E+04	2.87E+04	3.30E+04	3.10E+04	2.74E+04	5.03E+04	3.37E+04	3.10E+04	1.78E+04	2.56E+04	3.14E+04	505.25594	3	36.5
NUP159	YIL115C	SLSPTSEK	[5] Phospho (ST)	0.75	0.05	0.31	0.70	0.073	0.460	0.327	0.01	2.58E+04	7.64E+03	1.43E+04	3.15E+04	2.21E+04	2.65E+04	1.65E+04	1.62E+04	1.68E+04	3.14E+04	1.59E+04	1.20E+04	464.70476	2	22.52
YLR257W	YLR257W	SNSLITSTDPVEDHISK	[1] Phospho (ST)	-0.04	0.02	0.03	-0.06	0.432	0.460	0.443	0.38	1.09E+05	1.31E+05	8.64E+04	9.47E+04	1.22E+05	1.01E+05	1.30E+05	1.11E+05	9.08E+04	9.67E+04	1.31E+05	1.06E+05	961.94277	2	53.83
STU2	YLR045C	RSSESIGDLPHR	[3] Phospho (ST)	-0.26	-0.18	-0.23	-0.08	0.106	0.260	0.162	0.38	3.55E+04	5.01E+04	4.24E+04	3.26E+04	3.52E+04	3.95E+04	4.64E+04	2.74E+04	3.95E+04	3.09E+04	3.44E+04	4.36E+04	717.33014	2	44.57
RDI1	YDL135C	NLDAEDESLAK	[8] Phospho (ST)	-0.06	-0.47	0.18	0.40	0.368	0.213	0.196	0.24	3.14E+04	2.78E+04	3.96E+04	3.29E+04	2.83E+04	3.34E+04	2.50E+04	6.49E+03	3.99E+04	4.35E+04	3.30E+04	3.57E+04	642.77214	2	28.73
MDS3	YGL197W	NNDEEDDEDPVSPKPVSK	[12] Phospho (ST)	-0.11	0.04	0.16	-0.16	0.293	0.420	0.242	0.14	7.50E+04	7.29E+04	1.04E+05	8.05E+04	7.17E+04	8.13E+04	9.74E+04	7.56E+04	8.71E+04	9.81E+04	7.93E+04	1.04E+05	1047.431	2	46.92
ZRT1	YGL255W	NTAAVSSENDNENGTANGSHDTK	[7] Phospho (ST)	-0.14	-1.44	-0.34	1.30	0.413	0.068	0.309	0.03	1.24E+05	4.40E+04	5.54E+04	5.75E+04	5.01E+04	9.55E+04	3.43E+04	2.29E+04	2.51E+04	8.00E+04	3.14E+04	6.53E+04	804.98953	3	72.6
NPL3	YDR432W	ENSLETTFSSVNTR	[3] Phospho (ST)	-5.21	-0.82	-0.01	-4.39	0.001	0.025	0.484	0.00	6.62E+04	1.12E+05	8.58E+04	1.22E+03	2.80E+03	3.07E+03	4.93E+04	5.61E+04	4.37E+04	6.04E+04	1.10E+05	9.12E+04	832.86303	2	55.1
ENT4	YLL038C	SELTRQSLEK	[7] Phospho (ST)	-0.21	-0.17	0.02	-0.03	0.091	0.209	0.442	0.43	1.69E+04	2.16E+04	1.93E+04	1.51E+04	1.79E+04	1.71E+04	1.96E+04	1.32E+04	1.85E+04	2.16E+04	1.71E+04	2.00E+04	635.80563	2	33.52
ORC2	YBR060C	NTSPDPALKPK	[3] Phospho (ST)	0.18	1.12	0.79	-0.94	0.404	0.052	0.099	0.03	7.10E+03	1.35E+04	3.52E+04	1.68E+04	1.68E+04	2.97E+04	4.62E+04	2.86E+04	4.66E+04	2.97E+04	3.02E+04	3.64E+04	624.3056	2	28.89
SUM1	YDR310C	RTAGDDGALDQTENTSISPKK	[18] Phospho (ST)	-0.29	-0.23	-0.01	-0.07	0.051	0.163	0.464	0.40	5.37E+04	5.86E+04	6.08E+04	5.51E+04	3.92E+04	4.68E+04	6.06E+04	3.60E+04	5.15E+04	6.54E+04	4.92E+04	5.71E+04	762.01954	3	45.57
MTC1	YJL123C	SENKNSEAEDVFEFLDSLPEAK	[N-term] Acetyl (Protein N-term)|[6] Phospho	-0.50	0.04	-0.37	-0.54	0.183	0.464	0.255	0.07	1.31E+05	2.04E+05	7.92E+04	7.80E+04	1.29E+05	8.69E+04	1.72E+05	1.45E+05	1.09E+05	8.36E+04	1.54E+05	8.22E+04	874.04977	3	16.37
RRP36	YOR287C	EIDEQESSDDELK	[7] Phospho (ST)|[8] Phospho (ST)	0.12	-0.19	0.04	0.31	0.335	0.369	0.451	0.25	1.29E+05	6.58E+04	1.21E+05	1.08E+05	1.25E+05	1.11E+05	3.99E+04	1.44E+05	9.32E+04	1.29E+05	1.06E+05	9.06E+04	848.79811	2	20.4
PDS1	YDR113C	KLSQISR	[3] Phospho (ST)	0.47	-1.17	-0.79	1.63	0.127	0.026	0.112	0.02	1.28E+04	9.90E+03	8.37E+03	1.96E+04	1.10E+04	1.23E+04	2.72E+03	3.16E+03	7.93E+03	2.41E+03	4.05E+03	1.14E+04	456.23895	2	21.02
MHP1	YJL042W	RIVTNNEEEVTVSK	[4] Phospho (ST)	0.36	-0.27	-0.17	0.62	0.018	0.120	0.228	0.00	4.61E+04	3.78E+04	5.10E+04	5.97E+04	5.52E+04	5.80E+04	4.46E+04	3.12E+04	3.62E+04	4.09E+04	3.16E+04	4.75E+04	849.40844	2	49.44
RAD16	YBR114W	SVNYNELSDDDTAVK	[8] Phospho (ST)	-0.33	-0.17	-0.02	-0.16	0.003	0.115	0.360	0.15	5.52E+04	5.80E+04	5.28E+04	4.55E+04	4.10E+04	4.56E+04	5.11E+04	5.51E+04	4.15E+04	5.63E+04	5.59E+04	5.12E+04	875.36549	2	48.87
SLN1	YIL147C	APGSDDEEGGNLGRPIENPK	[4] Phospho (ST)	-0.24	-0.16	0.03	-0.09	0.101	0.180	0.414	0.26	6.63E+04	8.95E+04	7.92E+04	6.01E+04	6.39E+04	7.44E+04	7.74E+04	6.34E+04	6.99E+04	7.87E+04	8.10E+04	8.00E+04	1066.4691	2	45.35
SMY2	YBR172C	SNTPLLGGR	[3] Phospho (ST)	-0.67	-0.74	-0.04	0.07	0.020	0.014	0.410	0.29	2.80E+04	4.07E+04	4.12E+04	2.39E+04	1.98E+04	2.52E+04	2.31E+04	2.04E+04	2.21E+04	3.42E+04	3.54E+04	3.71E+04	497.7402	2	34.26
BUD27	YFL023W	ILENISDDDYDDDDDGNKK	[6] Phospho (ST)	0.50	0.20	0.24	0.31	0.002	0.166	0.092	0.04	5.50E+04	4.54E+04	4.58E+04	6.82E+04	6.84E+04	7.07E+04	4.46E+04	6.25E+04	6.05E+04	6.48E+04	5.82E+04	4.94E+04	760.30149	3	30.12
EDE1	YBL047C	RANSNEDGESVSSIQESPK	[10] Phospho (ST)|[13] Phospho (ST)	-0.29	-0.51	-0.10	0.22	0.144	0.090	0.371	0.23	5.52E+04	3.71E+04	5.95E+04	4.75E+04	3.89E+04	3.76E+04	2.37E+04	4.49E+04	3.81E+04	5.82E+04	3.61E+04	4.76E+04	731.96171	3	29.23
TIF3	YPR163C	SGGFGGSFGGR	[7] Phospho (ST)	-0.57	-0.02	-0.33	-0.55	0.071	0.467	0.139	0.07	1.38E+04	1.52E+04	2.08E+04	1.05E+04	8.04E+03	1.50E+04	1.27E+04	1.78E+04	1.85E+04	1.65E+04	1.12E+04	1.17E+04	533.21112	2	32.52
PSK1	YAL017W	GDYGNNISPERPSFR	[8] Phospho (ST)	0.56	1.00	0.50	-0.44	0.002	0.001	0.006	0.00	1.36E+04	1.63E+04	1.79E+04	2.39E+04	2.38E+04	2.28E+04	3.14E+04	3.50E+04	2.92E+04	2.39E+04	2.30E+04	2.10E+04	596.9286	3	18.74
IGO1	YNL157W	RISTCPSTASTAGVVDNATLIQK	[10] Phospho (ST)	0.26	0.41	0.07	-0.15	0.157	0.072	0.414	0.24	3.36E+04	5.13E+04	4.00E+04	5.03E+04	5.77E+04	4.11E+04	6.59E+04	4.82E+04	5.16E+04	2.84E+04	5.38E+04	4.92E+04	824.07253	3	57.22
MSN2	YMR037C	DNRLSLPNGANSNLFIDTNPNNLNEK	[12] Phospho (ST)	-0.49	-0.34	-0.52	-0.16	0.021	0.054	0.045	0.10	1.49E+05	1.39E+05	1.08E+05	9.43E+04	1.01E+05	8.64E+04	1.11E+05	1.09E+05	9.37E+04	8.55E+04	1.17E+05	7.35E+04	988.80098	3	54.64
SEC9	YGR009C	NSLNHSNSTLNVGPSR	[6] Phospho (ST)|[9] Phospho (ST)	0.10	0.02	0.17	0.08	0.371	0.470	0.323	0.37	2.48E+04	2.14E+04	3.64E+04	3.53E+04	2.38E+04	2.95E+04	2.42E+04	3.31E+04	2.66E+04	4.02E+04	2.29E+04	2.96E+04	619.59489	3	19.23
YMR045C	YMR045C	VSTQANSQQPTTPLSSAVPENHHHASPQAAQVPLPQNGPYI	[26] Phospho (ST)	-1.36	-0.48	0.09	-0.88	0.003	0.037	0.370	0.00	3.45E+05	2.76E+05	2.41E+05	1.39E+05	1.01E+05	9.56E+04	2.19E+05	1.79E+05	2.22E+05	2.25E+05	3.50E+05	3.41E+05	1194.5688	4	24.62
ATG13	YPR185W	HASVSHNSQGPQNQPEQEGQSDQDIGK	[3] Phospho (ST)	-0.24	-0.30	0.12	0.06	0.153	0.178	0.376	0.40	9.74E+04	6.17E+04	8.48E+04	7.29E+04	6.68E+04	6.69E+04	6.02E+04	5.19E+04	8.60E+04	1.02E+05	5.16E+04	1.12E+05	994.7592	3	43.99
GCN2	YDR283C	SIQNVPR	[1] Phospho (ST)	0.18	-0.08	0.04	0.26	0.214	0.392	0.451	0.16	1.29E+04	9.35E+03	1.43E+04	1.59E+04	1.23E+04	1.32E+04	8.15E+03	1.24E+04	1.39E+04	1.60E+04	1.20E+04	9.48E+03	447.21549	2	18.63
RCK2	YLR248W	DVSQITSSPK	[8] Phospho (ST)	1.34	1.40	1.43	-0.06	0.009	0.014	0.004	0.41	3.67E+03	8.64E+03	1.39E+04	2.20E+04	1.91E+04	2.52E+04	2.70E+04	1.71E+04	2.48E+04	2.52E+04	2.22E+04	2.31E+04	571.26092	2	20.07
MAM3	YOL060C	AADQADESSPLLSPSNSNHPSEHPQQDLNNK	[17] Phospho (ST)	-0.27	-0.17	0.10	-0.10	0.077	0.089	0.172	0.25	1.19E+05	9.72E+04	1.02E+05	9.50E+04	9.66E+04	7.20E+04	9.51E+04	8.82E+04	9.88E+04	1.13E+05	1.10E+05	1.19E+05	1136.4971	3	44.54
GIP4	YAL031C	SSSLQSYTNK	[3] Phospho (ST)	-0.48	-0.42	-0.49	-0.06	0.179	0.263	0.205	0.46	3.58E+04	1.52E+04	2.41E+04	2.43E+04	1.59E+04	1.37E+04	1.05E+04	3.22E+04	1.35E+04	2.80E+04	1.26E+04	1.26E+04	597.75585	2	42.03
MAM3	YOL060C	AADQADESSPLLSPSNSNHPSEHPQQDLNNK	[13] Phospho (ST)	-0.11	0.00	0.14	-0.11	0.299	0.486	0.048	0.28	6.30E+04	5.44E+04	5.72E+04	6.57E+04	5.43E+04	4.20E+04	5.96E+04	5.73E+04	5.80E+04	6.44E+04	6.22E+04	6.64E+04	852.62497	4	15.16
BDP1	YNL039W	EIEEDNSDNDKGVDENETAIVEK	[7] Phospho (ST)	-0.39	-0.32	-0.11	-0.07	0.067	0.093	0.329	0.35	8.88E+04	6.14E+04	8.19E+04	6.94E+04	5.53E+04	5.25E+04	5.26E+04	6.36E+04	6.97E+04	8.71E+04	5.61E+04	7.14E+04	891.37541	3	25.3
VHS2	YIL135C	RYSNTTINNANGGTSAGSTTGAALSR	[2] Phospho (Y)	-0.06	-0.46	0.01	0.40	0.372	0.053	0.474	0.08	8.91E+04	6.97E+04	7.37E+04	7.64E+04	6.31E+04	8.40E+04	7.08E+04	4.27E+04	5.61E+04	7.57E+04	7.12E+04	8.72E+04	874.73374	3	80.65
CHS3	YBR023C	RASTFDLLK	[3] Phospho (ST)	0.05	0.46	0.59	-0.41	0.451	0.180	0.074	0.13	1.21E+04	3.26E+04	2.33E+04	2.26E+04	2.52E+04	2.24E+04	4.25E+04	2.43E+04	2.67E+04	3.57E+04	3.73E+04	2.94E+04	565.78518	2	34.89
EFR3	YMR212C	DANEDLHSLSSR	[8] Phospho (ST)	0.04	-0.07	0.06	0.11	0.331	0.357	0.236	0.29	3.22E+04	2.97E+04	3.33E+04	3.48E+04	2.99E+04	3.30E+04	2.58E+04	2.75E+04	3.74E+04	3.09E+04	3.28E+04	3.57E+04	712.29732	2	39.78
VMA2	YBR127C	ARDDADEDEEDPDTRSSGK	[17] Phospho (ST)	1.47	0.45	0.54	1.02	0.007	0.113	0.055	0.02	4.19E+04	6.15E+04	6.37E+04	1.42E+05	1.25E+05	1.98E+05	9.71E+04	5.33E+04	7.87E+04	1.00E+05	6.70E+04	7.48E+04	1094.4193	2	48.67
SYP1	YCR030C	DSQLYDSLPNHGSGATPTSSSLSSIPQERPVSTLSSQITGELR	[32] Phospho (ST)	-0.20	0.06	-0.52	-0.26	0.313	0.442	0.165	0.10	1.42E+05	2.42E+05	1.12E+05	1.31E+05	1.61E+05	1.39E+05	1.86E+05	1.89E+05	1.40E+05	7.32E+04	1.48E+05	1.24E+05	1145.7999	4	21.44
NTH1	YDR001C	TMSVFDNVSPFK	[3] Phospho (ST)	0.32	0.91	1.04	-0.59	0.343	0.062	0.099	0.19	2.84E+04	5.81E+04	3.18E+04	3.53E+04	8.92E+04	2.29E+04	8.82E+04	8.98E+04	4.38E+04	6.00E+04	1.31E+05	5.17E+04	726.31835	2	59.43
RCN2	YOR220W	SRSTDDAVSLQDNNLALLEDHR	[1] Phospho (ST)	0.63	0.68	0.37	-0.05	0.025	0.086	0.113	0.44	2.89E+04	4.54E+04	2.69E+04	4.93E+04	5.88E+04	4.87E+04	7.43E+04	4.96E+04	3.80E+04	3.72E+04	4.91E+04	4.42E+04	638.04658	4	32.14
TOM71	YHR117W	RQSEAFAGQNEDEADLKDDGSVVSGSNK	[3] Phospho (ST)	-0.34	-0.37	-0.21	0.04	0.068	0.054	0.221	0.37	8.63E+04	6.06E+04	7.00E+04	5.78E+04	5.19E+04	6.21E+04	5.65E+04	5.08E+04	6.02E+04	5.11E+04	5.71E+04	7.94E+04	1011.7746	3	60.31
IRR1	YIL026C	SQVIEEDYDDEQNTSAQHVESDK	[8] Phospho (Y)	0.06	0.99	0.78	-0.93	0.431	0.030	0.034	0.03	6.07E+04	3.74E+04	4.00E+04	6.23E+04	4.52E+04	3.64E+04	6.97E+04	1.23E+05	8.24E+04	9.62E+04	5.83E+04	8.29E+04	916.0385	3	30.7
GIS4	YML006C	SLSGIDNPTHATNK	[3] Phospho (ST)	-0.06	0.26	-0.09	-0.33	0.334	0.077	0.321	0.05	2.49E+04	3.10E+04	2.97E+04	2.60E+04	2.49E+04	3.10E+04	3.77E+04	2.90E+04	3.60E+04	2.27E+04	2.50E+04	3.25E+04	767.8486	2	55.04
YDJ1	YNL064C	GGANYDSDEEEQGGEGVQCASQ	[5] Phospho (Y)	0.23	-0.14	0.52	0.37	0.131	0.269	0.168	0.09	1.23E+05	9.83E+04	1.09E+05	1.31E+05	1.07E+05	1.50E+05	7.29E+04	1.17E+05	1.10E+05	2.39E+05	9.39E+04	1.40E+05	1183.9223	2	44.44
INP52	YNL106C	RKSSTAPDEISTSTK	[4] Phospho (ST)|[5] Phospho (ST)	-0.26	-0.37	-0.12	0.11	0.114	0.145	0.356	0.38	2.42E+04	1.81E+04	2.01E+04	2.04E+04	1.50E+04	1.68E+04	1.02E+04	2.20E+04	1.62E+04	2.66E+04	1.61E+04	1.49E+04	589.92376	3	25.44
YSP2	YDR326C	SFSPSNLGNK	[3] Phospho (ST)	-0.36	-0.42	-0.16	0.06	0.069	0.044	0.272	0.38	2.78E+04	3.21E+04	3.86E+04	2.94E+04	2.14E+04	2.60E+04	2.07E+04	2.66E+04	2.63E+04	3.75E+04	2.70E+04	2.36E+04	565.74842	2	24.01
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALR	[N-term] Acetyl (Protein N-term)|[6] Phospho	0.13	0.28	-0.09	-0.15	0.434	0.275	0.449	0.41	4.08E+04	6.62E+04	1.18E+05	4.99E+04	1.51E+05	4.58E+04	7.64E+04	1.08E+05	8.79E+04	4.78E+04	1.14E+05	4.97E+04	746.5497	4	39.38
DRS1	YLL008W	GGKDDEIDEEDDSEEAK	[13] Phospho (ST)	1.94	0.90	0.65	1.04	0.001	0.006	0.038	0.00	2.14E+04	1.71E+04	2.35E+04	9.21E+04	7.91E+04	6.65E+04	3.11E+04	4.33E+04	4.11E+04	4.14E+04	2.61E+04	3.00E+04	980.86331	2	84.71
NRD1	YNL251C	SRSPPAPFSQPSTGR	[3] Phospho (ST)	0.98	0.57	-0.29	0.41	0.010	0.040	0.204	0.05	1.79E+04	3.09E+04	3.32E+04	5.56E+04	4.41E+04	6.18E+04	3.59E+04	4.62E+04	3.95E+04	2.07E+04	1.87E+04	2.75E+04	551.25884	3	32.98
GDE1	YPL110C	STSPNANANDNTEFFK	[3] Phospho (ST)	0.31	0.94	0.72	-0.63	0.020	0.008	0.002	0.02	5.67E+04	5.24E+04	6.06E+04	6.57E+04	7.79E+04	6.71E+04	8.97E+04	1.33E+05	1.03E+05	8.75E+04	1.05E+05	8.65E+04	918.87612	2	59.11
PBP2	YBR233W	DADSHSDNDHDSPDNVPSDVHLR	[6] Phospho (ST)	0.13	-0.01	0.09	0.14	0.269	0.486	0.383	0.33	7.06E+04	7.23E+04	8.25E+04	7.28E+04	7.18E+04	1.02E+05	9.95E+04	6.24E+04	6.21E+04	7.51E+04	5.71E+04	1.08E+05	875.3502	3	20.95
NPL6	YMR091C	HVDEEEDLSEDK	[9] Phospho (ST)	0.19	0.19	0.39	-0.01	0.147	0.162	0.041	0.48	2.51E+04	1.84E+04	2.52E+04	2.37E+04	2.60E+04	2.85E+04	2.60E+04	2.30E+04	2.95E+04	3.33E+04	2.59E+04	3.11E+04	762.79094	2	66

LEM3	YNL323W	GAIVSGDNPEEEEDVDASEFEEDEVKPVR	[18] Phospho (ST)	-0.40	0.03	-0.15	-0.43	0.167	0.461	0.325	0.08	6.40E+04	9.56E+04	5.27E+04	4.63E+04	7.11E+04	4.37E+04	8.43E+04	6.81E+04	6.43E+04	4.99E+04	7.41E+04	6.68E+04	818.35302	4	34.49
NOT3	YIL038C	TPTTAAATTTSSNANSR	[16] Phospho (ST)	-0.35	-0.63	-0.58	0.28	0.120	0.039	0.062	0.14	7.57E+04	5.29E+04	5.16E+04	4.75E+04	3.81E+04	5.59E+04	3.05E+04	4.56E+04	4.05E+04	5.01E+04	2.78E+04	4.29E+04	866.38141	2	48.26
SPB1	YCL054W	DYIEDNDDEGVEGDSDDDEAITNLISK	[15] Phospho (ST)	0.09	0.34	0.13	-0.25	0.423	0.247	0.352	0.30	1.88E+05	2.85E+05	1.29E+05	1.70E+05	3.09E+05	1.64E+05	1.59E+05	3.52E+05	2.54E+05	2.26E+05	2.25E+05	2.08E+05	1022.743	3	77.58
SHS1	YDL225W	KNDTYTDLASIASGRD	[10] Phospho (ST)|[13] Phospho (ST)	-0.95	-0.56	-0.50	-0.38	0.009	0.077	0.016	0.24	1.02E+05	9.61E+04	8.35E+04	3.29E+04	6.79E+04	4.54E+04	4.60E+04	9.63E+04	4.82E+04	7.30E+04	7.32E+04	5.36E+04	943.88268	2	39.32
TAF12	YDR145W	KISSSNSTEIPSVTGPDALK	[5] Phospho (ST)	-0.57	-0.40	-0.44	-0.18	0.026	0.068	0.064	0.11	5.68E+04	7.78E+04	5.47E+04	4.48E+04	3.98E+04	4.26E+04	5.44E+04	4.69E+04	4.24E+04	4.19E+04	5.55E+04	4.26E+04	704.34743	3	15.89
SOK2	YMR016C	SQVDGAGDVSNEEIAADDTK	[10] Phospho (ST)	0.18	1.10	0.76	-0.92	0.119	0.000	0.003	0.00	4.19E+04	4.64E+04	5.50E+04	5.96E+04	5.13E+04	5.18E+04	1.04E+05	1.03E+05	1.01E+05	8.74E+04	7.13E+04	8.35E+04	1050.9349	2	88.49
DEF1	YKL054C	NNYNYYQTQNGQEQQSPNQGVAQHSEDSQQK	[6] Phospho (Y)	-0.50	-0.89	-0.26	0.39	0.118	0.051	0.268	0.08	2.79E+05	1.48E+05	1.70E+05	1.59E+05	1.21E+05	1.41E+05	7.77E+04	1.33E+05	1.10E+05	1.91E+05	1.12E+05	1.95E+05	923.8874	4	17.46
MRL1	YPR079W	LRSSPSASSSSLANR	[4] Phospho (ST)	-0.15	-0.12	-0.35	-0.03	0.316	0.362	0.162	0.46	1.03E+04	1.19E+04	1.72E+04	1.26E+04	8.91E+03	1.39E+04	1.21E+04	8.97E+03	1.52E+04	1.00E+04	7.98E+03	1.29E+04	533.92128	3	15.85
ENT5	YDR153C	IDDLLDWDGPKSDTDTTAAAQTSLPFAEK	[17] Phospho (ST)	-0.65	-0.06	-0.22	-0.59	0.116	0.447	0.325	0.03	2.21E+05	3.36E+05	1.37E+05	1.42E+05	1.75E+05	1.26E+05	2.61E+05	2.24E+05	1.82E+05	1.66E+05	2.62E+05	1.70E+05	1067.8199	3	63.3
SKG1	YKR100C	DALEDVFATPK	[9] Phospho (ST)	0.07	0.61	0.25	-0.53	0.443	0.140	0.325	0.14	2.41E+04	5.89E+04	3.20E+04	3.04E+04	5.56E+04	3.51E+04	8.26E+04	4.88E+04	4.40E+04	2.74E+04	6.38E+04	4.57E+04	643.29015	2	31.75
RLM1	YPL089C	LLSPTALISK	[3] Phospho (ST)	-0.11	0.11	0.00	-0.22	0.412	0.418	0.499	0.32	2.50E+04	4.86E+04	2.27E+04	2.40E+04	4.04E+04	2.49E+04	5.05E+04	2.45E+04	2.90E+04	2.07E+04	4.20E+04	3.35E+04	561.81281	2	54.66
RGA1	YOR127W	TFSRPASLVNEIPSGSEPSK	[3] Phospho (ST)|[7] Phospho (ST)	-0.14	0.43	0.17	-0.57	0.344	0.191	0.275	0.14	5.44E+04	8.14E+04	5.29E+04	4.88E+04	7.70E+04	4.51E+04	6.62E+04	1.24E+05	6.29E+04	7.53E+04	8.12E+04	5.58E+04	755.00727	3	23.6
APL5	YPL195W	DNLSDTEEVIVIK	[4] Phospho (ST)	-0.02	0.20	0.04	-0.23	0.470	0.223	0.435	0.21	1.04E+05	1.36E+05	8.61E+04	9.57E+04	1.38E+05	8.66E+04	1.19E+05	1.50E+05	1.06E+05	1.09E+05	1.21E+05	1.03E+05	777.86948	2	67.74
KIN1	YDR122W	AVSDFVPGFAK	[3] Phospho (ST)	0.00	0.33	-0.13	-0.33	0.499	0.171	0.401	0.12	3.04E+04	6.06E+04	3.32E+04	3.02E+04	5.54E+04	3.88E+04	5.67E+04	5.21E+04	4.77E+04	2.60E+04	5.50E+04	3.27E+04	609.28453	2	58.4
CPR1	YDR155C	KVESLGSPSGATK	[7] Phospho (ST)	0.23	0.35	0.46	-0.11	0.050	0.098	0.038	0.30	1.77E+04	1.97E+04	2.22E+04	2.43E+04	2.14E+04	2.44E+04	2.92E+04	1.89E+04	2.78E+04	2.66E+04	2.28E+04	3.27E+04	670.82654	2	48.05
CDC34	YDR054C	AEDESEDVEDVER	[5] Phospho (ST)	0.08	0.44	0.30	-0.36	0.327	0.033	0.102	0.01	2.99E+04	2.38E+04	3.54E+04	3.26E+04	3.12E+04	3.02E+04	3.52E+04	4.32E+04	4.20E+04	4.27E+04	3.34E+04	3.36E+04	801.29701	2	60.9
STV1	YMR054W	NQSVEDLSFLEQGYQHR	[3] Phospho (ST)	-0.50	-0.17	-0.32	-0.33	0.034	0.243	0.092	0.05	1.61E+05	2.21E+05	1.58E+05	1.31E+05	1.33E+05	1.19E+05	1.63E+05	1.85E+05	1.33E+05	1.30E+05	1.59E+05	1.44E+05	1065.4672	2	88.59
STE12	YHR084W	SDNSPPKLESENFK	[4] Phospho (ST)	0.20	0.12	-0.09	0.08	0.129	0.283	0.298	0.30	1.71E+04	2.40E+04	2.36E+04	2.62E+04	2.51E+04	2.30E+04	2.47E+04	2.63E+04	1.95E+04	1.94E+04	2.04E+04	2.09E+04	557.91387	3	29.54
UTP14	YML093W	TAQSNGNDDEDASPQLK	[13] Phospho (ST)	-0.35	-0.44	0.07	0.09	0.193	0.147	0.429	0.36	8.13E+04	3.86E+04	7.52E+04	6.26E+04	4.48E+04	4.53E+04	4.08E+04	4.60E+04	5.72E+04	7.98E+04	4.96E+04	7.51E+04	935.37875	2	35.03
SSD1	YDR293C	TSSQSSIYGHSR	[3] Phospho (ST)	0.27	0.12	0.17	0.14	0.289	0.423	0.387	0.37	7.65E+03	2.60E+04	2.68E+04	2.95E+04	2.17E+04	2.17E+04	1.35E+04	3.34E+04	1.90E+04	3.29E+04	1.68E+04	1.84E+04	695.29345	2	32.7
BLM10	YFL007W	ARSATPTLQDQK	[3] Phospho (ST)|[7] Phospho (ST)	0.10	-0.73	0.03	0.83	0.381	0.063	0.475	0.01	2.18E+04	2.00E+04	3.64E+04	3.42E+04	2.52E+04	2.47E+04	1.32E+04	1.60E+04	1.80E+04	3.88E+04	1.97E+04	2.13E+04	738.31738	2	19.38
TAF7	YMR227C	IPGEAYDSEASDIEDDPLIESGVILR	[6] Phospho (Y)|[8] Phospho (ST)	-0.45	-0.33	-0.63	-0.12	0.174	0.264	0.110	0.40	2.42E+05	2.89E+05	1.31E+05	1.57E+05	2.16E+05	1.11E+05	1.33E+05	2.66E+05	1.27E+05	1.53E+05	1.81E+05	9.44E+04	988.43749	3	42.84
SPC110	YDR356W	SIDDTIDSTR	[1] Phospho (ST)	-0.33	-0.85	-0.67	0.52	0.109	0.020	0.021	0.04	4.16E+04	2.89E+04	4.43E+04	2.86E+04	2.73E+04	3.54E+04	1.52E+04	2.40E+04	2.47E+04	2.57E+04	2.40E+04	2.23E+04	601.75112	2	53.78
IES1	YFL013C	NDLNLTPLKK	[6] Phospho (ST)	-0.40	0.00	0.11	-0.40	0.043	0.498	0.322	0.18	1.57E+04	2.01E+04	1.82E+04	1.09E+04	1.43E+04	1.57E+04	2.55E+04	1.15E+04	1.69E+04	1.44E+04	2.16E+04	2.21E+04	618.32362	2	30.62
YPR137C-B	R137C-B	AVSPTDSTPPSTHTEDSK	[5] Phospho (ST)|[7] Phospho (ST)	-0.10	-0.13	0.29	0.03	0.385	0.358	0.238	0.44	9.78E+04	5.81E+04	1.23E+05	1.02E+05	7.84E+04	7.96E+04	6.79E+04	8.55E+04	1.01E+05	1.44E+05	8.27E+04	1.13E+05	672.9327	3	19.62
RSN1	YMR266W	YKEEESRSAV	[6] Phospho (ST)|[8] Phospho (ST)	-0.70	-1.15	-0.65	0.45	0.128	0.066	0.151	0.22	3.48E+04	1.41E+04	2.16E+04	1.94E+04	1.54E+04	8.54E+03	5.78E+03	1.64E+04	9.51E+03	2.28E+04	1.17E+04	1.03E+04	679.2571	2	15.15
YAP1802	YGR241C	TGSNNPFSLENIAR	[3] Phospho (ST)	-0.27	0.08	-0.20	-0.35	0.217	0.409	0.280	0.18	6.49E+04	7.31E+04	4.23E+04	4.54E+04	6.41E+04	4.04E+04	5.99E+04	8.36E+04	4.71E+04	4.87E+04	6.76E+04	4.10E+04	800.36296	2	56.22
ASK10	YGR097W	RGNNSAQNLTTSSSTASR	[5] Phospho (ST)	0.01	-0.54	0.17	0.55	0.483	0.034	0.344	0.02	5.62E+04	3.87E+04	5.06E+04	4.36E+04	4.53E+04	5.76E+04	2.91E+04	3.14E+04	3.97E+04	7.84E+04	3.29E+04	5.26E+04	966.43252	2	47.18
YMR178W	YMR178W	IYNLDK	[2] Phospho (Y)	-0.84	-0.99	-0.34	0.15	0.114	0.105	0.286	0.38	4.44E+04	2.26E+04	1.69E+04	1.84E+04	1.13E+04	1.73E+04	1.76E+04	6.24E+03	1.86E+04	1.65E+04	1.80E+04	3.17E+04	423.19483	2	20.52
PIG2	YIL045W	SVHFDR	[1] Phospho (ST)	-0.87	-1.26	-0.63	0.40	0.056	0.032	0.134	0.28	1.46E+04	1.20E+04	7.88E+03	9.55E+03	4.20E+03	5.16E+03	3.46E+03	2.60E+03	8.27E+03	4.64E+03	5.35E+03	1.24E+04	420.67359	2	19.33
VID27	YNL212W	TPSPLK	[3] Phospho (ST)	0.77	0.08	0.01	0.69	0.041	0.411	0.493	0.03	1.34E+04	9.68E+03	2.01E+04	2.20E+04	2.09E+04	3.07E+04	1.58E+04	1.26E+04	1.73E+04	1.59E+04	1.32E+04	1.43E+04	361.67798	2	19.19
CAF20	YOR276W	KKGSGEDDEEETETTPTSTVPVATIAQETLK	[12] Phospho (ST)|[14] Phospho (ST)	0.46	0.55	0.04	-0.09	0.160	0.044	0.427	0.40	8.13E+04	1.04E+05	6.34E+04	9.59E+04	1.63E+05	8.34E+04	1.18E+05	1.44E+05	1.02E+05	8.79E+04	9.34E+04	7.54E+04	863.63875	4	28.4
EIS1	YMR031C	ISIGNK	[2] Phospho (ST)	0.93	-1.41	0.18	2.34	0.122	0.069	0.381	0.03	9.95E+03	4.22E+03	4.02E+03	1.85E+04	7.23E+03	8.93E+03	3.48E+03	2.07E+03	1.27E+03	9.76E+03	4.79E+03	6.03E+03	356.17562	2	18.32
INP53	YOR109W	EKSPTPQTSTASLSSVTK	[8] Phospho (ST)	-0.24	0.52	-0.02	-0.76	0.204	0.090	0.473	0.03	1.47E+04	2.62E+04	2.08E+04	1.85E+04	1.55E+04	1.81E+04	3.79E+04	2.37E+04	2.66E+04	2.02E+04	2.06E+04	2.01E+04	643.64571	3	49.22
GIN4	YDR507C	RASIFSTTK	[3] Phospho (ST)	0.32	0.04	-0.41	0.28	0.266	0.458	0.070	0.31	1.59E+04	2.04E+04	2.23E+04	1.73E+04	1.79E+04	3.77E+04	2.66E+04	1.30E+04	2.05E+04	1.26E+04	1.31E+04	1.83E+04	545.76843	2	32.39
EDE1	YBL047C	RANSNEDGESVSSIQESPK	[10] Phospho (ST)|[12] Phospho (ST)	-0.42	-0.79	-0.30	0.37	0.075	0.027	0.154	0.07	1.05E+05	6.71E+04	1.01E+05	7.63E+04	6.67E+04	6.22E+04	3.82E+04	6.19E+04	5.83E+04	8.32E+04	5.80E+04	8.15E+04	1097.4395	2	28.47
UIP4	YPL186C	GNVTFPSPK	[7] Phospho (ST)	0.86	1.12	0.67	-0.26	0.003	0.008	0.009	0.14	1.19E+04	1.69E+04	1.81E+04	2.54E+04	3.00E+04	2.97E+04	3.87E+04	2.58E+04	3.76E+04	2.27E+04	2.79E+04	2.42E+04	513.73662	2	20.19
SIW14	YNL032W	EFDEDEDDGYDSNEHHQK	[10] Phospho (Y)	0.09	0.23	0.21	-0.14	0.351	0.039	0.047	0.27	2.61E+04	2.63E+04	2.85E+04	3.64E+04	2.31E+04	2.65E+04	2.81E+04	3.40E+04	3.28E+04	3.36E+04	2.78E+04	3.19E+04	763.60101	3	18.71
GRR1	YJR090C	IDNSPQAISYLHK	[4] Phospho (ST)	0.65	0.39	-0.15	0.26	0.013	0.044	0.275	0.03	9.19E+03	1.42E+04	1.44E+04	1.78E+04	2.17E+04	1.98E+04	1.70E+04	1.58E+04	1.69E+04	9.44E+03	1.23E+04	1.22E+04	522.58373	3	26.08
UTP14	YML093W	DVNPWLANESDEEHTVK	[10] Phospho (ST)	-0.18	-0.16	0.02	-0.03	0.258	0.238	0.457	0.46	6.20E+04	8.62E+04	6.47E+04	6.05E+04	7.91E+04	4.80E+04	6.18E+04	7.35E+04	5.58E+04	5.81E+04	8.21E+04	7.64E+04	1031.942	2	25.61
HMG1	YML075C	SLSSAQSSSSGPSSSSEEDDSRDIESLDK	[15] Phospho (ST)|[16] Phospho (ST)	-1.33	-0.63	-0.65	-0.70	0.021	0.108	0.036	0.20	1.73E+05	1.41E+05	1.12E+05	1.43E+04	9.47E+04	5.97E+04	5.48E+04	1.49E+05	7.10E+04	1.13E+05	8.00E+04	7.84E+04	1045.413	3	35.69
BUD27	YFL023W	ILENISDDDYDDDDDGNKK	[6] Phospho (ST)	0.49	-0.06	0.27	0.55	0.000	0.260	0.049	0.00	8.77E+04	7.90E+04	7.81E+04	1.16E+05	1.16E+05	1.12E+05	7.42E+04	8.54E+04	7.52E+04	1.12E+05	9.82E+04	8.63E+04	1139.9477	2	85.79
SEC16	YPL085W	LPWEVSDGEVSSGK	[6] Phospho (ST)	-0.47	-0.12	-0.05	-0.35	0.096	0.339	0.430	0.09	5.42E+04	8.80E+04	6.05E+04	4.34E+04	6.08E+04	4.26E+04	5.20E+04	7.19E+04	6.30E+04	5.15E+04	7.60E+04	6.82E+04	785.34601	2	49.08
STB3	YDR169C	SQVVFADSTPENIEHEIIAQK	[1] Phospho (ST)	-0.33	-0.26	-0.49	-0.07	0.157	0.159	0.094	0.41	7.01E+04	8.38E+04	5.67E+04	4.61E+04	7.50E+04	4.69E+04	5.71E+04	7.03E+04	4.89E+04	3.64E+04	6.97E+04	4.35E+04	812.3886	3	29.04
NUP2	YLR335W	YELYIK	[1] Phospho (Y)	0.35	0.61	0.42	-0.26	0.142	0.103	0.087	0.24	1.22E+04	1.08E+04	1.91E+04	1.66E+04	1.56E+04	2.15E+04	1.53E+04	1.96E+04	2.94E+04	2.10E+04	1.62E+04	1.93E+04	454.71002	2	16.19
NSR1	YGR159C	NTASFAGSK	[4] Phospho (ST)	-4.73	-4.34	-1.09	-0.39	0.027	0.028	0.121	0.05	5.46E+04	1.24E+04	3.59E+04	1.42E+03	1.15E+03	1.28E+03	1.37E+03	1.69E+03	1.99E+03	2.63E+04	1.16E+04	1.05E+04	481.70242	2	19.16
YDR348C	YDR348C	NPFLDDVSSATDFRR	[9] Phospho (ST)	-0.26	0.11	-0.35	-0.37	0.234	0.342	0.213	0.07	2.89E+04	4.94E+04	3.34E+04	2.38E+04	3.95E+04	2.99E+04	4.31E+04	3.71E+04	4.01E+04	1.61E+04	3.88E+04	3.25E+04	607.27272	3	33.62
YDR089W	YDR089W	SFNDLQHTLSLSK	[1] Phospho (ST)	-0.30	0.05	-0.23	-0.35	0.193	0.422	0.259	0.08	5.56E+04	7.54E+04	4.36E+04	3.93E+04	5.95E+04	4.32E+04	6.78E+04	6.01E+04	5.31E+04	3.83E+04	6.40E+04	4.68E+04	785.36941	2	47.79
CHS2	YBR038W	DNADLPVDPYHLSPQQQPSNNLFGSGR	[10] Phospho (Y)	0.57	2.36	1.67	-1.78	0.045	0.001	0.001	0.00	5.48E+04	4.17E+04	2.70E+04	5.29E+04	6.60E+04	6.51E+04	1.78E+05	2.50E+05	2.04E+05	1.17E+05	1.52E+05	1.24E+05	1016.1287	3	65.68
NOP12	YOL041C	EASKPDVSDEQTEEVALPK	[8] Phospho (ST)	0.89	-0.05	0.23	0.95	0.018	0.365	0.149	0.02	6.03E+04	6.49E+04	5.51E+04	1.05E+05	8.70E+04	1.43E+05	5.39E+04	5.16E+04	6.83E+04	8.07E+04	5.43E+04	7.65E+04	1076.4873	2	51.4
ZRC1	YMR243C	RFSIIAGGSPSSSQEAFDSHGNTEHGR	[3] Phospho (ST)	1.10	0.16	0.65	0.94	0.004	0.409	0.061	0.04	2.88E+04	4.20E+04	5.32E+04	9.15E+04	7.60E+04	9.86E+04	8.10E+04	2.25E+04	3.47E+04	5.86E+04	5.19E+04	8.40E+04	728.57455	4	66.58
UTP14	YML093W	MLDRNSDDEEDGRVQTLSDVENEEK	[6] Phospho (ST)|[16] Phospho (ST)	-1.28	-0.69	-0.12	-0.59	0.031	0.102	0.379	0.16	2.23E+05	1.23E+05	1.29E+05	5.10E+04	9.81E+04	4.64E+04	9.50E+04	1.40E+05	5.94E+04	1.16E+05	1.80E+05	1.43E+05	1028.4135	3	25.25
DCS2	YOR173W	HDGIATSPEK	[7] Phospho (ST)	1.49	0.00	0.45	1.49	0.010	0.500	0.147	0.03	1.73E+04	6.70E+03	8.60E+03	2.61E+04	2.67E+04	3.90E+04	2.32E+04	4.18E+03	5.26E+03	1.42E+04	1.50E+04	1.54E+04	567.74475	2	27.28
MSN2	YMR037C	NSISHSLDLWNHPK	[2] Phospho (ST)	-0.16	-0.03	-0.36	-0.13	0.301	0.464	0.203	0.23	3.47E+04	6.14E+04	4.16E+04	3.77E+04	4.66E+04	3.90E+04	5.08E+04	4.67E+04	3.75E+04	2.13E+04	4.16E+04	4.45E+04	576.6019	3	32.65
BUD6	YLR319C	RLSSVVTTSPDK	[3] Phospho (ST)|[8] Phospho (ST)	0.45	0.70	0.39	-0.25	0.024	0.007	0.013	0.09	3.21E+04	2.72E+04	3.62E+04	4.53E+04	3.72E+04	4.79E+04	4.38E+04	5.60E+04	5.50E+04	4.38E+04	4.17E+04	3.98E+04	725.3194	2	22.6
PMD1	YER132C	FSQAPSTQISPR	[10] Phospho (ST)	-0.03	0.02	0.38	-0.05	0.461	0.435	0.042	0.44	2.77E+04	3.33E+04	3.19E+04	2.33E+04	2.50E+04	4.26E+04	3.39E+04	3.20E+04	2.83E+04	4.64E+04	3.35E+04	4.10E+04	699.82494	2	19.67
VTS1	YOR359W	SAEPHVNSSPNLIPVQK	[8] Phospho (ST)	-0.67	-0.47	-0.37	-0.20	0.017	0.035	0.065	0.07	4.03E+04	5.91E+04	4.83E+04	3.32E+04	3.28E+04	2.65E+04	3.78E+04	3.50E+04	3.36E+04	3.39E+04	4.02E+04	4.01E+04	632.97939	3	21.55
YDR333C	YDR333C	DKGSDDDDDDEEFDK	[4] Phospho (ST)	0.52	0.34	0.38	0.18	0.108	0.219	0.139	0.32	2.28E+04	1.35E+04	2.64E+04	3.89E+04	2.83E+04	2.25E+04	1.64E+04	3.36E+04	2.93E+04	3.34E+04	2.56E+04	2.26E+04	608.8708	3	18.91
PAN1	YIR006C	NEEQSSFSSPSAK	[9] Phospho (ST)	0.31	0.45	0.41	-0.14	0.170	0.110	0.145	0.23	3.22E+04	1.56E+04	3.31E+04	3.67E+04	3.04E+04	3.32E+04	3.19E+04	3.43E+04	4.45E+04	4.44E+04	2.91E+04	3.39E+04	739.29612	2	40.79
MCM1	YMR043W	SDIEEGTPTNNGQQK	[1] Phospho (ST)	-0.54	-0.72	-0.33	0.18	0.178	0.138	0.276	0.29	5.83E+04	1.84E+04	4.61E+04	3.36E+04	2.30E+04	2.81E+04	1.78E+04	2.28E+04	3.39E+04	4.06E+04	2.33E+04	3.39E+04	849.35503	2	55.49
CHO1	YER026C	RASSIFSINTTPLAPPNATDIQK	[3] Phospho (ST)|[4] Phospho (ST)	-0.26	-0.06	-0.32	-0.20	0.171	0.412	0.161	0.23	1.19E+05	1.09E+05	7.72E+04	9.41E+04	9.39E+04	6.56E+04	9.83E+04	1.18E+05	7.57E+04	8.23E+04	1.03E+05	5.95E+04	868.08302	3	21.62
SSD1	YDR293C	RHSLGLNEAK	[3] Phospho (ST)	0.05	-0.51	-0.28	0.55	0.341	0.117	0.205	0.10	3.81E+04	4.02E+04	4.24E+04	3.75E+04	4.05E+04	4.68E+04	4.32E+04	1.41E+04	2.77E+04	2.12E+04	3.08E+04	4.74E+04	602.79522	2	24.47
PLP2	YOR281C	DLSDLEELEDDEDEDFLEAYK	[3] Phospho (ST)	-0.11	0.52	-0.09	-0.62	0.423	0.193	0.438	0.11	1.31E+05	2.53E+05	8.91E+04	1.38E+05	1.87E+05	1.15E+05	2.25E+05	3.13E+05	1.39E+05	1.18E+05	2.13E+05	1.12E+05	871.35102	3	68.61
KRE6	YPR159W	NDILSPPEFDRYPLVGSR	[12] Phospho (Y)	-0.53	-0.13	0.17	-0.40	0.040	0.304	0.313	0.06	1.17E+05	1.51E+05	1.02E+05	9.53E+04	8.98E+04	7.16E+04	1.19E+05	1.30E+05	9.04E+04	1.40E+05	1.84E+05	9.35E+04	719.01247	3	36.8
CMS1	YLR003C	EERNSEDDSNRPISK	[5] Phospho (ST)	1.98	0.35	0.60	1.63	0.033	0.395	0.126	0.07	2.88E+04	2.00E+04	1.37E+04	1.18E+05	3.64E+04	9.31E+04	6.59E+04	9.71E+03	4.11E+03	4.48E+04	2.41E+04	2.57E+04	619.26421	3	18.62
FAR11	YNL127W	SVSLEDLK	[3] Phospho (ST)	-0.45	0.19	-0.06	-0.64	0.102	0.263	0.424	0.01	1.25E+04	2.30E+04	2.16E+04	1.25E+04	1.39E+04	1.53E+04	1.93E+04	2.56E+04	2.01E+04	1.65E+04	2.26E+04	1.55E+04	485.72848	2	39.8
PRT1	YOR361C	LEDIPVDDIDFSDLEEQYK	[12] Phospho (ST)	0.29	0.11	-0.24	0.17	0.238	0.374	0.298	0.26	1.74E+05	2.66E+05	1.25E+05	2.04E+05	2.95E+05	1.91E+05	2.08E+05	2.29E+05	1.74E+05	1.61E+05	2.06E+05	1.13E+05	1182.0131	2	68.62
GIN4	YDR507C	RQSISSVSVSPSK	[3] Phospho (ST)|[10] Phospho (ST)	-0.12	-0.24	0.04	0.13	0.316	0.219	0.433	0.34	8.74E+04	5.86E+04	7.19E+04	8.10E+04	5.88E+04	6.13E+04	7.81E+04	6.26E+04	4.36E+04	7.24E+04	6.00E+04	9.24E+04	761.33984	2	17.01
CAB3	YKL088W	RFSPSLPSAVSFTVPEVER	[5] Phospho (ST)	-0.30	0.03	-0.28	-0.34	0.317	0.478	0.353	0.26	3.75E+04	8.94E+04	3.51E+04	3.26E+04	6.10E+04	3.79E+04	8.34E+04	3.79E+04	4.46E+04	2.09E+04	7.39E+04	3.85E+04	729.0286	3	40.03
STE2	YFL026W	FYPGTLSSFQTDSINNDAK	[13] Phospho (ST)	0.13	-0.03	-0.21	0.16	0.295	0.405	0.190	0.24	6.08E+04	7.59E+04	6.35E+04	6.03E+04	9.16E+04	6.69E+04	6.05E+04	7.12E+04	6.43E+04	4.62E+04	7.25E+04	5.49E+04	728.98822	3	45.4
VPS13	YLL040C	LAVLDPSILGER	[7] Phospho (ST)	-0.06	0.41	0.23	-0.47	0.453	0.167	0.327	0.11	3.49E+04	7.73E+04	4.01E+04	3.53E+04	6.92E+04	4.14E+04	8.17E+04	6.37E+04	5.72E+04	4.39E+04	8.37E+04	5.10E+04	681.85584	2	31.47
UTP22	YGR090W	RKASETSDQNIVK	[4] Phospho (ST)	0.30	-0.16	0.28	0.46	0.190	0.355	0.221	0.04	2.50E+04	1.08E+04	2.34E+04	2.52E+04	2.20E+04	2.57E+04	2.12E+04	1.26E+04	1.92E+04	2.75E+04	2.02E+04	2.41E+04	519.25372	3	21.28
INN1	YNL152W	LDSSSPNSHPHPSGLNSPK	[5] Phospho (ST)	0.48	0.48	0.30	0.01	0.083	0.158	0.235	0.49	1.36E+04	1.89E+04	2.93E+04	2.72E+04	2.74E+04	3.19E+04	3.51E+04	1.81E+04	3.27E+04	2.13E+04	2.17E+04	3.33E+04	679.97225	3	19.82
CHO1	YER026C	VESDEDFAPQEFPHTDTDVIVNEHR	[3] Phospho (ST)	0.09	0.38	-0.09	-0.29	0.370	0.087	0.397	0.11	5.23E+04	8.35E+04	6.38E+04	5.61E+04	7.40E+04	8.23E+04	1.01E+05	7.22E+04	8.77E+04	4.15E+04	7.40E+04	7.25E+04	1002.7636	3	69.92
DEF1	YKL054C	KTESPLENVAELK	[4] Phospho (ST)	-0.02	0.15	-0.30	-0.17	0.457	0.255	0.204	0.13	2.36E+04	3.55E+04	3.55E+04	2.82E+04	3.29E+04	3.19E+04	3.96E+04	3.04E+04	3.49E+04	1.55E+04	3.22E+04	2.90E+04	769.37724	2	40.69
CHS1	YNL192W	NEPSYELQNAHSGLFHSSNEELTNR	[18] Phospho (ST)	-0.11	-0.01	-0.19	-0.09	0.174	0.449	0.109	0.15	1.83E+05	1.65E+05	1.54E+05	1.66E+05	1.41E+05	1.59E+05	1.56E+05	1.72E+05	1.70E+05	1.24E+05	1.60E+05	1.56E+05	985.09353	3	22.57
SSB1	YDL229W	SSNITISNAVGRLSSEEIEK	[15] Phospho (ST)	0.30	-0.62	0.01	0.92	0.121	0.114	0.470	0.05	2.97E+04	2.50E+04	2.36E+04	3.63E+04	2.41E+04	3.60E+04	2.83E+04	1.55E+04	7.08E+03	2.74E+04	2.74E+04	2.40E+04	738.69437	3	31.1
HOG1	YLR113W	IQDPQMTGYVSTR	[9] Phospho (Y)	-0.35	-0.43	0.10	0.08	0.140	0.000	0.131	0.40	4.51E+04	4.48E+04	4.45E+04	3.03E+04	5.02E+04	2.51E+04	3.41E+04	3.36E+04	3.20E+04	4.47E+04	4.65E+04	5.25E+04	788.34835	2	45.85
PEA2	YER149C	NTSSPPISPNAAAIQEEDSSK	[3] Phospho (ST)|[4] Phospho (ST)	-0.50	-0.21	-0.16	-0.28	0.028	0.287	0.204	0.26	7.61E+04	5.74E+04	6.39E+04	5.16E+04	5.10E+04	3.75E+04	4.06E+04	8.40E+04	4.59E+04	5.83E+04	6.80E+04	5.02E+04	768.31944	3	20.03
GYP1	YOR070C	RTSNSYSPLR	[3] Phospho (ST)|[6] Phospho (Y)	0.28	-0.12	-0.24	0.40	0.074	0.364	0.249	0.13	2.52E+04	2.01E+04	2.43E+04	3.29E+04	2.63E+04	2.55E+04	1.25E+04	2.84E+04	2.32E+04	2.86E+04	1.49E+04	1.56E+04	670.77415	2	33.44
HPC2	YBR215W	RLVAAPTVSPPK	[9] Phospho (ST)	-0.24	0.14	-0.05	-0.38	0.166	0.354	0.424	0.16	2.58E+04	3.91E+04	3.50E+04	2.45E+04	2.69E+04	3.29E+04	4.71E+04	2.29E+04	3.98E+04	2.55E+04	3.01E+04	4.06E+04	658.36065	2	21.02
NOP12	YOL041C	EASKPDVSDEQTEEVALPK	[3] Phospho (ST)	1.05	0.60	0.35	0.45	0.002	0.036	0.059	0.03	1.94E+04	2.92E+04	2.68E+04	5.82E+04	5.19E+04	4.66E+04	4.45E+04	2.95E+04	4.06E+04	3.05E+04	2.99E+04	3.58E+04	717.99504	3	21.67
PMD1	YER132C	RSSSFTETVPTEPTR	[3] Phospho (ST)|[4] Phospho (ST)	-0.64	-0.13	-0.09	-0.51	0.001	0.275	0.327	0.05	5.37E+04	4.74E+04	5.22E+04	3.29E+04	3.46E+04	3.11E+04	4.26E+04	5.95E+04	3.79E+04	6.04E+04	4.00E+04	4.33E+04	927.88715	2	31.59
CMP2	YML057W	SEATPQPATSASPK	[12] Phospho (ST)	0.17	0.36	0.05	-0.19	0.145	0.074	0.270	0.22	2.59E+04	2.45E+04	2.33E+04	2.57E+04	2.48E+04	3.25E+04	3.27E+04	2.44E+04	3.73E+04	2.55E+04	2.36E+04	2.72E+04	726.32447	2	35.09

SWI4	YER111C	ITSPSSYNK	[3] Phospho (ST)	-0.22	0.49	0.59	-0.71	0.320	0.112	0.103	0.01	8.49E+03	8.15E+03	1.73E+04	1.15E+04	9.59E+03	8.05E+03	1.37E+04	1.69E+04	1.69E+04	2.16E+04	1.43E+04	1.50E+04	538.73681	2	24.56
UBP1	YDL122W	DNEELQEIDNVSLDEPK	[12] Phospho (ST)	0.31	0.47	0.12	-0.17	0.242	0.063	0.328	0.32	4.62E+04	7.14E+04	4.74E+04	5.70E+04	9.72E+04	4.98E+04	7.49E+04	8.97E+04	6.43E+04	5.72E+04	6.98E+04	5.21E+04	689.6324	3	64.11
BCK1	YJL095W	REAPKPPANTSPQR	[10] Phospho (ST)	0.38	-0.03	-0.09	0.41	0.153	0.464	0.410	0.11	4.10E+04	2.13E+04	2.80E+04	3.58E+04	3.24E+04	4.92E+04	2.76E+04	2.31E+04	3.74E+04	3.53E+04	2.03E+04	2.93E+04	543.60133	3	21.35
HMG1	YML075C	SLSSAQSSSSGPSSSSEEDDSRDIESLDK	[14] Phospho (ST)	-0.68	-0.07	-0.18	-0.61	0.005	0.393	0.136	0.05	1.08E+05	8.93E+04	8.46E+04	5.42E+04	6.06E+04	6.16E+04	7.46E+04	1.18E+05	7.56E+04	9.13E+04	7.59E+04	8.24E+04	1018.757	3	47.96
SEC7	YDR170C	VANPRVSYESSR	[7] Phospho (ST)	-0.29	-0.26	0.26	-0.03	0.088	0.098	0.099	0.45	1.82E+04	2.14E+04	2.00E+04	1.98E+04	1.28E+04	1.59E+04	1.94E+04	1.29E+04	1.73E+04	2.86E+04	2.08E+04	2.20E+04	722.83268	2	25.46
MAP2	YBL091C	ADESDPVESK	[4] Phospho (ST)	0.43	-1.16	-0.31	1.59	0.253	0.142	0.363	0.01	3.12E+04	5.86E+03	1.37E+04	2.89E+04	2.18E+04	1.79E+04	8.05E+03	8.97E+03	5.72E+03	2.25E+04	9.33E+03	9.10E+03	578.72371	2	42.64
SKT5	YBL061C	ASSPQVHPYKK	[N-term] Acetyl (Protein N-term)||[2] Phospho	-0.41	0.06	0.27	-0.47	0.020	0.337	0.139	0.01	1.86E+04	1.49E+04	1.78E+04	1.39E+04	1.12E+04	1.36E+04	1.90E+04	1.57E+04	1.88E+04	2.29E+04	1.55E+04	2.36E+04	682.32384	2	21.56
HPR1	YDR138W	INSASQTEGDELK	[5] Phospho (ST)	2.78	-0.11	-1.04	2.89	0.000	0.332	0.042	0.00	6.93E+03	7.24E+03	1.04E+04	6.08E+04	4.88E+04	6.00E+04	6.85E+03	7.39E+03	8.60E+03	6.87E+03	2.25E+03	2.83E+03	736.31905	2	66.79
PPZ1	YML016C	SLPSSSTTNTNSNVPDPSTPSKPNLEVNHQR	[1] Phospho (ST)	-0.29	-0.58	-0.14	0.29	0.081	0.010	0.241	0.04	1.28E+05	1.01E+05	1.35E+05	1.03E+05	8.43E+04	1.10E+05	7.69E+04	8.50E+04	8.06E+04	1.13E+05	9.10E+04	1.26E+05	1129.1941	3	66.67
RSC3	YDR303C	KLSEDGVTDGDGKPIPESER	[3] Phospho (ST)	-0.09	-0.26	-0.28	0.17	0.248	0.164	0.186	0.24	3.57E+04	4.35E+04	4.65E+04	3.77E+04	3.83E+04	4.18E+04	4.13E+04	2.46E+04	3.91E+04	2.20E+04	3.61E+04	4.51E+04	737.00557	3	47.62
CHS3	YBR023C	DGDVDNFEESSTQPINK	[12] Phospho (ST)	0.07	0.18	0.23	-0.12	0.331	0.222	0.113	0.29	6.53E+04	5.07E+04	6.84E+04	6.06E+04	6.20E+04	7.06E+04	5.47E+04	7.17E+04	8.30E+04	7.90E+04	6.28E+04	7.38E+04	987.90277	2	57.23
NIP1	YMR309C	SSNYDSSDEESDEEDGKK	[4] Phospho (Y)||[7] Phospho (ST)||[11] Phosph	-0.73	-0.68	-1.08	-0.05	0.223	0.279	0.152	0.48	3.00E+05	5.01E+04	1.57E+05	1.05E+05	1.58E+05	4.22E+04	1.84E+04	2.41E+05	5.70E+04	1.20E+05	7.27E+04	4.65E+04	1130.841	2	23.06
RIM15	YFL033C	SQEDEEHTILSDSDETH	[11] Phospho (ST)	-0.29	0.69	1.01	-0.97	0.068	0.032	0.002	0.01	4.57E+04	3.51E+04	4.68E+04	3.77E+04	3.18E+04	3.53E+04	7.21E+04	8.29E+04	5.06E+04	9.61E+04	7.32E+04	8.82E+04	1026.3901	2	73.14
NAB6	YML117W	TSTHRLSVPSVTAGNNNDSNNNGNNNK	[10] Phospho (ST)	-0.39	-0.86	-0.03	0.47	0.130	0.044	0.464	0.10	1.41E+05	8.33E+04	9.49E+04	9.70E+04	6.98E+04	7.58E+04	4.26E+04	8.22E+04	5.04E+04	1.20E+05	7.52E+04	1.17E+05	969.43015	3	55.37
AVT4	YNL101W	RAQSTVLNSNPFYSR	[4] Phospho (ST)	-0.53	-0.39	-0.61	-0.14	0.072	0.115	0.057	0.25	5.07E+04	8.30E+04	5.74E+04	4.04E+04	5.28E+04	3.93E+04	5.55E+04	4.91E+04	4.11E+04	3.84E+04	5.06E+04	3.65E+04	910.42522	2	22.29
ISW2	YOR304W	VTSYDITGDIRNEGSDAEEEEGEYK	[15] Phospho (ST)	-0.38	0.24	-0.05	-0.61	0.022	0.152	0.320	0.02	6.93E+04	7.72E+04	6.15E+04	5.00E+04	5.97E+04	5.04E+04	7.86E+04	9.95E+04	6.71E+04	6.47E+04	6.77E+04	6.85E+04	962.73299	3	38.8
ERB1	YMR049C	KRAASEESDVEEDEDK	[5] Phospho (ST)||[8] Phospho (ST)	-0.30	-0.99	-0.60	0.70	0.235	0.049	0.130	0.01	6.44E+04	2.97E+04	4.12E+04	4.19E+04	3.30E+04	3.53E+04	1.80E+04	2.51E+04	2.49E+04	3.99E+04	1.95E+04	2.97E+04	666.25194	3	32.07
ESF1	YDR365C	EAENDEDSEVNAK	[8] Phospho (ST)	-1.40	0.28	0.77	-1.68	0.181	0.377	0.253	0.01	7.11E+04	2.23E+03	2.66E+04	1.35E+04	1.11E+04	1.32E+04	2.78E+04	5.00E+04	4.35E+04	1.05E+05	4.51E+04	2.03E+04	765.28592	2	35.3
MOB1	YIL106W	SFLQNFHISPGQTIR	[N-term] Acetyl (Protein N-term)||[9] Phospho	0.28	1.69	0.89	-1.41	0.236	0.003	0.037	0.00	2.26E+04	3.47E+04	1.66E+04	2.47E+04	3.79E+04	2.73E+04	9.65E+04	7.37E+04	6.84E+04	3.85E+04	5.96E+04	3.90E+04	622.96897	3	27.67
NUP145	YGL092W	TDGTFGTLSGKDDSIVEEK	[14] Phospho (ST)	-0.22	0.45	-0.10	-0.67	0.247	0.132	0.368	0.06	3.84E+04	5.38E+04	3.10E+04	4.25E+04	3.38E+04	2.95E+04	6.40E+04	6.76E+04	3.72E+04	3.33E+04	4.43E+04	3.75E+04	693.64394	3	23.55
HAL5	YJL165C	NHSDSISASSLPK	[3] Phospho (ST)	0.39	0.29	0.10	0.10	0.007	0.027	0.333	0.17	3.63E+04	4.31E+04	4.30E+04	5.32E+04	4.99E+04	5.68E+04	4.48E+04	5.25E+04	5.23E+04	4.10E+04	3.54E+04	5.46E+04	711.81728	2	68.99
PAB1	YER165W	SQLAQQIQAR	[1] Phospho (ST)	0.51	0.05	-0.08	0.45	0.070	0.447	0.396	0.09	8.72E+03	1.16E+04	1.69E+04	1.74E+04	1.51E+04	2.04E+04	8.24E+03	1.42E+04	1.62E+04	1.06E+04	1.30E+04	1.16E+04	611.80097	2	37.79
KEL1	YHR158C	NNSPILETLPSNEIK	[3] Phospho (ST)	-0.51	-2.24	-0.48	1.73	0.011	0.000	0.000	0.00	8.19E+04	8.64E+04	7.93E+04	6.65E+04	6.18E+04	4.53E+04	1.78E+04	1.30E+04	2.15E+04	6.04E+04	5.95E+04	5.81E+04	874.92825	2	24.33
YPR137C-B	R137C-B	AHNVSTSNNSPSTDNDSISK	[7] Phospho (ST)||[10] Phospho (ST)	0.13	-0.22	-0.27	0.35	0.396	0.356	0.330	0.18	4.62E+04	1.37E+04	3.13E+04	4.09E+04	3.22E+04	2.67E+04	1.51E+04	3.20E+04	3.12E+04	3.61E+04	1.65E+04	2.28E+04	745.62529	3	18.05
SIP5	YMR140W	NTSHSITPIHDESTSASR	[5] Phospho (ST)	0.17	-0.12	0.28	0.29	0.176	0.290	0.087	0.09	3.92E+04	3.20E+04	4.34E+04	4.79E+04	3.77E+04	4.31E+04	3.70E+04	2.75E+04	4.08E+04	4.79E+04	3.94E+04	5.17E+04	673.96438	3	42.19
POL1	YNL102W	LRENLNSSPTSEFK	[7] Phospho (ST)||[8] Phospho (ST)	1.92	2.42	1.77	-0.50	0.000	0.001	0.000	0.02	2.12E+04	1.36E+04	1.57E+04	6.10E+04	6.13E+04	6.97E+04	7.48E+04	1.04E+05	9.31E+04	5.64E+04	5.34E+04	6.22E+04	891.37939	2	30.27
SLA1	YBL007C	SNANASWKDDELQNDVVGSAAGK	[1] Phospho (ST)	-0.33	-0.30	-0.28	-0.03	0.087	0.087	0.096	0.45	5.07E+04	5.99E+04	4.71E+04	4.75E+04	4.67E+04	3.11E+04	3.40E+04	4.95E+04	4.47E+04	3.43E+04	4.85E+04	4.71E+04	819.36217	3	49.81
KSP1	YHR082C	KRSDVSQNQNVASGFFK	[3] Phospho (ST)	0.34	0.08	0.31	0.27	0.060	0.348	0.114	0.07	3.50E+04	4.46E+04	5.03E+04	6.22E+04	4.91E+04	5.34E+04	4.96E+04	4.82E+04	3.91E+04	5.82E+04	4.22E+04	6.10E+04	664.6495	3	46.71
TSL1	YML100W	IASPIQHEHDSGSR	[3] Phospho (ST)	0.34	-1.22	-0.24	1.55	0.010	0.004	0.035	0.00	2.31E+04	2.80E+04	2.44E+04	3.15E+04	3.35E+04	3.02E+04	1.52E+04	6.89E+03	1.03E+04	2.12E+04	2.23E+04	2.04E+04	807.35662	2	33.97
NDC1	YML031W	DNGLLDESPNRLR	[8] Phospho (ST)	-0.22	0.80	0.23	-1.02	0.186	0.005	0.208	0.00	1.86E+04	2.82E+04	2.90E+04	1.92E+04	2.39E+04	2.19E+04	4.07E+04	4.25E+04	4.89E+04	2.26E+04	3.42E+04	3.23E+04	789.86772	2	27.74
BEM3	YPL115C	ALGFSPASK	[5] Phospho (ST)	-0.05	0.19	-0.09	-0.25	0.440	0.304	0.400	0.15	9.50E+03	2.11E+04	1.86E+04	1.52E+04	1.49E+04	1.73E+04	2.21E+04	1.42E+04	1.99E+04	1.30E+04	1.73E+04	1.58E+04	479.22588	2	15.36
ERB1	YMR049C	KRAASEESDVEEDEDK	[5] Phospho (ST)||[8] Phospho (ST)	-0.31	-0.97	-0.69	0.65	0.254	0.074	0.126	0.03	1.08E+05	4.46E+04	6.35E+04	6.84E+04	5.30E+04	5.22E+04	2.49E+04	4.36E+04	4.18E+04	5.71E+04	2.92E+04	4.77E+04	998.87509	2	20.14
ACC1	YNR016C	AVSVSDLSYVANSQSSPLR	[3] Phospho (ST)	-0.11	0.08	-0.16	-0.19	0.389	0.391	0.340	0.26	3.65E+04	4.49E+04	6.59E+04	3.55E+04	6.08E+04	4.05E+04	4.39E+04	5.93E+04	5.29E+04	3.66E+04	5.86E+04	3.69E+04	687.32873	3	64.26
GPH1	YPR160W	RLTGFLPQEIK	[3] Phospho (ST)	1.19	1.74	0.71	-0.54	0.040	0.029	0.190	0.15	4.41E+03	1.64E+04	6.73E+03	1.61E+04	2.79E+04	1.91E+04	4.44E+04	1.94E+04	2.83E+04	6.65E+03	2.27E+04	1.57E+04	461.24639	3	20.98
ATO3	YDR384C	TSSASSPQDLEK	[5] Phospho (ST)	0.36	-0.06	0.15	0.42	0.173	0.435	0.315	0.15	2.39E+04	1.40E+04	2.47E+04	3.54E+04	2.27E+04	2.23E+04	1.24E+04	2.53E+04	2.22E+04	2.82E+04	2.04E+04	2.08E+04	665.28242	2	55.64
TAF3	YPL011C	RTSLDYGGYF	[6] Phospho (Y)	-0.12	0.25	-0.26	-0.36	0.412	0.320	0.330	0.13	1.75E+04	4.73E+04	2.19E+04	2.52E+04	3.15E+04	2.33E+04	4.30E+04	3.48E+04	2.50E+04	2.09E+04	3.22E+04	1.93E+04	629.76136	2	26.35
CST6	YIL036W	FGSDTDDDDIDLKPVEGGKDPDNQSLPNSEK	[3] Phospho (ST)||[5] Phospho (ST)	-0.74	-0.26	-0.62	-0.48	0.141	0.335	0.068	0.31	1.15E+05	1.72E+05	1.41E+05	6.19E+03	1.53E+05	9.75E+04	3.03E+04	1.96E+05	1.32E+05	5.21E+04	1.22E+05	1.05E+05	1169.8147	3	38.91
HAL5	YJL165C	KNSLSTPR	[3] Phospho (ST)	1.02	0.07	0.03	0.96	0.017	0.446	0.471	0.02	1.65E+04	8.36E+03	9.13E+03	2.05E+04	2.02E+04	2.82E+04	1.69E+04	7.66E+03	1.10E+04	1.28E+04	1.18E+04	1.00E+04	491.73917	2	38.58
SET3	YKR029C	TPSLSNFNK	[3] Phospho (ST)	-0.18	-0.34	-0.23	0.16	0.178	0.103	0.189	0.23	1.95E+04	2.31E+04	2.70E+04	2.18E+04	1.79E+04	2.20E+04	1.42E+04	2.25E+04	1.84E+04	2.50E+04	1.85E+04	1.57E+04	544.24485	2	31.5
YDR365W-B	R365W-B	EVHTNQDPLDVSASK	[12] Phospho (ST)	-0.67	0.88	1.09	-1.55	0.003	0.003	0.000	0.00	4.32E+04	4.55E+04	4.73E+04	2.34E+04	2.80E+04	3.40E+04	8.51E+04	7.09E+04	9.44E+04	9.28E+04	9.42E+04	1.03E+05	860.38418	2	20.08
MCK1	YNL307C	GSEFIADDVTSNK	[11] Phospho (ST)	0.43	0.16	0.01	0.27	0.006	0.130	0.458	0.01	4.53E+04	4.00E+04	5.12E+04	6.25E+04	5.84E+04	6.28E+04	4.69E+04	5.03E+04	5.50E+04	4.08E+04	4.79E+04	4.92E+04	731.81	2	50.07
REG1	YDR028C	RSDSGVHSPITDNSSVASSTTSR	[8] Phospho (ST)	0.09	0.11	0.26	-0.02	0.157	0.374	0.025	0.48	3.47E+04	3.21E+04	3.62E+04	3.95E+04	3.42E+04	3.61E+04	5.13E+04	2.50E+04	3.47E+04	4.03E+04	3.80E+04	4.54E+04	810.02971	3	62.44
HSF1	YGL073W	ANSSTSSENPSLTPFDIESNNDRK	[4] Phospho (ST)	-0.03	0.01	0.00	-0.05	0.426	0.476	0.497	0.42	4.81E+04	5.80E+04	4.44E+04	5.02E+04	5.52E+04	4.18E+04	5.08E+04	6.14E+04	3.98E+04	4.08E+04	6.64E+04	4.35E+04	897.39122	3	57.77
DIG2	YDR480W	EEDHSGKPPTITTSPAEK	[10] Phospho (ST)	-0.44	-0.16	0.18	-0.29	0.024	0.300	0.292	0.18	3.71E+04	4.68E+04	5.12E+04	3.32E+04	3.43E+04	3.19E+04	5.18E+04	2.78E+04	4.18E+04	3.49E+04	5.18E+04	6.62E+04	1002.4513	2	31.8
ENO2	YHR174W	IGSEVYHNLK	[3] Phospho (ST)	-0.62	-0.03	-0.40	-0.59	0.074	0.462	0.176	0.01	1.52E+04	2.92E+04	2.56E+04	1.21E+04	1.85E+04	1.49E+04	2.33E+04	2.03E+04	2.51E+04	1.09E+04	2.02E+04	2.19E+04	620.29258	2	18.47
STF2	YGR008C	DRRGSNLQSHEQK	[5] Phospho (ST)	0.28	-0.48	-1.20	0.76	0.255	0.248	0.062	0.11	5.78E+04	4.00E+04	2.34E+04	4.54E+04	6.21E+04	3.97E+04	1.44E+04	2.02E+04	5.22E+04	2.92E+04	7.32E+03	1.62E+04	817.87388	2	16.46
ESF2	YNR054C	KVEDIESENESDIEEEQK	[7] Phospho (ST)||[11] Phospho (ST)	-0.08	-0.12	0.00	0.04	0.403	0.403	0.499	0.46	8.06E+04	3.83E+04	6.70E+04	5.88E+04	6.45E+04	5.23E+04	3.03E+04	7.62E+04	6.47E+04	7.69E+04	5.39E+04	5.52E+04	1155.4519	2	30.86
YPI1	YFR003C	KRSYSPNAYEIQPDYSEYR	[4] Phospho (Y)||[9] Phospho (Y)	-0.90	-0.45	-1.11	-0.45	0.027	0.238	0.016	0.28	1.00E+05	1.33E+05	7.61E+04	4.79E+04	6.78E+04	5.01E+04	5.01E+04	1.37E+05	3.90E+04	5.70E+04	4.50E+04	4.11E+04	842.68448	3	42.03
SYP1	YCR030C	TKPLPVEPASPSISLPTATVDNQPSGQVDSRPLHIR	[12] Phospho (ST)||[14] Phospho (ST)	0.58	0.47	-0.09	0.11	0.036	0.072	0.404	0.31	7.41E+04	1.14E+05	7.34E+04	1.09E+05	1.34E+05	1.48E+05	1.08E+05	1.47E+05	1.08E+05	1.11E+05	7.70E+04	5.83E+04	991.99705	4	34.32
GLC8	YMR311C	NPLALSPEQLAQQDPETLEEFRR	[6] Phospho (ST)	-0.14	-0.07	-0.07	-0.07	0.367	0.414	0.421	0.40	7.91E+04	8.73E+04	4.14E+04	5.70E+04	8.46E+04	4.64E+04	7.03E+04	6.82E+04	5.93E+04	7.52E+04	7.18E+04	5.06E+04	691.08591	4	31.41
BUD22	YMR014W	SNAIGAQTQSNKETTSDNEDLLIK	[16] Phospho (ST)	-0.38	-0.32	-0.06	-0.06	0.012	0.017	0.234	0.36	8.87E+04	8.98E+04	9.17E+04	6.62E+04	6.12E+04	8.04E+04	6.56E+04	8.34E+04	6.80E+04	8.87E+04	7.73E+04	9.28E+04	886.41443	3	28.53
YMR045C	YMR045C	VSTQANSQQPTTPLSSAVPENHHHASPQAAQVPLPQNGPYI	[26] Phospho (ST)	-1.17	-0.15	0.46	-1.01	0.001	0.152	0.017	0.00	1.52E+05	1.34E+05	1.24E+05	7.54E+04	5.72E+04	5.00E+04	1.28E+05	1.06E+05	1.34E+05	1.62E+05	2.09E+05	1.91E+05	955.8614	5	19.37
VPS13	YLL040C	ASQSSDSESIEVPTAILK	[9] Phospho (ST)	-0.21	-0.18	0.01	-0.03	0.314	0.300	0.493	0.48	1.12E+05	1.55E+05	9.13E+04	9.14E+04	1.50E+05	6.89E+04	1.36E+05	9.97E+04	8.06E+04	8.37E+04	1.54E+05	1.22E+05	971.4566	2	16.66
NRG1	YDR043C	NTLSDEEDLEQR	[4] Phospho (ST)	-0.50	-0.22	-0.48	-0.28	0.030	0.161	0.033	0.09	3.22E+04	2.31E+04	3.04E+04	2.03E+04	1.73E+04	2.30E+04	2.06E+04	2.48E+04	2.82E+04	2.33E+04	1.76E+04	2.03E+04	764.81238	2	53.7
IDS2	YJL146W	SSFSGASSNEPTNSPGDFLNQSR	[1] Phospho (ST)	-0.15	0.37	-0.36	-0.52	0.263	0.154	0.072	0.09	4.92E+04	6.75E+04	4.91E+04	4.70E+04	5.99E+04	4.20E+04	5.90E+04	9.57E+04	5.90E+04	4.67E+04	4.50E+04	3.78E+04	822.67896	3	52.9
YBT1	YLL048C	SSTSLSNLPAVK	[1] Phospho (ST)||[2] Phospho (ST)	-0.31	-0.18	-0.05	-0.13	0.129	0.333	0.422	0.39	4.82E+04	6.24E+04	4.78E+04	3.53E+04	5.46E+04	3.79E+04	3.38E+04	7.10E+04	3.54E+04	5.33E+04	6.19E+04	3.78E+04	682.29945	2	26.44
PSP2	YML017W	SNPFGSAKPVDTQSK	[1] Phospho (ST)	-1.21	-0.70	-0.40	-0.50	0.000	0.000	0.048	0.01	3.72E+04	3.66E+04	3.70E+04	1.69E+04	1.28E+04	1.83E+04	2.46E+04	2.22E+04	2.13E+04	2.24E+04	2.58E+04	3.60E+04	821.87743	2	48.93
PAT1	YCR077C	RSSYAFNNGNGATNLNK	[4] Phospho (Y)	-0.67	-0.98	-0.34	0.31	0.053	0.023	0.150	0.17	7.42E+04	4.86E+04	8.54E+04	4.72E+04	3.21E+04	5.15E+04	2.68E+04	3.44E+04	4.42E+04	5.64E+04	4.39E+04	6.38E+04	954.42408	2	55.11
NCB2	YDR397C	LHHNSVSDPVKSEDSS	[12] Phospho (ST)||[16] Phospho (ST)	0.23	0.03	-0.05	0.20	0.178	0.454	0.427	0.05	6.48E+04	4.63E+04	8.21E+04	7.67E+04	7.14E+04	7.81E+04	5.86E+04	6.69E+04	7.18E+04	6.36E+04	5.18E+04	7.08E+04	949.37143	2	21.47
UBP3	YER151C	KEPEESVEENTSK	[12] Phospho (ST)	0.06	-0.23	-0.08	0.29	0.420	0.250	0.411	0.07	1.05E+05	5.50E+04	8.26E+04	9.06E+04	7.88E+04	8.23E+04	6.28E+04	5.94E+04	8.38E+04	9.34E+04	5.70E+04	7.90E+04	793.33555	2	37.14
FBA1	YKL060C	VNLDTDCQYAYLTGIR	[5] Phospho (ST)	-0.82	-0.28	-0.68	-0.55	0.072	0.245	0.088	0.04	8.25E+04	1.38E+05	6.82E+04	4.35E+04	7.17E+04	4.81E+04	8.18E+04	8.86E+04	6.80E+04	4.96E+04	6.92E+04	6.14E+04	991.44154	2	62.16
LSB3	R024C-A	LAPTNSGGSGGKLDDPSGASSYYASHR	[9] Phospho (ST)	-0.89	-0.45	-0.35	-0.44	0.002	0.036	0.069	0.07	8.27E+04	9.75E+04	8.17E+04	5.09E+04	3.94E+04	5.15E+04	7.73E+04	6.55E+04	4.92E+04	5.30E+04	6.81E+04	8.39E+04	911.40351	3	46.09
SNC1	YAL030W	SSSTPFDPYALSEHDEERPQNVQSK	[N-term] Acetyl (Protein N-term)||[12] Phosph	-0.28	-0.22	-0.14	-0.07	0.105	0.206	0.296	0.35	7.49E+04	9.72E+04	6.54E+04	6.65E+04	6.37E+04	6.48E+04	8.25E+04	6.47E+04	5.74E+04	6.35E+04	8.78E+04	6.48E+04	990.76535	3	38.06
TAT1	YBR069C	NIFVSPSLTEIDKVDDNDDLK	[9] Phospho (ST)	0.13	-0.08	0.17	0.20	0.255	0.348	0.282	0.18	7.00E+04	7.37E+04	5.66E+04	6.72E+04	8.62E+04	6.52E+04	7.31E+04	6.57E+04	5.10E+04	6.30E+04	1.01E+05	6.24E+04	819.72017	3	22.73
SBE22	YHR103W	SSDFLPIELK	[2] Phospho (ST)	-0.52	0.47	0.55	-0.99	0.063	0.061	0.148	0.01	3.10E+04	3.76E+04	2.37E+04	2.02E+04	2.66E+04	1.75E+04	4.41E+04	5.00E+04	3.42E+04	3.68E+04	6.69E+04	3.12E+04	614.79741	2	38.33
ECM21	YBL101C	NSSHSLSETDLNQSK	[5] Phospho (ST)	-0.30	-0.33	0.03	0.03	0.013	0.007	0.421	0.25	4.04E+04	3.42E+04	3.76E+04	3.22E+04	2.96E+04	2.95E+04	2.99E+04	2.97E+04	2.97E+04	4.11E+04	3.22E+04	4.12E+04	863.86776	2	55.81
LCB5	YLR260W	SSIDNISR	[2] Phospho (ST)	0.90	0.96	0.89	-0.05	0.042	0.036	0.040	0.44	6.81E+03	3.48E+03	7.05E+03	1.46E+04	8.71E+03	9.18E+03	7.86E+03	1.45E+04	1.13E+04	1.43E+04	9.06E+03	8.84E+03	486.21314	2	32.48
RPL32	YBL092W	FLSPSGHK	[3] Phospho (ST)	0.81	1.71	1.39	-0.90	0.110	0.021	0.024	0.03	6.89E+02	5.87E+03	1.08E+04	9.63E+03	9.39E+03	1.14E+04	2.26E+04	1.22E+04	2.22E+04	1.20E+04	1.64E+04	1.71E+04	476.71794	2	20.08
SUI3	YPL237W	ENGSGDDLFAGLK	[4] Phospho (ST)	-0.75	-0.12	-0.04	-0.63	0.014	0.268	0.404	0.02	5.36E+04	7.22E+04	6.17E+04	3.10E+04	4.75E+04	3.33E+04	5.44E+04	6.75E+04	5.05E+04	5.98E+04	6.79E+04	5.47E+04	701.79883	2	57.05
NOC2	YOR206W	DLLDFAGTNPLDGIDSQDEGEDAERNSNIEEK	[16] Phospho (ST)||[27] Phospho (ST)	-0.37	-0.26	-0.48	-0.11	0.242	0.317	0.163	0.41	2.06E+05	2.66E+05	1.05E+05	1.29E+05	2.10E+05	1.08E+05	1.23E+05	2.40E+05	1.20E+05	1.30E+05	1.64E+05	1.19E+05	917.38204	4	25.58
MRC1	YCL061C	HIINESDSDTEVEAKPK	[6] Phospho (ST)||[8] Phospho (ST)	-1.02	-0.58	-0.74	-0.43	0.002	0.047	0.004	0.14	6.54E+04	5.08E+04	5.78E+04	2.42E+04	3.14E+04	3.03E+04	2.57E+04	5.24E+04	3.80E+04	3.13E+04	3.42E+04	3.89E+04	691.29248	3	30.19
SAP190	YKR028W	NYYNNVETNDDDYDSDDGK	[13] Phospho (Y)	-0.58	-0.37	-0.20	-0.21	0.006	0.188	0.173	0.32	1.20E+05	1.00E+05	9.31E+04	6.83E+04	7.08E+04	7.03E+04	5.36E+04	1.25E+05	6.38E+04	1.10E+05	8.30E+04	7.97E+04	1168.4136	2	50.81
YGR054W	YGR054W	SSETSPDSTPAPSAPASTNAPTNNK	[8] Phospho (ST)||[9] Phospho (ST)	0.50	0.13	0.02	0.37	0.073	0.356	0.472	0.15	4.71E+04	2.87E+04	4.16E+04	6.92E+04	4.56E+04	5.12E+04	3.18E+04	5.77E+04	3.92E+04	4.81E+04	3.26E+04	3.83E+04	863.68477	3	25.62
PEA2	YER149C	NTSSPPISPNAAAIQEEDSSK	[4] Phospho (ST)||[8] Phospho (ST)	-0.53	-0.38	-0.46	-0.15	0.013	0.097	0.024	0.32	1.47E+05	1.22E+05	1.25E+05	9.72E+04	1.01E+05	7.41E+04	7.53E+04	1.35E+05	9.15E+04	8.49E+04	1.15E+05	8.60E+04	1151.9783	2	34.55
EFR3	YMR212C	DANEDLHSLSSR	[8] Phospho (ST)||[11] Phospho (ST)	-0.26	-0.35	-0.53	0.09	0.096	0.164	0.023	0.39	2.84E+04	2.35E+04	3.33E+04	2.36E+04	2.20E+04	2.56E+04	1.36E+04	3.01E+04	2.31E+04	1.83E+04	2.20E+04	1.85E+04	752.28025	2	18.38
TPS3	YMR261C	SSSVTSASSHYIGLPQEAQINGEPLQR	[3] Phospho (ST)||[5] Phospho (ST)	-0.40	0.50	0.13	-0.91	0.271	0.230	0.395	0.11	8.40E+04	1.67E+05	6.03E+04	5.13E+04	1.17E+05	6.73E+04	8.18E+04	2.25E+05	1.35E+05	1.09E+05	1.25E+05	1.06E+05	1006.1203	3	36.45
SEC7	YDR170C	SSLSNDVR	[2] Phospho (ST)	-1.55	-0.38	-1.55	-1.18	0.221	0.395	0.218	0.14	3.07E+04	2.07E+03	4.11E+03	8.76E+03	1.89E+03	1.89E+03	2.54E+03	1.08E+04	1.51E+04	7.17E+03	3.40E+03	2.03E+03	479.20587	2	19.83
BBC1	YJL020C	STTHDVGEISNNVK	[3] Phospho (ST)	-0.08	-0.73	-0.09	0.66	0.241	0.139	0.340	0.17	2.81E+04	2.66E+04	3.03E+04	2.41E+04	2.72E+04	2.94E+04	3.03E+04	2.08E+04	7.66E+01	2.22E+04	2.41E+04	3.37E+04	790.85141	2	39.71
SKG6	YHR149C	VSGILEETDVVQPPSVGGILPHSGSQDDLRK	[25] Phospho (ST)	-0.14	0.01	-0.22	-0.16	0.354	0.486	0.296	0.27	8.75E+04	1.25E+05	6.25E+04	6.80E+04	1.06E+05	7.49E+04	1.08E+05	8.28E+04	8.65E+04	5.75E+04	1.02E+05	7.72E+04	828.16537	4	15.22
AGP1	YCL025C	NESSDNIGANTGHK	[3] Phospho (ST)	-0.60	-1.45	-0.60	0.85	0.215	0.095	0.237	0.04	6.78E+04	2.21E+04	2.49E+04	2.37E+04	2.32E+04	2.87E+04	2.00E+04	1.62E+04	5.71E+03	3.96E+04	1.83E+04	1.79E+04	762.30964	2	58.31
GGA1	YDR358W	VSLSSPKSPQENDTVVDILGDAHSK	[2] Phospho (ST)||[8] Phospho (ST)	-0.07	0.45	-0.05	-0.53	0.378	0.069	0.407	0.05	7.98E+04	9.29E+04	6.32E+04	7.01E+04	9.07E+04	6.31E+04	9.09E+04	1.33E+05	9.82E+04	7.09E+04	8.66E+04	7.07E+04	928.42318	3	45.13
ACF4	YJR083C	SINDFFSK	[1] Phospho (ST)	-0.01	0.05	-0.21	-0.06	0.491	0.448	0.307	0.43	1.70E+04	3.66E+04	2.40E+04	1.73E+04	3.55E+04	2.42E+04	2.21E+04	3.21E+04	2.61E+04	2.08E+04	2.83E+04	1.78E+04	519.2209	2	37.75
REG1	YDR028C	ANLDQNLNSPDNNRFPSSTSSSNR	[9] Phospho (ST)	0.11	0.32	0.23	-0.20	0.244	0.139	0.177	0.21	6.50E+04	5.73E+04	7.84E+04	7.75E+04	6.57E+04	7.38E+04	6.16E+04	8.75E+04	1.01E+05	7.92E+04	6.23E+04	9.34E+04	905.73075	3	44.18
TAO3	YIL129C	SQQIFTVQHQK	[1] Phospho (ST)	0.26	0.18	0.07	0.08	0.206	0.343	0.414	0.40	1.46E+04	1.79E+04	2.84E+04	2.23E+04	2.38E+04	2.68E+04	1.93E+04	1.77E+04	3.20E+04	2.22E+04	2.13E+04	2.04E+04	712.33925	2	31.76

RHO5	YNL180C	SANHTLTDELTTATTNTNGDK	[15] Phospho (ST)	-0.52	-0.68	-0.03	0.16	0.082	0.042	0.465	0.23	9.44E+04	5.39E+04	7.21E+04	5.39E+04	5.98E+04	3.99E+04	4.99E+04	4.04E+04	4.73E+04	7.20E+04	5.71E+04	8.72E+04	1143.0005	2	41.06
RMT2	YDR465C	EESVGSDDDATAANQQVYLK	[6] Phospho (ST)	0.18	0.19	0.11	-0.01	0.048	0.063	0.101	0.46	3.89E+04	4.45E+04	4.53E+04	4.59E+04	4.82E+04	5.14E+04	4.59E+04	5.34E+04	4.72E+04	4.81E+04	4.43E+04	4.69E+04	740.64973	3	27.44
YSP2	YDR326C	ALENAVGDEGNSK	[12] Phospho (ST)	0.22	0.28	0.53	-0.06	0.213	0.125	0.047	0.33	2.24E+04	1.59E+04	2.79E+04	2.89E+04	2.13E+04	2.70E+04	2.56E+04	2.66E+04	2.83E+04	3.77E+04	2.82E+04	3.00E+04	692.29356	2	48.91
BNA7	YDR428C	AISPDITLFNK	[3] Phospho (ST)	-1.57	0.38	-0.03	-1.95	0.012	0.151	0.464	0.00	2.90E+04	4.91E+04	2.94E+04	1.15E+04	1.41E+04	1.06E+04	5.90E+04	3.92E+04	4.15E+04	2.64E+04	4.61E+04	3.25E+04	649.82419	2	55.96
YLR057W	YLR057W	GDTVGSSKSIAEIDGDEVTQIR	[9] Phospho (ST)	-0.77	-0.94	0.10	0.18	0.184	0.155	0.433	0.39	1.53E+05	5.56E+04	5.30E+04	7.78E+04	3.68E+04	3.91E+04	2.77E+04	7.43E+04	3.40E+04	1.06E+05	1.03E+05	7.19E+04	786.36432	3	15.41
YMR086W	YMR086W	INSLTQR	[3] Phospho (ST)	-0.81	-1.97	-1.57	1.16	0.242	0.103	0.126	0.16	2.79E+04	9.05E+03	5.57E+03	1.56E+04	3.22E+03	5.44E+03	2.88E+03	2.46E+03	5.47E+03	6.15E+03	2.61E+03	5.57E+03	456.22079	2	30.54
SFK1	YKL051W	SFNQDYNTVDELPWYK	[1] Phospho (ST)	0.14	0.14	-0.29	0.00	0.368	0.367	0.257	0.50	9.78E+04	1.45E+05	6.68E+04	1.18E+05	1.41E+05	8.12E+04	1.12E+05	1.42E+05	8.59E+04	7.88E+04	1.09E+05	6.62E+04	1049.9445	2	89.09
PAR32	YDL173W	SHQSLHATTSSPNNNAPIVVGR	[4] Phospho (ST)|[11] Phospho (ST)	0.23	-0.20	-0.26	0.42	0.137	0.191	0.166	0.08	3.70E+04	3.21E+04	3.24E+04	4.38E+04	4.38E+04	3.11E+04	2.55E+04	3.77E+04	2.52E+04	2.34E+04	2.37E+04	3.78E+04	816.36858	3	17.1
AIM21	YIR003W	IFQNPTDEESTTSLNEK	[6] Phospho (ST)	-0.23	0.15	-0.01	-0.37	0.163	0.253	0.480	0.02	8.79E+04	9.72E+04	1.32E+05	9.55E+04	8.53E+04	9.04E+04	1.15E+05	1.05E+05	1.32E+05	8.93E+04	1.01E+05	1.24E+05	1016.9419	2	69.39
TRM2	YKR056W	LSSPLTDSGNR	[3] Phospho (ST)	0.16	-0.12	-0.22	0.28	0.282	0.297	0.236	0.11	1.83E+04	1.61E+04	2.50E+04	2.32E+04	1.72E+04	2.62E+04	1.78E+04	1.91E+04	1.78E+04	1.33E+04	1.65E+04	2.12E+04	613.77457	2	33.12
AXL2	YIL140W	EELLAKPPVQPPESPFFDPQNR	[14] Phospho (ST)	-0.22	0.01	-0.49	-0.23	0.133	0.479	0.043	0.13	9.57E+04	1.12E+05	8.11E+04	7.56E+04	9.30E+04	8.02E+04	1.00E+05	7.96E+04	1.11E+05	5.65E+04	8.44E+04	6.53E+04	872.42327	3	15.88
CDC3	YLR314C	DYEEELANDQEEEEGQGEGHENQSQEQR	[24] Phospho (ST)	1.05	-0.25	-0.40	1.30	0.015	0.254	0.108	0.01	1.11E+05	6.65E+04	8.54E+04	2.27E+05	1.77E+05	1.39E+05	4.82E+04	9.70E+04	7.61E+04	7.77E+04	5.51E+04	6.64E+04	1129.4337	3	20.36
YPK1	YKL126W	EEQQNNQATAGEHDASITRSSLDRK	[21] Phospho (ST)	-0.28	-0.36	0.32	0.09	0.067	0.074	0.073	0.36	5.01E+04	4.01E+04	4.79E+04	4.33E+04	3.79E+04	3.30E+04	4.37E+04	2.70E+04	3.67E+04	6.56E+04	4.68E+04	6.02E+04	955.76387	3	16.44
NTH1	YDR001C	RGSEDDTYSSSQGNRR	[3] Phospho (ST)	0.43	0.56	-0.42	-0.13	0.227	0.156	0.324	0.34	4.42E+04	2.41E+04	1.14E+04	4.72E+04	3.02E+04	2.99E+04	3.29E+04	3.51E+04	4.95E+04	3.92E+04	1.06E+04	1.00E+04	632.26039	3	23.71
MSS4	YDR208W	RNTQDSNLPNIPFHASK	[3] Phospho (ST)|[6] Phospho (ST)	-0.48	-0.28	-0.66	-0.21	0.007	0.226	0.003	0.31	6.48E+04	6.25E+04	5.39E+04	4.25E+04	4.78E+04	3.93E+04	3.39E+04	7.38E+04	4.19E+04	3.90E+04	4.15E+04	3.41E+04	700.30917	3	34.17
HNM1	YGL077C	VEEEIKPLDDMDSK	[13] Phospho (ST)	-0.86	-0.28	0.07	-0.58	0.080	0.191	0.405	0.22	3.58E+04	3.69E+04	3.69E+04	1.70E+04	3.79E+04	5.54E+03	3.17E+04	4.06E+04	1.83E+04	2.66E+04	5.11E+04	3.74E+04	576.58691	3	15.72
GSY2	YLR258W	PLSVPGSPR	[7] Phospho (ST)	0.72	1.13	0.69	-0.40	0.020	0.024	0.114	0.15	3.73E+03	3.52E+03	4.98E+03	5.40E+03	8.02E+03	6.79E+03	9.77E+03	5.73E+03	1.13E+04	3.26E+03	7.63E+03	8.80E+03	495.24351	2	16.69
LDB16	YCL005W	NASDADIVNIK	[3] Phospho (ST)	-0.24	-0.45	-0.39	0.21	0.126	0.003	0.020	0.19	4.13E+04	3.67E+04	3.98E+04	4.11E+04	2.64E+04	3.23E+04	2.60E+04	3.13E+04	2.91E+04	3.52E+04	2.89E+04	2.59E+04	620.28527	2	31.49
TIF4631	YGR162W	APPPKEEPAAPTSTATNMFSALMGESDDEE	[26] Phospho (ST)	-1.54	-0.91	-0.03	-0.63	0.018	0.052	0.477	0.19	3.56E+05	2.95E+05	1.90E+05	1.04E+05	1.51E+05	3.43E+04	1.36E+05	2.24E+05	8.73E+04	2.15E+05	4.23E+05	1.87E+05	1067.4488	3	53.43
GIP4	YAL031C	LPASSSPSPSPTSSASPSR	[16] Phospho (ST)	-0.37	0.18	0.02	-0.55	0.009	0.167	0.385	0.03	6.82E+04	6.33E+04	6.72E+04	4.99E+04	4.59E+04	5.81E+04	7.66E+04	6.06E+04	8.75E+04	6.63E+04	6.22E+04	7.35E+04	940.42587	2	51.06
PRK1	YIL095W	HGFTGNSVNNSR	[4] Phospho (ST)	0.37	0.49	0.64	-0.12	0.346	0.280	0.207	0.40	6.88E+03	3.90E+03	2.85E+04	1.12E+04	1.36E+04	2.60E+04	1.58E+04	1.49E+04	2.44E+04	2.39E+04	1.59E+04	2.16E+04	685.28618	2	68.68
GPT2	YKR067W	SEGETSEDEDEFDEK	[6] Phospho (ST)	-0.07	0.16	-0.27	-0.22	0.397	0.245	0.167	0.20	3.95E+04	2.78E+04	3.54E+04	4.12E+04	2.65E+04	3.03E+04	3.34E+04	4.58E+04	3.52E+04	3.66E+04	2.42E+04	2.42E+04	913.31298	2	42.59
GAT1	YFL021W	IASPSIPQYLR	[3] Phospho (ST)	-1.11	-0.59	-0.76	-0.53	0.056	0.139	0.116	0.04	2.33E+04	5.51E+04	3.18E+04	1.97E+04	1.87E+04	1.25E+04	2.88E+04	2.10E+04	2.36E+04	1.37E+04	3.07E+04	2.05E+04	662.83793	2	36.85
IRA2	YOL081W	NSDNVNSLNSSPK	[11] Phospho (ST)	0.27	0.23	0.74	0.04	0.272	0.324	0.063	0.46	1.22E+04	6.14E+03	1.63E+04	1.77E+04	1.16E+04	1.24E+04	9.89E+03	1.18E+04	1.89E+04	2.25E+04	1.40E+04	2.12E+04	728.30945	2	42.41
YSP2	YDR326C	NVNANSNSETENDNDRDDRSNVGK	[20] Phospho (ST)	-0.51	-0.61	-0.07	0.11	0.177	0.153	0.443	0.32	6.71E+04	2.41E+04	4.21E+04	3.42E+04	2.95E+04	3.01E+04	2.52E+04	2.44E+04	3.75E+04	5.40E+04	3.17E+04	4.13E+04	915.37599	3	28.22
NPR1	YNL183C	AIPSLSSSIPYSVPNSNK	[11] Phospho (Y)	-0.68	-0.16	-0.51	-0.53	0.091	0.353	0.152	0.03	1.03E+05	1.79E+05	8.59E+04	7.55E+04	7.89E+04	7.44E+04	1.22E+05	1.23E+05	8.48E+04	8.75E+04	1.06E+05	6.50E+04	970.97443	2	54.6
BUD3	YCL014W	AADVENLSDDDEHRQNESR	[8] Phospho (ST)	0.80	0.78	0.86	0.03	0.014	0.056	0.046	0.46	2.38E+04	1.72E+04	3.30E+04	3.90E+04	4.16E+04	4.85E+04	5.09E+04	2.76E+04	4.82E+04	3.76E+04	3.62E+04	6.03E+04	1140.4621	2	29.06
BCD1	YHR040W	FIDNAREEEDAEEDSQPTEEPVQK	[15] Phospho (ST)	1.01	-1.44	-1.16	2.45	0.001	0.004	0.006	0.00	6.13E+04	4.76E+04	7.41E+04	1.29E+05	1.22E+05	1.17E+05	2.30E+04	2.10E+04	2.34E+04	2.56E+04	2.55E+04	3.05E+04	962.4076	3	53.88
DIG1	YPL049C	TSQPQQQSPSLLQGEIR	[8] Phospho (ST)	-0.20	0.09	-0.45	-0.28	0.136	0.412	0.012	0.26	2.96E+04	3.69E+04	3.36E+04	3.23E+04	3.10E+04	2.41E+04	2.21E+04	5.09E+04	3.32E+04	2.72E+04	2.34E+04	2.26E+04	659.65322	3	24.16
ORC1	YML065W	ATQTAQISDAETR	[8] Phospho (ST)	-0.27	0.20	0.34	-0.47	0.202	0.296	0.174	0.10	2.31E+04	1.29E+04	2.19E+04	1.81E+04	1.36E+04	1.64E+04	1.54E+04	2.26E+04	2.85E+04	3.04E+04	1.80E+04	2.49E+04	736.32515	2	44.89
UBP1	YDL122W	RIIEHSDVENENVK	[6] Phospho (ST)	0.23	0.28	0.33	-0.05	0.138	0.193	0.077	0.42	2.25E+04	2.98E+04	3.51E+04	3.30E+04	3.22E+04	3.72E+04	3.91E+04	2.49E+04	4.21E+04	3.38E+04	3.51E+04	4.09E+04	881.41189	2	47.97
BUD27	YFL023W	ILENISDDDYDDDDDGNK	[6] Phospho (ST)	0.41	0.38	0.10	0.02	0.128	0.042	0.305	0.47	7.83E+04	1.02E+05	8.26E+04	7.67E+04	1.44E+05	1.28E+05	9.99E+04	1.31E+05	1.12E+05	9.08E+04	1.09E+05	8.12E+04	1075.9003	2	86.56
BNI1	YNL271C	KQPSLNNIYR	[4] Phospho (ST)	-0.13	-0.34	-0.09	0.21	0.191	0.033	0.265	0.03	2.63E+04	3.43E+04	3.01E+04	2.54E+04	2.85E+04	2.92E+04	2.21E+04	2.43E+04	2.54E+04	2.59E+04	2.88E+04	3.05E+04	656.82434	2	15.53
STB1	YNL309W	FSHIKPSASSPQSTFK	[10] Phospho (ST)	-0.72	-1.70	-0.09	0.99	0.012	0.032	0.367	0.16	3.41E+04	4.77E+04	4.23E+04	2.71E+04	2.06E+04	2.78E+04	3.38E+04	1.62E+03	2.65E+03	3.30E+04	3.41E+04	4.96E+04	610.29284	3	19.02
YDR365W-B	R365W-B	RSSTPQISNIESTGSGGMHK	[3] Phospho (ST)	0.07	-0.16	0.80	0.23	0.462	0.295	0.005	0.39	2.72E+04	3.16E+04	2.49E+04	2.15E+04	5.69E+04	9.66E+03	2.74E+04	3.14E+04	1.62E+04	4.43E+04	5.66E+04	4.49E+04	718.65924	3	58.29
YBR197C	YBR197C	SSSQEGNPQLVQLK	[3] Phospho (ST)	-0.35	-0.22	-0.51	-0.14	0.019	0.156	0.006	0.24	3.54E+04	4.39E+04	4.40E+04	3.35E+04	3.16E+04	3.15E+04	2.94E+04	4.32E+04	3.34E+04	2.85E+04	2.93E+04	2.85E+04	797.87758	2	53.8
PRR1	YKL116C	VVSELIAPANLSPQR	[12] Phospho (ST)	-0.05	0.13	-0.19	-0.18	0.424	0.230	0.185	0.22	1.63E+04	2.32E+04	2.05E+04	1.49E+04	2.46E+04	1.83E+04	1.95E+04	2.32E+04	2.30E+04	1.46E+04	1.81E+04	1.97E+04	558.62592	3	24.37
HEK2	YBL032W	SDSASFLEEKEEPQENHDNKEEQS	[5] Phospho (ST)	0.25	0.02	0.09	0.22	0.218	0.458	0.331	0.24	9.46E+04	7.75E+04	6.49E+04	1.22E+05	7.55E+04	8.29E+04	7.87E+04	9.65E+04	6.59E+04	8.80E+04	7.04E+04	9.43E+04	962.7249	3	28.26
NET1	YJL076W	GTTSFNEEGNRK	[2] Phospho (ST)	-4.29	-1.89	0.00	-2.40	0.065	0.109	0.499	0.00	2.17E+04	5.86E+03	4.98E+04	1.26E+03	8.78E+02	1.79E+03	8.19E+03	4.83E+03	7.87E+03	3.73E+04	1.84E+04	2.18E+04	710.29756	2	40.67
PPZ1	YML016C	HISNDDDIENSSQLSNIHASMENVNDK	[12] Phospho (ST)|[15] Phospho (ST)	-0.55	-0.35	0.02	-0.20	0.130	0.234	0.474	0.34	1.86E+05	1.00E+05	1.15E+05	8.87E+04	1.24E+05	6.12E+04	8.14E+04	1.53E+05	8.04E+04	1.33E+05	1.47E+05	1.27E+05	1062.7648	3	17.52
SKY1	YMR216C	GSSINYPGFVTK	[3] Phospho (ST)	-0.54	-0.11	-0.22	-0.43	0.079	0.384	0.262	0.14	2.17E+04	3.17E+04	1.94E+04	1.31E+04	2.07E+04	1.62E+04	1.91E+04	3.08E+04	1.76E+04	1.89E+04	2.69E+04	1.67E+04	675.31125	2	40.76
YPL077C	YPL077C	RNSVDIPLQTHNR	[3] Phospho (ST)	-0.12	0.10	-0.28	-0.22	0.290	0.359	0.177	0.17	1.85E+04	2.85E+04	2.67E+04	2.17E+04	2.08E+04	2.51E+04	2.94E+04	1.99E+04	2.94E+04	1.48E+04	2.21E+04	2.37E+04	543.93369	3	31.01
KEL1	YHR158C	HYNESSELSQNNTEIDK	[6] Phospho (ST)	-0.04	-0.66	-0.10	0.62	0.431	0.156	0.349	0.16	2.89E+04	1.99E+04	3.08E+04	2.46E+04	2.39E+04	2.90E+04	2.71E+04	2.16E+04	1.69E+03	2.64E+04	1.95E+04	2.84E+04	696.6233	3	38.43
GNP1	YDR508C	RAEGSHANSPDSSNSNGTTPISTKDSSSQLDNELNR	[22] Phospho (ST)|[23] Phospho (ST)	-0.69	-1.13	-0.11	0.45	0.038	0.012	0.350	0.07	1.44E+05	8.64E+04	1.22E+05	8.82E+04	6.94E+04	6.20E+04	4.43E+04	6.72E+04	4.94E+04	1.29E+05	8.26E+04	1.15E+05	984.16876	4	36.86
PAR32	YDL173W	SHQSLHATTSSPNNNAPIVVGR	[8] Phospho (ST)|[9] Phospho (ST)|[10] Phosp	-0.44	-0.47	-0.66	0.03	0.004	0.058	0.006	0.46	5.37E+04	5.26E+04	5.98E+04	3.84E+04	4.49E+04	3.92E+04	2.75E+04	5.31E+04	3.94E+04	3.17E+04	3.02E+04	4.31E+04	843.02297	3	18.08
SRP40	YKR092C	GGSITLESGSYK	[3] Phospho (ST)	-0.10	0.29	-0.18	-0.40	0.326	0.070	0.219	0.02	1.73E+04	2.61E+04	2.24E+04	1.75E+04	2.00E+04	2.37E+04	2.67E+04	2.55E+04	2.84E+04	2.24E+04	1.90E+04	1.65E+04	639.7848	2	57.55
YKL105C	YKL105C	TTSLGNSGSTIR	[3] Phospho (ST)	-0.45	-0.21	-0.03	-0.24	0.018	0.052	0.412	0.07	3.88E+04	3.34E+04	3.24E+04	2.43E+04	2.22E+04	2.99E+04	2.98E+04	2.84E+04	3.22E+04	3.28E+04	2.99E+04	3.94E+04	637.29693	2	50.87
ALY2	YJL084C	KNSISGLSSLNLSPLGAPGNSSVNVK	[3] Phospho (ST)	-0.13	0.11	0.19	-0.23	0.291	0.374	0.296	0.21	6.21E+04	7.90E+04	4.88E+04	6.02E+04	5.76E+04	5.63E+04	9.00E+04	6.28E+04	5.18E+04	5.75E+04	9.79E+04	6.16E+04	874.11736	3	35.18
GIN4	YDR507C	RQSISSVSVSPSK	[10] Phospho (ST)	0.19	-0.20	-0.20	0.39	0.043	0.074	0.151	0.00	1.82E+04	2.23E+04	2.09E+04	2.34E+04	2.26E+04	2.40E+04	1.73E+04	1.65E+04	1.96E+04	2.08E+04	1.45E+04	1.83E+04	721.35548	2	62.83
DEF1	YKL054C	KTESPLENVAELKK	[4] Phospho (ST)	0.01	0.23	0.35	-0.22	0.477	0.268	0.047	0.28	2.62E+04	2.92E+04	3.07E+04	2.53E+04	2.78E+04	3.36E+04	4.62E+04	2.10E+04	3.40E+04	2.99E+04	4.02E+04	4.00E+04	555.95374	3	28.07
ENP2	YGR145W	GHYDYEDEESDEEESDDETNQK	[5] Phospho (Y)|[15] Phospho (ST)	0.19	-0.26	0.01	0.44	0.323	0.365	0.492	0.22	1.11E+05	4.34E+04	6.62E+04	9.46E+04	7.96E+04	7.73E+04	2.73E+04	1.12E+05	4.62E+04	8.95E+04	5.51E+04	7.77E+04	941.63792	3	26.64
SPA2	YLL021W	PASFLNDVEEEESPVKPLK	[13] Phospho (ST)	-0.28	0.45	0.20	-0.73	0.266	0.185	0.326	0.08	2.51E+04	4.24E+04	2.14E+04	2.69E+04	2.97E+04	1.69E+04	5.77E+04	3.01E+04	3.38E+04	2.31E+04	4.51E+04	3.40E+04	736.6883	3	50.9
PSK1	YAL017W	GLSPLEEEK	[3] Phospho (ST)	0.65	0.68	0.19	-0.02	0.013	0.020	0.173	0.45	9.15E+03	1.26E+04	1.37E+04	1.66E+04	1.79E+04	2.14E+04	2.01E+04	1.52E+04	2.16E+04	1.27E+04	1.48E+04	1.29E+04	541.2434	2	34.33
YPT11	YNL304W	RYSSNDFEK	[3] Phospho (ST)	-0.29	-0.48	-0.32	0.18	0.008	0.005	0.036	0.06	1.60E+04	1.41E+04	1.59E+04	1.23E+04	1.32E+04	1.21E+04	1.11E+04	9.80E+03	1.22E+04	1.45E+04	1.13E+04	1.11E+04	613.24803	2	26.91
NOP53	YPL146C	NIDLSDVEQYMEK	[5] Phospho (ST)	-0.27	-0.28	0.69	0.01	0.320	0.241	0.090	0.49	4.54E+04	5.98E+04	3.14E+04	3.44E+04	6.19E+04	1.69E+04	3.15E+04	5.04E+04	3.03E+04	5.94E+04	1.03E+05	5.72E+04	832.35167	2	68.9
TPS3	YMR261C	SSSVTSASSHYIGLPQEAQINGEPLQR	[2] Phospho (ST)	-0.66	0.18	-0.23	-0.84	0.055	0.286	0.238	0.01	7.09E+04	1.17E+05	7.34E+04	4.96E+04	6.35E+04	5.26E+04	9.65E+04	1.20E+05	8.03E+04	6.61E+04	8.80E+04	6.83E+04	979.46449	3	50.44
KCS1	YDR017C	RSLSSSNQPSLLPEVVLNDNR	[6] Phospho (ST)	-0.46	-0.32	-0.54	-0.14	0.057	0.086	0.050	0.17	9.35E+04	1.17E+05	7.71E+04	6.91E+04	8.03E+04	5.94E+04	7.49E+04	7.94E+04	7.52E+04	5.99E+04	8.16E+04	5.68E+04	802.39734	3	51.22
FAR11	YNL127W	NSSSQDLLNK	[3] Phospho (ST)	-0.11	-0.21	0.04	0.10	0.391	0.305	0.459	0.37	2.04E+04	9.92E+03	2.16E+04	2.04E+04	1.39E+04	1.39E+04	1.08E+04	1.73E+04	1.68E+04	2.07E+04	1.45E+04	1.81E+04	593.26145	2	48.65
ZEO1	YOL109W	NEATPEAEQVKKEEQNIADGVEQK	[4] Phospho (ST)	-0.75	-0.49	-0.34	-0.26	0.005	0.010	0.096	0.14	4.90E+04	5.47E+04	4.69E+04	3.66E+04	2.44E+04	2.87E+04	4.12E+04	3.54E+04	3.08E+04	2.86E+04	4.04E+04	5.02E+04	691.8222	4	16.64
NTC20	YBR188C	RVLQEPDRDNDDSG	[13] Phospho (ST)	-0.17	-0.24	-0.01	0.08	0.271	0.198	0.485	0.33	3.81E+04	2.36E+04	3.87E+04	3.30E+04	2.54E+04	3.11E+04	2.41E+04	2.83E+04	3.23E+04	3.53E+04	2.46E+04	3.97E+04	848.35243	2	30.85
MNR2	YKL064W	SFVDENSPTDR	[7] Phospho (ST)	0.03	0.01	-0.10	0.02	0.420	0.492	0.269	0.47	2.76E+04	2.58E+04	3.19E+04	2.57E+04	2.95E+04	3.17E+04	1.83E+04	3.15E+04	3.59E+04	2.26E+04	2.88E+04	2.85E+04	673.76678	2	24.35
HOM3	YER052C	KGESTPPHPPENLSSSFYEK	[4] Phospho (ST)	-0.61	-0.27	-0.59	-0.34	0.134	0.321	0.171	0.25	7.11E+04	1.69E+05	9.78E+04	6.16E+04	7.14E+04	8.82E+04	1.42E+05	5.96E+04	7.86E+04	3.69E+04	9.07E+04	9.75E+04	1156.0172	2	19.62
SLG1	YOR008C	LYASSFSSNHGPSSGSFEEEHTK	[5] Phospho (ST)|[7] Phospho (ST)	-0.98	-0.09	-0.60	-0.90	0.001	0.316	0.004	0.01	5.56E+04	4.72E+04	5.02E+04	2.90E+04	2.71E+04	2.12E+04	3.92E+04	5.74E+04	4.74E+04	2.96E+04	3.23E+04	3.86E+04	882.34734	3	20.83
ECM3	YOR092W	RNSITGSLR	[3] Phospho (ST)	-0.91	-0.75	-0.58	-0.16	0.026	0.025	0.077	0.34	1.80E+04	1.38E+04	1.20E+04	5.27E+03	6.85E+03	1.11E+04	1.03E+04	6.44E+03	9.33E+03	7.67E+03	7.73E+03	1.40E+04	542.26871	2	30.12
YKL105C	YKL105C	EDQEEALSDNEPESSEK	[8] Phospho (ST)	-0.25	-0.21	-0.06	-0.04	0.178	0.247	0.424	0.43	1.03E+05	6.63E+04	1.09E+05	8.69E+04	7.25E+04	7.49E+04	6.29E+04	8.01E+04	9.77E+04	1.05E+05	6.85E+04	9.41E+04	1008.3872	2	63.91
YKL105C	YKL105C	AYSLPTR	[2] Phospho (Y)	-0.29	0.25	-0.01	-0.53	0.233	0.236	0.486	0.01	4.78E+03	9.59E+03	1.08E+04	6.39E+03	6.60E+03	7.62E+03	1.11E+04	8.48E+03	1.03E+04	7.34E+03	9.46E+03	8.11E+03	444.20487	2	17.69
YDR239C	YDR239C	SHSIQAPLQK	[3] Phospho (ST)	-0.08	-0.09	-0.19	0.01	0.115	0.176	0.098	0.45	1.69E+04	1.56E+04	1.51E+04	1.47E+04	1.48E+04	1.55E+04	1.38E+04	1.62E+04	1.48E+04	1.58E+04	1.19E+04	1.41E+04	594.79247	2	30.24
IMH1	YLR309C	SGSIGTLANANIDSSPANNSNPTK	[3] Phospho (ST)	0.00	-0.04	-0.20	0.04	0.495	0.425	0.191	0.43	4.71E+04	5.14E+04	4.14E+04	4.58E+04	5.18E+04	4.22E+04	3.64E+04	5.62E+04	4.34E+04	5.08E+04	3.89E+04	3.19E+04	804.03483	3	54.87
MUK1	YPL070W	SNSYDGFR	[3] Phospho (ST)	0.36	0.91	0.53	-0.55	0.084	0.035	0.118	0.09	5.98E+03	8.67E+03	6.91E+03	1.10E+04	7.76E+03	9.00E+03	1.11E+04	1.84E+04	1.11E+04	1.45E+04	9.03E+03	7.52E+03	513.19025	2	20.3
AKR1	YDR264C	AIRSGNEEESGNEQVNHNDEAEEDPLLTR	[10] Phospho (ST)	0.32	0.27	0.10	0.05	0.098	0.098	0.259	0.42	3.84E+04	3.76E+04	4.54E+04	6.09E+04	5.02E+04	4.03E+04	5.57E+04	3.97E+04	5.09E+04	3.96E+04	4.07E+04	4.96E+04	833.86352	4	19.13
MSN4	YKL062W	SSPAQDQQFIK	[2] Phospho (ST)	-0.20	-0.10	-0.22	-0.10	0.288	0.360	0.277	0.37	5.33E+04	3.16E+04	3.91E+04	4.80E+04	3.04E+04	2.98E+04	3.26E+04	4.55E+04	3.75E+04	4.83E+04	2.73E+04	3.09E+04	664.79987	2	44.73
LCB3	YJL134W	TLSNPNDFQEPNYLLDPGNHPSDHFR	[1] Phospho (ST)|[3] Phospho (ST)	-0.41	-0.72	-0.95	0.32	0.098	0.036	0.021	0.11	1.75E+05	2.12E+05	1.28E+05	1.18E+05	1.53E+05	1.17E+05	9.47E+04	1.30E+05	8.74E+04	6.34E+04	1.10E+05	9.32E+04	1062.1129	3	31.99
SDS3	YIL084C	AIQKVSNKDLSR	[6] Phospho (ST)	-0.44	-0.14	0.03	-0.30	0.064	0.291	0.463	0.05	4.28E+04	2.92E+04	2.95E+04	2.54E+04	2.27E+04	2.68E+04	3.25E+04	2.58E+04	3.40E+04	3.14E+04	2.86E+04	4.33E+04	480.25467	3	16.44
SSE2	YBR169C	GAAFICAIHSPTLR	[10] Phospho (ST)	0.26	0.46	0.14	-0.20	0.258	0.147	0.389	0.30	1.79E+04	3.40E+04	2.26E+04	2.55E+04	3.96E+04	2.41E+04	4.50E+04	2.42E+04	3.31E+04	1.47E+04	3.73E+04	2.99E+04	797.38444	2	33.85
HPC2	YBR215W	ETGSDSEDLFNK	[4] Phospho (ST)	-0.38	0.01	-0.03	-0.39	0.021	0.482	0.424	0.04	3.60E+04	3.45E+04	4.40E+04	2.98E+04	2.84E+04	2.96E+04	3.08E+04	4.06E+04	4.38E+04	4.18E+04	3.65E+04	3.39E+04	711.27771	2	28.91
SUB1	YMR039C	KEDIVSNINESK	[11] Phospho (ST)	1.13	2.04	1.96	-0.90	0.005	0.000	0.003	0.00	9.14E+03	6.37E+03	1.10E+04	2.15E+04	1.58E+04	2.09E+04	3.23E+04	3.54E+04	4.12E+04	3.24E+04	2.77E+04	4.33E+04	728.33889	2	49.63
VPS74	YDR372C	ADSGDTSSIHSSANNTK	[3] Phospho (ST)	0.20	-1.73	-0.99	1.93	0.410	0.142	0.214	0.02	4.21E+04	1.14E+04	6.42E+03	3.28E+04	1.52E+04	2.09E+04	5.31E+03	3.23E+03	9.50E+03	1.17E+04	7.04E+03	1.14E+04	591.24216	3	58.97
SFL1	YOR140W	KNSSNQNYDIDSGAR	[3] Phospho (ST)	0.12	-0.41	-0.45	0.53	0.264	0.069	0.041	0.02	2.96E+04	2.22E+04	3.17E+04	3.47E+04	2.79E+04	2.84E+04	1.63E+04	2.34E+04	2.32E+04	2.12E+04	1.76E+04	2.24E+04	874.86545	2	64.1
DNF1	YER166W	ARTSLDLPGVTNAASLIGTQQNN	[4] Phospho (ST)	-0.65	-0.43	-0.21	-0.22	0.021	0.063	0.184	0.12	8.15E+04	6.99E+04	5.41E+04	4.23E+04	4.88E+04	4.02E+04	4.76E+04	5.98E+04	4.51E+04	5.97E+04	6.65E+04	5.19E+04	807.73199	3	40.84
NUP159	YIL115C	LPETPSDEDGEVVEEEAQK	[6] Phospho (ST)	-0.20	-0.31	-0.81	0.10	0.213	0.160	0.039	0.27	5.84E+04	8.47E+04	9.81E+04	6.53E+04	7.05E+04	7.39E+04	5.13E+04	7.31E+04	7.07E+04	2.84E+04	5.76E+04	5.18E+04	1090.9603	2	75.25
ENT1	YDL161W	NQLVAASSPQQLQQQK	[8] Phospho (ST)	0.31	0.45	0.27	-0.14	0.087	0.126	0.168	0.32	1.57E+04	1.91E+04	2.45E+04	2.57E+04	2.62E+04	2.19E+04	1.76E+04	3.01E+04	3.36E+04	2.54E+04	1.86E+04	2.75E+04	616.63908	3	16.23
LSP1	YPL004C	KLSQLVK	[3] Phospho (ST)	0.52	0.16	-0.04	0.36	0.024	0.312	0.447	0.12	5.89E+03	8.18E+03	8.53E+03	1.03E+04	9.74E+03	1.24E+04	1.10E+04	5.78E+03	8.57E+03	4.95E+03	7.62E+03	9.39E+03	448.25423	2	35.27
EAP1	YKL204W	GPSSITDFLNLK	[4] Phospho (ST)	0.08	0.47	0.16	-0.39	0.435	0.180	0.388	0.16	2.07E+04	4.64E+04	2.06E+04	2.61E+04	4.07E+04	2.61E+04	5.14E+04	4.27E+04	2.78E+04	2.54E+04	4.75E+04	2.52E+04	686.33236	2	61.26
YLR108C	YLR108C	MSGQKGEIVVYTK	[11] Phospho (Y)	-0.20	0.00	0.16	-0.20	0.241	0.498	0.383	0.35	5.72E+04	5.03E+04	3.45E+04	3.28E+04	4.61E+04	4.47E+04	4.44E+04	2.43E+04	7.35E+04	2.20E+04	6.07E+04	7.59E+04	760.3679	2	20.95

SOD1	YJR104C	FEQASESEPTTVSYEIAGNSPNAER	[14] Phospho (Y)	0.89	0.48	0.37	0.41	0.020	0.047	0.021	0.12	2.44E+04	1.94E+04	2.21E+04	3.41E+04	5.32E+04	3.53E+04	2.66E+04	3.81E+04	2.74E+04	2.52E+04	3.08E+04	2.91E+04	699.05298	4	20.25
TRM44	YPL030W	KFEIDNGNESGEEDVK	[10] Phospho (ST)	-0.59	-0.32	0.03	-0.26	0.017	0.114	0.436	0.13	4.25E+04	3.17E+04	4.44E+04	2.44E+04	2.59E+04	2.85E+04	2.85E+04	2.69E+04	3.94E+04	3.84E+04	3.93E+04	4.31E+04	945.39456	2	54.39
RCN2	YOR220W	SNAASCTENDVNATASNPPKSPSITVNEFFH	[21] Phospho (ST)	-0.18	-0.14	-0.20	-0.03	0.310	0.320	0.293	0.45	8.17E+04	1.21E+05	6.82E+04	8.55E+04	9.59E+04	5.85E+04	9.33E+04	7.37E+04	7.84E+04	6.56E+04	1.02E+05	6.90E+04	1129.4933	3	40.54
RIM15	YFL033C	SQEDEEHTILSDSDETH	[11] Phospho (ST)	-0.13	1.20	1.26	-1.33	0.285	0.002	0.002	0.00	1.48E+04	1.13E+04	1.61E+04	1.56E+04	1.17E+04	1.14E+04	2.96E+04	3.76E+04	3.01E+04	3.91E+04	2.87E+04	3.35E+04	684.59547	3	32.05
IGD1	YFR017C	VPHGSPPQLGTR	[5] Phospho (ST)	0.80	0.80	0.58	0.00	0.010	0.028	0.085	0.49	1.20E+04	2.28E+04	2.18E+04	2.99E+04	3.36E+04	3.53E+04	3.42E+04	2.54E+04	3.89E+04	2.34E+04	2.42E+04	3.68E+04	663.32196	2	23.21
CRP1	YHR146W	SPALPQADDPIVETK	[1] Phospho (ST)	0.33	0.09	-0.36	0.24	0.129	0.297	0.055	0.20	3.29E+04	4.31E+04	3.88E+04	4.47E+04	6.12E+04	3.82E+04	3.57E+04	4.70E+04	3.98E+04	2.76E+04	3.55E+04	2.62E+04	830.89558	2	41.04
BUG1	YDL099W	SENNDQNDVDEESEEK	[13] Phospho (ST)	-0.37	-0.69	-0.27	0.32	0.327	0.223	0.380	0.29	8.03E+04	1.67E+04	3.66E+04	5.02E+04	3.41E+04	1.90E+04	1.77E+04	4.06E+04	2.47E+04	6.33E+04	2.44E+04	2.33E+04	980.85048	2	61.25
DEF1	YKL054C	KTESPLENVAELK	[4] Phospho (ST)	0.48	0.46	0.26	0.02	0.061	0.129	0.253	0.47	6.53E+03	1.18E+04	1.08E+04	1.18E+04	1.57E+04	1.33E+04	1.75E+04	9.70E+03	1.30E+04	7.64E+03	1.45E+04	1.28E+04	513.25542	3	30.59
SDS24	YBR214W	LSAVPMTQTPSQCLSCVHAQK	[15] Phospho (ST)	-0.61	-0.25	0.16	-0.36	0.096	0.028	0.273	0.22	4.20E+04	4.73E+04	3.98E+04	3.06E+04	4.28E+04	1.12E+04	3.46E+04	3.87E+04	3.54E+04	3.37E+04	5.76E+04	5.29E+04	808.36757	3	17.25
STE2	YFL026W	TFVSETADDIEK	[4] Phospho (ST)	-0.16	-0.24	-0.30	0.09	0.350	0.257	0.220	0.38	2.31E+04	4.66E+04	3.26E+04	2.25E+04	3.96E+04	2.98E+04	3.17E+04	3.18E+04	2.30E+04	2.32E+04	3.36E+04	2.63E+04	717.80601	2	58.76
ESF1	YDR365C	SSEDKEETTIEK	[2] Phospho (ST)	1.11	0.10	0.39	1.02	0.128	0.447	0.317	0.12	7.11E+03	1.16E+04	3.12E+04	2.89E+04	1.86E+04	6.07E+04	2.07E+04	1.13E+04	2.15E+04	1.77E+04	1.26E+04	3.52E+04	738.31138	2	39.71
FAS1	YKL182W	IPAVEYFGGESPVDVQSQVDSSSVSEDSAVFK	[25] Phospho (ST)	0.08	0.16	-0.23	-0.08	0.410	0.312	0.267	0.37	1.46E+05	1.94E+05	9.41E+04	1.44E+05	1.92E+05	1.24E+05	1.62E+05	1.86E+05	1.38E+05	1.26E+05	1.42E+05	1.04E+05	860.64325	4	46.68
YTA6	YPL074W	RNEQNLEPSSPVLVSATAVPAESK	[10] Phospho (ST)	0.01	0.09	-0.16	-0.08	0.467	0.249	0.209	0.11	3.69E+04	4.11E+04	3.08E+04	3.72E+04	3.69E+04	3.55E+04	3.79E+04	4.14E+04	3.68E+04	2.63E+04	3.46E+04	3.62E+04	868.42857	3	42.97
STB6	YKL072W	RNSIPFCNDGIHDTK	[3] Phospho (ST)	0.31	0.39	0.23	-0.07	0.159	0.179	0.238	0.42	1.28E+04	2.16E+04	1.55E+04	2.09E+04	2.47E+04	1.63E+04	2.98E+04	1.61E+04	1.92E+04	1.48E+04	2.38E+04	2.00E+04	618.6051	3	29.67
SPA2	YLL021W	AINSPIIRPSSSNGVPTTSR	[4] Phospho (ST)	0.26	0.09	0.10	0.17	0.042	0.387	0.348	0.26	2.24E+04	2.84E+04	2.81E+04	3.35E+04	3.03E+04	3.05E+04	3.60E+04	1.91E+04	2.88E+04	2.10E+04	2.84E+04	3.54E+04	712.02673	3	23.17
AKR1	YDR264C	AIRSGNEEESGNEQVNHNDEAEEDPLLTR	[4] Phospho (ST)|[10] Phospho (ST)	-0.62	-0.30	-0.33	-0.32	0.024	0.127	0.115	0.04	8.96E+04	6.14E+04	6.44E+04	4.59E+04	4.72E+04	4.68E+04	5.04E+04	6.75E+04	5.66E+04	6.21E+04	4.65E+04	6.26E+04	853.85525	4	27.6
PRK1	YIL095W	SVESFQSPQRK	[7] Phospho (ST)	-0.66	-0.08	-0.38	-0.58	0.121	0.433	0.226	0.03	2.91E+04	1.25E+04	1.60E+04	1.31E+04	1.01E+04	1.33E+04	1.46E+04	1.80E+04	2.21E+04	1.58E+04	1.16E+04	1.70E+04	686.81663	2	17.68
PCT1	YGR202C	EASPATEFANEFTGENSTAK	[3] Phospho (ST)	-1.18	-0.55	-0.76	-0.63	0.008	0.020	0.019	0.04	1.72E+05	1.87E+05	1.31E+05	7.08E+04	9.96E+04	4.58E+04	1.14E+05	1.16E+05	1.03E+05	7.91E+04	1.25E+05	8.58E+04	1090.9561	2	76.67
ASM4	YDL088C	EDDNTPAGHAGNPTNISSPIVANSPNK	[17] Phospho (ST)	0.30	0.02	-0.31	0.28	0.115	0.467	0.166	0.06	2.06E+04	3.18E+04	3.73E+04	3.75E+04	3.69E+04	3.61E+04	2.56E+04	2.89E+04	3.68E+04	2.12E+04	2.69E+04	2.44E+04	933.08577	3	32.21
SEC31	YDL195W	EALAFDNDESDAQDDANNEK	[10] Phospho (ST)	-0.14	-0.27	-0.03	0.12	0.293	0.207	0.450	0.33	1.09E+05	6.79E+04	9.19E+04	7.98E+04	9.59E+04	6.79E+04	5.44E+04	7.57E+04	9.39E+04	9.33E+04	8.50E+04	8.60E+04	1145.9355	2	63.1
DLD3	YEL071W	SCGYGHVGDGNIHLNIAVR	[1] Phospho (ST)|[4] Phospho (Y)	-0.31	-0.02	-0.57	-0.29	0.170	0.437	0.002	0.20	1.62E+04	1.82E+04	1.63E+04	1.08E+04	1.95E+04	1.06E+04	1.48E+04	1.94E+04	1.58E+04	1.11E+04	1.04E+04	1.27E+04	550.48718	4	17.57
CLA4	YNL298W	YAQNSSPTAAHFQPQR	[5] Phospho (ST)	0.09	0.32	0.30	-0.24	0.256	0.069	0.155	0.10	3.99E+04	4.51E+04	5.20E+04	4.54E+04	4.81E+04	5.21E+04	6.37E+04	4.70E+04	6.09E+04	5.09E+04	4.51E+04	7.29E+04	941.91531	2	23.19
DIG2	YDR480W	SAPPNITR	[1] Phospho (ST)	-1.25	-0.12	0.22	-1.13	0.065	0.412	0.329	0.02	2.42E+04	1.46E+04	4.27E+04	1.14E+04	9.76E+03	1.31E+04	1.88E+04	2.36E+04	3.25E+04	3.95E+04	2.84E+04	2.67E+04	468.22069	2	20.09
RPS6A	YPL090C	RASSLKA	[3] Phospho (ST)	-0.18	-0.03	0.43	-0.15	0.349	0.476	0.135	0.36	2.34E+04	1.08E+04	1.77E+04	1.97E+04	9.20E+03	1.70E+04	2.28E+04	1.30E+04	1.53E+04	2.88E+04	1.90E+04	2.21E+04	406.70485	2	15.11
SEC31	YDL195W	VATPLSGGVPPAPLPK	[3] Phospho (ST)	-1.01	-0.81	-0.48	-0.20	0.036	0.067	0.175	0.32	9.71E+04	1.56E+05	8.72E+04	3.77E+04	7.06E+04	6.03E+04	9.28E+04	4.44E+04	5.71E+04	4.14E+04	8.57E+04	1.16E+05	790.92638	2	37.08
CLA4	YNL298W	ISDNDFQNIGPAPRPPSSNSQGR	[20] Phospho (ST)	-0.28	0.03	-0.23	-0.30	0.056	0.443	0.120	0.06	5.10E+04	6.35E+04	6.70E+04	5.00E+04	4.68E+04	5.31E+04	5.07E+04	6.57E+04	6.86E+04	4.31E+04	5.39E+04	5.76E+04	845.38588	3	25.56
PAN1	YIR006C	GLDEDEDDGWSDEDESNNR	[11] Phospho (ST)	-0.15	0.32	0.22	-0.48	0.086	0.150	0.009	0.09	3.38E+04	3.19E+04	3.33E+04	2.60E+04	3.17E+04	3.15E+04	3.02E+04	5.42E+04	3.96E+04	3.87E+04	3.62E+04	4.06E+04	759.59609	3	15.6
PIB2	YGL023C	KPSLEFLPQPASSTNLNFNSNK	[3] Phospho (ST)	0.01	0.07	-0.01	-0.06	0.469	0.345	0.484	0.35	1.20E+05	1.40E+05	1.01E+05	1.15E+05	1.38E+05	1.11E+05	1.36E+05	1.36E+05	1.08E+05	9.77E+04	1.57E+05	1.04E+05	838.4082	3	59.44
RCN2	YOR220W	PFSYQEPLPKLSR	[12] Phospho (ST)	-0.02	0.38	0.37	-0.40	0.484	0.184	0.244	0.04	1.52E+04	4.23E+04	2.47E+04	2.70E+04	3.24E+04	2.17E+04	3.98E+04	3.48E+04	3.26E+04	2.57E+04	4.87E+04	3.20E+04	821.40669	2	26.5
SEC9	YGR009C	NSLNHSNSTLNVGPSR	[2] Phospho (ST)	-0.08	-0.10	0.04	0.02	0.273	0.223	0.457	0.46	3.09E+04	3.14E+04	3.36E+04	2.83E+04	2.69E+04	3.53E+04	3.17E+04	2.50E+04	3.28E+04	2.30E+04	2.90E+04	4.64E+04	888.90545	2	40.88
SEC18	YBR080C	SNAVIRPDFK	[1] Phospho (ST)	-0.17	-0.13	-0.32	-0.04	0.179	0.284	0.062	0.41	1.24E+04	1.51E+04	1.74E+04	1.27E+04	1.28E+04	1.45E+04	1.35E+04	1.13E+04	1.63E+04	1.20E+04	1.10E+04	1.29E+04	613.80014	2	17.09
FLC3	YGL139W	DHDDNSDYESNDTGVNDELK	[8] Phospho (Y)	-0.11	-0.02	-0.06	-0.09	0.298	0.459	0.400	0.29	4.84E+04	3.64E+04	3.69E+04	4.22E+04	3.19E+04	3.90E+04	3.76E+04	4.51E+04	3.74E+04	4.78E+04	3.74E+04	3.15E+04	787.95973	3	33.1
SCD5	YOR329C	IEPSNISPQHTYSNNVR	[7] Phospho (ST)	-0.05	0.38	0.13	-0.43	0.399	0.055	0.282	0.04	2.95E+04	3.69E+04	3.98E+04	3.23E+04	3.10E+04	3.95E+04	4.84E+04	3.79E+04	5.19E+04	3.26E+04	3.63E+04	4.73E+04	1018.4649	2	21.51
STF2	YGR008C	RGSNLQSHEQK	[3] Phospho (ST)	1.18	0.82	0.32	0.37	0.039	0.020	0.220	0.21	6.68E+03	9.20E+03	7.17E+03	1.97E+04	9.58E+03	2.31E+04	1.58E+04	9.97E+03	1.48E+04	1.35E+04	6.21E+03	9.14E+03	455.20889	3	20.02
SFL1	YOR140W	KNSSNQNYDIDSGAR	[4] Phospho (ST)	0.14	-0.39	-0.50	0.53	0.318	0.145	0.055	0.08	1.61E+04	1.04E+04	1.63E+04	1.99E+04	1.43E+04	1.30E+04	6.99E+03	1.32E+04	1.25E+04	1.06E+04	9.00E+03	1.08E+04	583.57941	3	44.12
BLM10	YFL007W	TANNDDDIKSPIPITNK	[10] Phospho (ST)	0.13	1.16	0.91	-1.03	0.187	0.004	0.001	0.01	1.24E+04	1.59E+04	1.36E+04	1.66E+04	1.36E+04	1.57E+04	3.64E+04	3.26E+04	2.50E+04	2.85E+04	2.56E+04	2.47E+04	645.97284	3	25.83
SNA2	R525W-A	YSHLSSSDDNYGSLA	[1] Phospho (Y)	0.18	0.75	0.19	-0.57	0.198	0.018	0.200	0.02	3.05E+04	4.91E+04	4.36E+04	4.76E+04	4.91E+04	4.30E+04	6.10E+04	8.34E+04	6.27E+04	4.58E+04	5.25E+04	4.25E+04	848.33172	2	37.86
SYP1	YCR030C	VSSTATSSIYQK	[10] Phospho (Y)	-0.20	0.16	0.00	-0.36	0.202	0.273	0.495	0.07	1.76E+04	1.33E+04	2.09E+04	1.46E+04	1.38E+04	1.68E+04	1.51E+04	2.07E+04	2.21E+04	2.21E+04	1.46E+04	1.53E+04	676.31072	2	46.81
BEM3	YPL115C	LRSPQNPNR	[3] Phospho (ST)	0.96	0.21	-0.11	0.75	0.078	0.362	0.394	0.14	1.51E+04	1.64E+04	8.36E+03	2.63E+04	1.39E+04	3.73E+04	2.45E+04	8.41E+03	1.30E+04	1.72E+04	9.91E+03	9.70E+03	581.27834	2	21.44
YMR086W	YMR086W	LDNSNSSESETVVNSENNLEK	[6] Phospho (ST)	-0.36	-0.50	-0.34	0.14	0.176	0.116	0.178	0.22	8.51E+04	4.27E+04	5.77E+04	5.46E+04	4.87E+04	4.11E+04	3.74E+04	4.74E+04	4.66E+04	5.19E+04	4.55E+04	4.89E+04	1195.0063	2	55.6
HNM1	YGL077C	VEEEIKPLDDMDSK	[13] Phospho (ST)	-0.79	-0.82	-0.34	0.02	0.054	0.050	0.167	0.49	7.69E+04	8.39E+04	7.41E+04	4.13E+04	7.43E+04	1.98E+04	4.89E+04	6.90E+04	1.56E+04	3.50E+04	8.53E+04	6.54E+04	864.37711	2	49.77
FAP7	YDL166C	MWLEQHPDGVTNEYQGPRSDDEDDEDSE	[19] Phospho (ST)|[27] Phospho (ST)	-1.01	-0.23	-0.19	-0.78	0.129	0.398	0.301	0.29	1.50E+05	2.35E+05	1.35E+05	1.11E+04	2.01E+05	4.57E+04	2.90E+04	3.18E+05	9.64E+04	1.10E+05	1.80E+05	1.66E+05	1151.752	3	24.19
YLR413W	YLR413W	AVQESDSTTSRIIEEHESPIDAEK	[5] Phospho (ST)|[10] Phospho (ST)|[18] Phos	-1.09	-0.58	-0.38	-0.51	0.024	0.138	0.041	0.27	1.74E+05	1.61E+05	1.29E+05	2.65E+04	1.17E+05	7.50E+04	5.16E+04	1.78E+05	8.14E+04	1.27E+05	1.26E+05	1.04E+05	971.06612	3	15.9
BRR2	YER172C	RELDSGDDQPQSSEAK	[5] Phospho (ST)	0.36	-0.12	0.04	0.48	0.041	0.288	0.407	0.04	2.72E+04	2.13E+04	2.39E+04	3.57E+04	2.87E+04	2.84E+04	1.90E+04	1.97E+04	2.77E+04	2.83E+04	2.11E+04	2.50E+04	921.38205	2	61.62
LSP1	YPL004C	ALLELLDDSPVTPGEARPAYDGYEASR	[12] Phospho (ST)	2.17	1.81	0.67	0.36	0.003	0.019	0.161	0.18	2.40E+04	4.08E+04	1.89E+04	1.14E+05	1.58E+05	1.05E+05	1.42E+05	7.53E+04	7.64E+04	3.03E+04	7.01E+04	3.25E+04	995.80293	3	52.04
YDR365W-B	R365W-B	DFRHSDSYSENETNHTNVPISSTGGTNNK	[7] Phospho (ST)|[8] Phospho (Y)	-1.59	-0.97	-0.32	-0.62	0.022	0.052	0.243	0.03	2.95E+05	1.57E+05	1.58E+05	8.08E+04	5.40E+04	6.83E+04	8.66E+04	1.27E+05	9.86E+04	2.07E+05	1.14E+05	1.67E+05	1123.4559	3	22.97
TOS4	YLR183C	TASESIGNFGK	[3] Phospho (ST)	-8.39	-9.36	-4.60	0.95	0.000	0.000	0.000	0.07	3.77E+04	5.43E+04	5.26E+04	1.97E+02	9.07E+01	1.14E+02	5.72E+01	2.75E+01	1.05E+02	2.08E+03	2.03E+03	1.81E+03	595.75836	2	60.57
IBD2	YNL164C	IDGQSAYHIDSAEEK	[11] Phospho (ST)	-0.05	-0.06	-0.06	0.01	0.409	0.410	0.399	0.47	1.97E+04	3.15E+04	2.58E+04	2.50E+04	2.30E+04	2.64E+04	2.87E+04	1.83E+04	2.67E+04	2.11E+04	2.58E+04	2.69E+04	871.86766	2	45.41
PTK2	YJR059W	SSVALQDLIK	[2] Phospho (ST)	-0.64	-0.51	-0.60	-0.13	0.019	0.057	0.032	0.31	2.18E+04	2.65E+04	1.85E+04	1.28E+04	1.65E+04	1.35E+04	1.79E+04	1.80E+04	1.10E+04	1.31E+04	1.84E+04	1.25E+04	577.2978	2	45.49
YLR257W	YLR257W	GESYQSAEQEIDHTAPEK	[6] Phospho (ST)	1.39	0.86	0.93	0.54	0.003	0.020	0.014	0.04	7.87E+03	1.05E+04	1.22E+04	3.00E+04	2.91E+04	2.12E+04	1.96E+04	2.19E+04	1.37E+04	1.45E+04	2.15E+04	2.22E+04	700.29204	3	48.46
SEC9	YGR009C	NSLNHSNSTLNVGPSR	[6] Phospho (ST)|[9] Phospho (ST)	-0.18	-0.23	-0.10	0.05	0.179	0.166	0.348	0.41	3.69E+04	2.92E+04	4.07E+04	3.45E+04	2.67E+04	3.28E+04	2.43E+04	3.59E+04	3.09E+04	4.08E+04	2.58E+04	3.33E+04	928.88879	2	16.35
PGM2	YMR105C	SQYQKTAEEYLK	[3] Phospho (Y)	0.29	0.23	0.69	0.06	0.321	0.375	0.085	0.46	2.36E+04	4.62E+03	1.74E+04	1.66E+04	1.33E+04	2.58E+04	2.75E+04	8.49E+03	1.76E+04	2.56E+04	2.35E+04	2.44E+04	523.24131	3	16.62
TYS1	YGR185C	GYPVATPQK	[6] Phospho (ST)	0.73	2.28	1.53	-1.56	0.030	0.004	0.004	0.01	2.34E+03	5.15E+03	5.93E+03	7.50E+03	6.88E+03	7.86E+03	2.77E+04	1.64E+04	2.14E+04	1.05E+04	1.32E+04	1.51E+04	520.74432	2	20.18
RPC31	YNL151C	ELAEDVDDASTGDGAAK	[10] Phospho (ST)	-0.53	-1.76	-0.04	1.23	0.010	0.000	0.427	0.00	3.14E+04	2.78E+04	3.52E+04	1.96E+04	2.42E+04	2.16E+04	1.15E+04	8.10E+03	8.25E+03	3.50E+04	2.29E+04	3.38E+04	872.35223	2	54.54
YTA7	YGR270W	EQSQENILQEPDLK	[3] Phospho (ST)	1.42	0.75	0.35	0.68	0.002	0.025	0.004	0.03	1.55E+04	1.83E+04	1.75E+04	4.14E+04	5.56E+04	4.09E+04	2.44E+04	3.70E+04	2.49E+04	2.25E+04	2.20E+04	2.11E+04	875.89944	2	53.49
NTH1	YDR001C	RGSEDDTYSSSQGNR	[3] Phospho (ST)	0.73	-1.41	-0.73	2.13	0.130	0.144	0.231	0.00	4.26E+04	1.39E+04	9.25E+03	4.15E+04	2.96E+04	3.80E+04	4.27E+03	4.43E+03	1.61E+04	1.65E+04	8.15E+03	1.49E+04	869.83692	2	82.02
IML2	YJL082W	SRTNDSSLLPGYMDSATLLHPGK	[6] Phospho (ST)|[7] Phospho (ST)	-1.06	-0.10	-0.21	-0.96	0.066	0.435	0.319	0.15	1.17E+05	1.39E+05	6.65E+04	4.17E+04	9.10E+04	2.17E+04	7.28E+04	1.70E+05	5.81E+04	7.73E+04	1.30E+05	7.20E+04	874.05617	3	53.17
SUP45	YBR143C	VNFEQLVDESEDEYYDEDEGSDYDFI	[10] Phospho (ST)|[23] Phospho (Y)	-0.92	-0.22	-0.77	-0.70	0.133	0.381	0.158	0.14	1.32E+06	7.13E+05	3.52E+05	4.80E+05	4.94E+05	2.88E+05	5.66E+05	1.06E+06	4.20E+05	4.54E+05	5.74E+05	3.65E+05	1108.7343	3	33.38
TCB3	YML072C	SPSNLNSTSVTPR	[9] Phospho (ST)|[11] Phospho (ST)	-0.34	-0.53	-0.24	0.19	0.209	0.156	0.278	0.27	6.68E+04	3.00E+04	4.56E+04	3.80E+04	3.31E+04	4.18E+04	1.99E+04	4.27E+04	3.60E+04	3.90E+04	3.47E+04	4.70E+04	760.31445	2	16.92
SCY1	YGL083W	ILNSPPQTPSSR	[4] Phospho (ST)	-0.34	0.19	0.17	-0.53	0.064	0.168	0.137	0.01	2.64E+04	3.57E+04	3.57E+04	2.57E+04	2.28E+04	2.89E+04	3.41E+04	3.47E+04	4.26E+04	3.65E+04	3.51E+04	3.87E+04	688.83259	2	43.49
MOB1	YIL106W	WNTANAANNAGSVSPTK	[12] Phospho (ST)	0.48	0.95	0.72	-0.47	0.001	0.002	0.001	0.01	8.02E+03	8.05E+03	9.30E+03	1.17E+04	1.17E+04	1.19E+04	1.40E+04	1.72E+04	1.78E+04	1.35E+04	1.32E+04	1.51E+04	594.93215	3	30.13
MAK5	YBR142W	AADELGIDVDSDEDDISK	[11] Phospho (ST)	-0.45	-0.18	0.20	-0.27	0.251	0.222	0.118	0.35	2.64E+04	3.71E+04	3.18E+04	4.26E+03	4.30E+04	2.24E+04	2.50E+04	3.43E+04	2.48E+04	3.39E+04	3.89E+04	3.68E+04	662.94078	3	21.38
NCB2	YDR397C	LHHNSVSDPVK	[5] Phospho (ST)	-0.43	-0.41	-0.45	-0.02	0.088	0.191	0.098	0.48	2.00E+04	3.23E+04	2.57E+04	1.53E+04	2.11E+04	2.16E+04	2.93E+04	1.03E+04	1.92E+04	1.47E+04	1.86E+04	2.41E+04	656.80603	2	26.76
GPT2	YKR067W	RDGYDVSSDAESSISR	[8] Phospho (ST)	0.18	0.23	0.02	-0.05	0.258	0.192	0.476	0.34	2.08E+04	3.51E+04	2.31E+04	2.61E+04	3.03E+04	3.30E+04	3.30E+04	3.15E+04	2.82E+04	2.97E+04	2.40E+04	2.63E+04	912.37645	2	46.31
BUD3	YCL014W	DFVALSDDEDEDGK	[6] Phospho (ST)	-0.32	0.37	0.21	-0.70	0.088	0.029	0.175	0.00	5.72E+04	7.88E+04	7.03E+04	4.54E+04	6.48E+04	5.46E+04	8.35E+04	9.77E+04	8.57E+04	7.84E+04	9.48E+04	6.61E+04	817.80935	2	67.43
MAM3	YOL060C	NSPDSISIPNSGANHGNENQNVTISTSYQNTK	[28] Phospho (Y)	-0.60	-0.43	-0.29	-0.18	0.006	0.032	0.063	0.18	8.71E+04	7.45E+04	6.96E+04	5.55E+04	4.56E+04	5.12E+04	4.82E+04	6.79E+04	5.60E+04	5.71E+04	7.32E+04	5.86E+04	1156.8471	3	21.13
PAR32	YDL173W	SHQSLHATTSSPNNNAPIVVGR	[10] Phospho (ST)	0.62	0.54	0.27	0.08	0.001	0.002	0.137	0.19	3.85E+04	4.18E+04	4.43E+04	6.66E+04	5.98E+04	6.46E+04	5.94E+04	5.62E+04	6.53E+04	5.10E+04	3.83E+04	6.08E+04	789.71206	3	30.4
HER1	YOR227W	IRTAQDQPVK	[3] Phospho (ST)	0.90	-0.48	-0.09	1.37	0.087	0.330	0.363	0.11	1.08E+04	1.03E+04	7.38E+03	1.30E+04	1.27E+04	2.74E+04	1.78E+04	1.85E+03	7.81E+02	7.10E+03	8.93E+03	1.08E+04	618.31019	2	22.63
PAF1	YBR279W	LDDGDSDDENLDVNHIISR	[6] Phospho (ST)	-0.49	-0.09	-0.28	-0.41	0.170	0.362	0.130	0.22	3.76E+04	5.23E+04	4.04E+04	1.21E+04	4.93E+04	3.11E+04	3.43E+04	5.04E+04	3.80E+04	3.09E+04	4.33E+04	3.28E+04	741.31449	3	62.09
PKH3	YDR466W	ASSEPSSPPPISR	[7] Phospho (ST)	-0.06	-0.08	-0.04	0.02	0.336	0.269	0.392	0.42	2.60E+04	3.04E+04	3.40E+04	2.58E+04	3.12E+04	2.96E+04	2.80E+04	2.73E+04	3.02E+04	3.15E+04	2.64E+04	3.01E+04	696.31453	2	21.79
MKT1	YNL085W	SNLSSPSSASSSASPATTVTK	[4] Phospho (ST)|[5] Phospho (ST)	-0.13	0.12	0.09	-0.25	0.276	0.389	0.388	0.28	6.14E+04	4.27E+04	5.93E+04	5.79E+04	4.72E+04	4.42E+04	4.17E+04	8.80E+04	4.79E+04	7.75E+04	4.51E+04	5.14E+04	709.63488	3	16.69
TOF1	YNL273W	RSLEASAADESDEDEEAIR	[11] Phospho (ST)	-0.15	-0.09	-0.23	-0.06	0.218	0.311	0.095	0.40	4.41E+04	5.62E+04	5.31E+04	4.00E+04	4.32E+04	5.50E+04	5.17E+04	3.85E+04	5.36E+04	3.76E+04	4.48E+04	4.83E+04	1086.9506	2	57.23
PEX25	YPL112C	FSAGSGSESHTESSRSDDEDSQAK	[21] Phospho (ST)	0.02	-0.43	-0.19	0.45	0.474	0.093	0.297	0.02	5.44E+04	3.19E+04	3.94E+04	4.88E+04	3.82E+04	4.02E+04	3.04E+04	2.85E+04	3.41E+04	4.69E+04	2.60E+04	3.72E+04	861.00346	3	42.03
UTP22	YGR090W	TVPEQENDESDTSPESNEVATNTAATR	[10] Phospho (ST)|[12] Phospho (ST)	-0.89	-0.32	0.13	-0.57	0.019	0.228	0.340	0.13	1.76E+05	1.05E+05	1.45E+05	6.53E+04	7.87E+04	8.67E+04	6.30E+04	1.58E+05	1.21E+05	1.97E+05	1.14E+05	1.57E+05	1018.0703	3	15.48
YJR029W	YJR029W	LTESTVNHTNHSDDELPGHLLLDSGASR	[2] Phospho (ST)	-0.73	0.06	0.08	-0.79	0.029	0.419	0.397	0.01	4.71E+04	7.66E+04	5.42E+04	3.74E+04	3.36E+04	3.63E+04	7.57E+04	5.34E+04	5.62E+04	4.73E+04	7.16E+04	6.88E+04	774.60766	4	32.43
DIG1	YPL049C	TSQPQQQSPSLLQGEIR	[8] Phospho (ST)	-0.49	-0.39	-0.81	-0.10	0.019	0.145	0.002	0.40	6.07E+04	6.50E+04	5.09E+04	4.66E+04	4.44E+04	3.48E+04	3.07E+04	6.56E+04	3.88E+04	3.26E+04	3.62E+04	3.17E+04	988.97622	2	35.5
NBP2	YDR162C	TKLDISD	[6] Phospho (ST)	0.42	0.52	0.28	-0.09	0.039	0.073	0.220	0.35	9.71E+03	6.59E+03	9.50E+03	1.20E+04	1.01E+04	1.25E+04	1.15E+04	1.58E+04	9.68E+03	1.43E+04	8.50E+03	8.58E+03	436.1942	2	21.6
SPT6	YGR116W	EEDDRLSEDDLDLLMENAGVER	[7] Phospho (ST)	-0.28	0.23	0.08	-0.51	0.281	0.212	0.428	0.14	1.08E+05	1.36E+05	8.32E+04	7.75E+04	1.41E+05	5.10E+04	1.49E+05	1.32E+05	1.01E+05	7.07E+04	1.72E+05	1.04E+05	881.71107	3	41.18
FYV8	YGR196C	EVGYLSDGVPK	[6] Phospho (ST)	-0.14	0.44	-0.09	-0.58	0.329	0.063	0.411	0.00	2.08E+04	3.98E+04	3.16E+04	2.36E+04	2.87E+04	3.15E+04	4.26E+04	3.90E+04	4.34E+04	2.01E+04	3.86E+04	2.81E+04	622.28463	2	23.74
MRD1	YPR112C	DEAPNLVIENESDDEYSALNR	[16] Phospho (Y)	0.53	0.48	0.15	0.05	0.115	0.056	0.243	0.45	4.94E+04	6.78E+04	4.88E+04	6.31E+04	1.12E+05	6.41E+04	6.93E+04	9.45E+04	6.74E+04	6.24E+04	6.82E+04	5.29E+04	825.01896	3	59.03
UIP4	YPL186C	EVDEHSNENNVATLNNEEDGGSAGEEK	[22] Phospho (ST)	1.15	0.96	0.67	0.19	0.000	0.001	0.030	0.02	2.59E+04	1.84E+04	2.47E+04	5.11E+04	5.19E+04	4.97E+04	4.33E+04	4.22E+04	4.85E+04	4.46E+04	2.84E+04	3.68E+04	989.73072	3	45.42
YNL054W-B	L054W-B	AHNVSTSNNSPSTDNDSISK	[5] Phospho (ST)	-0.37	-0.71	-0.46	0.34	0.180	0.083	0.140	0.09	9.97E+04	4.88E+04	6.41E+04	6.15E+04	5.07E+04	5.25E+04	3.84E+04	3.61E+04	5.56E+04	5.66E+04	4.53E+04	5.27E+04	1077.9512	2	61.36
SWI4	YER111C	ILENSPILYR	[5] Phospho (ST)	0.83	2.17	1.69	-1.35	0.204	0.006	0.027	0.03	1.61E+03	8.52E+03	1.28E+04	2.50E+03	1.93E+04	1.89E+04	4.48E+04	2.81E+04	3.07E+04	1.49E+04	3.35E+04	2.58E+04	649.33182	2	31.71
GCS1	YDL226C	SATPANSSNGANFQK	[3] Phospho (ST)	0.53	-0.66	0.09	1.19	0.103	0.117	0.417	0.01	1.56E+04	7.52E+03	1.88E+04	2.46E+04	1.66E+04	1.92E+04	6.40E+03	8.37E+03	1.17E+04	1.55E+04	1.07E+04	1.84E+04	787.33612	2	57.96

ASF1	YJL115W	IEGGSTDIESTPK	[6] Phospho (ST)	0.56	0.66	0.71	-0.09	0.015	0.064	0.028	0.38	1.34E+04	1.67E+04	2.01E+04	2.70E+04	2.21E+04	2.50E+04	1.84E+04	2.62E+04	3.45E+04	2.71E+04	2.15E+04	3.37E+04	707.31044	2	41.31
YLR257W	YLR257W	GSTPCLIGDSIR	[3] Phospho (ST)	-0.09	0.31	-0.11	-0.40	0.387	0.092	0.356	0.06	1.89E+04	2.71E+04	1.79E+04	1.57E+04	2.58E+04	1.85E+04	2.88E+04	2.57E+04	2.47E+04	1.53E+04	2.49E+04	1.90E+04	678.30529	2	57.07
FPK1	YNR047W	TNSFVGTEEYIAPEVIR	[3] Phospho (ST)	-0.15	0.17	-0.30	-0.31	0.365	0.357	0.251	0.19	9.73E+04	1.62E+05	7.16E+04	9.36E+04	1.19E+05	8.60E+04	1.38E+05	1.53E+05	8.08E+04	8.82E+04	1.04E+05	7.67E+04	1002.9703	2	69.28
KCS1	YDR017C	LGSSPSFLTQK	[4] Phospho (ST)	-0.12	0.30	-0.46	-0.42	0.375	0.150	0.120	0.06	1.97E+04	3.52E+04	2.28E+04	1.65E+04	2.87E+04	2.63E+04	2.97E+04	3.08E+04	3.51E+04	1.67E+04	2.28E+04	1.69E+04	622.80053	2	49.15
PTK2	YJR059W	SLGSPSVSSSK	[4] Phospho (ST)	0.81	1.08	0.84	-0.27	0.017	0.003	0.022	0.08	1.39E+04	8.42E+03	1.57E+04	2.47E+04	1.81E+04	2.39E+04	2.37E+04	2.78E+04	2.88E+04	2.76E+04	1.84E+04	2.22E+04	558.2524	2	33.07
JIP4	YDR475C	ALSLGPEESDNK	[3] Phospho (ST)	0.26	0.57	0.56	-0.31	0.276	0.103	0.103	0.06	7.60E+03	1.95E+04	2.50E+04	2.04E+04	1.88E+04	2.32E+04	2.18E+04	2.62E+04	2.93E+04	2.89E+04	2.48E+04	2.30E+04	670.29355	2	48.24
TIF4632	YGL049C	TVNKSDDETINSVITTEENTVK	[5] Phospho (ST)	-0.48	0.31	-0.22	-0.79	0.099	0.181	0.214	0.04	3.91E+04	5.31E+04	3.32E+04	2.98E+04	3.85E+04	2.19E+04	5.03E+04	6.62E+04	3.91E+04	3.03E+04	4.09E+04	3.67E+04	839.72656	3	41.83
MAK11	YKL021C	KRDAETADIGDQSEVESDTEELK	[17] Phospho (ST)	0.13	-0.29	0.82	0.42	0.292	0.225	0.061	0.07	2.67E+04	2.52E+04	4.04E+04	3.48E+04	3.53E+04	3.11E+04	3.40E+04	1.85E+04	2.31E+04	7.51E+04	3.78E+04	4.99E+04	882.38613	3	60.34
MAK11	YKL021C	DAETADIGDQSEVESDTEELK	[15] Phospho (ST)	-0.67	-0.20	-0.11	-0.47	0.008	0.021	0.192	0.03	7.93E+04	7.53E+04	7.35E+04	4.37E+04	6.10E+04	3.89E+04	6.17E+04	7.14E+04	6.56E+04	6.28E+04	8.11E+04	6.71E+04	1180.9792	2	49.9
MCH4	YOL119C	LTNVTSR	[6] Phospho (ST)	-0.02	-0.03	-0.16	0.01	0.485	0.477	0.384	0.48	1.51E+04	5.75E+03	9.35E+03	9.77E+03	9.53E+03	1.06E+04	7.18E+03	8.52E+03	1.39E+04	1.28E+04	6.89E+03	7.33E+03	435.70754	2	24.57
YMR114C	YMR114C	REEANLSPK	[7] Phospho (ST)	0.38	-0.61	0.15	0.99	0.141	0.203	0.355	0.04	2.10E+04	1.03E+04	1.13E+04	1.84E+04	1.75E+04	1.96E+04	1.68E+04	2.97E+03	8.14E+03	1.40E+04	1.36E+04	1.98E+04	562.26062	2	34.19
PAF1	YBR279W	TEGSEQEGENEKDEEIK	[4] Phospho (ST)	0.18	-0.14	-0.53	0.32	0.199	0.304	0.041	0.09	2.03E+04	1.38E+04	1.94E+04	2.31E+04	1.80E+04	1.96E+04	1.32E+04	1.54E+04	2.01E+04	1.43E+04	1.01E+04	1.26E+04	677.6075	3	28.2
MSH6	YDR097C	STTTDEDLSSSQSRR	[11] Phospho (ST)	0.49	-1.11	-0.85	1.60	0.055	0.019	0.053	0.00	2.82E+04	1.61E+04	1.90E+04	3.27E+04	2.59E+04	3.02E+04	9.84E+03	8.37E+03	1.10E+04	1.67E+04	7.41E+03	1.09E+04	875.36828	2	26.73
PIL1	YGR086C	ALLELLDDSPVTPGETRPAYDGYEASK	[12] Phospho (ST)	0.75	0.48	-0.35	0.27	0.078	0.243	0.323	0.25	1.87E+04	4.90E+04	1.68E+04	4.48E+04	5.43E+04	4.30E+04	5.99E+04	2.85E+04	2.97E+04	1.32E+04	3.40E+04	1.93E+04	747.60441	4	52.6
YLR407W	YLR407W	LTDESEESSSANNTTTTASHTLSNSK	[10] Phospho (ST)	0.05	-0.14	0.63	0.19	0.430	0.327	0.064	0.15	4.34E+04	2.32E+04	3.51E+04	3.90E+04	3.01E+04	3.63E+04	2.73E+04	2.97E+04	3.55E+04	5.38E+04	3.85E+04	6.55E+04	931.39626	3	52.01
BBC1	YJL020C	ARLSMFNQDITEQVPLPK	[4] Phospho (ST)	-0.30	0.12	0.38	-0.43	0.248	0.401	0.133	0.23	8.00E+04	6.00E+04	4.22E+04	5.34E+04	6.55E+04	2.89E+04	5.64E+04	9.99E+04	4.24E+04	8.62E+04	8.93E+04	6.13E+04	723.02588	3	20.49
SSD1	YDR293C	RSSTINNDSDSLSSPTK	[14] Phospho (ST)	-0.24	-0.08	0.32	-0.16	0.216	0.375	0.108	0.30	1.97E+04	1.30E+04	1.49E+04	1.69E+04	1.01E+04	1.33E+04	1.56E+04	1.16E+04	1.76E+04	2.19E+04	1.62E+04	2.11E+04	630.28145	3	33.42
SNT1	YCR033W	SVSKPNAPLEPDNIK	[1] Phospho (ST)	-0.53	-0.26	-0.28	-0.27	0.006	0.011	0.005	0.08	2.37E+04	2.39E+04	2.39E+04	1.41E+04	1.97E+04	1.58E+04	2.02E+04	1.79E+04	2.15E+04	1.97E+04	1.81E+04	2.12E+04	844.91614	2	25.47
ZUO1	YGR285C	NHTWSEFERIEAEK	[5] Phospho (ST)	-0.16	-0.56	0.03	0.40	0.304	0.199	0.464	0.27	1.43E+05	1.63E+05	9.48E+04	1.48E+05	9.54E+04	1.15E+05	1.70E+05	3.42E+04	6.68E+04	8.48E+04	1.59E+05	1.66E+05	928.40505	2	29.67
PEX19	YDL065C	DSDGVQVANESEEDPELK	[11] Phospho (ST)	-0.09	0.22	0.02	-0.31	0.317	0.094	0.447	0.03	8.71E+04	7.00E+04	9.60E+04	7.65E+04	7.13E+04	9.06E+04	9.41E+04	9.37E+04	1.08E+05	9.24E+04	7.28E+04	9.22E+04	1020.9189	2	45.92
SPC110	YDR356W	RNTTQTQVVSPTK	[10] Phospho (ST)	0.87	0.61	0.61	0.26	0.071	0.137	0.111	0.23	4.14E+03	4.65E+03	1.14E+04	1.06E+04	1.01E+04	1.62E+04	1.16E+04	7.28E+03	1.19E+04	1.16E+04	8.89E+03	1.04E+04	513.92224	3	15.85
UBP1	YDL122W	AAQQDSSEDENIGGEYYTK	[6] Phospho (ST)|[7] Phospho (ST)	-1.26	-0.68	-0.97	-0.58	0.024	0.135	0.002	0.29	1.86E+05	1.46E+05	1.56E+05	8.19E+03	1.14E+05	8.18E+04	3.63E+04	1.91E+05	7.78E+04	8.88E+04	8.72E+04	7.27E+04	1132.918	2	31.92
PCM1	YEL058W	LQGQYVGVMITASHNPYQDNGVK	[13] Phospho (ST)	-1.19	-0.94	-0.47	-0.25	0.017	0.020	0.073	0.27	1.44E+05	1.66E+05	9.95E+04	5.16E+04	8.67E+04	4.14E+04	8.87E+04	6.99E+04	5.50E+04	8.79E+04	1.12E+05	9.62E+04	867.07136	3	22.89
YBR085C-A	R085C-A	QSTNFTHSTGSFLQSAPVELTTVSGYQEFLK	[11] Phospho (ST)	-0.61	0.28	0.02	-0.89	0.140	0.268	0.480	0.02	2.32E+05	2.64E+05	9.50E+04	1.46E+05	1.44E+05	9.75E+04	2.94E+05	2.49E+05	1.75E+05	1.92E+05	2.56E+05	1.53E+05	1162.2157	3	52.85
DOA1	YKL213C	NTNGISLDQPNDNASSSAVSPSK	[20] Phospho (ST)	-0.19	0.56	0.26	-0.75	0.272	0.062	0.207	0.01	5.51E+04	2.80E+04	5.09E+04	4.02E+04	3.88E+04	3.82E+04	5.51E+04	6.36E+04	7.87E+04	5.68E+04	4.41E+04	5.93E+04	1192.0247	2	28.56
JIP4	YDR475C	SADASIPTISNIK	[1] Phospho (ST)	-0.53	0.02	-0.12	-0.56	0.044	0.450	0.296	0.03	3.39E+04	4.08E+04	3.03E+04	2.41E+04	3.07E+04	1.78E+04	3.55E+04	4.03E+04	3.09E+04	2.83E+04	3.98E+04	2.83E+04	698.84016	2	29.7
IST2	YBR086C	SSAESSNATNNNTLGTESK	[5] Phospho (ST)	0.24	0.38	0.74	-0.13	0.300	0.171	0.102	0.32	1.79E+04	8.10E+03	2.13E+04	2.44E+04	1.76E+04	1.38E+04	1.68E+04	2.18E+04	2.27E+04	3.77E+04	1.85E+04	2.30E+04	664.61111	3	32.67
NPR3	YHL023C	KVNSGEADTVYDSNIGHEASTDTPNLR	[4] Phospho (ST)	-0.35	-0.36	-0.58	0.00	0.003	0.056	0.032	0.49	4.92E+04	5.44E+04	5.55E+04	4.32E+04	4.00E+04	4.16E+04	5.16E+04	3.33E+04	3.95E+04	2.30E+04	3.79E+04	4.56E+04	990.77587	3	54.58
ARP4	YJL081C	STSPAANSADTPNETGK	[3] Phospho (ST)	-0.04	-0.04	-0.28	0.00	0.415	0.402	0.137	0.49	3.44E+04	2.44E+04	2.86E+04	3.25E+04	2.45E+04	2.79E+04	2.76E+04	2.80E+04	2.95E+04	2.97E+04	2.17E+04	2.08E+04	864.36127	2	55.91
UME6	YDR207C	RDSDNAVHAAASPLAPSNTPSDPK	[3] Phospho (ST)	0.45	-0.24	-0.16	0.69	0.033	0.081	0.077	0.02	3.09E+04	3.05E+04	3.35E+04	3.74E+04	4.03E+04	5.21E+04	3.21E+04	2.49E+04	2.36E+04	2.56E+04	2.81E+04	3.13E+04	833.38078	3	30.54
SUI3	YPL237W	DSSVDAFEK	[3] Phospho (ST)	0.84	0.60	0.28	0.24	0.008	0.079	0.138	0.20	7.57E+03	4.72E+03	8.18E+03	1.39E+04	1.14E+04	1.15E+04	6.89E+03	1.22E+04	1.21E+04	8.92E+03	8.64E+03	7.34E+03	539.21073	2	32.93
BBC1	YJL020C	NGSINSLTK	[3] Phospho (ST)	0.55	0.61	0.69	-0.06	0.089	0.119	0.062	0.42	7.50E+03	2.69E+03	6.96E+03	9.55E+03	7.46E+03	8.16E+03	5.73E+03	9.47E+03	1.11E+04	1.02E+04	7.28E+03	1.02E+04	507.23705	2	20.55
BFR2	YDR299W	NGESDLSDYGNSNTEETK	[4] Phospho (ST)|[7] Phospho (ST)	0.04	-0.30	-0.26	0.35	0.454	0.320	0.300	0.25	7.82E+04	3.26E+04	5.61E+04	6.56E+04	5.35E+04	5.29E+04	1.73E+04	7.31E+04	4.49E+04	6.56E+04	3.84E+04	3.51E+04	1060.3735	2	44.58
RTC1	YOL138C	LSSHTAPIIGSPR	[11] Phospho (ST)	0.04	0.53	0.31	-0.49	0.441	0.063	0.190	0.05	1.10E+04	1.89E+04	1.34E+04	1.23E+04	1.67E+04	1.56E+04	2.42E+04	1.62E+04	2.21E+04	1.30E+04	2.20E+04	1.86E+04	708.35594	2	26.45
ECM21	YBL101C	TTSVSGPSGYSDDAGVPNVNR	[3] Phospho (ST)	0.03	0.08	-0.15	-0.05	0.438	0.183	0.003	0.40	4.68E+04	4.71E+04	4.45E+04	4.48E+04	3.83E+04	5.83E+04	4.49E+04	5.38E+04	4.81E+04	4.19E+04	4.06E+04	4.18E+04	1080.4681	2	54.04
QDR3	YBR043C	TNLESTASNSR	[8] Phospho (ST)	0.02	-0.31	-0.52	0.33	0.475	0.167	0.129	0.20	1.18E+04	7.91E+03	1.16E+04	1.43E+04	9.05E+03	8.46E+03	5.88E+03	1.04E+04	8.91E+03	1.13E+04	5.68E+03	4.79E+03	630.26668	2	23.74
UPS3	YDR185C	FSDNAVK	[2] Phospho (ST)	-0.05	-0.04	0.05	-0.02	0.417	0.442	0.399	0.48	5.43E+03	6.64E+03	8.01E+03	5.30E+03	6.17E+03	7.90E+03	5.56E+03	5.94E+03	8.07E+03	7.56E+03	6.71E+03	6.48E+03	430.68116	2	16.47
MSS4	YDR208W	AKEDDLQLADTASIEEQPQTQGPIR	[13] Phospho (ST)	0.26	0.58	0.11	-0.32	0.133	0.011	0.353	0.05	2.99E+04	4.32E+04	3.46E+04	3.58E+04	4.90E+04	4.42E+04	5.74E+04	4.77E+04	5.61E+04	2.77E+04	4.78E+04	4.07E+04	945.11265	3	48.61
BUD3	YCL014W	SINVTTSNNK	[1] Phospho (ST)	-0.77	0.97	0.59	-1.74	0.186	0.110	0.240	0.03	1.66E+04	2.08E+03	1.65E+04	7.27E+03	6.90E+03	6.49E+03	1.09E+04	2.84E+04	2.98E+04	2.86E+04	1.53E+04	8.93E+03	579.26368	2	36.18
LAG1	YHL003C	RNSSVGKIDLGDTVPGFAAMPESAASK	[3] Phospho (ST)|[4] Phospho (ST)	-1.79	-0.94	-0.90	-0.86	0.014	0.061	0.064	0.11	1.23E+05	1.32E+05	6.49E+04	2.56E+04	4.58E+04	2.09E+04	5.35E+04	8.31E+04	3.06E+04	4.23E+04	8.74E+04	4.17E+04	955.76813	3	29.94
ENT1	YDL161W	LNELLATGTGIDTFGNVGEAR	[9] Phospho (ST)	-0.22	0.21	-0.02	-0.43	0.340	0.327	0.485	0.13	6.03E+04	1.35E+05	6.52E+04	6.52E+04	1.01E+05	5.78E+04	1.30E+05	9.12E+04	8.05E+04	6.64E+04	1.18E+05	7.28E+04	1114.5342	2	59.43
TVP18	YMR071C	NPTDDDFPHEAVVR	[3] Phospho (ST)	0.55	0.66	0.59	-0.11	0.058	0.032	0.069	0.19	5.85E+03	1.23E+04	1.26E+04	1.32E+04	1.61E+04	1.56E+04	1.75E+04	1.47E+04	1.64E+04	1.31E+04	1.43E+04	1.87E+04	564.5739	3	37.63
BOI2	YER114C	RTSYIDQYSSSDSNFNSR	[8] Phospho (Y)	-0.10	-0.26	0.32	0.16	0.393	0.235	0.209	0.29	4.62E+04	2.79E+04	2.84E+04	4.10E+04	2.71E+04	2.79E+04	3.14E+04	3.30E+04	2.13E+04	5.52E+04	3.03E+04	4.24E+04	736.30768	3	51.58
YBT1	YLL048C	SSTSLSNLPAVK	[3] Phospho (ST)	-0.36	0.05	-0.26	-0.41	0.102	0.429	0.174	0.06	1.57E+04	2.56E+04	1.96E+04	1.58E+04	1.46E+04	1.70E+04	2.02E+04	2.58E+04	1.72E+04	1.45E+04	1.85E+04	1.80E+04	642.3162	2	33.72
NAP1	YKR048C	LGSLVGQDSGYVGGLPK	[3] Phospho (ST)	-0.99	-0.27	-0.39	-0.72	0.013	0.157	0.094	0.00	6.28E+04	9.36E+04	6.23E+04	3.44E+04	4.12E+04	3.43E+04	6.52E+04	5.41E+04	6.19E+04	5.44E+04	6.22E+04	5.01E+04	863.92511	2	86.54
HAA1	YPR008W	SSSIDVNHR	[3] Phospho (ST)	0.71	0.95	1.25	-0.24	0.046	0.128	0.012	0.34	1.23E+04	5.34E+03	6.33E+03	1.34E+04	1.15E+04	1.42E+04	2.57E+04	1.07E+04	9.75E+03	1.69E+04	1.66E+04	2.34E+04	547.73511	2	37.31
FLC2	YAL053W	DDRVSFIPK	[5] Phospho (ST)	0.02	0.50	0.33	-0.48	0.477	0.095	0.266	0.03	7.12E+03	1.66E+04	1.42E+04	1.15E+04	1.42E+04	1.28E+04	2.09E+04	1.50E+04	1.76E+04	9.33E+03	2.27E+04	1.56E+04	578.77401	2	22.49
VTC3	YPL019C	SNSLSSDGNSNQDVEIGK	[10] Phospho (ST)	-1.55	-1.00	-0.28	-0.55	0.004	0.012	0.184	0.05	7.21E+04	4.66E+04	6.61E+04	2.53E+04	1.76E+04	2.02E+04	2.63E+04	3.84E+04	2.79E+04	6.49E+04	3.99E+04	4.74E+04	965.90598	2	33.85
KIN4	YOR233W	HTSVAGLVTIPGSPTTAR	[16] Phospho (ST)	0.00	0.72	0.38	-0.72	0.497	0.057	0.181	0.03	1.02E+04	2.21E+04	1.32E+04	1.16E+04	1.94E+04	1.45E+04	3.12E+04	2.27E+04	2.07E+04	1.48E+04	2.41E+04	2.05E+04	615.6476	3	31.1
BUL1	YMR275C	SASATGILGLR	[3] Phospho (ST)	0.22	0.46	0.35	-0.24	0.296	0.135	0.217	0.15	9.69E+03	2.01E+04	9.91E+03	1.31E+04	1.81E+04	1.50E+04	2.10E+04	1.90E+04	1.47E+04	1.48E+04	2.15E+04	1.42E+04	563.28737	2	69.91
HXT1	YHR094C	NESFHDNLSESQVQPAVAPPNTGK	[11] Phospho (ST)	-0.23	-1.10	-0.44	0.88	0.295	0.013	0.081	0.07	3.87E+04	2.38E+04	3.56E+04	3.38E+04	1.47E+04	3.54E+04	1.21E+04	1.92E+04	1.43E+04	2.57E+04	2.02E+04	2.66E+04	662.30192	4	22.72
MYO5	YMR109W	SVPNPASTLTASQSNARPSPPTAATR	[1] Phospho (ST)	-0.83	-0.29	-0.33	-0.54	0.012	0.096	0.113	0.01	4.96E+04	6.13E+04	4.18E+04	2.94E+04	3.27E+04	2.37E+04	4.47E+04	4.18E+04	3.80E+04	3.72E+04	4.95E+04	3.47E+04	887.09723	3	31.55
BMH1	YER177W	IVSSIEQKEESK	[11] Phospho (ST)	-0.34	-0.42	-0.16	0.08	0.142	0.108	0.300	0.31	1.26E+04	1.23E+04	1.95E+04	1.16E+04	1.04E+04	1.32E+04	1.10E+04	9.43E+03	1.27E+04	1.32E+04	1.10E+04	1.56E+04	728.84961	2	37.38
NUP60	YAR002W	ISPSAPSK	[2] Phospho (ST)	0.51	-0.74	0.19	1.25	0.173	0.201	0.373	0.03	1.14E+04	3.74E+03	5.08E+03	1.04E+04	6.99E+03	1.15E+04	7.33E+03	2.52E+03	2.26E+03	1.07E+04	5.65E+03	6.79E+03	433.70437	2	17.61
PFK1	YGR240C	DAFLEATSEDEIISR	[8] Phospho (ST)	-0.58	0.04	-0.13	-0.62	0.069	0.446	0.295	0.05	2.60E+05	2.32E+05	1.60E+05	1.58E+05	1.81E+05	9.71E+04	2.29E+05	2.65E+05	1.76E+05	1.80E+05	2.17E+05	2.00E+05	888.39432	2	32.46
MAK21	YDR060W	SLPVFASADDYAQYLDQDSD	[19] Phospho (ST)	-0.53	-0.13	-1.06	-0.40	0.251	0.441	0.117	0.31	1.50E+05	2.24E+05	4.54E+04	8.21E+04	1.48E+05	6.14E+04	7.93E+04	2.33E+05	7.13E+04	5.63E+04	7.26E+04	7.18E+04	767.31536	3	34.23
GPT2	YKR067W	VNSRGSLTDIPIFSDAK	[3] Phospho (ST)|[6] Phospho (ST)	-0.42	-0.13	-0.45	-0.29	0.126	0.305	0.074	0.19	5.07E+04	4.93E+04	3.32E+04	3.28E+04	4.42E+04	2.27E+04	3.65E+04	4.88E+04	3.63E+04	2.84E+04	3.95E+04	2.97E+04	660.6354	3	36.69
SDS23	YGL056C	HTSIVEMLSTPPQLPNSTDLNSLSEQTDK	[3] Phospho (ST)	0.11	0.23	0.41	-0.12	0.423	0.236	0.191	0.41	9.25E+04	1.01E+05	5.39E+04	9.09E+04	1.37E+05	3.93E+04	1.06E+05	1.07E+05	7.63E+04	8.68E+04	1.56E+05	8.53E+04	1088.1797	3	16.95
MSC3	YLR219W	RNVYHTDAASDNASAPLGSNK	[10] Phospho (ST)	0.30	-0.32	-0.04	0.62	0.040	0.036	0.406	0.01	2.90E+04	2.69E+04	3.13E+04	3.82E+04	3.06E+04	3.84E+04	2.72E+04	2.20E+04	2.07E+04	2.90E+04	2.27E+04	3.30E+04	756.67338	3	67.62
EFB1	YAL003W	ADEFDSFPAASAAAAEEEEDDDVDLFGSDDEEADAEAEK	[28] Phospho (ST)	-0.06	0.31	-0.29	-0.37	0.458	0.215	0.332	0.23	1.03E+05	1.97E+05	2.37E+05	1.14E+05	2.79E+05	1.22E+05	1.71E+05	2.30E+05	2.64E+05	1.20E+05	2.56E+05	6.39E+04	1051.4077	4	24.7
RPS6A	YPL090C	LVTPQR	[3] Phospho (ST)	2.55	-0.33	0.26	2.88	0.005	0.338	0.331	0.01	3.52E+03	2.99E+03	1.69E+03	1.62E+04	1.11E+04	2.10E+04	4.39E+03	1.01E+03	1.13E+03	1.94E+03	2.61E+03	5.28E+03	397.2017	2	15.24
STE20	YHL007C	RATPVSTPVISK	[3] Phospho (ST)	0.08	-0.02	-0.35	0.10	0.329	0.488	0.215	0.43	1.25E+04	1.88E+04	1.57E+04	1.52E+04	1.75E+04	1.70E+04	2.58E+04	5.85E+03	1.47E+04	6.53E+03	1.18E+04	1.84E+04	668.35536	2	26.97
RRP5	YMR229C	VEDAEYESSDDEDEK	[8] Phospho (ST)|[9] Phospho (ST)	-0.03	0.12	-0.26	-0.15	0.476	0.446	0.325	0.42	6.00E+04	1.64E+04	4.74E+04	4.39E+04	4.87E+04	2.84E+04	1.07E+04	8.39E+04	3.99E+04	4.42E+04	3.13E+04	2.77E+04	960.30342	2	36.51
SIS2	YKR072C	SPNSNPAPVSNSIPGNHAVIPNHTNTSR	[1] Phospho (ST)	-0.26	-0.35	0.11	0.09	0.129	0.012	0.244	0.37	6.35E+04	6.15E+04	6.21E+04	6.77E+04	4.43E+04	4.42E+04	4.68E+04	4.37E+04	5.61E+04	6.66E+04	5.65E+04	7.88E+04	987.13182	3	56.97
EFR3	YMR212C	TQTRTIGLDK	[3] Phospho (ST)	0.10	-0.37	0.03	0.47	0.324	0.034	0.455	0.05	1.45E+04	1.19E+04	1.18E+04	1.63E+04	1.07E+04	1.40E+04	1.02E+04	8.41E+03	1.10E+04	1.65E+04	9.60E+03	1.29E+04	606.80296	2	37.11
BCK1	YJL095W	HYETNVSSPLK	[8] Phospho (ST)	-0.13	-0.05	0.16	-0.07	0.305	0.363	0.295	0.36	2.18E+04	1.57E+04	1.80E+04	2.09E+04	1.37E+04	1.62E+04	1.70E+04	1.83E+04	1.80E+04	2.73E+04	1.82E+04	1.66E+04	677.80478	2	19.21
TOP1	YOL006C	VASMNSASLQDEAEPYDSDEAISK	[16] Phospho (Y)	-0.48	0.78	0.81	-1.26	0.354	0.101	0.096	0.10	1.06E+04	4.79E+04	2.62E+04	2.47E+03	5.35E+04	4.82E+03	4.39E+04	6.32E+04	3.82E+04	4.01E+04	6.60E+04	4.26E+04	879.70226	3	45.62
POL12	YBL035C	LHGPFSLSDSK	[6] Phospho (ST)	0.77	2.01	1.40	-1.24	0.003	0.001	0.002	0.00	6.00E+03	8.72E+03	6.35E+03	1.13E+04	1.21E+04	1.25E+04	3.35E+04	2.58E+04	2.56E+04	1.57E+04	2.15E+04	1.86E+04	634.28969	2	15.17
PSK1	YAL017W	RSSLPR	[3] Phospho (ST)	1.08	0.66	0.22	0.43	0.022	0.130	0.319	0.16	1.68E+04	9.20E+03	8.52E+03	2.32E+04	1.90E+04	3.10E+04	2.62E+04	1.16E+04	1.66E+04	1.86E+04	1.18E+04	9.90E+03	398.19677	2	30.9
RPN1	YHR027C	GEEDADEEETAEGQTNSISDFLGEQVNEPTK	[17] Phospho (ST)	0.67	0.61	0.22	0.06	0.029	0.036	0.103	0.42	8.65E+04	7.62E+04	6.37E+04	1.11E+05	1.51E+05	9.86E+04	9.58E+04	1.45E+05	1.05E+05	9.80E+04	8.08E+04	8.53E+04	1150.1423	3	21.3
KCC4	YCL024W	IAASLSDDDLK	[6] Phospho (ST)	0.10	0.32	-0.19	-0.21	0.353	0.140	0.229	0.19	1.06E+04	1.58E+04	1.81E+04	1.29E+04	1.64E+04	1.86E+04	1.96E+04	1.47E+04	2.12E+04	1.28E+04	1.40E+04	1.21E+04	614.27959	2	30.34
MRC1	YCL061C	NVSSSFTQTQR	[5] Phospho (ST)	-4.88	-4.86	-1.56	-0.02	0.001	0.001	0.004	0.47	5.14E+04	3.31E+04	4.60E+04	1.31E+03	1.30E+03	1.81E+03	1.15E+03	1.57E+03	1.75E+03	1.83E+04	1.18E+04	1.43E+04	667.79085	2	41.06
SHE3	YBR130C	SASPVLPGVK	[3] Phospho (ST)	0.33	0.10	-0.48	0.23	0.057	0.284	0.034	0.04	1.27E+04	1.81E+04	1.45E+04	1.81E+04	2.11E+04	1.77E+04	1.71E+04	1.52E+04	1.61E+04	9.46E+03	1.18E+04	1.12E+04	517.76805	2	39.61
APL6	YGR261C	LTGINDGDSNSISGK	[11] Phospho (ST)	-0.17	-0.23	-0.01	0.07	0.180	0.110	0.487	0.31	3.75E+04	3.44E+04	4.60E+04	3.57E+04	3.09E+04	3.85E+04	3.14E+04	3.15E+04	3.75E+04	4.95E+04	3.14E+04	3.63E+04	779.34235	2	42.89
NUP2	YLR335W	KDESDSENDIEIK	[4] Phospho (ST)	1.02	0.52	0.27	0.50	0.007	0.067	0.209	0.00	1.12E+04	1.09E+04	2.06E+04	3.18E+04	2.84E+04	2.65E+04	1.92E+04	1.99E+04	2.23E+04	1.86E+04	1.56E+04	1.75E+04	801.33284	2	59
ISW2	YOR304W	NEGSDAEEEEGEYK	[4] Phospho (ST)	-0.01	0.09	-0.24	-0.10	0.482	0.337	0.094	0.32	2.18E+04	1.62E+04	1.96E+04	2.19E+04	1.73E+04	1.80E+04	1.59E+04	2.25E+04	2.31E+04	1.78E+04	1.60E+04	1.50E+04	833.29436	2	66.58
INP52	YNL106C	EISIVSVSPR	[3] Phospho (ST)	-0.25	0.55	-0.02	-0.80	0.245	0.057	0.483	0.01	1.42E+04	2.77E+04	2.06E+04	1.51E+04	2.16E+04	1.59E+04	3.57E+04	2.57E+04	3.04E+04	1.27E+04	2.70E+04	2.20E+04	583.79467	2	29.68
YMR295C	YMR295C	SSISNTSDHDGANR	[7] Phospho (ST)	1.05	0.17	0.31	0.88	0.038	0.322	0.285	0.04	2.91E+04	1.97E+04	1.31E+04	5.05E+04	2.67E+04	5.10E+04	2.86E+04	2.10E+04	2.03E+04	3.83E+04	1.90E+04	1.92E+04	770.80534	2	65
PHO91	YNR013C	INNDENSSGNEEDEDGNRQEVLDFQDAER	[8] Phospho (ST)	-0.21	-0.29	-0.18	0.07	0.153	0.146	0.230	0.40	1.17E+05	8.98E+04	1.02E+05	8.09E+04	1.07E+05	7.84E+04	6.32E+04	1.08E+05	8.11E+04	6.79E+04	1.10E+05	9.49E+04	1140.1253	3	33.85
NOT3	YIL038C	TPTTAAATTTSSNANSR	[12] Phospho (ST)	-0.37	-0.77	-0.56	0.39	0.138	0.029	0.080	0.07	2.65E+04	1.78E+04	1.65E+04	1.60E+04	1.22E+04	1.88E+04	1.11E+04	1.28E+04	1.18E+04	1.65E+04	9.53E+03	1.52E+04	577.92281	3	21.85
EXO1	YOR033C	YSSSFSGVNANR	[4] Phospho (ST)	-0.59	-0.07	-0.15	-0.52	0.003	0.368	0.182	0.04	3.44E+04	3.22E+04	3.98E+04	2.38E+04	2.36E+04	2.31E+04	2.80E+04	3.08E+04	4.23E+04	3.70E+04	2.95E+04	2.96E+04	684.78357	2	56.23
PLM2	YDR501W	NNTIQETPLPK	[7] Phospho (ST)	-5.07	-3.45	-1.25	-1.63	0.000	0.001	0.003	0.04	4.82E+04	5.40E+04	6.89E+04	1.28E+03	1.25E+03	2.52E+03	4.14E+03	3.35E+03	8.17E+03	2.36E+04	2.05E+04	2.75E+04	667.82187	2	20.51
YLR227W-B	R227W-B	AVSPTDSTPPSTHTEDSKPISEINLR	[3] Phospho (ST)	-1.20	-0.18	0.24	-1.02	0.002	0.297	0.260	0.03	5.81E+04	7.54E+04	5.84E+04	2.53E+04	2.99E+04	2.84E+04	7.90E+04	4.11E+04	4.95E+04	4.46E+04	9.07E+04	9.13E+04	953.78498	3	15.7
PHO84	YML123C	ASTAVESLDNHPPK	[7] Phospho (ST)	-2.17	-0.99	-0.55	-1.18	0.001	0.007	0.074	0.00	1.86E+04	2.70E+04	2.31E+04	4.83E+03	4.80E+03	5.64E+03	1.41E+04	9.54E+03	1.09E+04	1.09E+04	1.41E+04	2.19E+04	773.35119	2	56.67

POM34	YLR018C	HSGISSTLVSANNDNNSPHTPVTR	[20] Phospho (ST)	0.48	0.43	0.55	0.05	0.026	0.064	0.052	0.41	4.67E+04	3.78E+04	5.40E+04	7.11E+04	5.53E+04	6.69E+04	7.28E+04	4.90E+04	6.53E+04	6.03E+04	5.69E+04	8.57E+04	862.39665	3	17.3
RIM11	YMR139W	QLKPTEPNVSYICSR	[11] Phospho (Y)	-0.28	-0.58	-0.40	0.30	0.121	0.046	0.112	0.10	3.90E+04	3.68E+04	2.58E+04	3.10E+04	2.60E+04	2.66E+04	1.99E+04	1.91E+04	2.87E+04	2.29E+04	2.09E+04	3.34E+04	936.43999	2	25.84
CBF5	YLR175W	EYVPLDNAEQSTSSSQETKETEEEPK	[14] Phospho (ST)	2.18	-0.73	-1.71	2.91	0.001	0.009	0.000	0.00	1.87E+04	1.92E+04	1.97E+04	1.07E+05	7.33E+04	8.04E+04	8.49E+03	1.10E+04	1.51E+04	5.73E+03	5.87E+03	5.91E+03	1012.4351	3	16.01
BOI2	YER114C	DVSDTLSPDFDSK	[7] Phospho (ST)	-0.42	-0.32	-0.18	-0.10	0.016	0.021	0.210	0.16	3.47E+04	4.33E+04	4.15E+04	3.05E+04	3.23E+04	2.62E+04	3.04E+04	3.20E+04	3.32E+04	3.31E+04	4.37E+04	2.89E+04	753.30657	2	47.15
FLC3	YGL139W	DHDDNSDYESNDTGVNDELK	[6] Phospho (ST)	-0.19	-0.20	-0.12	0.01	0.053	0.012	0.054	0.47	6.23E+04	5.93E+04	5.83E+04	5.70E+04	4.57E+04	5.45E+04	4.99E+04	5.59E+04	5.03E+04	5.68E+04	5.76E+04	5.16E+04	1181.4363	2	63.24
SKG6	YHR149C	VSGILEETDVVQPPSVGGILPHSGSQDDLRK	[25] Phospho (ST)	-0.13	0.00	-0.17	-0.13	0.362	0.496	0.323	0.33	8.26E+04	1.06E+05	5.50E+04	6.61E+04	9.64E+04	6.01E+04	9.98E+04	7.08E+04	7.26E+04	5.80E+04	9.27E+04	6.61E+04	1103.8843	3	24
YLR257W	YLR257W	GESYQSAEQEIDHTAPEK	[4] Phospho (Y)|[6] Phospho (ST)	1.67	0.94	0.89	0.72	0.001	0.086	0.001	0.06	1.12E+04	1.13E+04	1.09E+04	3.32E+04	4.12E+04	3.16E+04	1.42E+04	3.37E+04	1.63E+04	2.33E+04	1.89E+04	1.97E+04	726.94761	3	30.42
ROX1	YPR065W	FSSSPNSSVLENNR	[4] Phospho (ST)	0.18	-0.08	-0.22	0.26	0.170	0.337	0.117	0.13	1.72E+04	1.70E+04	2.05E+04	2.08E+04	1.72E+04	2.39E+04	1.48E+04	1.63E+04	2.07E+04	1.81E+04	1.32E+04	1.57E+04	809.34835	2	37.51
RPS21A	YKR057W	NVWSYSR	[5] Phospho (Y)	-0.30	-0.19	-0.37	-0.11	0.190	0.325	0.151	0.35	7.02E+03	1.37E+04	1.00E+04	8.04E+03	8.69E+03	8.26E+03	6.57E+03	1.21E+04	8.32E+03	7.58E+03	8.73E+03	7.43E+03	496.20563	2	17.38
TSL1	YML100W	SPSAFNR	[1] Phospho (ST)	0.03	-0.45	-0.19	0.48	0.480	0.241	0.358	0.14	7.73E+03	2.25E+03	6.08E+03	6.33E+03	3.74E+03	6.29E+03	2.11E+03	4.58E+03	5.06E+03	5.40E+03	3.93E+03	4.77E+03	429.67878	2	24.29
DGK1	YOR311C	EEISSSDDDAHVPVTEIHLK	[6] Phospho (ST)	-0.35	-0.18	-0.28	-0.17	0.083	0.161	0.101	0.17	4.21E+04	4.08E+04	3.08E+04	2.51E+04	3.59E+04	2.83E+04	3.63E+04	3.27E+04	3.16E+04	3.11E+04	3.56E+04	2.70E+04	767.6815	3	21.79
MKC7	YDR144C	KYGSSFENALDDTKGR	[2] Phospho (Y)	-0.47	0.54	1.37	-1.02	0.146	0.227	0.019	0.12	9.16E+03	4.63E+03	9.77E+03	6.43E+03	4.01E+03	6.50E+03	1.90E+04	5.16E+03	1.02E+04	1.46E+04	1.89E+04	2.73E+04	623.27714	3	19.07
VTC2	YFL004W	LMGVDSEEEEIELPPGVK	[6] Phospho (ST)	-1.20	-0.06	0.22	-1.15	0.037	0.441	0.341	0.06	1.82E+05	2.49E+05	1.52E+05	6.92E+04	1.52E+05	3.20E+04	2.13E+05	2.35E+05	1.12E+05	1.43E+05	3.54E+05	1.80E+05	1025.9708	2	54.25
CTF4	YPR135W	YNIDSSQEELLAR	[1] Phospho (Y)	3.96	1.85	1.24	2.12	0.072	0.092	0.140	0.11	1.68E+03	1.81E+03	2.06E+03	1.65E+04	1.18E+04	5.88E+04	1.23E+04	1.96E+03	5.85E+03	3.53E+03	1.38E+03	8.28E+03	539.9083	3	15.01
CBF5	YLR175W	VNENTPEQWK	[5] Phospho (ST)	0.46	0.22	-0.03	0.24	0.005	0.226	0.431	0.17	2.69E+04	2.39E+04	2.98E+04	3.66E+04	3.48E+04	3.92E+04	2.59E+04	2.66E+04	4.12E+04	2.46E+04	2.42E+04	3.03E+04	662.78251	2	29.08
RGA2	YDR379W	VHDELPSPGKVPLSPSPK	[7] Phospho (ST)|[14] Phospho (ST)	-0.41	-0.08	-0.26	-0.33	0.027	0.243	0.065	0.03	3.40E+04	3.19E+04	2.72E+04	2.14E+04	2.74E+04	2.14E+04	2.90E+04	3.11E+04	2.78E+04	2.37E+04	2.94E+04	2.47E+04	681.99082	3	25.84
MRL1	YPR079W	LRSSPSASSSSLANR	[4] Phospho (ST)	0.20	0.28	0.12	-0.07	0.303	0.248	0.400	0.40	8.52E+03	9.17E+03	1.66E+04	1.33E+04	1.01E+04	1.61E+04	1.47E+04	1.02E+04	1.67E+04	1.07E+04	8.91E+03	1.77E+04	800.37756	2	24.44
NGR1	YBR212W	NGSHSDLVNLQR	[3] Phospho (ST)	-0.36	-0.37	-0.07	0.00	0.079	0.080	0.334	0.49	2.14E+04	1.81E+04	2.43E+04	1.68E+04	1.28E+04	1.99E+04	1.23E+04	1.83E+04	1.88E+04	1.91E+04	1.83E+04	2.31E+04	710.32321	2	31.87
CYC8	YBR112C	AASVSPSTKPLNTEPESSSVQPTVSSESSTTK	[3] Phospho (ST)	-0.83	-0.92	-0.32	0.10	0.004	0.003	0.000	0.39	6.47E+04	6.32E+04	6.34E+04	4.75E+04	3.14E+04	2.90E+04	4.44E+04	2.93E+04	2.70E+04	5.23E+04	5.01E+04	5.10E+04	1100.8503	3	32.28
YOR352W	YOR352W	SEPNTPLHAQPNEQLDLNNLNDLDEK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.53	-0.18	-0.25	-0.34	0.092	0.218	0.114	0.19	1.04E+05	1.04E+05	7.65E+04	5.72E+04	9.61E+04	4.38E+04	7.57E+04	1.02E+05	7.22E+04	7.88E+04	8.93E+04	7.18E+04	1054.1232	3	24.52
RPL43A	YPR043W	YGSSLRRQVK	[1] Phospho (Y)	0.07	0.39	0.44	-0.32	0.432	0.245	0.244	0.27	8.29E+03	1.21E+04	5.83E+03	6.34E+03	1.13E+04	9.84E+03	1.60E+04	5.66E+03	1.27E+04	4.51E+03	1.58E+04	1.53E+04	637.3241	2	16.06
BEM3	YPL115C	ITIKSPNK	[2] Phospho (ST)	-0.78	-2.33	-1.01	1.55	0.056	0.006	0.032	0.03	1.54E+04	1.13E+04	8.70E+03	9.58E+03	4.78E+03	6.34E+03	2.59E+03	6.60E+02	3.80E+03	4.15E+03	5.12E+03	8.38E+03	490.7625	2	16.51
PAF1	YBR279W	RLDDGDSDDENLDVNHIISR	[7] Phospho (ST)	-0.42	-0.41	-0.59	0.00	0.174	0.077	0.106	0.50	4.56E+04	7.36E+04	5.50E+04	2.21E+04	5.90E+04	4.92E+04	4.48E+04	4.22E+04	4.37E+04	1.80E+04	4.65E+04	5.09E+04	1189.5163	2	47.37
SEC53	YFL045C	TIGHSVQSPDDTVK	[8] Phospho (ST)	-0.35	-0.28	-0.66	-0.07	0.116	0.112	0.021	0.39	1.47E+04	2.15E+04	1.89E+04	1.38E+04	1.15E+04	1.82E+04	1.71E+04	1.34E+04	1.49E+04	1.02E+04	1.08E+04	1.39E+04	782.35592	2	38.63
KIN2	YLR096W	SASPVVGEHQEK	[3] Phospho (ST)	0.70	-0.77	-0.43	1.46	0.076	0.095	0.092	0.03	8.13E+03	4.93E+03	5.78E+03	9.34E+03	7.24E+03	1.40E+04	6.36E+03	2.45E+03	2.25E+03	5.25E+03	4.59E+03	4.13E+03	449.8693	3	29.59
HYP2	YEL034W	MSDEEHTFETADAGSSATYPMQCSALRK	[2] Phospho (ST)	-2.91	-1.93	-0.73	-0.98	0.037	0.056	0.175	0.10	2.44E+05	1.02E+05	8.30E+04	3.03E+04	1.87E+04	7.95E+03	4.73E+04	4.77E+04	1.77E+04	7.09E+04	1.20E+05	6.82E+04	1067.4405	3	35.7
YOR1	YGR281W	TITVGDAVSETELENK	[9] Phospho (ST)	-0.17	0.42	0.34	-0.59	0.327	0.087	0.123	0.06	3.98E+04	6.20E+04	4.47E+04	5.09E+04	5.34E+04	2.61E+04	6.49E+04	7.84E+04	5.28E+04	5.33E+04	7.49E+04	5.70E+04	893.41018	2	50.89
VPS74	YDR372C	VNRADSGDTSSIHSSANNTK	[6] Phospho (ST)	0.14	-0.15	0.13	0.29	0.350	0.356	0.391	0.13	3.36E+04	1.80E+04	1.80E+04	2.51E+04	2.13E+04	3.05E+04	2.34E+04	1.59E+04	2.35E+04	3.60E+04	1.84E+04	2.19E+04	714.31273	3	58.49
YMR086W	YMR086W	TSSLPNQR	[3] Phospho (ST)	0.19	0.14	-0.04	0.05	0.355	0.420	0.485	0.46	1.42E+04	3.88E+03	7.94E+03	1.10E+04	9.16E+03	9.55E+03	6.48E+03	1.52E+04	7.03E+03	1.69E+04	4.91E+03	3.61E+03	491.7213	2	24.59
SSD1	YDR293C	TSSQSSIYGHSR	[3] Phospho (ST)|[8] Phospho (Y)	0.33	-0.07	0.53	0.40	0.229	0.462	0.216	0.28	1.44E+04	5.89E+03	1.41E+04	1.84E+04	1.43E+04	1.05E+04	3.78E+03	2.02E+04	8.61E+03	2.67E+04	1.17E+04	1.11E+04	735.2771	2	30.44
MIG1	YGL035C	SLTDFQGLNNANPNNNGSLR	[1] Phospho (ST)	-1.11	-0.98	-0.37	-0.13	0.001	0.003	0.030	0.18	9.12E+04	7.88E+04	6.90E+04	3.51E+04	3.93E+04	3.66E+04	3.42E+04	4.49E+04	4.23E+04	5.76E+04	6.16E+04	6.60E+04	1113.5008	2	69.76
MLF3	YNL074C	TNSATLPSSESSPASPDLK	[3] Phospho (ST)	-0.84	-0.60	-0.41	-0.24	0.000	0.002	0.010	0.09	4.62E+04	4.67E+04	4.63E+04	2.79E+04	2.47E+04	2.51E+04	3.46E+04	3.14E+04	2.55E+04	3.34E+04	3.07E+04	4.09E+04	984.94425	2	52.29
IBD2	YNL164C	IDGQSAYHIDSAEEK	[7] Phospho (Y)	-0.04	0.06	-0.09	-0.10	0.426	0.423	0.340	0.35	8.02E+03	1.25E+04	1.22E+04	9.59E+03	1.11E+04	1.12E+04	1.32E+04	7.88E+03	1.31E+04	1.06E+04	1.01E+04	1.00E+04	581.58087	3	28.64
RPL25	YOL127W	VRTSATFR	[6] Phospho (ST)	-0.03	0.57	0.64	-0.60	0.479	0.192	0.151	0.10	1.49E+03	4.25E+03	7.18E+03	4.23E+03	3.43E+03	4.99E+03	6.45E+03	4.00E+03	8.74E+03	4.76E+03	6.49E+03	8.98E+03	509.24738	2	15.83
SKG6	YHR149C	SHGSPIHNNQLSR	[4] Phospho (ST)	0.32	0.24	0.29	0.09	0.233	0.307	0.267	0.31	4.30E+03	1.34E+04	1.49E+04	1.37E+04	1.24E+04	1.46E+04	1.53E+04	1.18E+04	1.12E+04	1.52E+04	1.06E+04	1.41E+04	509.56662	3	24.64
AVT3	YKL146W	SFIIQK	[1] Phospho (ST)	0.77	0.55	0.07	0.23	0.031	0.078	0.431	0.08	2.37E+03	5.01E+03	6.23E+03	7.79E+03	6.82E+03	8.70E+03	6.17E+03	6.37E+03	7.35E+03	5.80E+03	4.36E+03	4.14E+03	408.20668	2	25.04
GGA1	YDR358W	SPQENDTVVDILGDAHSK	[1] Phospho (ST)	0.20	0.30	0.23	-0.10	0.303	0.210	0.225	0.40	1.95E+04	3.31E+04	3.34E+04	4.07E+04	3.73E+04	2.08E+04	2.87E+04	4.65E+04	3.05E+04	3.04E+04	4.11E+04	2.94E+04	668.97049	3	21.03
SUM1	YDR310C	RTAGDDGALDQTENTSISPK	[18] Phospho (ST)	-0.17	0.02	-0.06	-0.19	0.213	0.468	0.402	0.20	1.82E+04	2.30E+04	2.64E+04	2.02E+04	1.71E+04	2.27E+04	2.56E+04	1.79E+04	2.51E+04	2.26E+04	1.64E+04	2.57E+04	719.32198	3	19.6
TAF12	YDR145W	KISSSNSTEIPSVTGPDALK	[3] Phospho (ST)	-0.90	-0.57	-0.78	-0.33	0.015	0.055	0.027	0.07	6.24E+04	7.75E+04	4.74E+04	3.25E+04	3.51E+04	3.27E+04	5.15E+04	3.93E+04	3.56E+04	3.11E+04	4.47E+04	3.30E+04	1056.0178	2	60.29
YLR177W	YLR177W	RNTQPVLNLHPAAAPTNDAGLAVVDGK	[3] Phospho (ST)	0.01	0.04	-0.31	-0.03	0.480	0.442	0.148	0.45	3.59E+04	4.84E+04	4.00E+04	4.38E+04	4.18E+04	3.94E+04	5.45E+04	3.06E+04	4.29E+04	2.26E+04	3.96E+04	3.84E+04	940.4785	3	35.54
AIM3	YBR108W	RAPTPPAPSR	[4] Phospho (ST)	0.58	1.59	0.98	-1.01	0.176	0.042	0.097	0.07	7.54E+02	5.58E+03	5.80E+03	4.92E+03	5.28E+03	7.95E+03	1.48E+04	5.90E+03	1.59E+04	4.67E+03	7.97E+03	1.12E+04	565.27892	2	17.67
RGA2	YDR379W	DHQVGDLESQQRSPNSSSGGTTNIAQK	[9] Phospho (ST)	0.15	-0.39	-0.46	0.54	0.312	0.029	0.226	0.10	4.36E+04	4.14E+04	4.57E+04	6.61E+04	4.43E+04	3.51E+04	2.60E+04	3.60E+04	3.78E+04	2.75E+04	9.55E+03	5.81E+04	974.43862	3	36.89
DNF1	YER166W	ETQDLLQSPQFQQAQTFGR	[8] Phospho (ST)	-0.42	-0.35	-0.53	-0.07	0.078	0.056	0.020	0.41	5.81E+04	6.35E+04	4.96E+04	3.15E+04	5.62E+04	4.02E+04	3.56E+04	5.07E+04	4.76E+04	4.57E+04	4.12E+04	3.14E+04	768.02215	3	32.67
PSH1	YOL054W	HVIITDDEEEEQR	[5] Phospho (ST)	0.57	0.29	0.27	0.29	0.020	0.183	0.194	0.14	1.41E+04	2.03E+04	2.01E+04	2.40E+04	2.59E+04	3.11E+04	2.33E+04	1.59E+04	2.73E+04	1.55E+04	2.46E+04	2.55E+04	846.86	2	53.36
BRE5	YNR051C	ESGNNASTPSSSPEPVANPPK	[2] Phospho (ST)|[12] Phospho (ST)	0.21	-0.12	-0.13	0.32	0.246	0.353	0.351	0.06	1.13E+05	5.94E+04	1.01E+05	1.23E+05	9.91E+04	9.32E+04	7.22E+04	9.08E+04	8.89E+04	1.01E+05	6.31E+04	8.49E+04	1113.9518	2	23.74
TDH3	YGR192C	IVSNASCTTNCLAPLAK	[6] Phospho (ST)	-0.51	-0.33	-0.21	-0.18	0.027	0.074	0.128	0.15	4.53E+04	4.52E+04	3.32E+04	3.13E+04	3.09E+04	2.48E+04	2.85E+04	3.71E+04	3.27E+04	3.61E+04	3.76E+04	3.31E+04	950.44044	2	40.64
ESBP6	YNL125C	KLSISR	[3] Phospho (ST)	-0.27	-1.09	-0.22	0.82	0.079	0.033	0.135	0.07	8.11E+03	6.12E+03	7.93E+03	5.73E+03	5.82E+03	6.84E+03	6.32E+03	1.95E+03	2.12E+03	5.69E+03	5.89E+03	7.39E+03	392.20849	2	22.36
FUI1	YBL042C	KDTDSENNITIAQDDEK	[5] Phospho (ST)	-0.09	-0.55	-0.06	0.46	0.385	0.165	0.381	0.22	2.28E+04	1.51E+04	2.27E+04	1.41E+04	1.81E+04	2.46E+04	9.46E+03	7.64E+03	2.41E+04	2.02E+04	2.04E+04	1.73E+04	1008.4234	2	41.03
YNL234W	YNL234W	VFQALLYSNK	[7] Phospho (Y)	-0.04	-0.57	-0.42	0.54	0.416	0.067	0.189	0.05	9.92E+03	1.35E+04	1.02E+04	1.07E+04	1.16E+04	1.05E+04	1.01E+04	4.63E+03	7.91E+03	4.00E+03	8.25E+03	1.29E+04	631.80993	2	25.17
DIP5	YPL265W	NSSSLDSDHDAYYSK	[7] Phospho (ST)	-0.34	-0.22	-0.64	-0.12	0.178	0.285	0.058	0.37	2.30E+04	3.32E+04	1.87E+04	2.47E+04	1.55E+04	1.87E+04	1.81E+04	2.91E+04	1.68E+04	1.78E+04	1.42E+04	1.62E+04	884.83898	2	39.75
MMP1	YLL061W	VQFSTSVLSTPSNEGNNLIHR	[12] Phospho (ST)	-0.82	-0.31	-0.79	-0.51	0.034	0.141	0.039	0.03	3.20E+04	5.36E+04	3.90E+04	2.95E+04	2.35E+04	1.74E+04	3.53E+04	3.44E+04	3.04E+04	2.14E+04	3.14E+04	1.92E+04	794.04847	3	30.73
YDR186C	YDR186C	FPNSQQPDSAGASSPK	[14] Phospho (ST)	-0.06	0.00	-0.06	-0.06	0.250	0.490	0.263	0.33	7.28E+04	6.73E+04	7.46E+04	7.36E+04	6.36E+04	6.93E+04	7.19E+04	6.24E+04	8.09E+04	7.06E+04	6.20E+04	7.35E+04	849.36134	2	62.95
SMY2	YBR172C	VSTPVQQHPLLQR	[3] Phospho (ST)	-0.21	-0.36	-0.35	0.15	0.272	0.206	0.256	0.27	1.15E+04	2.43E+04	1.84E+04	1.59E+04	1.49E+04	1.61E+04	1.79E+04	1.02E+04	1.43E+04	6.35E+03	1.66E+04	1.95E+04	791.90928	2	36.17
PLM2	YDR501W	FVPVEHSPR	[7] Phospho (ST)	-3.28	-4.50	-1.73	1.22	0.000	0.000	0.003	0.02	2.58E+04	3.46E+04	3.49E+04	4.15E+03	2.62E+03	2.99E+03	1.56E+03	7.64E+02	1.86E+03	6.80E+03	6.73E+03	1.51E+04	574.26864	2	32.21
YOL087C	YOL087C	QQYMNTSSLK	[8] Phospho (ST)	-0.36	-0.09	0.23	-0.27	0.227	0.437	0.368	0.31	1.10E+04	4.45E+03	9.31E+03	8.35E+03	6.06E+03	4.83E+03	5.44E+03	1.23E+04	5.48E+03	1.66E+04	5.62E+03	6.82E+03	640.2759	2	22.5
SLK19	YOR195W	EKEDEENDITNSHINR	[10] Phospho (ST)	1.23	1.17	1.27	0.06	0.002	0.003	0.003	0.34	8.18E+03	4.23E+03	7.57E+03	1.72E+04	1.57E+04	1.39E+04	1.66E+04	1.32E+04	1.51E+04	1.74E+04	1.34E+04	1.76E+04	674.95131	3	36.8
PUF6	YDR496C	ISIDSSDEESELSKK	[5] Phospho (ST)|[6] Phospho (ST)	-0.85	-0.21	-0.59	-0.65	0.054	0.320	0.004	0.20	2.26E+04	2.15E+04	2.66E+04	3.57E+03	1.95E+04	1.61E+04	1.25E+04	3.22E+04	1.66E+04	1.52E+04	1.60E+04	1.59E+04	609.58347	3	18.77
CLA4	YNL298W	NGHSPTNGQFPR	[4] Phospho (ST)	-0.26	-0.33	-0.19	0.07	0.052	0.150	0.208	0.41	2.57E+04	3.01E+04	2.50E+04	2.53E+04	2.12E+04	2.12E+04	2.11E+04	1.42E+04	2.91E+04	2.83E+04	1.71E+04	2.53E+04	696.30037	2	20.02
ARE2	YNR019W	SSPDAVDSVGK	[2] Phospho (ST)	0.51	0.43	0.29	0.09	0.059	0.098	0.147	0.36	1.50E+04	9.07E+03	1.59E+04	2.26E+04	1.61E+04	1.83E+04	1.43E+04	1.81E+04	2.13E+04	1.80E+04	1.40E+04	1.68E+04	571.24216	2	36.78
NET1	YJL076W	SQSSIADNNGSPVK	[11] Phospho (ST)	2.75	1.24	0.84	1.51	0.001	0.010	0.031	0.00	6.91E+03	2.33E+03	4.94E+03	3.71E+04	2.60E+04	3.26E+04	9.00E+03	1.28E+04	1.17E+04	9.62E+03	8.09E+03	7.68E+03	742.32497	2	29.44
ALR1	YOL130W	SSLVSPVLEIPHESK	[2] Phospho (ST)	-0.36	0.27	-0.17	-0.63	0.288	0.306	0.395	0.04	1.63E+04	5.36E+04	2.66E+04	2.03E+04	3.17E+04	2.32E+04	4.77E+04	3.41E+04	3.45E+04	1.95E+04	4.07E+04	2.53E+04	851.42737	2	41.27
SEC16	YPL085W	TSPAIYAR	[2] Phospho (ST)	0.17	0.19	-0.21	-0.02	0.271	0.245	0.223	0.45	5.11E+03	8.37E+03	8.52E+03	8.38E+03	6.85E+03	9.48E+03	6.84E+03	9.48E+03	8.79E+03	6.78E+03	5.43E+03	6.76E+03	479.72312	2	19.19
SLG1	YOR008C	RISNGTFINGGPGGK	[3] Phospho (ST)	-0.12	-0.03	0.28	-0.10	0.256	0.444	0.162	0.35	1.98E+04	1.66E+04	2.03E+04	1.37E+04	1.87E+04	1.97E+04	2.27E+04	1.55E+04	1.75E+04	1.62E+04	2.62E+04	2.66E+04	777.87509	2	47.63
RAD9	YDR217C	RNSDLDAASIK	[3] Phospho (ST)	-1.84	-1.26	-0.94	-0.58	0.005	0.004	0.007	0.16	1.93E+04	2.03E+04	2.69E+04	3.41E+03	4.05E+03	1.11E+04	1.14E+04	7.22E+03	9.15E+03	1.09E+04	1.10E+04	1.28E+04	635.29663	2	38.57
DUN1	YDL101C	REHSGDVTDSSFK	[4] Phospho (ST)	-1.80	-1.83	-0.76	0.04	0.001	0.003	0.004	0.48	5.48E+04	4.80E+04	4.16E+04	1.62E+04	1.22E+04	1.31E+04	2.46E+04	7.60E+03	8.25E+03	2.67E+04	2.78E+04	3.05E+04	772.82673	2	66.95
ALR1	YOL130W	STSQKSDADDDTLER	[3] Phospho (ST)|[6] Phospho (ST)	-0.33	-0.70	-0.12	0.38	0.286	0.153	0.420	0.20	3.35E+04	1.05E+04	3.34E+04	2.66E+04	2.12E+04	1.40E+04	8.96E+03	2.12E+04	1.74E+04	3.44E+04	1.67E+04	2.03E+04	914.33759	2	18.75
BSP1	YPR171W	PAGEALSPVR	[7] Phospho (ST)	0.24	0.54	0.10	-0.29	0.312	0.102	0.356	0.28	1.27E+04	1.24E+04	1.75E+04	1.15E+04	1.29E+04	2.60E+04	2.38E+04	1.29E+04	2.51E+04	1.19E+04	1.49E+04	1.90E+04	538.76048	2	42.66
NOP8	YOL144W	DFDFDKPMTLNDSDEELLTEQR	[13] Phospho (ST)	-0.12	-0.02	0.33	-0.10	0.374	0.467	0.251	0.39	4.35E+04	5.91E+04	4.35E+04	3.69E+04	6.40E+04	3.39E+04	4.80E+04	5.69E+04	3.92E+04	4.24E+04	9.38E+04	4.77E+04	913.38964	3	47.93
IDS2	YJL146W	RSSIQDVQWIR	[3] Phospho (ST)	-0.19	-0.04	-0.47	-0.15	0.291	0.451	0.155	0.08	2.33E+04	4.31E+04	2.53E+04	2.53E+04	2.83E+04	2.68E+04	3.03E+04	3.19E+04	2.70E+04	1.53E+04	2.85E+04	2.23E+04	734.35846	2	33.36
HER1	YOR227W	TIASPQRPLSGQNVNNELSNSK	[4] Phospho (ST)	0.40	1.37	1.08	-0.97	0.030	0.003	0.007	0.00	9.31E+03	1.05E+04	1.36E+04	1.41E+04	1.54E+04	1.45E+04	2.35E+04	3.37E+04	2.90E+04	2.81E+04	1.86E+04	2.42E+04	812.06223	3	42.07
VTS1	YOR359W	SAEPHVNSSPNLIPVQK	[1] Phospho (ST)	-1.04	-0.82	-0.67	-0.22	0.020	0.030	0.063	0.12	4.01E+04	6.80E+04	4.63E+04	2.38E+04	3.00E+04	2.14E+04	2.87E+04	2.70E+04	3.17E+04	2.21E+04	3.80E+04	3.71E+04	948.96521	2	25.46
PAF1	YBR279W	TEGSEQEGENEKDEEIK	[4] Phospho (ST)	0.37	-0.01	-0.57	0.38	0.032	0.490	0.018	0.08	2.47E+04	1.93E+04	2.13E+04	3.20E+04	2.52E+04	2.76E+04	1.67E+04	2.06E+04	2.78E+04	1.58E+04	1.15E+04	1.68E+04	1015.9084	2	44.66
MTR4	YJL050W	NADTNVGDTPDHTQDK	[9] Phospho (ST)	0.09	-0.84	-0.48	0.94	0.453	0.218	0.305	0.04	5.45E+04	7.74E+03	2.15E+04	3.16E+04	1.97E+04	3.81E+04	2.17E+04	1.05E+04	1.44E+04	2.65E+04	1.75E+04	1.61E+04	904.36296	2	20
YJR056C	YJR056C	LDSDSEVDIR	[3] Phospho (ST)	1.00	0.76	0.08	0.25	0.005	0.007	0.353	0.10	1.04E+04	1.32E+04	1.61E+04	2.42E+04	2.42E+04	3.11E+04	2.49E+04	1.99E+04	2.23E+04	1.28E+04	1.41E+04	1.49E+04	614.75869	2	49.28
STE13	YOR219C	SFESLK	[1] Phospho (ST)	-0.30	-0.06	-0.21	-0.24	0.189	0.407	0.244	0.11	4.75E+03	4.74E+03	7.48E+03	5.63E+03	3.69E+03	4.48E+03	5.35E+03	5.33E+03	5.61E+03	5.31E+03	5.29E+03	4.08E+03	395.67257	2	24.55
CTR9	YOL145C	TLSDSDEDDDDVVK	[5] Phospho (ST)	-0.19	-0.31	-0.16	0.12	0.113	0.011	0.136	0.26	3.89E+04	4.15E+04	4.01E+04	4.10E+04	2.95E+04	3.54E+04	2.88E+04	3.57E+04	3.30E+04	4.21E+04	3.43E+04	3.17E+04	816.81243	2	61.8
NIC96	YFR002W	SISSLDPK	[1] Phospho (ST)	0.47	0.62	0.37	-0.15	0.010	0.004	0.068	0.01	7.45E+03	5.79E+03	8.34E+03	9.84E+03	1.01E+04	9.97E+03	1.12E+04	1.16E+04	1.05E+04	1.03E+04	1.00E+04	7.60E+03	463.7153	2	22.35
CWC22	YGR278W	KIYLVLKSSLSGDEAAHK	[3] Phospho (Y)	-1.42	-3.07	-0.54	1.64	0.172	0.102	0.322	0.02	1.33E+05	2.99E+04	2.19E+04	1.99E+04	1.69E+04	3.21E+04	5.16E+03	8.82E+03	8.09E+03	2.05E+04	3.92E+04	6.76E+04	680.35348	3	22.23
APA1	YCL050C	GQTPEGEDPLGKPEEELTVIPEFGGADNK	[3] Phospho (ST)	0.28	0.28	-0.15	0.00	0.242	0.228	0.379	0.50	6.56E+04	1.05E+05	5.25E+04	8.52E+04	1.16E+05	7.02E+04	1.04E+05	9.91E+04	6.83E+04	5.44E+04	9.71E+04	5.04E+04	1045.1455	3	22.29
KRE6	YPR159W	AVSTANDNSFLQPPHR	[3] Phospho (ST)	-0.51	-0.26	-0.41	-0.25	0.037	0.126	0.154	0.03	5.81E+04	8.88E+04	7.64E+04	4.73E+04	5.68E+04	5.23E+04	5.74E+04	6.28E+04	6.60E+04	2.96E+04	6.69E+04	7.10E+04	917.41777	2	27.38
SRC1	YML034W	VSASFADK	[4] Phospho (ST)	-3.84	-2.19	-0.70	-1.66	0.001	0.003	0.033	0.01	1.22E+04	1.11E+04	1.72E+04	1.19E+03	8.05E+02	7.96E+02	2.89E+03	2.09E+03	3.88E+03	9.78E+03	6.82E+03	8.31E+03	452.69432	2	34.5
AIM7	YDR063W	LIEVSSGLEDDSDVEELREQLENC	[12] Phospho (ST)	-0.36	0.17	-0.40	-0.53	0.207	0.306	0.136	0.08	2.06E+05	2.40E+05	1.22E+05	1.33E+05	2.05E+05	1.04E+05	2.08E+05	2.57E+05	1.73E+05	1.52E+05	1.54E+05	1.24E+05	953.41653	3	21.51
PHO84	YML123C	ASTAVESLDNHPPK	[3] Phospho (ST)	-2.28	-1.33	-0.78	-0.95	0.003	0.020	0.070	0.11	1.46E+04	2.21E+04	2.55E+04	4.91E+03	3.86E+03	4.01E+03	1.32E+04	7.47E+03	3.98E+03	8.63E+03	8.51E+03	1.90E+04	515.90312	3	26.41
YDR239C	YDR239C	ITNEIDSGSSNEDDDDGLQEK	[9] Phospho (ST)	0.09	-0.41	0.18	0.49	0.250	0.059	0.128	0.05	4.40E+04	3.95E+04	4.45E+04	5.00E+04	4.69E+04	3.91E+04	2.26E+04	3.42E+04	3.98E+04	5.59E+04	4.20E+04	4.73E+04	1180.9676	2	26.58

SEC3	YER008C	NVSQGAVPSSAPPVSGGNYSHK	[3] Phospho (ST)	-0.49	-0.42	-0.31	-0.07	0.002	0.001	0.078	0.15	5.05E+04	4.51E+04	4.64E+04	3.21E+04	3.64E+04	3.26E+04	3.46E+04	3.54E+04	3.63E+04	2.94E+04	3.90E+04	4.64E+04	1110.5084	2	30.19
ENT1	YDL161W	LNELLATGTGIDTFGNVGEAR	[9] Phospho (ST)	-0.16	0.46	0.07	-0.63	0.394	0.170	0.453	0.05	2.67E+04	6.55E+04	2.73E+04	2.91E+04	5.05E+04	2.71E+04	6.48E+04	5.38E+04	4.62E+04	2.92E+04	6.05E+04	3.58E+04	743.35871	3	58.89
SKN7	YHR206W	SFSTINSNVNK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-4.75	-4.18	-1.88	-0.57	0.000	0.000	0.000	0.19	4.44E+04	4.76E+04	4.25E+04	2.07E+03	1.81E+03	1.09E+03	2.67E+03	3.64E+03	1.07E+03	1.57E+04	1.15E+04	9.29E+03	666.79578	2	23.42
YSC84	YHR016C	GYSLGHGPTHPSNMSNVDDLSHK	[3] Phospho (ST)	-0.38	-0.43	0.18	0.04	0.225	0.233	0.260	0.48	1.78E+04	2.40E+04	1.78E+04	1.68E+04	2.33E+04	5.63E+03	2.67E+04	9.28E+03	8.39E+03	1.64E+04	2.54E+04	2.57E+04	633.27603	4	17.94
SHO1	YER118C	NTTPYQNNVYNDAIR	[3] Phospho (ST)	-0.66	-0.50	-0.14	-0.16	0.024	0.059	0.249	0.26	4.13E+04	3.78E+04	5.53E+04	2.75E+04	2.51E+04	3.26E+04	2.49E+04	3.15E+04	3.86E+04	4.26E+04	4.15E+04	3.79E+04	931.90772	2	52.95
NUP145	YGL092W	AYEPDLSDADFEGIEASPK	[2] Phospho (Y)	0.03	0.41	0.12	-0.38	0.473	0.149	0.404	0.08	2.26E+04	4.52E+04	2.19E+04	2.35E+04	3.90E+04	2.91E+04	4.47E+04	3.93E+04	3.49E+04	2.23E+04	4.23E+04	3.26E+04	711.96904	3	24.78
HRD1	YOL013C	STSTPSPTWYTFPLHK	[3] Phospho (ST)	-1.28	-0.26	-1.10	-1.03	0.123	0.374	0.146	0.05	1.57E+04	5.28E+04	1.64E+04	1.15E+04	1.31E+04	1.02E+04	2.29E+04	3.38E+04	1.43E+04	8.64E+03	1.60E+04	1.49E+04	643.96515	3	18.92
ITR1	YDR497C	TSQSNVGDAVGNADSVEFNSEHDSPSK	[2] Phospho (ST)	-0.38	-0.42	-0.58	0.05	0.059	0.010	0.018	0.41	4.34E+04	3.85E+04	3.49E+04	3.65E+04	2.99E+04	2.35E+04	2.72E+04	3.04E+04	2.94E+04	3.26E+04	2.23E+04	2.30E+04	953.39765	3	45.8
GAT1	YFL021W	INNNITPPPSSSLNPGAAGK	[6] Phospho (ST)	-0.64	-0.19	-0.56	-0.46	0.007	0.167	0.012	0.02	7.67E+04	6.08E+04	8.09E+04	4.56E+04	4.96E+04	4.46E+04	5.38E+04	7.00E+04	6.83E+04	4.46E+04	4.92E+04	5.41E+04	1014.9916	2	15.73
STU1	YBL034C	SEGDEESDDAVDENDVKK	[7] Phospho (ST)	0.31	0.23	0.23	0.08	0.160	0.132	0.154	0.37	2.44E+04	1.71E+04	2.67E+04	3.57E+04	2.30E+04	2.59E+04	2.57E+04	2.57E+04	2.89E+04	2.77E+04	2.33E+04	2.90E+04	1030.8945	2	64.58
YJL049W	YJL049W	ESSSEDLLK	[2] Phospho (ST)	1.28	0.63	0.30	0.65	0.001	0.031	0.179	0.00	7.32E+03	7.30E+03	1.16E+04	2.34E+04	1.96E+04	2.07E+04	1.14E+04	1.38E+04	1.55E+04	1.31E+04	1.06E+04	8.58E+03	544.23173	2	20.53
UME6	YDR207C	RLSAPEQQQQLEVPPLK	[3] Phospho (ST)	0.29	0.43	-0.17	-0.14	0.230	0.102	0.344	0.26	1.66E+04	3.74E+04	2.85E+04	2.96E+04	4.27E+04	2.87E+04	3.83E+04	3.37E+04	3.90E+04	1.74E+04	2.92E+04	2.69E+04	681.02076	3	26.21
RRD1	YIL153W	EEESIEQANAGSPGREQTSTR	[12] Phospho (ST)	0.22	0.80	0.27	-0.57	0.248	0.096	0.180	0.14	1.34E+04	1.07E+04	1.98E+04	1.55E+04	1.49E+04	2.10E+04	1.52E+04	2.40E+04	3.72E+04	1.72E+04	1.60E+04	1.97E+04	786.00602	3	25.2
ECM3	YOR092W	EYSNVDQYGR	[3] Phospho (ST)	-0.33	-0.07	-0.60	-0.26	0.111	0.404	0.042	0.15	8.68E+03	1.39E+04	1.13E+04	8.90E+03	9.94E+03	8.13E+03	8.74E+03	1.35E+04	1.01E+04	6.72E+03	8.94E+03	6.70E+03	655.75655	2	45.23
RPL24B	YGR148C	VEVDSFSGAK	[5] Phospho (ST)	1.05	0.28	-0.02	0.77	0.003	0.076	0.479	0.00	7.84E+03	9.78E+03	1.17E+04	2.17E+04	2.20E+04	1.71E+04	1.19E+04	1.12E+04	1.25E+04	8.62E+03	1.26E+04	7.74E+03	559.74229	2	22.44
YDR090C	YDR090C	YSRLSV	[5] Phospho (ST)	-0.18	0.33	-0.33	-0.51	0.299	0.136	0.184	0.04	3.44E+03	5.21E+03	6.28E+03	3.97E+03	3.62E+03	5.58E+03	5.61E+03	5.75E+03	7.45E+03	2.81E+03	4.54E+03	4.52E+03	402.68606	2	16.22
DCS2	YOR173W	STPIFFHR	[1] Phospho (ST)	0.08	0.22	-0.41	-0.13	0.436	0.348	0.282	0.29	3.92E+03	1.21E+04	5.53E+03	7.13E+03	7.83E+03	7.90E+03	1.02E+04	8.85E+03	6.03E+03	2.81E+03	7.38E+03	6.02E+03	542.75281	2	30.49
SSD1	YDR293C	SSTINNDSDSLSSPTK	[13] Phospho (ST)	-0.22	-0.19	-0.13	-0.03	0.158	0.183	0.289	0.46	4.34E+04	3.73E+04	3.81E+04	4.29E+04	2.97E+04	2.96E+04	2.65E+04	4.15E+04	3.61E+04	3.88E+04	2.57E+04	4.38E+04	866.87007	2	24.02
GIN4	YDR507C	FTASSASSSNLTTPGSSK	[2] Phospho (ST)	-0.46	-0.74	0.03	0.28	0.023	0.006	0.437	0.03	6.21E+04	5.48E+04	7.40E+04	5.05E+04	4.25E+04	4.59E+04	3.50E+04	3.68E+04	4.23E+04	6.84E+04	5.55E+04	7.08E+04	905.39754	2	32.16
SPT6	YGR116W	LEDFFSEDEEEEESGLR	[6] Phospho (ST)	1.74	1.21	0.21	0.53	0.012	0.003	0.273	0.10	3.24E+04	5.20E+04	3.60E+04	1.02E+05	1.85E+05	1.16E+05	9.61E+04	1.03E+05	7.84E+04	3.15E+04	5.49E+04	5.29E+04	1070.4189	2	58.92
RLP7	YNL002C	EVSGFGSLNR	[3] Phospho (ST)	-3.64	-1.19	-0.21	-2.45	0.000	0.002	0.135	0.00	1.37E+04	1.66E+04	1.87E+04	1.56E+03	8.88E+02	1.46E+03	6.51E+03	8.58E+03	6.32E+03	1.24E+04	1.58E+04	1.41E+04	573.25343	2	29.08
FIR1	YER032W	VDTSPVNQSFESR	[4] Phospho (ST)	-0.04	0.63	0.55	-0.66	0.469	0.043	0.086	0.04	1.75E+04	8.00E+03	1.34E+04	9.77E+03	1.01E+04	1.81E+04	1.85E+04	1.86E+04	2.29E+04	2.18E+04	1.43E+04	2.08E+04	773.33458	2	39.06
PHO84	YML123C	ASTAVESLDNHPPK	[3] Phospho (ST)	-2.15	-0.99	-0.60	-1.16	0.001	0.016	0.077	0.03	2.92E+04	4.10E+04	4.32E+04	7.29E+03	8.71E+03	9.47E+03	2.61E+04	1.27E+04	1.82E+04	1.63E+04	2.25E+04	3.62E+04	773.35072	2	49.82
SNF2	YOR290C	NAPLDSKDENFASVSPAGPSSVHNAK	[15] Phospho (ST)	-0.30	-0.13	-0.10	-0.17	0.036	0.304	0.201	0.27	2.27E+04	2.72E+04	2.71E+04	2.03E+04	1.90E+04	2.34E+04	2.98E+04	1.73E+04	2.34E+04	2.16E+04	2.58E+04	2.43E+04	907.08316	3	24.55
SMC4	YLR086W	RLELLQLSPVK	[8] Phospho (ST)	-0.28	0.19	-0.05	-0.47	0.206	0.272	0.451	0.05	1.73E+04	2.77E+04	1.67E+04	1.53E+04	2.04E+04	1.50E+04	2.79E+04	1.96E+04	2.28E+04	1.38E+04	2.67E+04	1.90E+04	688.38939	2	36.22
SPA2	YLL021W	PASFLNDVEEEESPVK	[13] Phospho (ST)	0.37	0.91	0.38	-0.54	0.202	0.020	0.201	0.07	2.31E+04	4.07E+04	2.20E+04	3.50E+04	4.96E+04	2.66E+04	6.51E+04	4.89E+04	4.72E+04	2.99E+04	5.14E+04	3.07E+04	935.41216	2	46.26
HAL5	YJL165C	SLSESIK	[1] Phospho (ST)	0.15	-0.09	-0.06	0.24	0.300	0.400	0.442	0.15	4.47E+03	3.17E+03	6.15E+03	5.53E+03	4.83E+03	4.94E+03	3.12E+03	4.50E+03	5.29E+03	6.34E+03	3.26E+03	3.58E+03	422.19645	2	17
PIB2	YGL023C	KGDEESGADTVTSPITFEK	[13] Phospho (ST)	0.31	0.85	0.39	-0.53	0.106	0.002	0.047	0.01	1.17E+04	1.49E+04	1.77E+04	1.90E+04	1.51E+04	2.08E+04	2.74E+04	2.49E+04	2.73E+04	1.82E+04	2.17E+04	1.81E+04	697.64408	3	27.68
NUP60	YAR002W	SAEGNNIDQSLILK	[1] Phospho (ST)	0.79	1.93	1.67	-1.14	0.029	0.001	0.008	0.00	5.16E+03	1.26E+04	7.12E+03	1.45E+04	1.53E+04	1.33E+04	3.09E+04	3.56E+04	2.83E+04	2.90E+04	3.14E+04	1.89E+04	791.37962	2	17.81
MRD1	YPR112C	DTDIGLVNDDANSDEK	[13] Phospho (ST)	0.42	0.25	0.21	0.17	0.005	0.070	0.088	0.10	6.07E+04	5.05E+04	6.06E+04	7.42E+04	7.40E+04	8.16E+04	5.88E+04	7.52E+04	7.03E+04	6.44E+04	7.39E+04	5.98E+04	900.86267	2	47.54
GPD1	YDL022W	SSSSVSLK	[1] Phospho (ST)|[6] Phospho (ST)	-0.87	-0.81	-0.41	-0.06	0.186	0.201	0.340	0.47	3.11E+04	4.49E+03	2.39E+04	1.89E+04	5.80E+03	7.87E+03	4.85E+03	1.96E+04	9.59E+03	3.02E+04	8.37E+03	6.12E+03	477.68264	2	18.78
PFK1	YGR240C	ASSDASDLLR	[3] Phospho (ST)	-1.64	-0.67	-0.49	-0.98	0.001	0.008	0.045	0.00	1.24E+04	1.33E+04	1.65E+04	3.86E+03	4.97E+03	4.67E+03	8.65E+03	8.31E+03	9.70E+03	7.74E+03	1.23E+04	1.01E+04	557.74263	2	38.48
TMA10	YLR327C	RLSDLQQYHI	[3] Phospho (ST)	-0.95	0.75	-0.80	-1.70	0.027	0.049	0.044	0.01	1.06E+04	1.97E+04	1.49E+04	7.48E+03	8.76E+03	7.12E+03	3.32E+04	2.21E+04	2.07E+04	6.40E+03	9.55E+03	1.00E+04	676.82187	2	25.31
ENT2	YLR206W	TRSNPHDSSPSYQDDLEK	[1] Phospho (ST)|[3] Phospho (ST)	-0.03	-1.00	-0.60	0.97	0.441	0.014	0.027	0.01	6.70E+04	4.95E+04	4.90E+04	5.48E+04	5.87E+04	4.89E+04	2.17E+04	3.91E+04	2.19E+04	3.89E+04	2.93E+04	4.13E+04	1118.4345	2	16.55
PAF1	YBR279W	RLDDGDSDDENLDVNHIISR	[7] Phospho (ST)	-0.14	0.05	-0.27	-0.19	0.402	0.432	0.260	0.36	1.08E+04	1.98E+04	1.72E+04	5.97E+03	2.30E+04	1.44E+04	1.35E+04	1.83E+04	1.77E+04	7.74E+03	1.63E+04	1.56E+04	595.26221	4	15.94
UTP22	YGR090W	TVPEQENDESDTSPESNEVATNTAATR	[13] Phospho (ST)	0.06	0.09	-0.58	-0.04	0.433	0.390	0.111	0.43	4.67E+04	4.90E+04	8.15E+04	5.12E+04	6.10E+04	7.20E+04	5.10E+04	6.47E+04	7.31E+04	4.95E+04	4.43E+04	2.52E+04	991.41527	3	22.79
MPT5	YGL178W	SNSSVTNNFSNQYAQDQK	[4] Phospho (ST)	-0.27	-0.37	-0.38	0.09	0.052	0.170	0.101	0.41	4.80E+04	4.05E+04	4.04E+04	4.01E+04	3.48E+04	3.16E+04	2.03E+04	4.95E+04	3.01E+04	4.50E+04	2.55E+04	2.82E+04	1056.4381	2	66.86
BRR2	YER172C	RELDSGDDQPQSSEAK	[5] Phospho (ST)	0.56	0.04	0.02	0.52	0.007	0.432	0.454	0.02	1.13E+04	9.03E+03	1.07E+04	1.71E+04	1.40E+04	1.46E+04	8.95E+03	9.76E+03	1.31E+04	1.25E+04	8.67E+03	1.04E+04	614.59012	3	16.6
IRA2	YOL081W	GSSPSLCSTTR	[3] Phospho (ST)	0.51	0.20	0.61	0.32	0.036	0.302	0.033	0.16	8.36E+03	5.71E+03	9.34E+03	1.23E+04	1.15E+04	9.53E+03	5.64E+03	9.84E+03	1.13E+04	1.43E+04	1.08E+04	1.06E+04	616.75267	2	42.52
NDD1	YOR372C	RSQSLLSDSGSK	[4] Phospho (ST)	0.53	-1.19	-1.64	1.72	0.057	0.017	0.009	0.00	9.47E+03	6.46E+03	1.19E+04	1.51E+04	1.08E+04	1.43E+04	3.68E+03	3.33E+03	5.13E+03	2.48E+03	2.65E+03	3.79E+03	672.8111	2	24.97
RAD53	YPL153C	LLHSNNTENVK	[4] Phospho (ST)	-7.69	-4.93	-1.77	-2.76	0.005	0.005	0.015	0.04	2.01E+04	3.87E+04	4.37E+04	2.12E+02	1.52E+02	1.02E+02	1.63E+03	3.41E+02	1.36E+03	1.28E+04	9.12E+03	8.19E+03	674.81611	2	24.92
NUP100	YKL068W	AHSPQTDLKDDHDESTPDPQSK	[3] Phospho (ST)	0.43	0.29	0.46	0.14	0.047	0.209	0.157	0.29	1.30E+04	1.27E+04	1.96E+04	2.18E+04	1.92E+04	1.98E+04	2.27E+04	1.27E+04	2.00E+04	1.68E+04	1.60E+04	2.94E+04	843.35675	3	19.39
GAT1	YFL021W	NSLNIVAPLK	[2] Phospho (ST)	-0.90	-0.31	-0.38	-0.59	0.016	0.123	0.137	0.02	2.03E+04	2.86E+04	1.96E+04	9.52E+03	1.45E+04	1.27E+04	1.88E+04	2.07E+04	1.58E+04	1.24E+04	1.74E+04	2.28E+04	574.80789	2	43.01
VPS68	YOL129W	MEADDHVSLFR	[N-term] Acetyl (Protein N-term)|[8] Phospho	0.27	0.77	0.47	-0.50	0.366	0.176	0.275	0.27	9.09E+03	2.45E+04	1.17E+04	1.26E+04	3.22E+04	9.83E+03	4.39E+04	1.72E+04	1.64E+04	8.40E+03	3.45E+04	1.99E+04	721.29561	2	36.82
GGA1	YDR358W	ELNLIDFDDDTTANTPSVTSPSK	[22] Phospho (ST)	-0.05	0.61	0.42	-0.66	0.425	0.043	0.111	0.03	5.08E+04	5.24E+04	3.46E+04	4.38E+04	5.37E+04	3.56E+04	8.75E+04	6.48E+04	5.77E+04	5.57E+04	7.88E+04	4.93E+04	854.05073	3	21.62
AVT4	YNL101W	AQSTVLNSNPFYSR	[3] Phospho (ST)	-0.64	0.00	-0.15	-0.64	0.080	0.498	0.357	0.01	3.21E+04	6.33E+04	4.33E+04	3.33E+04	3.22E+04	2.34E+04	4.63E+04	5.14E+04	4.12E+04	3.48E+04	5.55E+04	3.51E+04	832.37864	2	82.53
JSN1	YJR091C	GLSVSSVK	[6] Phospho (ST)	0.90	0.75	0.16	0.14	0.004	0.004	0.222	0.16	3.48E+03	3.47E+03	4.88E+03	7.83E+03	6.28E+03	7.96E+03	6.76E+03	6.05E+03	7.15E+03	3.98E+03	4.29E+03	4.94E+03	428.71226	2	17.84
PIB2	YGL023C	KGDEESGADTVTSPITFEK	[13] Phospho (ST)	-0.07	0.26	-0.29	-0.32	0.399	0.155	0.115	0.13	3.03E+04	4.39E+04	3.92E+04	2.80E+04	3.55E+04	4.47E+04	5.26E+04	3.59E+04	4.68E+04	2.58E+04	3.58E+04	3.09E+04	1045.9624	2	27.41
VCX1	YDL128W	MDATTPLLTVANSHPAR	[N-term] Acetyl (Protein N-term)|[13] Phosph	-0.63	-0.23	0.07	-0.40	0.141	0.282	0.430	0.23	5.60E+04	7.23E+04	3.65E+04	3.03E+04	5.79E+04	1.82E+04	5.85E+04	4.94E+04	3.29E+04	4.04E+04	7.87E+04	5.43E+04	958.95206	2	28.96
YLR257W	YLR257W	GESYQSAEQEIDHTAPEK	[4] Phospho (Y)|[6] Phospho (ST)	1.31	0.43	0.54	0.89	0.003	0.153	0.005	0.02	2.48E+04	2.04E+04	1.90E+04	5.15E+04	6.37E+04	4.44E+04	2.20E+04	4.08E+04	2.35E+04	3.18E+04	3.24E+04	2.88E+04	1089.9183	2	44.71
EDC1	YGL222C	KHSPPSSPSSTTTLGK	[6] Phospho (ST)	-0.34	-0.69	-0.62	0.35	0.053	0.052	0.030	0.17	1.23E+04	1.65E+04	1.28E+04	1.16E+04	1.09E+04	1.05E+04	1.28E+04	5.84E+03	7.13E+03	7.33E+03	8.15E+03	1.16E+04	564.60512	3	31.58
UTP14	YML093W	IVDPYGGSDDEQGDNVFMFK	[8] Phospho (ST)	-0.42	-0.12	0.24	-0.31	0.238	0.381	0.296	0.33	5.12E+04	6.32E+04	4.20E+04	3.10E+04	6.91E+04	1.66E+04	5.13E+04	6.52E+04	2.78E+04	4.43E+04	9.20E+04	4.89E+04	771.65311	3	42.52
YNL054W-B	L054W-B	IQEYDKASTK	[8] Phospho (ST)	0.61	0.41	1.53	0.19	0.104	0.284	0.006	0.34	9.53E+03	3.28E+03	4.64E+03	7.77E+03	8.56E+03	1.03E+04	1.22E+04	7.20E+03	3.79E+03	2.00E+04	1.63E+04	1.42E+04	631.78711	2	26.6
YRO2	YBR054W	KAQEEEEDVATDSE	[11] Phospho (ST)	-1.01	0.00	-0.95	-1.00	0.075	0.499	0.082	0.01	3.16E+04	1.13E+04	2.02E+04	1.25E+04	1.03E+04	8.60E+03	1.63E+04	2.13E+04	2.55E+04	1.26E+04	8.44E+03	1.16E+04	830.31767	2	39
RPN13	YLR421C	MIGVLNNSSESDEEESNDEK	[11] Phospho (ST)	-0.35	0.07	0.42	-0.42	0.277	0.442	0.103	0.27	4.63E+04	2.94E+04	5.49E+04	3.48E+04	5.54E+04	1.25E+04	4.07E+04	6.75E+04	2.89E+04	4.64E+04	6.84E+04	6.05E+04	769.30631	3	44.23
OSH2	YDL019C	SREDLSIAEDLNQVSK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.72	-0.05	0.14	-0.67	0.060	0.452	0.350	0.08	4.29E+04	3.57E+04	2.32E+04	2.07E+04	2.68E+04	1.45E+04	2.98E+04	4.45E+04	2.43E+04	4.84E+04	3.79E+04	2.62E+04	669.28931	3	25.42
UTP14	YML093W	IVDPYGGSDDEQGDNVFMFK	[8] Phospho (ST)	-0.41	-0.24	0.22	-0.17	0.218	0.290	0.338	0.40	1.22E+05	1.22E+05	7.89E+04	6.73E+04	1.34E+05	4.17E+04	8.65E+04	1.34E+05	5.31E+04	9.39E+04	1.96E+05	8.50E+04	1156.9775	2	85.83
DUS4	YLR405W	SASVVERQE	[3] Phospho (ST)	0.15	0.35	0.51	-0.20	0.419	0.306	0.266	0.17	3.97E+03	2.49E+03	1.21E+04	6.20E+03	6.33E+03	8.02E+03	6.44E+03	8.15E+03	9.03E+03	1.36E+04	6.49E+03	6.33E+03	542.73721	2	32.34
COG3	YER157W	KNSLVR	[3] Phospho (ST)	0.97	-0.93	-1.13	1.90	0.114	0.027	0.004	0.05	1.06E+04	1.21E+04	8.50E+03	1.03E+04	1.72E+04	3.38E+04	8.41E+03	3.36E+03	4.60E+03	5.54E+03	4.77E+03	3.96E+03	398.70747	2	26.27
MLF3	YNL074C	SQAYSCPFILK	[5] Phospho (ST)	-0.66	0.78	0.19	-1.44	0.205	0.104	0.371	0.01	1.40E+04	4.57E+04	1.81E+04	1.26E+04	2.20E+04	1.47E+04	3.98E+04	5.95E+04	3.47E+04	2.71E+04	3.57E+04	2.60E+04	697.31514	2	39.95
NUP159	YIL115C	LPETPSDEDGEVVEEEAQK	[6] Phospho (ST)	0.15	0.10	-0.28	0.05	0.253	0.320	0.150	0.40	1.44E+04	2.06E+04	2.13E+04	1.73E+04	2.29E+04	2.23E+04	1.71E+04	2.29E+04	2.05E+04	1.21E+04	1.77E+04	1.65E+04	727.64296	3	26.71
FBA1	YKL060C	VNLDTDCQYAYLTGIR	[9] Phospho (Y)	-0.89	-0.33	-0.68	-0.56	0.091	0.260	0.126	0.06	2.16E+04	4.05E+04	1.72E+04	1.06E+04	1.87E+04	1.36E+04	2.25E+04	2.45E+04	1.61E+04	1.26E+04	1.85E+04	1.84E+04	661.29708	3	37.61
HEK2	YBL032W	SDSASFLEEKEEPQENHDNK	[5] Phospho (ST)	0.62	0.25	0.12	0.37	0.029	0.212	0.329	0.08	1.50E+04	2.56E+04	1.90E+04	3.55E+04	2.67E+04	2.93E+04	2.80E+04	2.50E+04	1.81E+04	2.56E+04	2.05E+04	1.89E+04	804.99981	3	52.35
TFG1	YGR186W	EMLQANAMGLRDEEAPSENEEDELFGEK	[17] Phospho (ST)	-0.32	0.29	0.64	-0.61	0.327	0.309	0.173	0.24	3.22E+04	4.82E+04	3.05E+04	2.30E+04	5.68E+04	8.68E+03	5.15E+04	6.57E+04	1.82E+04	3.28E+04	9.37E+04	4.61E+04	1087.7948	3	34.73
FUN30	YAL019W	VASSSPLKPTSPTVPDASVASLR	[5] Phospho (ST)|[10] Phospho (ST)	-4.18	-3.82	-2.28	-0.36	0.000	0.000	0.000	0.08	8.63E+04	9.47E+04	8.14E+04	4.29E+03	6.02E+03	4.14E+03	6.16E+03	7.03E+03	5.34E+03	1.96E+04	1.93E+04	1.50E+04	809.72435	3	19.83
MSB3	YNL293W	SPSVPNFHDK	[3] Phospho (ST)	0.14	0.39	0.37	-0.25	0.310	0.080	0.101	0.04	1.01E+04	1.80E+04	1.87E+04	1.85E+04	1.48E+04	1.83E+04	2.11E+04	2.07E+04	1.94E+04	2.23E+04	1.96E+04	1.84E+04	604.26149	2	24.99
HRP1	YOL123W	SSDEEDFNDIYGDDKPTTTEEVK	[1] Phospho (ST)|[2] Phospho (ST)	-0.36	0.07	0.00	-0.42	0.285	0.463	0.499	0.34	3.95E+04	3.67E+04	3.11E+04	7.66E+03	5.08E+04	2.52E+04	1.82E+04	7.07E+04	2.34E+04	4.56E+04	3.63E+04	2.54E+04	932.0256	3	35.39
RPP1A	YDL081C	EEEEAKEESDDDMGFGLFD	[9] Phospho (ST)	-0.58	0.00	0.20	-0.58	0.097	0.500	0.294	0.13	3.43E+05	3.74E+05	2.56E+05	1.90E+05	3.30E+05	1.29E+05	3.25E+05	4.26E+05	2.22E+05	3.17E+05	5.14E+05	2.83E+05	1136.4127	2	47.69
ENT1	YDL161W	RGTGRSDENDDDLQR	[6] Phospho (ST)	0.49	-0.25	-0.03	0.74	0.071	0.261	0.465	0.02	2.54E+04	1.48E+04	2.83E+04	3.50E+04	2.61E+04	3.52E+04	1.74E+04	1.49E+04	2.53E+04	2.75E+04	1.60E+04	2.35E+04	605.25345	3	33.41
YRB1	YDR002W	KEGDDAPESPDIHFEPVVHLEK	[9] Phospho (ST)	1.79	0.68	1.04	1.11	0.001	0.157	0.018	0.01	3.21E+03	7.14E+03	7.26E+03	1.78E+04	2.20E+04	2.14E+04	1.49E+04	6.24E+03	7.04E+03	9.28E+03	1.25E+04	1.44E+04	514.43918	5	24.8
MRE11	YMR224C	TGSPDITQSHVDNESR	[3] Phospho (ST)	0.23	0.61	-0.09	-0.38	0.224	0.027	0.373	0.08	1.24E+04	1.54E+04	1.98E+04	1.67E+04	1.57E+04	2.35E+04	2.45E+04	2.03E+04	2.78E+04	1.50E+04	1.23E+04	1.76E+04	911.88402	2	51.21
REG1	YDR028C	SDSGVHSPITDNSSVASSTTSR	[10] Phospho (ST)	-0.15	0.49	0.23	-0.64	0.128	0.001	0.057	0.00	2.30E+04	2.13E+04	2.15E+04	1.73E+04	1.91E+04	2.27E+04	3.19E+04	3.20E+04	2.83E+04	2.93E+04	2.33E+04	2.46E+04	757.99597	3	49.77
TRS33	YOR115C	SSTHSNNVGHPQSSPQGPLTEQQR	[N-term] Acetyl (Protein N-term)|[14] Phosph	-0.24	0.44	0.23	-0.68	0.081	0.115	0.196	0.06	3.28E+04	3.05E+04	3.73E+04	3.11E+04	3.02E+04	2.39E+04	3.71E+04	3.74E+04	6.17E+04	3.98E+04	2.93E+04	4.86E+04	899.06682	3	22.91
PGM2	YMR105C	CTGGIILTASHNPGGPENDMGIK	[10] Phospho (ST)	-0.21	0.16	0.56	-0.36	0.313	0.344	0.157	0.23	1.89E+04	2.21E+04	1.31E+04	1.68E+04	2.15E+04	8.53E+03	2.79E+04	1.71E+04	1.52E+04	1.57E+04	3.95E+04	2.46E+04	807.03094	3	44.68
YDR348C	YDR348C	NSSTSSRPFSVNNPFR	[10] Phospho (ST)	-0.53	-0.22	-0.18	-0.31	0.103	0.275	0.324	0.07	2.77E+04	5.23E+04	3.22E+04	2.35E+04	2.70E+04	2.71E+04	3.37E+04	3.66E+04	2.58E+04	2.35E+04	4.12E+04	3.40E+04	938.92126	2	22.3
IRS4	YKR019C	VVLVDHNSSS	[9] Phospho (ST)	-0.38	-0.13	0.01	-0.25	0.086	0.315	0.482	0.12	1.76E+04	1.21E+04	1.97E+04	1.30E+04	1.27E+04	1.22E+04	1.21E+04	1.50E+04	1.79E+04	1.98E+04	1.35E+04	1.66E+04	568.75278	2	29.02
SYF2	YGR129W	NLATQTQNSSKQDSSADEEDNK	[9] Phospho (ST)|[10] Phospho (ST)	-0.83	-0.97	-0.84	0.14	0.081	0.084	0.083	0.38	6.42E+04	2.61E+04	4.25E+04	2.85E+04	2.59E+04	2.06E+04	1.04E+04	3.28E+04	2.48E+04	2.95E+04	1.84E+04	2.62E+04	857.33661	3	30.89
MNR2	YKL064W	AETVSQLQGLTAK	[5] Phospho (ST)	0.42	0.24	-0.11	0.18	0.138	0.252	0.399	0.14	4.77E+03	1.17E+04	8.04E+03	1.12E+04	1.24E+04	9.23E+03	8.91E+03	1.03E+04	9.82E+03	5.75E+03	9.20E+03	7.74E+03	713.3531	2	55.41
MED2	YDL005C	VVQNSPVSSVHTANFSER	[5] Phospho (ST)	-0.13	-0.01	-0.11	-0.13	0.306	0.492	0.351	0.36	1.81E+04	2.97E+04	3.06E+04	2.12E+04	2.55E+04	2.48E+04	3.65E+04	1.86E+04	2.29E+04	1.89E+04	2.59E+04	2.76E+04	1019.4745	2	65.41
SSB1	YDL229W	SSNITISNAVGRLSSEEIEK	[14] Phospho (ST)	0.35	-0.65	0.06	1.00	0.103	0.162	0.410	0.07	1.83E+04	1.85E+04	1.32E+04	2.26E+04	1.64E+04	2.46E+04	2.06E+04	7.45E+03	3.72E+03	1.41E+04	2.16E+04	1.63E+04	1107.5367	2	18.37
CAF120	YNL278W	PFASSVNDSPSDR	[9] Phospho (ST)	-0.39	0.49	0.59	-0.89	0.090	0.017	0.015	0.00	1.62E+04	1.14E+04	1.78E+04	1.37E+04	1.11E+04	9.73E+03	2.12E+04	2.19E+04	2.08E+04	2.28E+04	2.05E+04	2.49E+04	729.79865	2	47.38
MLP1	YKR095W	SSSGGFNPFTSPSPNK	[11] Phospho (ST)	-0.64	0.62	0.30	-1.25	0.085	0.228	0.218	0.11	1.70E+04	3.09E+04	1.72E+04	1.46E+04	1.42E+04	1.30E+04	1.81E+04	5.96E+04	2.20E+04	3.29E+04	2.65E+04	2.06E+04	845.8597	2	19.26
FEN1	YCR034W	NVPTPSPSPKPQHR	[8] Phospho (ST)	-1.06	-2.15	-1.59	1.09	0.013	0.004	0.004	0.03	3.98E+04	3.69E+04	2.47E+04	2.00E+04	1.62E+04	1.24E+04	1.23E+04	2.93E+03	7.59E+03	9.84E+03	1.23E+04	1.17E+04	811.39654	2	20.58
KCC4	YCL024W	IAASLSDDDLKEDNDKK	[6] Phospho (ST)	-0.25	-0.44	-0.18	0.19	0.153	0.003	0.037	0.25	1.48E+04	1.51E+04	1.54E+04	1.46E+04	8.72E+03	1.50E+04	1.17E+04	9.73E+03	1.21E+04	1.26E+04	1.28E+04	1.48E+04	652.96476	3	44.24

YGR125W	YGR125W	LLLSPASSNVDDDRNR	[7] Phospho (ST)|[8] Phospho (ST)	-0.43	0.06	-0.16	-0.49	0.137	0.427	0.064	0.19	3.59E+04	3.90E+04	3.87E+04	1.45E+04	4.07E+04	2.92E+04	2.77E+04	5.63E+04	3.47E+04	3.08E+04	3.70E+04	3.39E+04	644.61442	3	17.08
KEL1	YHR158C	VEEDGNVADEDDEIGVAQMASSPSK	[22] Phospho (ST)	-0.14	0.61	0.49	-0.75	0.351	0.013	0.068	0.04	3.58E+04	4.27E+04	4.34E+04	3.23E+04	5.42E+04	2.39E+04	6.27E+04	7.18E+04	5.18E+04	4.20E+04	7.11E+04	5.80E+04	891.37204	3	19.33
CAF20	YOR276W	KKGSGEDDEEETETTPTSTVPVATIAQETLK	[19] Phospho (ST)	0.09	-0.15	-0.02	0.24	0.310	0.265	0.461	0.16	6.58E+04	7.18E+04	5.42E+04	7.38E+04	7.20E+04	5.77E+04	7.14E+04	5.65E+04	4.47E+04	7.60E+04	6.00E+04	5.32E+04	843.64674	4	23.3
MLF3	YNL074C	NRSSSILFQR	[3] Phospho (ST)	-0.33	-0.12	-0.16	-0.21	0.079	0.337	0.256	0.24	9.42E+03	1.16E+04	1.32E+04	9.23E+03	7.69E+03	1.04E+04	7.19E+03	1.19E+04	1.24E+04	1.11E+04	7.84E+03	1.18E+04	644.31411	2	32.78
NPR1	YNL183C	AIPSLSSSIPYSVPNSNK	[4] Phospho (ST)	-0.64	-0.09	-0.38	-0.55	0.078	0.398	0.160	0.03	3.07E+04	5.11E+04	2.86E+04	2.08E+04	2.84E+04	2.14E+04	3.71E+04	3.89E+04	2.77E+04	2.74E+04	3.28E+04	2.45E+04	647.65115	3	25.35
SKG3	YLR187W	SANEFSTTPEDK	[1] Phospho (ST)	-0.28	-0.35	0.15	0.07	0.240	0.175	0.321	0.40	1.66E+04	1.00E+04	2.03E+04	1.17E+04	1.02E+04	1.66E+04	1.01E+04	1.31E+04	1.36E+04	2.00E+04	1.41E+04	1.80E+04	703.28014	2	48.12
RPL3	YOR063W	ALEEVSLK	[6] Phospho (ST)	-0.44	0.10	0.38	-0.53	0.112	0.381	0.103	0.03	5.01E+03	8.31E+03	9.44E+03	5.06E+03	5.41E+03	6.34E+03	9.19E+03	6.26E+03	8.88E+03	8.41E+03	1.09E+04	1.04E+04	484.73881	2	19.72
ASK10	YGR097W	VNTPAIDDYGNLITVER	[9] Phospho (Y)	-0.02	0.42	0.46	-0.44	0.479	0.140	0.137	0.13	2.01E+04	3.55E+04	2.00E+04	1.57E+04	3.37E+04	2.49E+04	4.23E+04	3.05E+04	2.82E+04	2.55E+04	4.40E+04	3.43E+04	657.31491	3	33.98
YMR295C	YMR295C	TASVADPILDAVQEAQPFEQAADTFHDNMNR	[3] Phospho (ST)	-1.25	0.17	-0.05	-1.42	0.112	0.381	0.472	0.04	5.61E+04	1.40E+05	5.60E+04	1.85E+04	7.38E+04	1.33E+04	1.03E+05	1.15E+05	6.45E+04	5.25E+04	1.33E+05	5.76E+04	871.14021	4	30.13
YMR295C	YMR295C	SSISNTSDHDGANRASDVK	[16] Phospho (ST)	-0.10	-0.18	-0.15	0.07	0.250	0.262	0.213	0.38	2.78E+04	2.98E+04	2.18E+04	2.33E+04	2.49E+04	2.56E+04	3.07E+04	1.94E+04	2.01E+04	2.64E+04	2.06E+04	2.45E+04	1020.935	2	39.84
APL5	YPL195W	NSPEPNEFLR	[2] Phospho (ST)	0.41	0.80	-0.03	-0.39	0.170	0.023	0.468	0.14	7.86E+03	1.36E+04	1.01E+04	9.75E+03	1.91E+04	1.31E+04	1.74E+04	2.25E+04	1.51E+04	5.52E+03	1.33E+04	1.20E+04	641.77746	2	23.06
LSB3	R024C-A	FTAPTSPSTSSPK	[5] Phospho (ST)|[6] Phospho (ST)	0.33	0.25	-0.19	0.08	0.065	0.238	0.212	0.39	1.73E+04	1.33E+04	1.98E+04	2.06E+04	1.92E+04	2.36E+04	1.36E+04	2.61E+04	2.02E+04	1.20E+04	1.69E+04	1.52E+04	734.29446	2	21.22
TPO2	YGR138C	SLQDLGVTSAAPVPDINAPQTAK	[1] Phospho (ST)	0.81	0.08	-0.34	0.73	0.075	0.427	0.208	0.09	3.57E+04	2.56E+04	1.82E+04	4.77E+04	6.32E+04	2.86E+04	3.81E+04	2.53E+04	2.04E+04	1.54E+04	2.72E+04	2.03E+04	791.72877	3	58.36
DNF2	YDR093W	DISTPDLSK	[3] Phospho (ST)	-0.19	-0.27	0.07	0.08	0.175	0.147	0.358	0.37	1.01E+04	8.72E+03	1.19E+04	1.05E+04	8.14E+03	8.33E+03	6.85E+03	8.04E+03	1.06E+04	1.26E+04	9.96E+03	9.73E+03	528.23681	2	23.46
YDR348C	YDR348C	NLSLSRDNYDVGHSNEGVR	[3] Phospho (ST)	-0.41	-1.94	-0.10	1.53	0.031	0.009	0.313	0.03	2.20E+04	2.16E+04	2.58E+04	2.04E+04	1.42E+04	1.77E+04	1.45E+04	1.58E+03	1.95E+03	2.46E+04	1.67E+04	2.35E+04	737.99778	3	31.47
STE20	YHL007C	APAQETVTTPTSKPAQAR	[9] Phospho (ST)	-0.52	-0.28	-0.25	-0.24	0.030	0.183	0.251	0.27	1.20E+04	1.28E+04	1.48E+04	8.98E+03	7.01E+03	1.16E+04	1.26E+04	6.58E+03	1.34E+04	7.30E+03	9.58E+03	1.64E+04	645.31748	3	27.45
PTR2	YKR093W	DSYVSDDVANSTER	[11] Phospho (ST)	0.65	0.37	0.03	0.28	0.025	0.129	0.459	0.04	1.30E+04	1.08E+04	2.02E+04	2.37E+04	2.10E+04	2.43E+04	1.59E+04	2.02E+04	2.06E+04	1.42E+04	1.62E+04	1.44E+04	819.32107	2	39.5
PMD1	YER132C	SVSLFSPATK	[1] Phospho (ST)	-0.23	0.38	0.26	-0.61	0.249	0.140	0.206	0.05	8.19E+03	1.32E+04	8.57E+03	8.04E+03	1.07E+04	6.77E+03	1.56E+04	1.40E+04	9.50E+03	1.17E+04	1.45E+04	9.66E+03	558.77069	2	26.52
YFR016C	YFR016C	ESTGIEVGNSPITR	[10] Phospho (ST)	-0.21	-0.76	-0.17	0.55	0.068	0.125	0.153	0.20	1.18E+04	1.23E+04	9.70E+03	9.68E+03	9.47E+03	1.01E+04	1.33E+04	4.30E+03	2.35E+03	1.14E+04	8.87E+03	9.73E+03	770.35734	2	18.2
HSP12	YFL014W	DNAEGQGESLADQAR	[9] Phospho (ST)	1.71	0.54	0.32	1.17	0.000	0.091	0.150	0.00	8.96E+03	4.90E+03	1.04E+04	2.47E+04	2.61E+04	2.84E+04	8.60E+03	1.31E+04	1.36E+04	1.05E+04	9.32E+03	1.05E+04	820.83201	2	58.31
HRP1	YOL123W	SSDEEDFNDIYGDDKPTTTEEVKK	[1] Phospho (ST)|[2] Phospho (ST)	-0.63	-0.63	-0.49	0.00	0.101	0.128	0.098	0.50	5.62E+04	3.93E+04	3.11E+04	1.68E+04	3.91E+04	2.56E+04	1.65E+04	4.41E+04	2.12E+04	2.53E+04	3.22E+04	3.27E+04	974.7225	3	34.63
STU1	YBL034C	SEGDEESDDAVDENDVKK	[7] Phospho (ST)	0.26	0.35	0.23	-0.09	0.219	0.134	0.243	0.36	1.03E+04	7.45E+03	1.32E+04	1.52E+04	9.54E+03	1.23E+04	1.07E+04	1.30E+04	1.57E+04	1.54E+04	1.00E+04	1.10E+04	687.5982	3	22.25
RGA1	YOR127W	TFSRPASLVNEIPSGSEPSK	[3] Phospho (ST)|[7] Phospho (ST)	-0.24	0.27	0.07	-0.51	0.195	0.282	0.414	0.17	6.30E+04	7.73E+04	5.45E+04	5.44E+04	6.88E+04	4.17E+04	6.66E+04	1.18E+05	5.04E+04	7.12E+04	8.55E+04	4.71E+04	1132.0063	2	31.3
SHS1	YDL225W	KNDTYTDLASIASGRD	[5] Phospho (Y)|[10] Phospho (ST)|[13] Phosp	-1.67	-0.50	-0.53	-1.17	0.008	0.231	0.009	0.18	8.67E+04	9.91E+04	8.44E+04	2.59E+03	5.25E+04	2.96E+04	1.89E+04	1.26E+05	4.66E+04	7.32E+04	5.69E+04	5.64E+04	983.86654	2	23.17
STF2	YGR008C	RGSNLQSHEQK	[3] Phospho (ST)	1.26	0.61	0.18	0.65	0.032	0.059	0.315	0.10	7.40E+03	1.18E+04	7.24E+03	2.42E+04	1.20E+04	2.71E+04	1.59E+04	9.87E+03	1.47E+04	1.26E+04	6.78E+03	1.06E+04	682.30969	2	21.39
NPR1	YNL183C	SSSHIGSVSNSSSSDR	[7] Phospho (ST)	0.35	0.25	0.45	0.09	0.185	0.272	0.155	0.35	1.28E+04	2.20E+04	3.17E+04	3.22E+04	2.38E+04	2.88E+04	2.19E+04	3.33E+04	2.43E+04	3.90E+04	2.52E+04	2.68E+04	837.34212	2	61.14
KIN1	YDR122W	YSPSSPLTTNSIHQR	[5] Phospho (ST)	0.13	0.23	-0.11	-0.11	0.317	0.233	0.350	0.34	1.23E+04	2.00E+04	1.45E+04	1.45E+04	2.00E+04	1.66E+04	2.34E+04	1.58E+04	1.58E+04	1.16E+04	1.58E+04	1.60E+04	884.40801	2	38.3
RLF2	YPR018W	SNSDLQAQTASQSQSPEK	[3] Phospho (ST)	-0.51	-1.05	-0.21	0.54	0.056	0.004	0.209	0.07	2.68E+04	2.07E+04	2.87E+04	2.03E+04	1.22E+04	2.10E+04	1.03E+04	1.29E+04	1.37E+04	2.49E+04	1.59E+04	2.50E+04	993.42617	2	73.98
LYP1	YNL268W	HGSLQGGAIADVNSITNSLTR	[14] Phospho (ST)|[18] Phospho (ST)	-0.86	-0.56	-0.74	-0.29	0.035	0.080	0.039	0.27	4.78E+04	5.67E+04	3.55E+04	2.18E+04	3.74E+04	1.80E+04	1.91E+04	3.91E+04	3.64E+04	3.74E+04	2.60E+04	2.02E+04	757.67801	3	27.38
POL1	YNL102W	NGTSIDDYEGDESDGDRIYDEIDEK	[8] Phospho (Y)	-0.63	0.00	-0.29	-0.63	0.073	0.498	0.198	0.04	2.72E+04	4.06E+04	2.15E+04	1.60E+04	2.07E+04	2.09E+04	2.48E+04	3.84E+04	2.60E+04	2.27E+04	2.35E+04	2.67E+04	977.38494	3	28.54
SCD5	YOR329C	NNHSNTAADNATNVSSPQK	[16] Phospho (ST)	-0.30	-0.16	-0.06	-0.14	0.243	0.352	0.442	0.28	5.51E+04	2.57E+04	3.22E+04	2.60E+04	3.01E+04	3.54E+04	3.21E+04	2.74E+04	4.14E+04	4.31E+04	2.78E+04	3.75E+04	1025.4332	2	57.11
PBS2	YJL128C	SNPGSLINGVQSTSTSSSTEGPHDTVGTTPR	[1] Phospho (ST)	-0.92	-0.15	-0.08	-0.76	0.002	0.134	0.372	0.00	4.07E+04	3.12E+04	3.67E+04	1.79E+04	1.81E+04	2.16E+04	3.20E+04	3.16E+04	3.40E+04	2.64E+04	3.42E+04	4.24E+04	1051.1444	3	59.1
YMR221C	YMR221C	LIEGDTGSGIIPDEQER	[8] Phospho (ST)	0.15	0.41	0.29	-0.26	0.274	0.038	0.202	0.06	2.68E+04	3.74E+04	2.53E+04	2.74E+04	3.79E+04	3.37E+04	4.23E+04	3.97E+04	3.69E+04	2.59E+04	4.69E+04	3.67E+04	954.93426	2	39.67
MTL1	YGR023W	HTNVEGYDDDDDDANDENLSSNFHNR	[21] Phospho (ST)	-0.46	-0.32	0.01	-0.15	0.029	0.089	0.489	0.17	3.06E+04	2.22E+04	3.05E+04	1.98E+04	2.16E+04	1.89E+04	1.99E+04	2.59E+04	2.11E+04	3.24E+04	2.76E+04	2.35E+04	1068.3976	3	33.14
RPL10	YLR075W	KGSLENNIR	[3] Phospho (ST)	-0.12	0.14	0.40	-0.26	0.436	0.422	0.247	0.31	7.96E+03	1.14E+03	8.59E+03	4.27E+03	3.82E+03	8.18E+03	4.12E+03	6.08E+03	9.27E+03	8.93E+03	6.40E+03	7.99E+03	555.7689	2	28.39
LCB3	YJL134W	ARTLSNPNDFQEPNYLLDPGNHPSDHFR	[3] Phospho (ST)|[5] Phospho (ST)	-0.30	-0.52	-0.89	0.23	0.054	0.013	0.005	0.04	6.50E+04	7.94E+04	6.09E+04	5.36E+04	6.08E+04	5.26E+04	5.14E+04	4.76E+04	4.38E+04	3.24E+04	4.48E+04	3.37E+04	853.62151	4	15.44
YPR137C-B	R137C-B	AHNVSTSNNSPSTDNDSISK	[7] Phospho (ST)|[10] Phospho (ST)	0.25	-0.06	-0.05	0.31	0.274	0.458	0.462	0.23	3.66E+04	1.29E+04	2.85E+04	3.66E+04	2.92E+04	2.70E+04	1.16E+04	3.25E+04	3.06E+04	3.43E+04	1.89E+04	2.23E+04	1117.9344	2	26.02
GNP1	YDR508C	NDLDDVSHYEMK	[7] Phospho (ST)	-0.50	-0.32	0.19	-0.19	0.222	0.253	0.323	0.39	1.27E+04	2.80E+04	2.08E+04	1.38E+04	2.45E+04	5.19E+03	2.01E+04	1.94E+04	9.84E+03	1.81E+04	3.10E+04	2.12E+04	773.30132	2	45.86
NTH1	YDR001C	TMSVFDNVSPFKK	[3] Phospho (ST)	-0.28	0.51	0.55	-0.78	0.297	0.230	0.155	0.12	1.53E+04	3.58E+04	1.75E+04	1.48E+04	2.28E+04	1.90E+04	4.02E+04	4.43E+04	1.30E+04	2.73E+04	4.66E+04	2.67E+04	790.36571	2	47.38
PHO91	YNR013C	FYISQETGLIANYNELK	[2] Phospho (Y)	-0.87	-1.80	-0.17	0.93	0.179	0.086	0.407	0.04	3.61E+04	8.84E+03	1.39E+04	1.45E+04	8.50E+03	9.15E+03	3.47E+03	7.29E+03	6.06E+03	1.93E+04	1.20E+04	2.07E+04	694.99601	3	17.39
SDS23	YGL056C	NTEANKSDTESLHK	[7] Phospho (ST)	0.85	-1.00	-0.37	1.85	0.062	0.111	0.267	0.01	1.18E+04	5.85E+03	4.70E+03	1.28E+04	1.01E+04	1.75E+04	4.29E+03	1.15E+03	5.74E+03	4.31E+03	4.76E+03	8.14E+03	551.90845	3	30.69
RTC1	YOL138C	SAQFHASPIAK	[7] Phospho (ST)	-1.25	-1.44	-1.03	0.19	0.027	0.013	0.062	0.40	5.07E+03	8.63E+03	7.06E+03	1.21E+03	2.62E+03	4.89E+03	3.98E+03	1.53E+03	2.12E+03	4.11E+03	5.55E+03	5.24E+02	618.79175	2	19
PPH22	YDL188C	ARSNDEDTDEELEDFNFKPGSSGIADHK	[8] Phospho (ST)	0.46	0.38	0.42	0.08	0.022	0.157	0.058	0.37	1.88E+04	2.93E+04	2.65E+04	3.51E+04	3.26E+04	3.49E+04	4.24E+04	3.13E+04	2.30E+04	3.49E+04	2.78E+04	3.70E+04	801.59163	4	29.54
INP53	YOR109W	EKSPTPQTSTASLSSVTK	[3] Phospho (ST)	-0.41	0.41	-0.22	-0.82	0.100	0.163	0.208	0.05	1.33E+04	2.01E+04	1.31E+04	1.01E+04	1.16E+04	1.33E+04	2.82E+04	1.46E+04	1.92E+04	1.22E+04	1.36E+04	1.42E+04	964.96555	2	30.7
TGL4	YKR089C	YSITSASLNPR	[2] Phospho (ST)	-0.23	0.19	-0.19	-0.42	0.222	0.274	0.271	0.08	1.18E+04	1.86E+04	1.19E+04	1.10E+04	1.41E+04	1.08E+04	1.99E+04	1.53E+04	1.30E+04	1.00E+04	1.49E+04	1.21E+04	644.80092	2	44.32
TFG1	YGR186W	DGSQTPTVDSVTK	[3] Phospho (ST)	3.37	0.39	-0.88	2.98	0.000	0.047	0.017	0.00	3.00E+03	2.88E+03	3.74E+03	3.60E+04	2.66E+04	3.74E+04	3.49E+03	4.39E+03	4.77E+03	1.87E+03	1.03E+03	2.32E+03	707.8087	2	43.85
MDS3	YGL197W	SSAFPQSPIR	[7] Phospho (ST)	0.46	1.38	0.65	-0.92	0.138	0.006	0.064	0.00	3.58E+03	1.06E+04	8.77E+03	1.01E+04	9.19E+03	1.24E+04	2.34E+04	1.76E+04	1.87E+04	1.11E+04	1.38E+04	1.11E+04	585.27172	2	15.67
YGR149W	YGR149W	LQPDSDAVISDASVNDK	[10] Phospho (ST)|[13] Phospho (ST)	-0.63	0.11	0.03	-0.74	0.020	0.218	0.341	0.02	6.23E+04	6.87E+04	6.85E+04	2.78E+04	5.03E+04	5.05E+04	7.58E+04	7.82E+04	6.07E+04	6.68E+04	7.09E+04	6.53E+04	967.39624	2	22.83
PMD1	YER132C	TSVTDFTASQQR	[2] Phospho (ST)	-0.29	0.18	0.03	-0.47	0.120	0.108	0.440	0.01	1.16E+04	1.57E+04	1.50E+04	1.41E+04	9.53E+03	1.10E+04	1.59E+04	1.59E+04	1.62E+04	1.46E+04	1.24E+04	1.61E+04	710.80916	2	42.03
AVT3	YKL146W	NPSNSLQLQGGDITR	[5] Phospho (ST)	-0.23	-0.08	-0.33	-0.15	0.181	0.382	0.104	0.25	1.75E+04	1.25E+04	1.96E+04	1.61E+04	1.37E+04	1.25E+04	1.24E+04	1.60E+04	1.85E+04	1.33E+04	1.17E+04	1.44E+04	840.39193	2	55.77
AGE2	YIL044C	SNTSLLNLQVSSLSK	[1] Phospho (ST)	-1.08	-0.19	-0.39	-0.89	0.033	0.331	0.163	0.06	4.32E+04	7.09E+04	4.08E+04	1.69E+04	3.36E+04	2.29E+04	3.78E+04	6.35E+04	3.47E+04	3.14E+04	4.90E+04	3.78E+04	835.92279	2	73.7
UTP22	YGR090W	RKASETSDQNIVK	[4] Phospho (ST)	0.49	-0.12	0.45	0.60	0.103	0.405	0.132	0.02	1.55E+04	5.99E+03	1.59E+04	1.65E+04	1.87E+04	1.72E+04	1.38E+04	7.85E+03	1.28E+04	1.81E+04	1.42E+04	1.89E+04	778.37759	2	37.69
PUF4	YGL014W	RQTFHALSPTDLINAANNVTLSK	[3] Phospho (ST)	0.34	0.04	0.17	0.29	0.205	0.476	0.366	0.28	2.85E+04	6.66E+04	3.40E+04	5.51E+04	5.94E+04	4.86E+04	7.59E+04	2.64E+04	3.07E+04	4.17E+04	6.62E+04	3.76E+04	864.43854	3	44.03
ROM2	YLR371W	TRVSSTSLALK	[4] Phospho (ST)	-0.02	0.04	-0.52	-0.06	0.482	0.444	0.110	0.37	4.67E+03	9.90E+03	8.88E+03	7.31E+03	6.54E+03	9.34E+03	8.63E+03	7.30E+03	8.27E+03	4.93E+03	5.32E+03	6.08E+03	621.82671	2	25.45
MTC4	YBR255W	IATTPEAQISR	[4] Phospho (ST)	0.17	0.51	0.12	-0.34	0.268	0.183	0.344	0.27	7.61E+03	1.08E+04	1.03E+04	8.21E+03	1.07E+04	1.35E+04	1.09E+04	8.77E+03	2.14E+04	7.01E+03	1.18E+04	1.25E+04	633.80777	2	24.59
VMA2	YBR127C	DDADEDEEDPDTRSSGK	[15] Phospho (ST)	0.61	-0.39	0.11	1.00	0.122	0.273	0.433	0.01	3.83E+04	1.10E+04	1.97E+04	4.25E+04	3.01E+04	3.28E+04	1.49E+04	1.94E+04	1.86E+04	3.64E+04	2.00E+04	1.80E+04	980.84998	2	41.83
GTS1	YGL181W	SHSFYK	[3] Phospho (ST)	0.56	-0.61	-0.12	1.17	0.010	0.100	0.340	0.01	4.71E+03	3.39E+03	3.30E+03	5.29E+03	5.68E+03	5.85E+03	3.49E+03	2.88E+03	1.07E+03	4.40E+03	2.60E+03	3.48E+03	424.67045	2	26.02
YNR014W	YNR014W	RASEPQLPSFDNR	[3] Phospho (ST)	-0.13	-0.09	-0.45	-0.04	0.197	0.334	0.064	0.42	2.13E+04	2.66E+04	2.75E+04	2.23E+04	2.51E+04	2.17E+04	1.96E+04	2.30E+04	2.83E+04	1.25E+04	2.13E+04	2.14E+04	798.86178	2	21.28
YNL095C	YNL095C	EYSNVDQYGHQR	[2] Phospho (Y)	-0.03	-0.71	-0.14	0.67	0.418	0.013	0.289	0.01	1.49E+04	1.92E+04	1.95E+04	1.97E+04	1.58E+04	1.68E+04	1.06E+04	8.84E+03	1.34E+04	1.55E+04	1.28E+04	2.04E+04	788.31531	2	17.59
SSD1	YDR293C	ATSNLSPPSFK	[3] Phospho (ST)	0.36	0.63	0.17	-0.28	0.146	0.041	0.328	0.05	8.40E+03	1.89E+04	1.53E+04	1.58E+04	1.96E+04	1.91E+04	2.41E+04	1.93E+04	2.27E+04	1.25E+04	1.95E+04	1.58E+04	614.78465	2	17.02
FLC3	YGL139W	NENASTDALR	[5] Phospho (ST)	-0.35	1.27	0.87	-1.62	0.341	0.078	0.107	0.04	5.10E+03	1.17E+03	9.99E+03	2.82E+03	4.62E+03	5.29E+03	6.09E+03	1.52E+04	1.80E+04	1.31E+04	9.44E+03	7.29E+03	585.7436	2	46.79
MSL5	YLR116W	SPSPPPVYDAQGK	[3] Phospho (ST)	-0.15	-0.47	-0.36	0.31	0.178	0.073	0.067	0.13	2.37E+04	3.19E+04	2.61E+04	2.66E+04	2.37E+04	2.32E+04	2.65E+04	1.60E+04	1.65E+04	1.99E+04	2.53E+04	1.86E+04	711.81931	2	31.32
FUN30	YAL019W	AVVEGFDETSAEPTPAPAPAPVER	[10] Phospho (ST)	0.14	0.57	0.28	-0.43	0.219	0.002	0.017	0.01	3.63E+04	4.50E+04	4.11E+04	3.75E+04	5.09E+04	4.60E+04	6.49E+04	5.85E+04	5.79E+04	5.10E+04	4.73E+04	5.02E+04	839.72379	3	19.09
RFM1	YOR279C	LGSEEDEEGDGHDGDEGETK	[3] Phospho (ST)	-0.27	-0.32	-0.17	0.05	0.181	0.152	0.286	0.42	2.60E+04	1.63E+04	2.49E+04	1.79E+04	1.52E+04	2.25E+04	1.86E+04	1.36E+04	2.13E+04	2.09E+04	1.48E+04	2.39E+04	1092.8909	2	61.88
GGA1	YDR358W	SLQPFDDLLGDFNK	[1] Phospho (ST)	-0.13	0.59	0.35	-0.72	0.365	0.074	0.232	0.03	4.71E+04	7.67E+04	3.97E+04	4.79E+04	6.16E+04	3.95E+04	7.71E+04	1.02E+05	6.69E+04	6.60E+04	9.66E+04	4.60E+04	844.88393	2	45.4
DNF1	YER166W	ETQDLLQSPQFQQAQTFGR	[8] Phospho (ST)	-0.46	-0.31	-0.70	-0.15	0.124	0.172	0.052	0.27	4.05E+04	5.32E+04	2.90E+04	2.81E+04	3.81E+04	2.30E+04	2.94E+04	3.66E+04	3.32E+04	2.46E+04	3.02E+04	2.10E+04	1151.5298	2	50.44
PSD2	YGR170W	RTISVSDENAK	[4] Phospho (ST)	0.02	-0.40	-0.14	0.42	0.466	0.028	0.078	0.10	6.05E+03	6.39E+03	7.13E+03	8.56E+03	5.23E+03	6.07E+03	5.23E+03	3.98E+03	5.63E+03	5.89E+03	5.64E+03	6.18E+03	650.30013	2	54.03
SYT1	YPR095C	SQSTSFVQGK	[3] Phospho (ST)	-0.10	-0.08	0.00	-0.02	0.351	0.354	0.498	0.48	1.07E+04	8.63E+03	1.03E+04	1.20E+04	8.51E+03	7.28E+03	7.90E+03	1.16E+04	8.51E+03	1.31E+04	7.33E+03	9.23E+03	574.75308	2	42.73
SIR4	YDR227W	VSLSQPVSASK	[2] Phospho (ST)	0.90	0.26	-0.34	0.64	0.001	0.056	0.015	0.00	1.38E+04	1.46E+04	1.33E+04	2.48E+04	2.87E+04	2.40E+04	1.92E+04	1.53E+04	1.54E+04	9.38E+03	1.19E+04	1.16E+04	591.79175	2	39.5
WHI4	YDL224C	PRPSLLSER	[4] Phospho (ST)	-0.37	-0.41	0.27	0.03	0.182	0.328	0.177	0.49	5.56E+03	8.21E+03	1.03E+04	3.93E+03	7.65E+03	7.00E+03	1.34E+04	4.37E+03	3.47E+02	9.97E+03	8.14E+03	1.10E+04	567.78679	2	17.25
YGR237C	YGR237C	VDKDEQDNSDDLKTEVR	[14] Phospho (ST)	0.14	-0.39	-0.04	0.54	0.223	0.067	0.442	0.02	9.50E+04	6.76E+04	8.66E+04	1.04E+05	8.15E+04	9.00E+04	5.06E+04	7.37E+04	6.54E+04	1.00E+05	5.78E+04	8.40E+04	695.97174	3	16.57
YMR086W	YMR086W	KVSQESLHSQPK	[6] Phospho (ST)	-1.12	0.12	-0.52	-1.24	0.063	0.423	0.152	0.08	1.18E+04	8.35E+03	5.07E+03	3.02E+03	2.09E+03	6.46E+03	1.40E+04	4.31E+03	9.03E+03	7.20E+03	6.40E+03	3.96E+03	483.2363	3	29.82
YGR054W	YGR054W	KSSETSPDSTPAPSAPASTNAPTNNK	[10] Phospho (ST)	-0.28	-0.06	0.00	-0.22	0.188	0.391	0.496	0.18	3.24E+04	2.09E+04	3.17E+04	2.95E+04	1.76E+04	2.27E+04	2.86E+04	2.45E+04	2.85E+04	2.70E+04	2.22E+04	3.60E+04	879.72683	3	16.8
KIN4	YOR233W	TSCGSPCYAAPELVVSTK	[1] Phospho (ST)	0.02	0.39	0.21	-0.37	0.487	0.194	0.319	0.09	2.85E+04	5.99E+04	2.46E+04	3.46E+04	4.88E+04	3.08E+04	4.41E+04	5.79E+04	4.57E+04	4.47E+04	4.74E+04	3.84E+04	1003.9347	2	26.29
ROD1	YOR018W	NNSGSSVSLQQLAR	[3] Phospho (ST)	-0.70	-0.48	-0.28	-0.21	0.006	0.059	0.061	0.25	2.27E+04	2.00E+04	1.73E+04	1.19E+04	1.41E+04	1.11E+04	1.04E+04	1.88E+04	1.38E+04	1.64E+04	1.82E+04	1.49E+04	770.85955	2	54.31
GAT1	YFL021W	KNSLNIVAPLK	[3] Phospho (ST)	-1.11	-0.31	-1.09	-0.80	0.075	0.291	0.086	0.02	7.45E+03	2.19E+04	1.30E+04	5.64E+03	7.93E+03	6.08E+03	1.46E+04	9.48E+03	1.02E+04	3.66E+03	9.30E+03	6.87E+03	638.85542	2	37.75
CCR4	YAL021C	KQQPTGDSTPSGTATNSAVSTPLTPK	[17] Phospho (ST)|[20] Phospho (ST)	-1.49	-0.59	-0.04	-0.91	0.000	0.004	0.448	0.00	5.15E+04	4.44E+04	4.85E+04	1.98E+04	1.47E+04	1.67E+04	2.71E+04	3.56E+04	3.34E+04	6.08E+04	3.29E+04	4.72E+04	911.07828	3	22.8
APL5	YPL195W	DNLSDTEEVIVIKK	[4] Phospho (ST)	0.01	-0.21	-0.01	0.21	0.490	0.174	0.487	0.09	1.23E+04	1.86E+04	1.64E+04	1.38E+04	1.74E+04	1.63E+04	1.52E+04	1.29E+04	1.28E+04	1.65E+04	1.52E+04	1.55E+04	841.9166	2	47.28
RPL24A	YGL031C	AQRPITGASLDLIK	[9] Phospho (ST)	0.18	0.23	0.19	-0.05	0.359	0.341	0.373	0.45	7.08E+03	1.65E+04	6.81E+03	9.75E+03	1.42E+04	1.05E+04	1.61E+04	8.43E+03	1.10E+04	7.10E+03	1.57E+04	1.17E+04	781.91878	2	23.51
AIM3	YBR108W	AYSGDISAADDNLNPFER	[3] Phospho (ST)	-1.15	-0.13	0.18	-1.02	0.020	0.323	0.297	0.02	4.30E+04	5.69E+04	3.41E+04	1.63E+04	2.95E+04	1.47E+04	3.92E+04	4.88E+04	3.42E+04	3.84E+04	6.62E+04	4.77E+04	1017.9261	2	59.22
MLF3	YNL074C	KNSNNVSSPLDNVIPTSR	[3] Phospho (ST)	-0.24	-0.03	0.64	-0.21	0.087	0.459	0.027	0.28	1.66E+04	1.99E+04	1.81E+04	1.78E+04	1.30E+04	1.54E+04	1.39E+04	2.48E+04	1.47E+04	2.36E+04	3.57E+04	2.61E+04	1011.4867	2	21.96
PRT1	YOR361C	LEDIPVDDIDFSDLEEQYK	[12] Phospho (ST)	0.69	0.49	-0.24	0.20	0.127	0.143	0.332	0.29	1.67E+04	3.93E+04	1.58E+04	2.70E+04	5.37E+04	3.51E+04	3.64E+04	3.40E+04	3.06E+04	1.97E+04	2.33E+04	1.78E+04	788.34638	3	47.34
GPT2	YKR067W	VNSRGSLTDIPIFSDAK	[3] Phospho (ST)|[6] Phospho (ST)	-0.72	-0.36	-0.45	-0.37	0.019	0.087	0.057	0.08	7.36E+04	6.58E+04	4.99E+04	3.65E+04	4.64E+04	3.18E+04	5.21E+04	5.55E+04	4.01E+04	4.65E+04	5.41E+04	3.75E+04	990.44995	2	18.55
IST2	YBR086C	LLPDGDAVDALSR	[12] Phospho (ST)	-0.45	0.04	-0.19	-0.48	0.069	0.435	0.246	0.03	2.62E+04	3.52E+04	2.42E+04	1.66E+04	2.45E+04	2.18E+04	3.15E+04	3.17E+04	2.46E+04	1.95E+04	3.07E+04	2.49E+04	711.33809	2	15.54

CDC24	YAL041W	TTSSSFESEIK	[4] Phospho (ST)	0.05	0.48	-0.34	-0.43	0.424	0.043	0.120	0.01	7.23E+03	1.22E+04	1.18E+04	1.11E+04	9.85E+03	1.13E+04	1.55E+04	1.51E+04	1.28E+04	8.48E+03	8.23E+03	7.87E+03	648.27448	2	18.5
ENT1	YDL161W	TGTFINSQGTGYR	[12] Phospho (Y)	0.12	0.70	-0.17	-0.58	0.377	0.155	0.329	0.18	6.87E+03	1.46E+04	1.01E+04	1.17E+04	8.78E+03	1.38E+04	1.17E+04	2.74E+04	1.21E+04	1.14E+04	8.70E+03	7.92E+03	741.32123	2	28.65
HXT1	YHR094C	NSTPDLISPQK	[2] Phospho (ST)	-0.05	-1.20	-0.47	1.15	0.464	0.049	0.226	0.06	1.16E+04	1.11E+04	2.27E+04	1.00E+04	1.14E+04	2.24E+04	9.13E+03	5.83E+03	4.76E+03	1.74E+04	6.05E+03	9.35E+03	640.30037	2	30.3
PUF3	YLL013C	TALSVGTAPPFSTNSK	[4] Phospho (ST)|[7] Phospho (ST)	-1.32	-0.45	-0.58	-0.88	0.012	0.160	0.061	0.10	4.25E+04	6.36E+04	4.35E+04	9.88E+03	2.60E+04	2.38E+04	2.92E+04	5.54E+04	2.51E+04	4.30E+04	3.04E+04	2.65E+04	869.37951	2	16.17
TAF2	YCR042C	LIGQNGEESEK	[9] Phospho (ST)	1.15	0.24	0.14	0.91	0.010	0.353	0.378	0.03	7.78E+03	3.79E+03	1.06E+04	1.82E+04	1.38E+04	1.72E+04	5.07E+03	7.30E+03	1.38E+04	8.08E+03	6.31E+03	1.00E+04	642.27933	2	27.99
YDJ1	YNL064C	GGANYDSDEEEQGGEGVQCASQ	[5] Phospho (Y)	0.29	0.08	0.78	0.21	0.128	0.423	0.131	0.30	2.01E+04	1.41E+04	1.74E+04	2.19E+04	1.67E+04	2.45E+04	9.56E+03	2.47E+04	2.04E+04	4.72E+04	1.56E+04	2.59E+04	789.61725	3	36.21
SIS2	YKR072C	SPNSNPAPVSNSIPGNHAVIPNHTNTSR	[4] Phospho (ST)	-0.42	-0.61	0.00	0.19	0.016	0.000	0.492	0.15	2.57E+04	2.41E+04	2.43E+04	2.22E+04	1.67E+04	1.65E+04	1.52E+04	1.64E+04	1.70E+04	2.44E+04	2.11E+04	2.88E+04	740.60098	4	22.56
YJL070C	YJL070C	VLSENDGDVSPSVLK	[10] Phospho (ST)	0.01	0.58	0.25	-0.58	0.494	0.020	0.167	0.03	2.38E+04	3.88E+04	2.54E+04	2.03E+04	3.81E+04	3.00E+04	4.47E+04	4.20E+04	4.51E+04	3.34E+04	3.77E+04	3.33E+04	819.88512	2	45.96
GLO3	YER122C	AISSDQLFGRGSFDEAANR	[12] Phospho (ST)	0.38	0.48	0.14	-0.11	0.042	0.043	0.130	0.32	1.24E+04	1.58E+04	1.44E+04	1.74E+04	2.16E+04	1.64E+04	2.41E+04	1.92E+04	1.63E+04	1.54E+04	1.68E+04	1.49E+04	707.65174	3	27.81
HRQ1	YDR291W	LKSAGQGSGK	[8] Phospho (ST)	-0.32	-0.58	-0.10	0.26	0.335	0.264	0.463	0.35	1.17E+04	2.41E+03	6.29E+03	7.63E+03	4.49E+03	4.24E+03	1.97E+03	8.14E+03	3.51E+03	1.35E+04	3.12E+03	2.43E+03	506.74405	2	28.36
PTK2	YJR059W	RPTSPSISGSGSGGNSPSSSAGAR	[4] Phospho (ST)	0.70	-0.13	0.29	0.83	0.002	0.331	0.209	0.01	1.71E+04	1.54E+04	1.94E+04	2.86E+04	2.55E+04	3.00E+04	1.83E+04	9.78E+03	1.93E+04	2.02E+04	1.46E+04	2.87E+04	1120.9988	2	26.05
MRS6	YOR370C	RPSFFSFTQNPSPLVVPHLAGIEDPLPATTPDK	[8] Phospho (ST)	0.21	0.31	-0.24	-0.10	0.342	0.272	0.336	0.39	6.17E+04	1.32E+05	5.57E+04	6.74E+04	1.26E+05	9.53E+04	1.40E+05	8.29E+04	8.73E+04	5.16E+04	9.81E+04	6.10E+04	914.71097	4	33.06
RPP2B	YDR382W	EESDDDMGFGLFD	[3] Phospho (ST)	-1.24	-0.26	0.01	-0.98	0.053	0.289	0.490	0.09	8.84E+04	7.33E+04	4.00E+04	2.52E+04	5.07E+04	9.47E+03	5.82E+04	7.53E+04	3.46E+04	5.64E+04	9.71E+04	4.98E+04	778.76171	2	25.37
YDR348C	YDR348C	SPPPVSR	[1] Phospho (ST)	0.86	0.53	0.26	0.33	0.127	0.062	0.266	0.30	9.08E+03	6.27E+03	7.78E+03	1.28E+04	6.57E+03	2.26E+04	1.36E+04	8.18E+03	1.17E+04	1.33E+04	7.32E+03	7.03E+03	410.19157	2	33.09
HSP42	YDR171W	KSSSFAHLQAPSPIPDPLQVSKPETR	[4] Phospho (ST)	0.08	0.22	0.61	-0.14	0.382	0.354	0.056	0.39	1.94E+04	3.19E+04	2.03E+04	2.60E+04	2.32E+04	2.65E+04	4.51E+04	1.93E+04	1.89E+04	2.83E+04	4.45E+04	3.65E+04	725.11951	4	39.15
RRP5	YMR229C	VEDAEYESSDDEDEKLDK	[8] Phospho (ST)|[9] Phospho (ST)	-0.98	-0.82	-0.67	-0.16	0.030	0.091	0.052	0.40	5.65E+04	3.21E+04	4.03E+04	1.44E+04	2.69E+04	2.39E+04	8.22E+03	3.96E+04	2.51E+04	2.18E+04	2.90E+04	3.02E+04	1138.407	2	28.5
PEX25	YPL112C	DDGSQSPIRK	[6] Phospho (ST)	1.99	1.22	0.99	0.76	0.034	0.001	0.028	0.12	5.49E+03	5.94E+03	5.36E+03	2.50E+04	9.46E+03	3.22E+04	1.46E+04	1.13E+04	1.34E+04	1.49E+04	7.69E+03	1.09E+04	591.7607	2	32.96
TOF1	YNL273W	SLEASAADESDEDEEAIR	[10] Phospho (ST)	-0.22	0.01	-0.47	-0.22	0.015	0.482	0.002	0.16	2.96E+04	3.00E+04	3.27E+04	2.80E+04	2.51E+04	2.64E+04	3.78E+04	3.05E+04	2.47E+04	2.38E+04	2.02E+04	2.25E+04	1008.9002	2	61.84
BNR1	YIL159W	SLSLHAR	[3] Phospho (ST)	0.55	0.18	0.12	0.37	0.200	0.394	0.432	0.09	3.10E+02	3.35E+03	4.72E+03	3.74E+03	3.47E+03	5.13E+03	3.43E+03	2.66E+03	3.44E+03	2.67E+03	3.15E+03	3.28E+03	432.21018	2	29.04
COG3	YER157W	SSSILTLAR	[2] Phospho (ST)	0.21	0.24	0.01	-0.03	0.261	0.231	0.482	0.45	5.86E+03	1.10E+04	7.42E+03	7.79E+03	1.13E+04	9.04E+03	1.06E+04	1.06E+04	7.52E+03	8.04E+03	9.97E+03	6.50E+03	514.26297	2	51.5
SYP1	YCR030C	SNNWTPGEASDTPPLPPHATPK	[5] Phospho (ST)	-0.63	-0.37	-0.30	-0.26	0.003	0.024	0.101	0.04	1.38E+05	1.55E+05	1.26E+05	8.75E+04	9.63E+04	8.74E+04	9.59E+04	1.22E+05	1.08E+05	8.38E+04	1.31E+05	1.26E+05	1197.5383	2	24.51
ENP2	YGR145W	HDNSSDEEGIDENGNKK	[4] Phospho (ST)|[5] Phospho (ST)	-1.65	-0.73	-0.90	-0.92	0.200	0.312	0.282	0.12	5.04E+04	1.81E+03	1.02E+04	5.70E+03	5.89E+03	8.30E+03	5.46E+03	2.03E+04	1.19E+04	1.75E+04	9.73E+03	6.11E+03	683.24711	3	43.07
MIG1	YGL035C	SLTDFQGLNNANPNNNGSLR	[3] Phospho (ST)	-1.02	-0.98	-0.44	-0.05	0.001	0.006	0.012	0.43	2.75E+04	2.53E+04	2.17E+04	1.10E+04	1.31E+04	1.26E+04	8.52E+03	1.60E+04	1.34E+04	1.69E+04	1.86E+04	1.94E+04	742.66942	3	50.57
YKL105C	YKL105C	TTSIAGINR	[3] Phospho (ST)	-0.40	0.01	-0.26	-0.41	0.040	0.485	0.135	0.06	6.24E+03	6.24E+03	7.98E+03	5.35E+03	4.44E+03	5.75E+03	5.29E+03	7.64E+03	7.65E+03	6.92E+03	4.70E+03	5.48E+03	506.74527	2	32.37
DLD3	YEL071W	YDMSLQLK	[1] Phospho (Y)	1.85	1.82	1.24	0.03	0.001	0.002	0.012	0.42	4.72E+02	1.03E+03	1.73E+03	4.29E+03	3.68E+03	3.82E+03	3.37E+03	4.46E+03	3.72E+03	2.76E+03	2.17E+03	2.78E+03	539.2397	2	15.69
RAV1	YJR033C	FGSPSASDIESPNPK	[3] Phospho (ST)	-0.18	0.45	0.11	-0.62	0.338	0.117	0.352	0.08	6.29E+03	7.27E+03	1.09E+04	4.14E+03	8.43E+03	9.09E+03	1.24E+04	7.99E+03	1.30E+04	8.97E+03	7.64E+03	9.79E+03	806.84931	2	52.6
VID30	YGL227W	SRSAINIETESR	[3] Phospho (ST)	-1.96	-1.03	-0.72	-0.92	0.000	0.003	0.003	0.02	1.51E+04	1.92E+04	1.59E+04	3.77E+03	3.63E+03	5.50E+03	1.03E+04	7.36E+03	6.88E+03	1.01E+04	9.92E+03	1.05E+04	721.83552	2	54.79
SEC31	YDL195W	EALAFDNDESDAQDDANNEK	[10] Phospho (ST)	0.11	0.41	0.28	-0.30	0.379	0.182	0.223	0.18	1.45E+04	8.64E+03	2.03E+04	1.44E+04	1.84E+04	1.43E+04	1.30E+04	2.15E+04	2.34E+04	2.06E+04	1.72E+04	1.52E+04	764.29277	3	23.51
IPL1	YPL209C	NSLVNIK	[2] Phospho (ST)	0.35	0.50	0.27	-0.16	0.063	0.032	0.110	0.12	3.83E+03	3.95E+03	5.69E+03	5.42E+03	6.15E+03	5.60E+03	5.72E+03	7.19E+03	6.22E+03	5.09E+03	5.77E+03	5.37E+03	434.22037	2	25.06
YSH1	YLR277C	IEPIKEENEDNLDSQAEK	[14] Phospho (ST)	2.54	-1.10	-1.77	3.64	0.000	0.006	0.003	0.00	9.71E+03	1.46E+04	1.43E+04	7.44E+04	7.11E+04	7.93E+04	6.21E+03	5.81E+03	6.03E+03	2.51E+03	4.04E+03	4.75E+03	1090.983	2	38.79
CTK3	YML112W	DSITSSSTTTPPSSQQK	[6] Phospho (ST)	0.09	-0.04	-0.27	0.13	0.110	0.408	0.030	0.22	2.44E+04	2.35E+04	2.64E+04	2.75E+04	2.64E+04	2.52E+04	2.01E+04	2.35E+04	2.87E+04	1.97E+04	1.87E+04	2.32E+04	916.40426	2	27.73
YOL103W-B	L103W-B	IIHRSPSIDASPPENNSSHNIVPIK	[5] Phospho (ST)	-0.31	0.08	0.51	-0.39	0.244	0.438	0.083	0.25	3.98E+04	2.41E+04	2.32E+04	3.07E+04	2.56E+04	1.38E+04	4.69E+04	1.67E+04	2.84E+04	3.37E+04	3.98E+04	5.03E+04	701.35301	4	25.48
OSH2	YDL019C	EVIQPSSVSLYR	[11] Phospho (Y)	-0.84	-0.46	-0.80	-0.39	0.006	0.041	0.066	0.06	2.16E+04	1.96E+04	1.57E+04	1.08E+04	1.19E+04	9.06E+03	1.66E+04	1.31E+04	1.19E+04	3.13E+03	1.54E+04	1.43E+04	729.35559	2	25.62
YOL019W	YOL019W	SSGSRDDDETEELEEK	[10] Phospho (ST)	-0.34	-0.42	-0.66	0.08	0.200	0.069	0.024	0.41	3.06E+04	2.15E+04	2.10E+04	2.80E+04	1.58E+04	1.41E+04	1.78E+04	2.04E+04	1.65E+04	1.64E+04	1.45E+04	1.54E+04	953.3704	2	50.97
RFA2	YNL312W	GYGSQVAQQFEIGGYVK	[4] Phospho (ST)	0.99	1.54	0.90	-0.55	0.056	0.017	0.075	0.11	3.02E+04	7.24E+04	2.94E+04	1.07E+05	9.84E+04	5.59E+04	1.56E+05	1.43E+05	8.34E+04	8.26E+04	1.09E+05	5.41E+04	955.9387	2	90.45
TOP1	YOL006C	VNHELSSDDDDDVPLSQTLK	[6] Phospho (ST)|[7] Phospho (ST)	-1.04	-0.23	-0.39	-0.80	0.005	0.297	0.007	0.13	8.93E+04	9.84E+04	8.13E+04	2.83E+04	5.91E+04	4.38E+04	3.59E+04	1.14E+05	7.85E+04	6.96E+04	6.93E+04	6.58E+04	1193.9883	2	24.03
TPS3	YMR261C	SSSVTSASSHYIGLPQEAQINGEPLQR	[3] Phospho (ST)|[5] Phospho (ST)|[11] Phosp	-0.35	-0.04	-0.50	-0.31	0.292	0.478	0.071	0.37	9.17E+04	8.66E+04	5.30E+04	2.93E+04	1.10E+05	4.26E+04	2.87E+04	1.33E+05	6.43E+04	5.92E+04	5.40E+04	5.01E+04	1032.7765	3	24.29
MHP1	YJL042W	RASFSLHNDKPQPAK	[3] Phospho (ST)	-0.10	-1.41	-0.83	1.31	0.131	0.003	0.021	0.00	2.07E+04	2.25E+04	1.93E+04	2.05E+04	1.91E+04	1.88E+04	1.24E+04	5.33E+03	5.68E+03	7.47E+03	1.03E+04	1.74E+04	592.62361	3	21.16
RTC1	YOL138C	FTYNSVSPR	[7] Phospho (ST)	0.56	0.77	0.43	-0.21	0.034	0.025	0.129	0.18	3.16E+03	5.50E+03	5.01E+03	5.73E+03	7.14E+03	7.23E+03	8.33E+03	6.01E+03	8.97E+03	5.36E+03	8.13E+03	5.00E+03	575.75049	2	25.8
KIN2	YLR096W	TISDYIPSAR	[3] Phospho (ST)	-0.02	0.48	-0.18	-0.51	0.483	0.195	0.387	0.08	5.11E+03	1.82E+04	9.39E+03	8.39E+03	1.28E+04	1.10E+04	1.65E+04	1.84E+04	1.08E+04	9.28E+03	1.27E+04	6.88E+03	601.77683	2	19.53
MAK21	YDR060W	LIQGLSDDDDAK	[6] Phospho (ST)	0.20	0.13	-0.20	0.08	0.146	0.372	0.142	0.42	1.65E+04	1.51E+04	1.99E+04	1.70E+04	1.99E+04	2.26E+04	1.17E+04	1.80E+04	2.66E+04	1.62E+04	1.60E+04	1.27E+04	685.29865	2	28.38
HAL5	YJL165C	AFSIIPSQR	[3] Phospho (ST)	-0.02	-0.17	-0.40	0.15	0.480	0.320	0.180	0.21	1.37E+04	2.76E+04	1.72E+04	1.59E+04	2.26E+04	1.93E+04	1.94E+04	1.64E+04	1.63E+04	1.13E+04	1.76E+04	1.55E+04	549.77113	2	24.41
MAK21	YDR060W	LEDVDDDDIEEESTSSK	[16] Phospho (ST)	0.37	0.22	0.11	0.15	0.072	0.229	0.318	0.23	1.88E+04	2.70E+04	3.14E+04	3.57E+04	3.51E+04	2.93E+04	2.45E+04	2.86E+04	3.69E+04	3.07E+04	2.75E+04	2.52E+04	1003.3872	2	58.96
TPK1	YJL164C	YVPDVTYTLCGTPDYIAPEVVSTK	[7] Phospho (Y)	0.38	1.26	0.68	-0.87	0.246	0.046	0.171	0.08	1.98E+04	3.80E+04	1.51E+04	3.10E+04	4.40E+04	2.03E+04	8.54E+04	4.38E+04	4.52E+04	2.40E+04	6.21E+04	3.10E+04	923.4314	3	32.89
DPS1	YLL018C	AYLAQSPQFNK	[6] Phospho (ST)	-0.03	0.05	0.00	-0.07	0.472	0.449	0.497	0.35	4.66E+03	9.07E+03	1.07E+04	6.92E+03	8.13E+03	8.99E+03	6.87E+03	9.46E+03	8.95E+03	6.60E+03	9.56E+03	8.28E+03	673.81101	2	27.35
MSN4	YKL062W	RGSTISPTTTINNSNPNFK	[6] Phospho (ST)|[8] Phospho (ST)	-0.37	-0.34	-0.50	-0.03	0.047	0.216	0.038	0.47	2.15E+04	1.69E+04	2.39E+04	1.67E+04	1.49E+04	1.66E+04	8.08E+03	2.35E+04	1.77E+04	1.76E+04	1.41E+04	1.25E+04	736.9954	3	20.48
MTC5	YDR128W	AFSSVHSESGK	[7] Phospho (ST)	-0.44	-1.78	-0.73	1.33	0.250	0.067	0.167	0.02	2.48E+04	8.46E+03	1.04E+04	1.12E+04	9.13E+03	1.17E+04	8.01E+03	2.25E+03	2.46E+03	1.01E+04	6.72E+03	9.55E+03	608.25565	2	39.14
YPK9	YOR291W	RLTESEPLVLSSAEQSR	[5] Phospho (ST)	-0.47	-0.46	-0.14	-0.01	0.030	0.147	0.314	0.49	1.44E+04	2.05E+04	1.73E+04	1.16E+04	1.27E+04	1.34E+04	1.91E+04	1.19E+04	7.07E+03	1.18E+04	2.03E+04	1.53E+04	661.3232	3	21.86
SPC29	YPL124W	NFASLEHSR	[8] Phospho (ST)	-0.33	-0.25	-0.16	-0.09	0.138	0.127	0.234	0.35	7.36E+03	9.11E+03	1.11E+04	5.38E+03	7.44E+03	9.02E+03	8.04E+03	7.53E+03	7.65E+03	9.26E+03	7.40E+03	8.00E+03	570.74561	2	20.75
AXL2	YIL140W	SNVNVGQVK	[1] Phospho (ST)	0.42	0.56	0.67	-0.14	0.269	0.216	0.162	0.30	1.52E+03	7.25E+03	1.55E+04	1.00E+04	1.03E+04	1.22E+04	1.47E+04	8.62E+03	1.26E+04	1.48E+04	1.08E+04	1.30E+04	512.74609	2	15.41
GIN4	YDR507C	KISEIR	[3] Phospho (ST)	-0.68	-1.23	-0.53	0.55	0.047	0.050	0.123	0.20	7.49E+03	5.61E+03	4.10E+03	3.43E+03	3.56E+03	3.73E+03	4.84E+03	1.32E+03	1.15E+03	2.27E+03	4.57E+03	5.06E+03	413.21507	2	28.63
YLR413W	YLR413W	IIEEHESPIDAEK	[7] Phospho (ST)	0.09	0.12	-0.37	-0.03	0.237	0.346	0.060	0.46	1.41E+04	1.71E+04	1.71E+04	1.64E+04	1.61E+04	1.89E+04	1.95E+04	1.13E+04	2.17E+04	9.44E+03	1.35E+04	1.44E+04	795.35803	2	23.87
IML2	YJL082W	TNDSSLLPGYMDSATLLHPGK	[4] Phospho (ST)	-0.51	0.91	0.69	-1.42	0.274	0.131	0.193	0.09	1.12E+04	2.30E+04	1.01E+04	8.18E+03	2.06E+04	2.32E+03	3.17E+04	4.12E+04	1.05E+04	1.41E+04	4.07E+04	1.70E+04	766.35692	3	55.73
ALR1	YOL130W	SESTNETEIHEK	[1] Phospho (ST)	-2.15	-0.12	-1.01	-2.03	0.130	0.452	0.226	0.03	3.32E+04	6.07E+03	6.63E+03	6.30E+03	1.76E+03	2.26E+03	7.39E+03	1.50E+04	1.98E+04	1.24E+04	6.16E+03	4.13E+03	742.30037	2	48.79
INP52	YNL106C	RKSSTAPDEISTSTK	[3] Phospho (ST)|[4] Phospho (ST)	-0.27	-0.46	-0.26	0.20	0.160	0.106	0.182	0.25	1.42E+04	1.21E+04	1.89E+04	1.41E+04	1.29E+04	1.06E+04	7.63E+03	1.44E+04	1.08E+04	1.52E+04	1.07E+04	1.19E+04	884.38161	2	17.39
SPA2	YLL021W	ITAQESIKSPEAAR	[9] Phospho (ST)	0.61	1.85	1.31	-1.24	0.022	0.020	0.023	0.03	2.05E+03	3.91E+03	3.34E+03	4.52E+03	4.70E+03	5.00E+03	1.46E+04	6.04E+03	1.31E+04	4.72E+03	8.85E+03	9.57E+03	527.5941	3	17.43
ALR1	YOL130W	SVASLPSR	[4] Phospho (ST)	0.22	0.24	0.19	-0.02	0.197	0.088	0.214	0.45	3.20E+03	4.65E+03	4.04E+03	3.88E+03	4.31E+03	5.63E+03	4.50E+03	4.93E+03	4.63E+03	5.49E+03	4.08E+03	4.02E+03	448.71562	2	32.77
GLE1	YDL207W	ASHSSLLDNAK	[4] Phospho (ST)	-5.40	-3.06	-0.96	-2.34	0.000	0.000	0.002	0.00	1.11E+04	1.02E+04	1.32E+04	1.29E+02	1.63E+02	4.97E+02	1.27E+03	1.39E+03	1.44E+03	5.24E+03	6.16E+03	6.32E+03	611.77599	2	21.5
CDC45	YLR103C	INNDNNDDTDGEEEEDNSAQK	[9] Phospho (ST)	-0.42	-1.34	-0.23	0.92	0.219	0.052	0.338	0.01	3.48E+04	1.16E+04	2.52E+04	2.15E+04	1.59E+04	1.62E+04	8.67E+03	7.23E+03	1.25E+04	2.64E+04	1.35E+04	2.14E+04	815.96525	3	20.55
HIF1	YLL022C	RPLSQPTTSIGFPALEK	[7] Phospho (ST)	2.23	0.66	-0.03	1.57	0.000	0.093	0.476	0.00	7.90E+03	1.49E+04	6.83E+03	4.72E+04	4.92E+04	4.30E+04	2.08E+04	1.33E+04	1.28E+04	1.39E+04	1.02E+04	4.74E+03	641.33242	3	24.38
GRH1	YDR517W	RPSSGEAHQFQALGFK	[3] Phospho (ST)	0.19	0.21	-0.44	-0.02	0.313	0.310	0.219	0.46	9.86E+03	2.59E+04	2.01E+04	1.87E+04	2.39E+04	2.10E+04	2.65E+04	1.75E+04	2.05E+04	7.20E+03	1.69E+04	1.70E+04	613.95645	3	26.36
AXL2	YIL140W	HLQNIQDSQSGK	[10] Phospho (ST)	0.28	0.37	0.63	-0.09	0.335	0.261	0.134	0.38	1.37E+04	2.19E+03	1.68E+04	1.08E+04	1.09E+04	1.81E+04	1.39E+04	1.25E+04	1.59E+04	1.94E+04	1.60E+04	1.52E+04	717.8216	2	39.68
POL3	YDL102W	RQSIDHGVGSEPVSTIEIIPSDSFR	[3] Phospho (ST)	0.32	0.27	-0.04	0.05	0.181	0.309	0.460	0.45	2.69E+04	5.17E+04	3.08E+04	3.71E+04	4.83E+04	5.12E+04	6.64E+04	3.11E+04	3.41E+04	2.51E+04	4.92E+04	3.18E+04	936.11939	3	32.47
EDE1	YBL047C	VATPSIPQQPIPLK	[3] Phospho (ST)	-0.24	-0.20	-0.32	-0.04	0.176	0.200	0.162	0.42	3.14E+04	4.22E+04	2.83E+04	2.76E+04	3.39E+04	2.45E+04	3.32E+04	2.55E+04	2.98E+04	1.99E+04	3.47E+04	2.70E+04	784.9266	2	22.85
SDS23	YGL056C	NTEANKSDTESLHK	[7] Phospho (ST)|[11] Phospho (ST)	1.14	-0.40	0.40	1.55	0.025	0.296	0.293	0.01	1.03E+04	3.46E+03	4.33E+03	1.61E+04	1.09E+04	1.30E+04	6.58E+03	5.02E+03	2.07E+03	1.28E+04	5.87E+03	5.20E+03	578.56398	3	24.72
GRS1	YBR121C	YDIGNPVTGETLESPR	[14] Phospho (ST)	-0.18	0.32	-0.08	-0.49	0.350	0.205	0.435	0.03	2.21E+04	5.07E+04	2.92E+04	2.36E+04	3.71E+04	2.96E+04	4.72E+04	3.73E+04	4.26E+04	2.31E+04	4.14E+04	3.23E+04	914.41242	2	28.76
PFK26	YIL107C	RYSVIPTAPPSAR	[3] Phospho (ST)	0.38	1.04	0.81	-0.66	0.121	0.096	0.038	0.16	8.13E+03	9.33E+03	5.15E+03	7.87E+03	1.17E+04	9.88E+03	2.48E+04	7.84E+03	1.40E+04	9.26E+03	1.44E+04	1.60E+04	747.87742	2	50.58
RPS9B	YBR189W	HIDFAPTSPFGGARPGR	[8] Phospho (ST)	0.65	0.28	-0.11	0.37	0.017	0.334	0.380	0.23	1.35E+04	1.93E+04	1.15E+04	2.07E+04	2.44E+04	2.43E+04	3.03E+04	9.61E+03	1.37E+04	8.82E+03	1.71E+04	1.49E+04	621.6285	3	26.61
AKL1	YBR059C	QSSDPTISEQSPR	[11] Phospho (ST)	-0.04	-0.34	0.07	0.30	0.465	0.250	0.438	0.18	1.80E+04	7.72E+03	9.73E+03	1.49E+04	1.00E+04	9.51E+03	7.26E+03	9.50E+03	1.12E+04	1.40E+04	9.68E+03	1.34E+04	756.32205	2	21.82
PIG2	YIL045W	SLPITPK	[1] Phospho (ST)	-0.85	0.14	0.07	-0.99	0.010	0.139	0.310	0.00	7.08E+03	7.93E+03	6.05E+03	2.66E+03	4.27E+03	4.76E+03	7.77E+03	7.35E+03	8.16E+03	7.16E+03	6.87E+03	8.08E+03	418.21989	2	15.65
CFT2	YLR115W	YSQLVDLR	[1] Phospho (Y)	-0.27	-0.51	-0.06	0.24	0.263	0.168	0.454	0.32	4.68E+03	3.45E+03	6.65E+03	3.31E+03	3.33E+03	5.63E+03	4.72E+03	1.58E+03	4.10E+03	2.96E+03	3.98E+03	7.25E+03	537.25245	2	20.9
DEP1	YAL013W	SQQTPQESEQTTAK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.45	-0.82	-1.32	1.27	0.167	0.111	0.053	0.02	2.01E+04	7.81E+03	2.15E+04	2.91E+04	2.04E+04	1.81E+04	4.56E+03	1.19E+04	1.15E+04	1.01E+04	3.58E+03	6.07E+03	842.85667	2	18.28
NUP145	YGL092W	TYSFSSSVSGNAPLPLASQSSLVSR	[3] Phospho (ST)	-0.87	-0.31	-0.53	-0.56	0.080	0.280	0.163	0.11	6.51E+04	1.09E+05	4.57E+04	4.94E+04	3.67E+04	3.39E+04	6.23E+04	7.84E+04	3.64E+04	5.68E+04	5.95E+04	3.59E+04	874.75444	3	61.75
AVT1	YJR001W	GVNSLSR	[4] Phospho (ST)	0.42	0.38	0.23	0.04	0.174	0.172	0.338	0.44	4.83E+03	1.89E+03	3.69E+03	6.11E+03	3.81E+03	4.07E+03	3.69E+03	4.51E+03	5.38E+03	6.15E+03	3.50E+03	2.61E+03	406.6868	2	35.6
YNL095C	YNL095C	ILTSDATVSK	[3] Phospho (ST)	0.49	0.57	0.70	-0.09	0.132	0.110	0.044	0.41	3.28E+03	6.65E+03	6.91E+03	6.50E+03	6.67E+03	1.04E+04	1.07E+04	5.65E+03	8.68E+03	7.38E+03	8.99E+03	1.09E+04	557.77347	2	33.71
SEC16	YPL085W	TSPSPTGPNPNNSPSPSSPISR	[6] Phospho (ST)	0.23	0.35	0.35	-0.12	0.103	0.045	0.009	0.25	1.28E+04	1.63E+04	1.54E+04	1.55E+04	2.00E+04	1.67E+04	1.70E+04	2.18E+04	1.79E+04	1.92E+04	1.87E+04	1.87E+04	753.34202	3	18.77
SCY1	YGL083W	DGSSDIPR	[3] Phospho (ST)	0.33	0.13	0.44	0.21	0.230	0.410	0.196	0.31	4.50E+03	2.18E+03	6.17E+03	6.53E+03	5.66E+03	4.01E+03	2.61E+03	4.85E+03	6.56E+03	8.09E+03	4.80E+03	4.60E+03	463.68435	2	34.9
SPO14	YKR031C	SVTEEVDRVNSRPDELENQEVLR	[11] Phospho (ST)	-0.85	-0.55	-0.84	-0.30	0.015	0.099	0.031	0.23	2.86E+04	3.39E+04	2.10E+04	1.58E+04	1.60E+04	1.44E+04	2.74E+04	1.29E+04	1.68E+04	1.05E+04	2.08E+04	1.55E+04	931.77371	3	28.05
HBT1	YDL223C	KYSGNTATGPPQDTIK	[3] Phospho (ST)	3.17	1.52	1.06	1.65	0.001	0.008	0.022	0.00	3.21E+03	4.63E+03	2.95E+03	3.04E+04	2.74E+04	3.96E+04	1.12E+04	7.21E+03	1.25E+04	6.15E+03	6.40E+03	1.00E+04	879.40918	2	33.83
SPA2	YLL021W	KPASFLNDVEEEESPVK	[14] Phospho (ST)	-0.38	0.34	0.35	-0.72	0.012	0.033	0.024	0.00	1.49E+04	1.82E+04	1.78E+04	1.32E+04	1.36E+04	1.23E+04	2.44E+04	2.00E+04	2.00E+04	1.91E+04	2.31E+04	2.26E+04	666.64202	3	26.93
YGR054W	YGR054W	ANKKSSETSPDSTPAPSAPASTNAPTNNK	[12] Phospho (ST)|[13] Phospho (ST)	0.27	-0.25	-0.21	0.52	0.135	0.169	0.294	0.04	2.26E+04	1.59E+04	1.84E+04	2.76E+04	1.99E+04	2.11E+04	1.26E+04	1.94E+04	1.59E+04	2.39E+04	1.15E+04	1.39E+04	1010.7751	3	20.84
VRP1	YLR337C	LFSTGGSTLQHK	[3] Phospho (ST)	-0.18	0.08	0.03	-0.25	0.364	0.443	0.474	0.34	4.91E+03	1.05E+04	9.39E+03	3.51E+03	8.47E+03	9.92E+03	1.32E+04	5.18E+03	7.70E+03	4.42E+03	8.44E+03	1.25E+04	678.32152	2	23.71
EIS1	YMR031C	EATETSSAVQTKEPEEK	[7] Phospho (ST)	0.19	-0.04	0.46	0.23	0.240	0.455	0.084	0.20	9.64E+03	9.66E+03	1.55E+04	1.36E+04	1.19E+04	1.41E+04	9.60E+03	9.06E+03	1.51E+04	1.54E+04	1.34E+04	1.90E+04	972.42822	2	41.41
HRB1	YNL004W	ESVHNHSDGDDVDIPMDDSPVNEEARK	[7] Phospho (ST)	-0.45	-0.48	0.44	0.03	0.207	0.093	0.000	0.48	1.74E+04	1.77E+04	1.82E+04	1.92E+04	1.73E+04	2.67E+03	1.90E+04	9.85E+03	9.36E+03	2.45E+04	2.40E+04	2.38E+04	772.57161	4	34.62

CHO1	YER026C	VESDEDFAPQEFPHTDTDVIVNEHR	[3] Phospho (ST)	0.15	0.39	-0.15	-0.25	0.380	0.179	0.397	0.25	1.00E+04	2.42E+04	1.62E+04	1.14E+04	2.25E+04	2.19E+04	2.71E+04	1.71E+04	2.19E+04	6.99E+03	1.95E+04	1.90E+04	752.32479	4	33.03
MLP2	YIL149C	GSGEDAEEELWNSPSK	[13] Phospho (ST)	-0.48	-0.09	-0.22	-0.39	0.077	0.392	0.176	0.15	2.19E+04	2.76E+04	1.72E+04	1.45E+04	1.99E+04	1.34E+04	1.65E+04	2.79E+04	1.83E+04	1.92E+04	1.94E+04	1.87E+04	907.86022	2	30.17
RIF1	YBR275C	SKVDDLRSDEDEHGTVAQEK	[8] Phospho (ST)	-0.01	-0.21	-0.29	0.21	0.492	0.293	0.215	0.25	1.29E+04	2.17E+04	1.35E+04	1.90E+04	1.46E+04	1.43E+04	1.86E+04	1.14E+04	1.14E+04	9.93E+03	1.29E+04	1.63E+04	780.01126	3	37.98
ZRG8	YER033C	RNNSDDETEHTSAIK	[4] Phospho (ST)	-1.34	0.12	0.06	-1.47	0.145	0.432	0.472	0.03	1.77E+04	4.55E+03	5.41E+03	2.16E+03	1.65E+03	7.09E+03	1.29E+04	7.02E+03	1.03E+04	1.49E+04	8.17E+03	5.79E+03	599.58591	3	32.53
BEM1	YBR200W	ITSADISTPSHDNGSVIK	[3] Phospho (ST)	-0.30	-0.10	-0.05	-0.20	0.141	0.375	0.430	0.27	1.27E+04	1.87E+04	1.92E+04	1.24E+04	1.20E+04	1.67E+04	1.92E+04	1.06E+04	1.74E+04	1.20E+04	1.76E+04	1.93E+04	961.4489	2	18.65
CMP2	YML057W	TERPQSSTTPIDSK	[9] Phospho (ST)	0.84	0.03	-0.07	0.82	0.023	0.473	0.428	0.01	1.08E+04	7.90E+03	4.76E+03	1.51E+04	1.15E+04	1.55E+04	9.83E+03	6.20E+03	7.84E+03	7.72E+03	6.23E+03	8.42E+03	813.87252	2	25.56
REG1	YDR028C	LLPDTTLNYGSDEESDNGEFNGYGNAVSHNVNTSR	[9] Phospho (Y)|[15] Phospho (ST)	-0.49	0.25	-0.08	-0.74	0.087	0.321	0.260	0.15	6.05E+04	6.85E+04	5.29E+04	2.79E+04	6.09E+04	4.05E+04	4.54E+04	1.17E+05	5.42E+04	5.66E+04	6.08E+04	5.42E+04	987.41073	4	22.62
YAK1	YJL141C	RLSAYPPSTSPPLQPPFK	[5] Phospho (Y)	0.19	0.72	0.08	-0.53	0.350	0.075	0.436	0.10	1.04E+04	1.97E+04	8.50E+03	9.63E+03	1.89E+04	1.55E+04	2.75E+04	1.69E+04	1.93E+04	9.33E+03	1.75E+04	1.39E+04	688.35054	3	16.32
GIC2	YDR309C	RRNSIATPSPQSK	[4] Phospho (ST)	0.95	0.37	0.25	0.58	0.002	0.166	0.194	0.03	4.92E+03	7.15E+03	8.04E+03	1.30E+04	1.21E+04	1.39E+04	1.13E+04	6.07E+03	8.62E+03	8.60E+03	6.15E+03	9.17E+03	507.92247	3	23.66
RPN4	YDL020C	KQSFVLNK	[3] Phospho (ST)	-0.16	-0.07	-0.27	-0.09	0.229	0.424	0.240	0.42	6.43E+03	6.13E+03	5.74E+03	5.38E+03	4.20E+03	6.80E+03	6.22E+03	3.12E+03	8.06E+03	3.12E+03	4.48E+03	7.58E+03	522.26769	2	37.38
WHI5	YOR083W	LRSPPTAAR	[3] Phospho (ST)	-0.28	0.79	0.57	-1.07	0.354	0.140	0.136	0.08	4.25E+03	2.51E+03	8.63E+03	2.28E+03	3.50E+03	6.87E+03	1.26E+04	4.38E+03	9.72E+03	6.26E+03	8.13E+03	8.41E+03	524.76851	2	19.07
LEO1	YOR123C	FYGEDANNFSDQDETTHTFKEENVELVR	[10] Phospho (ST)	-0.42	-0.42	-0.47	0.00	0.142	0.113	0.114	0.49	5.50E+04	3.13E+04	5.45E+04	4.06E+04	2.42E+04	4.07E+04	3.84E+04	3.72E+04	2.95E+04	2.76E+04	3.11E+04	4.32E+04	854.36825	4	23.99
SSK2	YNR031C	RPSNIGLPLPK	[3] Phospho (ST)	-0.62	-0.14	-0.46	-0.48	0.100	0.357	0.220	0.04	7.79E+03	1.62E+04	1.00E+04	7.08E+03	8.59E+03	6.37E+03	1.24E+04	9.09E+03	9.28E+03	3.42E+03	1.23E+04	9.03E+03	636.3476	2	17.09
YDR210W-B	R210W-B	TTNSTPSIDDR	[7] Phospho (ST)	-0.95	-0.55	-0.12	-0.39	0.015	0.095	0.345	0.17	1.18E+04	8.15E+03	1.33E+04	6.59E+03	5.00E+03	5.67E+03	4.43E+03	9.80E+03	8.47E+03	1.30E+04	8.25E+03	9.33E+03	643.76692	2	16.61
CBF5	YLR175W	VNENTPEQWKK	[5] Phospho (ST)	0.21	-0.22	-0.10	0.43	0.114	0.116	0.206	0.03	1.22E+04	9.85E+03	1.15E+04	1.38E+04	1.40E+04	1.10E+04	9.79E+03	7.92E+03	1.11E+04	9.88E+03	1.01E+04	1.13E+04	726.83006	2	29.99
LCB3	YJL134W	TLSNPNDFQEPNYLLDPGNHPSDHFR	[3] Phospho (ST)	-0.46	-0.25	-0.44	-0.21	0.175	0.288	0.203	0.20	6.14E+04	1.35E+05	7.70E+04	6.32E+04	5.44E+04	8.07E+04	8.80E+04	8.01E+04	6.18E+04	5.28E+04	9.33E+04	5.47E+04	1035.4576	3	42.15
YFR016C	YFR016C	DQLTESDLDEAINATENFAQELSSQR	[6] Phospho (ST)	-0.59	-0.25	-0.19	-0.34	0.102	0.278	0.348	0.13	1.13E+05	1.80E+05	8.89E+04	8.71E+04	9.57E+04	7.17E+04	1.23E+05	1.23E+05	7.66E+04	1.07E+05	1.58E+05	7.05E+04	1002.1083	3	49.37
MLF3	YNL074C	NSNNVSSPLDNVIPTSR	[2] Phospho (ST)	0.16	0.56	0.72	-0.40	0.324	0.064	0.016	0.14	1.93E+04	2.98E+04	2.46E+04	2.23E+04	3.69E+04	2.28E+04	3.22E+04	4.67E+04	2.97E+04	3.96E+04	4.76E+04	3.43E+04	947.43696	2	32.12
SSD1	YDR293C	IPGQLFSGTLGLLRPSQQANSDNNKPPQSPK	[29] Phospho (ST)	0.29	-0.20	-0.52	0.49	0.070	0.260	0.106	0.03	5.05E+04	5.72E+04	3.77E+04	5.81E+04	6.22E+04	5.76E+04	2.90E+04	5.04E+04	4.74E+04	2.02E+04	4.83E+04	3.26E+04	843.1804	4	18.57
GCN2	YDR283C	TLSQSSIR	[3] Phospho (ST)	0.54	0.45	0.24	0.09	0.131	0.153	0.324	0.34	1.23E+03	3.72E+03	4.30E+03	4.32E+03	3.67E+03	5.49E+03	4.09E+03	3.86E+03	4.75E+03	4.94E+03	2.61E+03	3.43E+03	486.23153	2	23.51
NUP2	YLR335W	GSQTTTNDSKEESTTEATGNESQDATK	[6] Phospho (ST)	-0.21	-1.12	-0.10	0.91	0.357	0.057	0.422	0.07	3.29E+04	1.42E+04	1.77E+04	2.81E+04	1.48E+04	1.30E+04	9.86E+03	8.55E+03	1.13E+04	2.87E+04	1.60E+04	1.55E+04	966.39765	3	23.47
PGA2	YNL149C	NQGLDPDSDADIEELLEE	[8] Phospho (ST)	0.03	0.47	0.21	-0.44	0.474	0.129	0.277	0.16	3.48E+04	4.47E+04	2.41E+04	2.83E+04	4.99E+04	2.73E+04	4.00E+04	6.41E+04	3.94E+04	3.27E+04	5.17E+04	3.54E+04	694.62026	3	25.05
NPR1	YNL183C	SQHSSIGDLK	[1] Phospho (ST)	0.49	0.30	0.13	0.19	0.220	0.339	0.425	0.24	1.12E+03	4.66E+03	9.53E+03	7.06E+03	7.26E+03	7.26E+03	4.41E+03	6.15E+03	8.35E+03	4.88E+03	5.58E+03	6.35E+03	576.25883	2	23.66
STE12	YHR084W	LVSPSDPTSYMK	[3] Phospho (ST)	-0.17	-0.14	0.33	-0.02	0.385	0.346	0.250	0.48	1.15E+04	2.09E+04	1.57E+04	1.34E+04	2.33E+04	6.16E+03	1.92E+04	1.25E+04	1.19E+04	1.25E+04	2.94E+04	1.88E+04	702.80978	2	45.97
ROD1	YOR018W	NNSGSSVSLQQLAR	[6] Phospho (ST)	-1.29	-0.58	-0.50	-0.71	0.003	0.076	0.046	0.08	1.74E+04	1.40E+04	1.18E+04	6.20E+03	6.10E+03	5.35E+03	6.68E+03	1.38E+04	8.34E+03	1.20E+04	1.01E+04	8.52E+03	770.86018	2	32.5
MTC1	YJL123C	QKESEDEDEDDEIIDPSEWVK	[4] Phospho (ST)	-0.04	0.27	0.18	-0.31	0.458	0.244	0.302	0.11	2.55E+04	4.11E+04	1.82E+04	2.56E+04	3.31E+04	2.36E+04	3.15E+04	4.09E+04	2.97E+04	3.24E+04	3.29E+04	3.10E+04	872.35811	3	20.02
SEC2	YNL272C	IGPLVEDDSDEDQNDAISVR	[9] Phospho (ST)	-0.33	0.13	-0.18	-0.46	0.261	0.349	0.250	0.21	6.59E+04	9.57E+04	8.28E+04	2.55E+04	1.02E+05	6.69E+04	5.56E+04	1.08E+05	1.04E+05	5.78E+04	6.83E+04	8.99E+04	1133.9908	2	68.69
KKQ8	YKL168C	SFSESFK	[3] Phospho (ST)	0.23	0.31	-0.44	-0.08	0.194	0.182	0.110	0.38	2.65E+03	4.63E+03	4.46E+03	4.52E+03	4.09E+03	5.19E+03	5.84E+03	5.11E+03	3.60E+03	2.50E+03	3.51E+03	2.63E+03	456.18109	2	22.81
GOS1	YHL031C	SQFHSQSNVLNTANNK	[1] Phospho (ST)	0.37	-0.75	-0.07	1.12	0.101	0.111	0.386	0.04	1.48E+04	1.59E+04	2.08E+04	1.74E+04	2.24E+04	2.70E+04	1.45E+04	1.49E+04	1.35E+03	1.53E+04	1.43E+04	1.97E+04	934.91878	2	62.36
RPG1	YBR079C	EVSEEENTEPEVQEEK	[3] Phospho (ST)	0.41	0.46	-0.04	-0.05	0.056	0.042	0.428	0.35	2.17E+04	1.39E+04	2.23E+04	2.75E+04	2.25E+04	2.69E+04	2.47E+04	2.50E+04	2.99E+04	2.00E+04	1.73E+04	1.90E+04	992.89992	2	35.71
SLK19	YOR195W	HVLALNYSPIR	[7] Phospho (Y)	0.02	0.86	0.15	-0.84	0.490	0.096	0.421	0.09	4.18E+03	1.10E+04	4.69E+03	3.70E+03	1.02E+04	6.12E+03	1.71E+04	8.33E+03	1.05E+04	2.49E+03	1.17E+04	7.86E+03	681.8502	2	27.88
EFB1	YAL003W	ADEFDSFPAASAAAAEEEEDDDVDLFGSDDEEADAEAEK	[11] Phospho (ST)	-0.34	0.16	-0.60	-0.50	0.287	0.371	0.183	0.07	5.77E+04	9.76E+04	3.05E+04	3.72E+04	6.60E+04	4.36E+04	7.09E+04	7.94E+04	5.74E+04	2.73E+04	4.68E+04	4.86E+04	701.27421	6	19.93
SFP1	YLR403W	RPSVSNPPYHR	[3] Phospho (ST)	0.33	-0.01	-0.06	0.34	0.236	0.493	0.455	0.16	5.69E+03	1.25E+04	1.83E+04	1.28E+04	1.55E+04	1.74E+04	1.66E+04	8.51E+03	1.11E+04	9.52E+03	1.04E+04	1.51E+04	695.32339	2	22.88
UBP1	YDL122W	AAQQDSSEDENIGGEYYTK	[7] Phospho (ST)	-0.10	-0.19	-0.19	0.09	0.316	0.281	0.234	0.40	2.63E+04	2.53E+04	2.00E+04	2.55E+04	2.38E+04	1.73E+04	1.36E+04	2.84E+04	2.05E+04	2.68E+04	1.95E+04	1.65E+04	1092.9348	2	55.45
JJJ1	YNL227C	GLQTDDDEDWSTK	[4] Phospho (ST)	-0.16	0.28	0.27	-0.45	0.214	0.054	0.050	0.06	1.90E+04	1.92E+04	1.91E+04	2.16E+04	1.39E+04	1.57E+04	1.93E+04	2.47E+04	2.58E+04	2.59E+04	1.97E+04	2.33E+04	795.30465	2	31.19
NOP7	YGR103W	EQNEETELDTFEDNNK	[10] Phospho (ST)	1.43	-0.99	-0.51	2.42	0.000	0.014	0.091	0.00	2.06E+04	1.45E+04	1.80E+04	4.77E+04	4.98E+04	4.58E+04	1.01E+04	1.15E+04	5.12E+03	7.10E+03	1.42E+04	1.60E+04	1017.9005	2	16.2
CMS1	YLR003C	EERNSEDDSNRPISK	[5] Phospho (ST)	2.36	0.49	0.78	1.88	0.018	0.360	0.052	0.04	1.17E+04	1.14E+04	6.52E+03	6.52E+04	2.46E+04	6.28E+04	3.40E+04	6.57E+03	1.00E+03	2.27E+04	1.30E+04	1.52E+04	928.39389	2	15.5
DIG1	YPL049C	RVNDSYDSPLSGTASTGK	[8] Phospho (ST)	-0.45	-0.51	-0.14	0.06	0.045	0.112	0.216	0.45	2.42E+04	2.84E+04	2.18E+04	1.52E+04	1.66E+04	2.26E+04	2.57E+04	1.73E+04	9.33E+03	2.15E+04	2.04E+04	2.58E+04	967.92932	2	30.18
PPZ1	YML016C	SLPSSSTTNTNSNVPDPSTPSKPNLEVNHQR	[19] Phospho (ST)	0.85	1.69	1.37	-0.84	0.001	0.002	0.003	0.01	1.36E+04	1.18E+04	9.84E+03	2.22E+04	1.94E+04	2.18E+04	3.71E+04	4.61E+04	3.05E+04	2.76E+04	2.63E+04	3.72E+04	1129.195	3	21.25
INP52	YNL106C	VSPSNSKSEEELPCK	[8] Phospho (ST)	0.03	-0.20	0.18	0.23	0.452	0.284	0.272	0.09	6.66E+03	1.21E+04	1.29E+04	1.05E+04	1.07E+04	1.12E+04	7.85E+03	8.71E+03	1.10E+04	1.06E+04	1.18E+04	1.34E+04	885.88448	2	24.89
BFR2	YDR299W	NGESDLSDYGNSNTEETKK	[4] Phospho (ST)|[7] Phospho (ST)	0.01	-0.82	-0.21	0.83	0.492	0.192	0.331	0.16	1.76E+04	7.78E+03	1.25E+04	1.18E+04	1.36E+04	1.27E+04	4.87E+03	1.65E+04	1.14E+02	1.53E+04	7.19E+03	1.02E+04	749.94953	3	18.5
VHS2	YIL135C	SLSSQSFDNETSPAHPR	[3] Phospho (ST)|[6] Phospho (ST)	-0.33	-0.86	-0.79	0.53	0.110	0.032	0.023	0.06	3.52E+04	2.26E+04	2.63E+04	2.37E+04	2.00E+04	2.33E+04	9.83E+03	2.09E+04	1.57E+04	1.77E+04	1.25E+04	1.83E+04	1010.396	2	27.05
SUM1	YDR310C	RTAGDDGALDQTENTSISPK	[18] Phospho (ST)	-0.18	-0.06	-0.05	-0.11	0.255	0.420	0.437	0.33	1.70E+04	2.86E+04	2.62E+04	1.85E+04	2.12E+04	2.37E+04	2.67E+04	1.62E+04	2.57E+04	2.01E+04	2.09E+04	2.85E+04	1078.4791	2	38.57
YMR086W	YMR086W	SNSAHSALNAR	[3] Phospho (ST)	0.18	-1.12	-0.77	1.30	0.344	0.080	0.130	0.00	1.90E+04	7.03E+03	9.80E+03	1.50E+04	1.19E+04	1.38E+04	7.17E+03	5.45E+03	3.85E+03	9.15E+03	6.15E+03	5.70E+03	604.26345	2	43.28
BFR2	YDR299W	NGESDLSDYGNSNTEETKK	[4] Phospho (ST)|[9] Phospho (Y)	0.07	-1.06	-0.35	1.13	0.401	0.100	0.189	0.07	3.80E+04	2.20E+04	2.77E+04	2.43E+04	3.33E+04	3.47E+04	1.09E+04	3.05E+04	7.67E+02	3.16E+04	1.75E+04	1.96E+04	1124.4211	2	51.39
PAM1	YDR251W	VPQINITQPSPIQTNFATSDNPAAVIK	[10] Phospho (ST)	-1.12	-0.40	-0.30	-0.72	0.040	0.168	0.203	0.08	5.71E+04	7.26E+04	3.61E+04	1.55E+04	3.95E+04	2.13E+04	5.38E+04	3.18E+04	3.97E+04	4.42E+04	5.12E+04	3.94E+04	982.16708	3	22.08
AGP1	YCL025C	NESSDNIGANTGHK	[3] Phospho (ST)	-0.45	-1.43	-0.76	0.98	0.259	0.093	0.192	0.03	1.50E+04	4.73E+03	6.10E+03	6.28E+03	5.48E+03	7.15E+03	5.15E+03	3.10E+03	1.34E+03	8.31E+03	3.22E+03	3.73E+03	508.54181	3	24.31
AHA1	YDR214W	SSFTEIK	[2] Phospho (ST)	-3.18	-3.61	-1.99	0.42	0.002	0.003	0.005	0.32	8.71E+03	1.39E+04	1.53E+04	1.43E+03	1.33E+03	1.38E+03	2.46E+03	3.50E+02	2.71E+02	4.08E+03	3.12E+03	2.34E+03	446.19671	2	18.98
MAM3	YOL060C	DWDESKSEYGNENINQENSNR	[9] Phospho (Y)	0.03	0.17	0.13	-0.14	0.444	0.312	0.335	0.35	1.59E+04	1.21E+04	1.32E+04	1.66E+04	1.42E+04	1.13E+04	1.08E+04	2.10E+04	1.45E+04	1.95E+04	1.05E+04	1.51E+04	870.01277	3	45.95
SEC16	YPL085W	TSPSPTGPNPNNSPSPSSPISR	[6] Phospho (ST)	-0.11	-0.21	-0.01	0.10	0.299	0.253	0.487	0.38	3.08E+04	3.97E+04	3.02E+04	3.21E+04	3.59E+04	2.53E+04	2.13E+04	3.94E+04	2.66E+04	3.21E+04	3.23E+04	3.60E+04	1129.5082	2	33.17
IST2	YBR086C	VPTVGSYGVAGATLPETIPTSK	[6] Phospho (ST)	-0.39	0.23	-0.04	-0.62	0.228	0.306	0.473	0.05	3.36E+04	6.89E+04	3.19E+04	2.89E+04	4.30E+04	3.08E+04	6.63E+04	4.89E+04	4.23E+04	3.01E+04	6.71E+04	3.35E+04	1113.0606	2	80.34
MRD1	YPR112C	EENNKDEAPNLVIENESDDEYSALNR	[17] Phospho (ST)	0.14	0.18	0.05	-0.05	0.314	0.287	0.412	0.45	1.66E+04	2.04E+04	1.38E+04	1.49E+04	2.37E+04	1.73E+04	1.75E+04	2.56E+04	1.47E+04	1.45E+04	1.77E+04	2.04E+04	772.58215	4	18.28
PFK26	YIL107C	KRSNPTSASSSQSELSEQPK	[7] Phospho (ST)	0.12	-0.04	-0.19	0.15	0.208	0.438	0.206	0.24	1.39E+04	1.15E+04	1.12E+04	1.45E+04	1.19E+04	1.34E+04	1.51E+04	1.07E+04	1.00E+04	1.10E+04	8.11E+03	1.30E+04	743.34408	3	43.13
SAK1	YER129W	SRSLTVAELNEEK	[3] Phospho (ST)	-0.04	0.14	-0.09	-0.17	0.435	0.305	0.359	0.23	1.43E+04	2.13E+04	1.60E+04	1.55E+04	1.57E+04	1.92E+04	2.26E+04	1.47E+04	1.95E+04	1.35E+04	1.59E+04	1.92E+04	778.36958	2	38.53
SLA1	YBL007C	SNANASWKDDELQNDVVGSAAGKR	[1] Phospho (ST)	-0.59	-0.52	-0.63	-0.07	0.018	0.017	0.005	0.39	1.72E+04	2.14E+04	1.87E+04	1.48E+04	1.39E+04	9.37E+03	1.12E+04	1.59E+04	1.28E+04	1.07E+04	1.33E+04	1.29E+04	871.39759	3	47.98
YHR162W	YHR162W	IANYRIR	[4] Phospho (Y)	-0.45	0.27	-0.32	-0.72	0.247	0.314	0.310	0.07	3.55E+03	8.72E+03	3.53E+03	2.45E+03	5.14E+03	3.95E+03	8.22E+03	4.22E+03	6.63E+03	2.55E+03	5.30E+03	4.86E+03	493.2527	2	22.86
CUE5	YOR042W	VVAETTYIDTPDTETK	[7] Phospho (Y)	-0.49	1.19	0.97	-1.69	0.187	0.032	0.078	0.01	2.94E+04	1.62E+04	1.14E+04	1.17E+04	1.27E+04	1.61E+04	5.75E+04	3.00E+04	4.30E+04	2.28E+04	3.52E+04	5.37E+04	931.92081	2	23.18
GIC2	YDR309C	SFDDVLYSFNQLEPLQT	[1] Phospho (ST)	-0.07	-0.20	-0.68	0.13	0.428	0.330	0.098	0.34	6.10E+04	6.53E+04	2.95E+04	4.69E+04	5.93E+04	4.24E+04	6.07E+04	4.48E+04	2.98E+04	3.21E+04	4.22E+04	2.26E+04	1048.462	2	27.62
CYR1	YJL005W	GSSVHDINNGIADK	[3] Phospho (ST)	-0.19	-0.59	-0.01	0.40	0.044	0.037	0.443	0.09	1.38E+04	1.32E+04	1.57E+04	1.25E+04	1.29E+04	1.21E+04	1.31E+04	7.18E+03	8.16E+03	1.36E+04	1.49E+04	1.40E+04	753.83153	2	41.09
YMR086W	YMR086W	RPQSVGQFR	[4] Phospho (ST)	0.00	-0.82	0.00	0.82	0.490	0.048	0.498	0.04	3.86E+03	4.43E+03	4.94E+03	4.50E+03	4.05E+03	4.71E+03	1.10E+03	2.42E+03	3.96E+03	3.63E+03	5.39E+03	4.22E+03	577.77698	2	21.39
HAA1	YPR008W	RISPISNSR	[3] Phospho (ST)	-0.63	0.87	0.45	-1.49	0.251	0.091	0.218	0.03	6.21E+03	1.19E+03	4.18E+03	9.98E+02	1.74E+03	4.75E+03	8.41E+03	4.37E+03	8.35E+03	6.04E+03	6.12E+03	3.72E+03	555.27676	2	16.68
BDF1	YLR399C	ALSQEEQSR	[3] Phospho (ST)	0.83	-0.72	-1.79	1.55	0.107	0.225	0.109	0.01	5.56E+03	5.32E+02	7.50E+03	8.33E+03	5.86E+03	1.01E+04	1.79E+03	3.21E+03	3.23E+03	2.81E+03	8.02E+02	2.92E+02	564.24118	2	31.66
PHO84	YML123C	NNDIESSSPSQLQHEA	[6] Phospho (ST)	-2.27	-1.28	-0.50	-0.99	0.003	0.009	0.065	0.00	4.46E+04	2.75E+04	3.12E+04	8.25E+03	7.20E+03	5.98E+03	1.26E+04	1.51E+04	1.48E+04	2.60E+04	2.16E+04	2.51E+04	918.37873	2	66.08
MPT5	YGL178W	RSNSSVTNNFSNQYAQDQK	[7] Phospho (ST)	0.00	-0.43	-0.03	0.43	0.499	0.046	0.470	0.10	1.91E+04	1.85E+04	1.78E+04	2.20E+04	1.45E+04	1.88E+04	1.16E+04	1.80E+04	1.16E+04	2.69E+04	1.32E+04	1.42E+04	756.66125	3	17.47
SFB2	YNL049C	ANSFTQLAQNQQFPGSGK	[3] Phospho (ST)	-0.55	-0.24	-0.07	-0.32	0.019	0.294	0.320	0.27	1.68E+04	2.20E+04	1.80E+04	1.07E+04	1.47E+04	1.33E+04	1.08E+04	2.52E+04	1.21E+04	1.91E+04	1.70E+04	1.81E+04	668.3061	3	36.19
NOT5	YPR072W	DVSISDR	[3] Phospho (ST)	-0.30	-0.18	0.35	-0.12	0.323	0.393	0.312	0.36	2.50E+03	2.48E+03	6.88E+03	3.65E+03	2.87E+03	3.13E+03	2.21E+03	3.79E+03	4.46E+03	7.68E+03	4.71E+03	2.73E+03	436.18138	2	26.62
DRE2	YKR071C	VVDDLIEDSDDDDFSSDSSK	[9] Phospho (ST)	-0.13	0.25	0.05	-0.38	0.406	0.185	0.417	0.23	3.45E+04	5.71E+04	4.33E+04	1.94E+04	6.74E+04	3.63E+04	4.57E+04	6.33E+04	5.13E+04	4.35E+04	4.85E+04	4.75E+04	761.62879	3	16.38
DNF2	YDR093W	ARASLDLPGINHAETLLSQR	[4] Phospho (ST)	-0.60	-0.38	-0.29	-0.23	0.109	0.250	0.282	0.31	1.42E+04	3.33E+04	2.45E+04	1.42E+04	1.61E+04	1.72E+04	2.75E+04	1.03E+04	1.78E+04	1.39E+04	2.76E+04	1.75E+04	748.05011	3	44.78
CCT3	YJL014W	KGESQTNIEIEK	[4] Phospho (ST)	1.84	0.45	0.72	1.39	0.005	0.071	0.084	0.01	2.18E+03	1.98E+03	3.55E+03	6.78E+03	9.49E+03	1.14E+04	3.28E+03	3.47E+03	3.78E+03	5.94E+03	3.04E+03	3.77E+03	728.33943	2	34.55
ASK10	YGR097W	KTNSTGNVPCLTAEK	[4] Phospho (ST)	-0.29	-0.30	0.48	0.01	0.099	0.048	0.018	0.49	1.34E+04	1.31E+04	1.15E+04	7.94E+03	1.04E+04	1.28E+04	9.28E+03	9.51E+03	1.22E+04	1.56E+04	1.68E+04	2.06E+04	850.38922	2	33.38
PRB1	YEL060C	VEFTKDDDEEPSDSEDK	[12] Phospho (ST)	0.04	0.51	0.01	-0.46	0.429	0.078	0.478	0.05	2.02E+04	1.18E+04	1.39E+04	1.60E+04	1.54E+04	1.59E+04	1.94E+04	1.86E+04	2.71E+04	1.70E+04	1.34E+04	1.59E+04	1032.8949	2	56.17
ASK1	YKL052C	LPDSSDEDTGSEAVPSR	[4] Phospho (ST)|[5] Phospho (ST)	-0.27	-0.20	-1.19	-0.07	0.197	0.347	0.003	0.46	3.34E+04	2.47E+04	3.21E+04	1.62E+04	3.20E+04	2.67E+04	9.33E+03	3.96E+04	2.95E+04	1.25E+04	1.66E+04	1.05E+04	961.35959	2	37.65
HSP150	YJL159W	IGSIVANR	[3] Phospho (ST)	1.86	1.90	1.61	-0.05	0.010	0.003	0.010	0.42	6.11E+02	8.75E+02	3.00E+03	4.69E+03	4.70E+03	6.95E+03	5.68E+03	5.27E+03	5.92E+03	4.46E+03	4.08E+03	5.19E+03	455.23151	2	50.1
YDR365W-B	R365W-B	EVHTNQDPLDVSASKTEECEK	[12] Phospho (ST)	-0.46	0.49	0.88	-0.95	0.067	0.137	0.017	0.06	1.05E+04	1.14E+04	1.15E+04	6.51E+03	6.52E+03	1.13E+04	2.26E+04	1.12E+04	1.30E+04	2.05E+04	1.55E+04	2.55E+04	832.6931	3	25.8
LTE1	YAL024C	SLTTAYYNK	[1] Phospho (ST)	-0.43	0.35	0.01	-0.78	0.042	0.185	0.490	0.06	5.10E+03	7.15E+03	5.97E+03	4.79E+03	3.84E+03	4.89E+03	7.70E+03	1.05E+04	5.09E+03	7.48E+03	6.66E+03	4.17E+03	570.75263	2	26.4
SAP155	YFR040W	RGSSSFGNDDINNNDDDDANEDDESAYLTK	[5] Phospho (ST)	0.04	0.09	-0.31	-0.05	0.438	0.349	0.137	0.39	3.05E+04	2.04E+04	2.13E+04	2.02E+04	2.77E+04	2.63E+04	2.13E+04	2.81E+04	2.76E+04	2.31E+04	1.72E+04	1.79E+04	1163.4436	3	25.53
FUI1	YBL042C	KDTDSENNITIAQDDEK	[5] Phospho (ST)|[10] Phospho (ST)	-0.48	-0.33	-0.07	-0.15	0.145	0.295	0.432	0.39	3.86E+04	1.67E+04	2.69E+04	2.05E+04	1.85E+04	2.01E+04	8.08E+03	3.14E+04	2.62E+04	3.38E+04	2.11E+04	2.33E+04	1048.4096	2	16.34
GGA1	YDR358W	VSLSSPKSPQENDTVVDILGDAHSK	[2] Phospho (ST)|[5] Phospho (ST)	0.11	0.86	0.13	-0.75	0.415	0.025	0.359	0.06	1.03E+04	1.74E+04	9.38E+03	8.47E+03	2.06E+04	1.11E+04	1.94E+04	2.78E+04	2.04E+04	9.98E+03	1.61E+04	1.47E+04	696.56931	4	20.24
VTS1	YOR359W	GAHPGAVLLSPQSSAINK	[10] Phospho (ST)	-0.77	-0.58	-0.28	-0.19	0.060	0.089	0.248	0.24	1.20E+04	2.43E+04	2.07E+04	1.13E+04	1.39E+04	8.35E+03	1.52E+04	1.11E+04	1.19E+04	1.05E+04	1.82E+04	1.83E+04	913.96197	2	21.01
IST2	YBR086C	SSAESSNATNNNTLGTESK	[2] Phospho (ST)|[5] Phospho (ST)	-0.41	-0.56	-0.30	0.15	0.246	0.208	0.328	0.38	5.08E+04	1.50E+04	4.01E+04	3.32E+04	2.84E+04	1.84E+04	1.34E+04	3.62E+04	2.24E+04	4.58E+04	1.88E+04	2.16E+04	1036.3972	2	40.74
NUP2	YLR335W	EESTTEATGNESQDATK	[4] Phospho (ST)	2.21	-0.18	0.29	2.39	0.001	0.375	0.345	0.00	8.98E+03	2.56E+03	5.28E+03	2.74E+04	2.82E+04	2.24E+04	4.11E+03	4.75E+03	5.98E+03	1.13E+04	4.54E+03	4.73E+03	939.36835	2	27.74
MSC3	YLR219W	TRSPELQDNLK	[3] Phospho (ST)	0.66	0.26	-0.06	0.40	0.016	0.284	0.425	0.11	2.79E+03	5.21E+03	4.77E+03	6.75E+03	6.42E+03	7.01E+03	7.36E+03	3.90E+03	4.03E+03	5.06E+03	3.76E+03	3.39E+03	690.82916	2	26.29
NVJ1	YHR195W	SLNQPSSLLHIQVSPTK	[14] Phospho (ST)	-0.75	0.70	0.09	-1.46	0.155	0.084	0.435	0.00	7.73E+03	2.39E+04	1.17E+04	5.90E+03	9.32E+03	1.05E+04	2.81E+04	2.13E+04	2.11E+04	1.09E+04	1.64E+04	1.89E+04	964.99688	2	23.32
HSP26	YBR072W	RQLANTPAK	[6] Phospho (ST)	3.14	2.21	1.11	0.94	0.039	0.037	0.019	0.16	1.10E+03	2.20E+03	1.30E+03	1.17E+04	5.86E+03	2.33E+04	1.15E+04	3.82E+03	5.96E+03	3.16E+03	2.57E+03	4.24E+03	539.77348	2	33.68

ATG13	YPR185W	HASVSHNSQGPQNQPEQEGQSDQDIGK	[5] Phospho (ST)	-0.05	-0.35	0.15	0.30	0.417	0.112	0.337	0.09	1.72E+04	1.13E+04	1.65E+04	1.68E+04	1.40E+04	1.28E+04	1.20E+04	9.50E+03	1.39E+04	1.94E+04	1.04E+04	2.03E+04	746.32168	4	17.81
KIN2	YLR096W	RISQSGQSQHPTR	[3] Phospho (ST)	1.22	-0.42	0.00	1.64	0.063	0.348	0.499	0.05	2.44E+03	7.51E+03	2.97E+03	1.05E+04	5.49E+03	1.41E+04	7.26E+03	1.27E+03	1.13E+03	4.76E+03	3.19E+03	4.99E+03	521.24547	3	21.04
TAF12	YDR145W	ISSSNSTEIPSVTGPDALK	[4] Phospho (ST)	0.46	0.28	-0.10	0.18	0.053	0.122	0.320	0.17	1.78E+04	2.87E+04	2.48E+04	2.90E+04	3.85E+04	3.08E+04	3.02E+04	3.14E+04	2.50E+04	2.24E+04	2.24E+04	2.17E+04	991.97114	2	52.82
FBA1	YKL060C	GISNEGQNASIK	[10] Phospho (ST)	-0.40	-1.51	-0.62	1.11	0.103	0.005	0.041	0.01	2.98E+04	1.94E+04	2.23E+04	2.24E+04	1.67E+04	1.51E+04	6.28E+03	7.98E+03	1.09E+04	1.89E+04	1.26E+04	1.51E+04	649.29214	2	23.98
UBP6	YFR010W	FNDDKVSVVEK	[7] Phospho (ST)	0.76	0.26	0.21	0.50	0.021	0.248	0.097	0.10	8.07E+03	7.23E+03	9.54E+03	1.13E+04	1.34E+04	1.76E+04	1.40E+04	7.25E+03	8.50E+03	9.85E+03	8.61E+03	1.04E+04	680.31197	2	55.43
NPR1	YNL183C	SSSHIGSVSNSSSSDR	[7] Phospho (ST)	0.30	0.14	0.37	0.16	0.202	0.358	0.225	0.26	6.53E+03	7.07E+03	1.26E+04	1.26E+04	9.96E+03	9.71E+03	7.67E+03	1.19E+04	9.34E+03	1.60E+04	8.64E+03	9.30E+03	558.56371	3	30.28
FPK1	YNR047W	TNSFVGTEEYIAPEVIR	[10] Phospho (Y)	0.05	0.40	-0.37	-0.35	0.466	0.242	0.292	0.17	1.35E+04	3.61E+04	1.39E+04	1.67E+04	2.82E+04	2.09E+04	3.44E+04	3.04E+04	1.91E+04	1.33E+04	2.22E+04	1.36E+04	668.98286	3	21.68
BCP1	YDR361C	YEVNFDTDDDTDSGK	[7] Phospho (ST)	0.65	0.60	0.24	0.05	0.023	0.083	0.274	0.43	1.01E+04	1.37E+04	1.90E+04	2.03E+04	2.42E+04	2.26E+04	1.54E+04	2.18E+04	2.76E+04	2.25E+04	1.35E+04	1.43E+04	900.82834	2	42.05
RRP36	YOR287C	REIDEQESSDDELK	[8] Phospho (ST)|[9] Phospho (ST)	0.63	0.23	-0.14	0.39	0.032	0.363	0.348	0.21	1.89E+04	9.95E+03	2.19E+04	2.55E+04	2.71E+04	2.57E+04	6.85E+03	3.05E+04	2.22E+04	1.70E+04	1.47E+04	1.45E+04	926.8486	2	15.48
SKO1	YNL167C	SGLTPNESNIR	[4] Phospho (ST)	-0.05	0.11	-0.09	-0.17	0.448	0.390	0.405	0.27	3.50E+03	8.46E+03	7.64E+03	5.96E+03	5.20E+03	7.72E+03	8.57E+03	5.44E+03	7.18E+03	5.44E+03	7.01E+03	5.92E+03	634.28811	2	25.71
NUP2	YLR335W	ADGTGEAQVDNSPTTESNSR	[12] Phospho (ST)	0.85	-0.01	0.03	0.86	0.024	0.488	0.473	0.02	1.77E+04	8.84E+03	1.73E+04	3.22E+04	2.24E+04	2.44E+04	1.06E+04	1.46E+04	1.83E+04	1.83E+04	1.09E+04	1.55E+04	1058.4274	2	36.82
GUK1	YDR454C	RLSAAQAELAYAETGAHDK	[3] Phospho (ST)	-0.69	-0.08	0.14	-0.61	0.084	0.442	0.364	0.22	1.59E+04	2.36E+04	1.66E+04	4.76E+03	1.60E+04	1.40E+04	3.01E+04	1.21E+04	1.08E+04	1.19E+04	2.29E+04	2.71E+04	694.65937	3	58.18
TIF4631	YGR162W	SPVPTK	[5] Phospho (ST)	1.31	-1.44	-0.98	2.75	0.016	0.029	0.069	0.00	4.50E+03	2.26E+03	5.47E+03	1.00E+04	7.36E+03	1.30E+04	1.54E+03	1.06E+03	1.90E+03	2.91E+03	2.22E+03	1.05E+03	354.66998	2	19.02
RPL13A	YDL082W	APEAEQVLSAAATFPIAQPATDVEAR	[21] Phospho (ST)	-0.58	-0.13	-0.20	-0.45	0.144	0.383	0.345	0.12	3.25E+04	5.82E+04	2.78E+04	2.03E+04	3.60E+04	2.32E+04	4.50E+04	2.73E+04	3.59E+04	2.22E+04	4.85E+04	3.21E+04	911.77731	3	52.62
PLM2	YDR501W	ELSSTTAIVSPAQK	[3] Phospho (ST)	-4.99	-3.19	-1.42	-1.79	0.000	0.000	0.001	0.02	3.23E+04	4.05E+04	4.15E+04	7.69E+02	1.34E+03	1.46E+03	5.28E+03	2.10E+03	5.08E+03	1.47E+04	1.27E+04	1.53E+04	756.37085	2	25.02
TAE2	YPL009C	NNSFEHDNLEK	[3] Phospho (ST)	-0.08	-0.06	-0.12	-0.01	0.377	0.413	0.333	0.47	8.79E+03	5.75E+03	9.87E+03	7.80E+03	7.31E+03	8.04E+03	6.64E+03	7.17E+03	9.54E+03	6.97E+03	6.61E+03	8.87E+03	713.78593	2	16.59
IST2	YBR086C	VPTVGSYGVAGATLPETIPTSK	[7] Phospho (Y)	-0.33	0.35	0.14	-0.68	0.275	0.239	0.398	0.07	1.27E+04	2.78E+04	1.31E+04	1.08E+04	1.90E+04	1.29E+04	3.04E+04	1.94E+04	1.84E+04	1.48E+04	2.79E+04	1.62E+04	742.37586	3	29.29
MSL5	YLR116W	NRSPSPPPVYDAQGK	[3] Phospho (ST)|[5] Phospho (ST)	0.41	0.44	-0.11	-0.03	0.015	0.108	0.292	0.45	2.01E+04	1.47E+04	1.97E+04	2.52E+04	2.31E+04	2.42E+04	1.71E+04	3.13E+04	2.57E+04	1.89E+04	1.40E+04	1.75E+04	886.87408	2	16.85
YGR130C	YGR130C	VSESTSIGK	[6] Phospho (ST)	-0.97	-0.95	-1.59	-0.02	0.270	0.270	0.201	0.49	2.56E+04	3.12E+03	3.18E+03	9.79E+03	2.71E+03	3.76E+03	3.21E+03	4.61E+03	8.68E+03	6.03E+03	2.62E+03	1.90E+03	494.22363	2	23.49
LEO1	YOR123C	KQSQILR	[3] Phospho (ST)	1.40	-1.15	-0.69	2.55	0.002	0.007	0.013	0.00	3.37E+03	2.32E+03	3.05E+03	7.47E+03	6.59E+03	9.06E+03	1.69E+03	1.35E+03	8.74E+02	1.96E+03	1.65E+03	1.80E+03	476.75194	2	41.17
RGA2	YDR379W	VHDELPSPGKVPLSPSPK	[7] Phospho (ST)|[14] Phospho (ST)|[16] Phos	-0.81	0.29	-1.12	-1.10	0.085	0.290	0.007	0.10	1.44E+04	2.07E+04	1.53E+04	3.35E+03	1.66E+04	8.80E+03	1.14E+04	3.18E+04	1.86E+04	8.82E+03	8.41E+03	5.90E+03	708.64584	3	16.75
PIN4	YBL051C	SLSHSGLDDGLEQGLNR	[1] Phospho (ST)	-0.33	-0.58	-0.16	0.25	0.085	0.016	0.324	0.10	1.57E+04	2.04E+04	1.51E+04	1.61E+04	1.22E+04	1.24E+04	1.19E+04	1.20E+04	1.01E+04	1.08E+04	2.18E+04	1.32E+04	939.42425	2	45.76
PAF1	YBR279W	RRLDDGDSDDENLDVNHIISR	[8] Phospho (ST)	0.56	-0.70	0.41	1.25	0.035	0.027	0.220	0.01	1.76E+04	2.18E+04	2.46E+04	3.71E+04	2.49E+04	3.20E+04	1.68E+04	1.36E+04	9.06E+03	4.37E+04	1.72E+04	2.42E+04	634.28767	4	55.47
YDR090C	YDR090C	GNTFDEESGQAQKEEPDEK	[8] Phospho (ST)	-0.68	-0.22	-0.07	-0.46	0.012	0.086	0.403	0.01	1.67E+04	1.29E+04	1.69E+04	1.04E+04	7.73E+03	1.09E+04	1.34E+04	1.32E+04	1.34E+04	1.90E+04	9.83E+03	1.54E+04	739.96602	3	33.36
RBS1	YDL189W	MTALDSRNWGLTPAMETGLFQK	[2] Phospho (ST)|[6] Phospho (ST)	-0.75	-1.23	-0.05	0.48	0.165	0.093	0.467	0.25	1.55E+04	5.01E+03	8.17E+03	8.81E+03	4.53E+03	3.71E+03	2.35E+03	7.01E+03	2.88E+03	7.85E+03	7.84E+03	1.21E+04	526.23734	5	15.85
MRC1	YCL061C	HPSIIK	[3] Phospho (ST)	-8.13	-7.74	-2.15	-0.41	0.000	0.000	0.004	0.32	1.33E+04	1.72E+04	1.30E+04	5.86E+01	1.26E+01	5.37E+01	0.00E+00	8.09E+01	9.21E+01	5.64E+02	2.41E+03	6.82E+03	387.69891	2	29.22
SSD1	YDR293C	SQSELTNLMIEQFTLQK	[6] Phospho (ST)	-0.21	0.02	-0.17	-0.22	0.386	0.488	0.404	0.35	2.57E+04	5.19E+04	2.06E+04	2.23E+04	4.85E+04	1.43E+04	3.86E+04	3.82E+04	2.25E+04	2.04E+04	4.88E+04	1.82E+04	697.33502	3	41.54
SEC16	YPL085W	SNSNVPSLFADFPAPPK	[1] Phospho (ST)	-1.32	-0.61	-0.45	-0.71	0.028	0.136	0.186	0.09	5.47E+04	8.07E+04	3.72E+04	2.71E+04	2.33E+04	1.87E+04	4.12E+04	5.14E+04	2.08E+04	4.36E+04	5.65E+04	2.60E+04	934.43857	2	58.96
RPC82	YPR190C	RSGSNAAASLPSK	[4] Phospho (ST)	0.46	-0.71	-0.64	1.17	0.091	0.015	0.024	0.02	2.62E+03	2.87E+03	3.45E+03	5.39E+03	3.52E+03	3.38E+03	1.63E+03	1.49E+03	2.31E+03	2.46E+03	1.79E+03	1.47E+03	442.54516	3	19.73
HPR1	YDR138W	INSASQTEGDELK	[3] Phospho (ST)	-1.89	-1.53	-0.64	-0.36	0.000	0.001	0.011	0.09	1.81E+04	1.70E+04	2.19E+04	4.85E+03	4.42E+03	6.04E+03	7.16E+03	5.07E+03	7.48E+03	1.41E+04	1.01E+04	1.24E+04	736.31976	2	61.55
CDC25	YLR310C	NSVNSVVTPR	[2] Phospho (ST)	0.38	0.15	0.25	0.23	0.030	0.277	0.182	0.15	6.73E+03	6.81E+03	8.71E+03	9.49E+03	8.79E+03	1.08E+04	8.34E+03	6.29E+03	1.01E+04	8.80E+03	6.74E+03	1.09E+04	576.77435	2	45.08
DEF1	YKL054C	KEISDIKK	[4] Phospho (ST)	-4.26	-3.53	-0.92	-0.73	0.002	0.002	0.021	0.23	1.51E+04	9.90E+03	9.91E+03	5.15E+02	5.40E+02	7.43E+02	1.75E+03	8.29E+01	1.16E+03	4.95E+03	6.38E+03	7.09E+03	520.77285	2	26.07
MAF1	YDR005C	SSNNNYSSGTATNNVNK	[2] Phospho (ST)	-1.03	-1.07	-0.77	0.04	0.117	0.124	0.160	0.47	2.76E+04	7.79E+03	1.49E+04	1.16E+04	8.25E+03	4.88E+03	2.91E+03	1.31E+04	7.89E+03	1.38E+04	8.06E+03	7.56E+03	926.3797	2	65.9
YPK2	YMR104C	DNDKTDTFCGTPEYLAPEILLGQGYTK	[7] Phospho (ST)	0.01	0.48	0.09	-0.46	0.483	0.119	0.398	0.09	7.45E+04	7.24E+04	3.76E+04	5.98E+04	7.42E+04	5.23E+04	9.22E+04	1.03E+05	6.11E+04	7.38E+04	7.52E+04	4.78E+04	1042.8065	3	53.55
GAT1	YFL021W	IKSSTSVQSSATPPSNTSSNPDIK	[9] Phospho (ST)|[10] Phospho (ST)	-0.86	-0.67	-0.41	-0.19	0.026	0.070	0.162	0.28	3.24E+04	1.90E+04	2.27E+04	1.44E+04	1.25E+04	1.41E+04	1.01E+04	2.02E+04	1.65E+04	2.44E+04	1.20E+04	1.95E+04	865.05246	3	27.47
SWH1	YAR042W	ESDEDSDADEFFDAEEAASDKK	[6] Phospho (ST)	-0.47	0.03	0.10	-0.50	0.234	0.472	0.360	0.22	1.56E+04	2.63E+04	1.80E+04	3.75E+03	2.50E+04	1.44E+04	1.55E+04	2.71E+04	1.84E+04	1.92E+04	2.41E+04	2.06E+04	843.98226	3	19.63
SAH1	YER043C	TGPFEVGVHVLPK	[1] Phospho (ST)	-0.51	-0.67	-0.27	0.16	0.150	0.012	0.252	0.38	2.28E+04	2.57E+04	1.83E+04	2.59E+04	1.11E+04	9.97E+03	1.56E+04	1.41E+04	1.22E+04	2.15E+04	2.47E+04	9.38E+03	730.3725	2	25.07
IOC4	YMR044W	QQAIDASEEEEEEEEK	[7] Phospho (ST)	-0.15	-0.43	-0.18	0.28	0.296	0.092	0.288	0.12	3.79E+04	2.55E+04	2.50E+04	3.15E+04	2.28E+04	2.54E+04	1.76E+04	2.39E+04	2.40E+04	3.26E+04	1.92E+04	2.61E+04	1051.4031	2	43.58
XRN1	YGL173C	SSENVQVDLANFEK	[2] Phospho (ST)	0.07	0.29	0.37	-0.22	0.408	0.166	0.099	0.24	1.11E+04	1.68E+04	1.65E+04	1.57E+04	1.95E+04	1.14E+04	1.70E+04	2.26E+04	1.46E+04	1.81E+04	2.30E+04	1.61E+04	830.36794	2	56.09
SOG2	YOR353C	AVSVSANSPE	[8] Phospho (ST)	0.49	-1.69	0.24	2.17	0.206	0.061	0.347	0.03	7.11E+03	3.13E+03	9.21E+03	1.32E+04	8.63E+03	5.49E+03	4.87E+03	7.79E+02	3.75E+02	1.20E+04	5.97E+03	5.06E+03	520.71855	2	31.65
IRA2	YOL081W	TSSFNNTAHETGSEK	[2] Phospho (ST)	0.11	-0.12	-0.03	0.22	0.254	0.312	0.444	0.12	1.62E+04	1.16E+04	1.58E+04	1.53E+04	1.50E+04	1.68E+04	1.37E+04	1.07E+04	1.59E+04	1.63E+04	1.31E+04	1.34E+04	845.3421	2	25.12
LTE1	YAL024C	VQSIAITPTK	[3] Phospho (ST)	0.03	0.36	0.39	-0.33	0.472	0.156	0.117	0.19	4.25E+03	6.75E+03	7.88E+03	4.74E+03	5.58E+03	8.93E+03	9.00E+03	5.88E+03	9.34E+03	6.81E+03	9.79E+03	8.08E+03	569.29885	2	23.35
GAL80	YML051W	RSSVSTVPNAAPIR	[3] Phospho (ST)	-0.02	1.16	-0.05	-1.18	0.478	0.010	0.458	0.01	3.51E+03	7.49E+03	6.67E+03	4.14E+03	5.98E+03	7.27E+03	1.43E+04	1.02E+04	1.49E+04	3.81E+03	5.87E+03	7.45E+03	767.89258	2	22.27
FAR11	YNL127W	SDGNISALTFK	[1] Phospho (ST)	-0.60	0.07	-0.27	-0.67	0.050	0.376	0.153	0.00	7.17E+03	1.17E+04	8.80E+03	4.77E+03	6.89E+03	6.60E+03	9.01E+03	1.02E+04	9.86E+03	7.86E+03	7.37E+03	7.76E+03	616.78212	2	51.91
REG1	YDR028C	SDSGVHSPITDNSSVASSTTSR	[7] Phospho (ST)|[10] Phospho (ST)	0.16	-0.16	-0.09	0.32	0.062	0.188	0.387	0.07	1.44E+04	1.45E+04	1.44E+04	1.76E+04	1.47E+04	1.60E+04	1.03E+04	1.56E+04	1.29E+04	1.93E+04	9.61E+03	1.18E+04	784.65149	3	20.7
HYP2	YEL034W	SDEEHTFETADAGSSATYPMQCSALR	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.08	-0.65	-0.84	0.58	0.404	0.034	0.022	0.05	4.11E+04	4.50E+04	6.40E+04	3.48E+04	4.87E+04	5.89E+04	2.80E+04	3.32E+04	3.42E+04	3.33E+04	2.66E+04	2.39E+04	995.06513	3	21.24
YOR304C-A	R304C-A	LEASEEPQAPLANTSETNSIKGDTENIVTVFDLANEIEK	[17] Phospho (ST)|[19] Phospho (ST)	0.06	-0.06	-0.44	0.12	0.447	0.458	0.218	0.38	8.47E+04	1.04E+05	3.54E+04	6.37E+04	9.69E+04	7.28E+04	8.90E+04	8.39E+04	4.23E+04	4.56E+04	7.57E+04	4.30E+04	1095.0054	4	35.76
ROX1	YPR065W	SLSGLPLTHDK	[3] Phospho (ST)	-3.17	-1.93	-1.31	-1.24	0.010	0.018	0.034	0.01	8.76E+03	2.13E+04	1.72E+04	1.87E+03	1.00E+03	2.35E+03	4.50E+03	4.60E+03	3.27E+03	5.68E+03	8.13E+03	5.22E+03	624.30553	2	34.05
BFR1	YOR198C	VVADDLVLVTPK	[10] Phospho (ST)	-0.25	1.13	0.18	-1.37	0.387	0.130	0.421	0.08	3.00E+03	2.07E+04	8.73E+03	6.12E+03	1.25E+04	8.71E+03	3.97E+04	1.21E+04	1.89E+04	3.39E+03	1.77E+04	1.56E+04	674.86036	2	52.33
KCC4	YCL024W	DNDTVNAPTTVK	[4] Phospho (ST)	0.14	-0.35	-0.24	0.49	0.392	0.279	0.334	0.02	4.36E+03	8.88E+03	1.52E+04	1.02E+04	9.27E+03	1.18E+04	7.91E+03	6.34E+03	8.07E+03	8.54E+03	7.70E+03	7.83E+03	677.79831	2	29.61
RGA2	YDR379W	AQSSLGSISK	[4] Phospho (ST)	0.24	0.51	0.04	-0.27	0.233	0.130	0.461	0.19	5.82E+03	5.57E+03	1.04E+04	8.63E+03	7.71E+03	9.34E+03	9.07E+03	8.12E+03	1.38E+04	9.55E+03	8.31E+03	4.56E+03	529.24992	2	32.48
XRS2	YDR369C	APEVEASPVVSK	[7] Phospho (ST)	-0.29	0.50	0.31	-0.79	0.118	0.152	0.047	0.09	1.24E+04	1.21E+04	1.31E+04	8.57E+03	8.79E+03	1.35E+04	1.53E+04	1.16E+04	2.65E+04	1.50E+04	1.36E+04	1.81E+04	646.81039	2	29.9
MSN2	YMR037C	SSVVIESTK	[2] Phospho (ST)	-0.11	0.93	0.49	-1.04	0.365	0.010	0.108	0.00	4.03E+03	2.25E+03	4.13E+03	3.43E+03	2.58E+03	3.63E+03	6.51E+03	5.65E+03	7.67E+03	3.62E+03	6.17E+03	4.85E+03	515.24676	2	24.03
ATR1	YML116W	GNQSLVVLTESK	[4] Phospho (ST)	-0.80	0.16	0.19	-0.96	0.014	0.304	0.167	0.02	8.12E+03	1.25E+04	1.07E+04	5.38E+03	6.50E+03	6.07E+03	1.51E+04	1.10E+04	8.91E+03	1.20E+04	1.24E+04	1.13E+04	677.83478	2	32.05
NTE1	YML059C	KFSSLSPELR	[6] Phospho (ST)	0.78	0.26	-0.10	0.52	0.040	0.344	0.433	0.11	2.05E+03	6.43E+03	4.06E+03	6.77E+03	7.79E+03	7.07E+03	7.84E+03	2.98E+03	4.23E+03	2.27E+03	5.06E+03	4.38E+03	622.30785	2	20.85
PSK1	YAL017W	ISLSPSTESLADSK	[2] Phospho (ST)|[6] Phospho (ST)	-0.20	0.13	0.18	-0.33	0.364	0.322	0.229	0.29	1.41E+04	1.86E+04	1.95E+04	5.87E+03	2.58E+04	1.39E+04	1.50E+04	2.45E+04	1.77E+04	1.91E+04	2.39E+04	1.62E+04	797.83307	2	19.71
NOT3	YIL038C	ETERSPSSSPIHNATKPEEAVK	[8] Phospho (ST)	-0.10	-0.49	-0.16	0.39	0.291	0.058	0.359	0.07	1.54E+04	2.08E+04	2.15E+04	1.99E+04	1.62E+04	1.77E+04	1.70E+04	1.01E+04	1.39E+04	8.71E+03	1.77E+04	2.53E+04	825.38982	3	15.58
SWI6	YLR182W	IDTSVIDAESDSTPNTAR	[12] Phospho (ST)	0.09	0.47	0.09	-0.38	0.178	0.006	0.347	0.01	1.79E+04	2.05E+04	1.89E+04	1.86E+04	2.17E+04	2.06E+04	2.86E+04	2.35E+04	2.73E+04	1.48E+04	2.48E+04	2.15E+04	986.43095	2	40.52
CDC33	YOL139C	KFEENVSVDDTTATPK	[14] Phospho (ST)	0.96	0.88	0.76	0.08	0.043	0.126	0.075	0.44	5.93E+03	1.86E+04	1.45E+04	2.03E+04	2.24E+04	3.30E+04	3.67E+04	1.17E+04	2.33E+04	1.61E+04	2.20E+04	2.80E+04	930.91739	2	18.14
PUF2	YPR042C	STDNYTLPQTAQLNSFLEK	[2] Phospho (ST)	0.03	0.01	-0.28	0.01	0.479	0.482	0.177	0.49	1.08E+04	1.72E+04	1.13E+04	1.07E+04	2.05E+04	8.75E+03	1.24E+04	1.46E+04	1.26E+04	1.02E+04	1.25E+04	9.58E+03	750.68293	3	37.21
PBS2	YJL128C	TSSTSSHYNNINADLHAR	[3] Phospho (ST)	-0.40	-0.24	-0.33	-0.16	0.106	0.246	0.171	0.30	1.39E+04	2.30E+04	1.68E+04	1.59E+04	1.28E+04	1.18E+04	1.91E+04	1.56E+04	1.06E+04	1.29E+04	1.15E+04	1.83E+04	689.96781	3	24.65
SHE3	YBR130C	LAPHHNIFMANLESSPTK	[15] Phospho (ST)	0.50	0.10	0.59	0.40	0.180	0.436	0.020	0.28	1.18E+04	1.59E+04	1.75E+04	2.17E+04	3.14E+04	1.11E+04	2.65E+04	1.59E+04	6.06E+03	1.98E+04	2.63E+04	2.22E+04	696.33101	3	33.09
PIB2	YGL023C	KLSSFK	[4] Phospho (ST)	0.64	-1.05	-0.18	1.70	0.016	0.042	0.254	0.01	2.53E+03	2.78E+03	2.94E+03	4.15E+03	3.58E+03	5.18E+03	2.36E+03	2.32E+02	1.36E+03	1.74E+03	2.31E+03	3.23E+03	395.19877	2	22.17
PSH1	YOL054W	DNNDDNTEELDDPQPK	[7] Phospho (ST)	-0.19	0.01	0.27	-0.20	0.343	0.493	0.248	0.28	2.20E+04	8.28E+03	2.15E+04	1.83E+04	1.19E+04	1.53E+04	1.14E+04	1.98E+04	2.09E+04	2.30E+04	1.72E+04	2.24E+04	969.86655	2	28.07
COX4	YGL187C	CWECGSVYK	[8] Phospho (Y)	1.10	0.87	1.30	0.23	0.048	0.144	0.004	0.34	1.35E+03	2.12E+03	3.83E+03	4.14E+03	4.20E+03	7.37E+03	7.23E+03	2.20E+03	3.93E+03	5.99E+03	6.18E+03	5.86E+03	634.73136	2	15.13
NGG1	YDR176W	GVQSPPKPPPSNEISGTIENDVESIK	[4] Phospho (ST)	-0.32	0.28	-0.25	-0.59	0.240	0.160	0.271	0.05	3.68E+04	4.09E+04	2.19E+04	2.10E+04	3.89E+04	2.01E+04	4.37E+04	4.09E+04	3.60E+04	1.81E+04	3.72E+04	2.82E+04	933.78577	3	41.91
SEC16	YPL085W	LLNDSDQHDITADSNDLPDNSIVEHDSVITQTK	[5] Phospho (ST)	-0.60	0.20	0.03	-0.80	0.049	0.216	0.457	0.02	1.78E+04	2.60E+04	2.19E+04	9.38E+03	1.66E+04	1.73E+04	2.53E+04	2.02E+04	2.98E+04	2.09E+04	1.91E+04	2.69E+04	933.1753	4	21.28
ZDS2	YML109W	RTSTDWSTENEK	[3] Phospho (ST)	0.48	0.56	0.99	-0.08	0.175	0.145	0.045	0.28	2.08E+03	3.64E+03	7.71E+03	6.51E+03	6.10E+03	6.14E+03	6.52E+03	5.71E+03	7.65E+03	1.10E+04	7.50E+03	8.20E+03	767.31453	2	36.6
MLF3	YNL074C	KVSNGGFSTEFNSCDT	[3] Phospho (ST)	-1.08	-0.08	-0.11	-1.00	0.002	0.384	0.060	0.03	1.85E+04	2.01E+04	1.86E+04	1.08E+04	1.02E+04	6.05E+03	1.39E+04	2.44E+04	1.59E+04	1.72E+04	1.86E+04	1.72E+04	915.35705	2	48.69
TOM71	YHR117W	RQSEAFAGQNEDEADLK	[3] Phospho (ST)	0.37	0.56	0.15	-0.19	0.082	0.053	0.272	0.18	8.34E+03	1.34E+04	1.45E+04	1.53E+04	1.43E+04	1.71E+04	1.83E+04	1.41E+04	2.10E+04	1.46E+04	1.20E+04	1.37E+04	663.28486	3	21.3
STU1	YBL034C	KSEGDEESDDAVDENDVKK	[8] Phospho (ST)	-0.12	-0.77	-0.28	0.65	0.371	0.046	0.219	0.02	1.34E+04	7.13E+03	9.12E+03	1.08E+04	9.73E+03	6.87E+03	6.03E+03	5.60E+03	5.73E+03	9.90E+03	7.01E+03	7.42E+03	730.29703	3	40.46
STE2	YFL026W	IGPFADASYK	[9] Phospho (Y)	-1.12	-0.33	-0.66	-0.79	0.090	0.279	0.175	0.04	5.17E+03	1.81E+04	1.28E+04	3.53E+03	8.21E+03	4.81E+03	1.10E+04	7.46E+03	1.02E+04	5.38E+03	1.13E+04	6.17E+03	574.75519	2	29.77
NUP60	YAR002W	ISSMPGGYFHSEISPDSTVNR	[8] Phospho (Y)	-0.47	0.55	0.50	-1.02	0.224	0.070	0.154	0.06	1.06E+04	1.53E+04	1.08E+04	6.72E+03	1.61E+04	3.69E+03	2.10E+04	2.01E+04	1.26E+04	1.03E+04	2.45E+04	1.73E+04	787.67907	3	16.93
HRK1	YOR267C	KLSMSQLR	[3] Phospho (ST)	-0.08	-1.10	0.51	1.02	0.464	0.020	0.212	0.20	2.94E+03	4.52E+03	2.78E+03	1.95E+03	6.73E+03	1.03E+03	1.77E+03	1.91E+03	1.07E+03	2.26E+03	7.58E+03	4.76E+03	521.75949	2	32.75
FLC2	YAL053W	NKNDSELFELRK	[5] Phospho (ST)	0.45	-0.23	0.47	0.68	0.000	0.246	0.058	0.03	8.95E+03	9.86E+03	9.36E+03	1.24E+04	1.29E+04	1.33E+04	1.14E+04	7.48E+03	5.12E+03	1.18E+04	1.07E+04	1.65E+04	786.87411	2	15.11
CRP1	YHR146W	EETPLAEPTNVSK	[12] Phospho (ST)	-0.03	-0.53	0.03	0.50	0.445	0.068	0.442	0.01	2.89E+04	1.68E+04	2.13E+04	2.07E+04	2.14E+04	2.32E+04	1.49E+04	1.76E+04	1.36E+04	2.26E+04	2.33E+04	2.27E+04	747.84024	2	19.71
SYP1	YCR030C	TKPLPVEPASPSISLPTATVDNQPSGQVDSRPLHIR	[12] Phospho (ST)	0.84	0.45	-0.08	0.39	0.088	0.222	0.444	0.18	1.11E+04	3.75E+04	1.81E+04	4.46E+04	2.56E+04	4.94E+04	4.17E+04	2.46E+04	2.51E+04	2.52E+04	1.52E+04	2.25E+04	972.00393	4	36.86
HSL1	YKL101W	SLNLNDLLVFDDPLPSK	[1] Phospho (ST)	-1.67	-1.09	-1.27	-0.58	0.007	0.023	0.018	0.10	4.08E+04	5.51E+04	3.18E+04	1.15E+04	1.63E+04	1.22E+04	2.54E+04	2.23E+04	1.21E+04	1.57E+04	2.58E+04	1.15E+04	990.49185	2	92.89
SYT1	YPR095C	SIEDEGYHNK	[1] Phospho (ST)	0.81	0.84	0.83	-0.03	0.154	0.132	0.138	0.44	0.00E+00	2.14E+03	5.04E+03	5.08E+03	4.32E+03	3.22E+03	4.49E+03	3.96E+03	4.45E+03	4.89E+03	4.05E+03	3.87E+03	636.25092	2	28.28
RTK1	YDL025C	KNTDSDQEDQIK	[5] Phospho (ST)	0.47	-0.76	0.17	1.23	0.215	0.204	0.418	0.01	1.21E+04	3.01E+03	4.76E+03	1.08E+04	8.61E+03	8.01E+03	5.37E+03	4.23E+03	2.11E+03	1.24E+04	5.03E+03	4.87E+03	750.81438	2	60.31
AIR2	YDL175C	YFGVSDDDK	[5] Phospho (ST)	0.08	0.27	-0.39	-0.18	0.274	0.049	0.063	0.11	7.09E+03	8.43E+03	8.72E+03	8.27E+03	9.63E+03	7.80E+03	8.74E+03	9.72E+03	1.07E+04	6.25E+03	7.61E+03	4.66E+03	563.21126	2	18.75
MDG1	YNL173C	VPVSSITSHAK	[8] Phospho (ST)	0.38	-0.03	-0.13	0.41	0.148	0.471	0.373	0.13	2.28E+03	4.76E+03	3.72E+03	5.34E+03	5.09E+03	3.59E+03	4.76E+03	2.29E+03	3.48E+03	2.26E+03	3.52E+03	4.05E+03	603.3002	2	22.62
REG1	YDR028C	SMGLLDEYIDPTK	[1] Phospho (ST)	-0.68	0.42	0.49	-1.10	0.166	0.176	0.230	0.07	1.46E+04	2.31E+04	1.36E+04	6.76E+03	2.06E+04	4.62E+03	2.88E+04	2.57E+04	1.40E+04	1.53E+04	3.96E+04	1.70E+04	781.34864	2	69.06
ENT2	YLR206W	YSDLNTLLATGTGIDTFGNTGEAR	[12] Phospho (ST)	0.25	0.50	0.20	-0.25	0.255	0.138	0.190	0.29	2.28E+04	2.85E+04	1.77E+04	2.20E+04	3.79E+04	2.24E+04	4.34E+04	3.49E+04	1.96E+04	2.61E+04	2.89E+04	2.42E+04	856.39349	3	31.65

TOM1	YDR457W	ADDDVSNNDEEVENGLDHGNSNDR	[6] Phospho (ST)	-0.17	0.01	0.17	-0.18	0.279	0.479	0.314	0.27	1.58E+04	1.07E+04	1.34E+04	1.27E+04	1.44E+04	8.41E+03	1.06E+04	1.65E+04	1.31E+04	1.01E+04	1.99E+04	1.49E+04	904.01015	3	20.45
RFM1	YOR279C	LGSEEDEEGDGHDGDEGETK	[3] Phospho (ST)	0.12	0.32	0.42	-0.21	0.384	0.232	0.139	0.24	4.17E+03	3.05E+03	7.07E+03	6.10E+03	4.99E+03	4.43E+03	6.56E+03	4.23E+03	7.12E+03	6.95E+03	5.50E+03	6.66E+03	728.92939	3	23.3
BUD3	YCL014W	ALTPER	[3] Phospho (ST)	0.55	1.30	0.71	-0.74	0.097	0.033	0.019	0.10	1.99E+03	1.62E+03	2.51E+03	2.34E+03	2.56E+03	4.10E+03	6.33E+03	2.70E+03	6.05E+03	2.85E+03	3.18E+03	3.98E+03	383.67809	2	19.47
MDS3	YGL197W	NNDEEDDEDPVSPKPVSK	[12] Phospho (ST)|[17] Phospho (ST)	-0.22	-0.58	-0.15	0.35	0.221	0.058	0.320	0.05	4.12E+04	2.38E+04	3.27E+04	3.23E+04	2.57E+04	2.56E+04	1.89E+04	2.13E+04	2.52E+04	3.37E+04	2.21E+04	3.24E+04	1087.4143	2	17.54
MPT5	YGL178W	SNSSVTNNFSNQYAQDQK	[3] Phospho (ST)	0.19	0.65	0.53	-0.46	0.243	0.185	0.016	0.25	7.17E+03	7.46E+03	8.37E+03	8.62E+03	1.12E+04	6.45E+03	5.87E+03	2.04E+04	9.88E+03	1.31E+04	1.04E+04	9.82E+03	704.62779	3	41.83
SFL1	YOR140W	SSLNEDSLYPK	[2] Phospho (ST)	-0.08	0.19	-1.01	-0.26	0.439	0.355	0.094	0.15	7.35E+03	2.31E+04	1.36E+04	1.41E+04	1.37E+04	1.40E+04	1.53E+04	2.13E+04	1.36E+04	7.80E+03	8.46E+03	5.68E+03	666.79039	2	25.88
UBP3	YER151C	TSSPSPSPPAAK	[3] Phospho (ST)	0.27	0.49	-0.01	-0.23	0.197	0.019	0.486	0.20	1.10E+04	8.27E+03	1.07E+04	1.01E+04	1.01E+04	1.59E+04	1.43E+04	1.22E+04	1.57E+04	1.35E+04	8.55E+03	7.68E+03	603.77374	2	28.78
EIS1	YMR031C	EATETSSAVQTK	[3] Phospho (ST)	1.37	0.17	0.68	1.20	0.028	0.385	0.191	0.02	6.59E+03	2.32E+03	2.06E+03	1.09E+04	6.24E+03	1.12E+04	3.84E+03	4.06E+03	4.46E+03	9.29E+03	4.15E+03	4.17E+03	666.28949	2	18.16
HPC2	YBR215W	LVAAPTVSPPK	[8] Phospho (ST)	-1.27	-0.64	-0.30	-0.63	0.001	0.024	0.220	0.11	1.39E+04	1.36E+04	1.34E+04	3.57E+03	5.92E+03	7.49E+03	1.22E+04	6.60E+03	7.43E+03	5.09E+03	1.48E+04	1.32E+04	580.31018	2	15.88
SUM1	YDR310C	TAGDDGALDQTENTSISPK	[15] Phospho (ST)	-0.68	-0.28	-0.44	-0.40	0.036	0.226	0.082	0.12	1.63E+04	2.42E+04	2.82E+04	1.41E+04	1.34E+04	1.54E+04	1.36E+04	1.79E+04	2.51E+04	1.75E+04	1.53E+04	1.77E+04	1000.4231	2	17.81
SSA2	YLL024C	NTISEAGDKLEQADK	[4] Phospho (ST)	-0.19	-0.13	0.05	-0.07	0.305	0.385	0.444	0.40	8.42E+03	1.50E+04	1.95E+04	1.24E+04	1.33E+04	1.19E+04	1.57E+04	1.46E+04	9.07E+03	1.36E+04	1.43E+04	1.66E+04	849.88395	2	37.21
ZRT2	YLR130C	DHYSHENDHQDVSQLATR	[3] Phospho (Y)	-0.53	-2.26	-0.79	1.73	0.085	0.002	0.014	0.04	2.51E+04	2.42E+04	2.95E+04	2.70E+04	1.22E+04	1.54E+04	1.17E+04	3.08E+03	1.65E+03	1.64E+04	9.67E+03	1.94E+04	558.73325	4	17.67
SEC16	YPL085W	HEDLFAASGNDEK	[8] Phospho (ST)	-0.07	-0.21	-0.08	0.14	0.355	0.147	0.337	0.11	1.03E+04	1.37E+04	1.46E+04	1.13E+04	1.33E+04	1.24E+04	1.03E+04	1.21E+04	1.12E+04	1.25E+04	1.32E+04	1.09E+04	756.80502	2	38.8
FIN1	YDR130C	HSIQVTPR	[6] Phospho (ST)	-1.21	1.08	0.69	-2.28	0.129	0.074	0.087	0.03	2.70E+03	7.93E+02	2.65E+03	0.00E+00	5.63E+02	2.09E+03	6.15E+03	2.32E+03	4.54E+03	2.45E+03	3.88E+03	3.61E+03	509.24758	2	21.67
NTH1	YDR001C	RGSEDDTYSSSQGNRR	[10] Phospho (ST)	0.44	0.50	-0.64	-0.06	0.239	0.200	0.256	0.44	2.37E+04	1.47E+04	5.30E+03	2.74E+04	1.79E+04	1.40E+04	1.49E+04	2.00E+04	2.68E+04	1.92E+04	4.79E+03	4.09E+03	947.88793	2	35.34
MHP1	YJL042W	IVTNNEEEVTVSK	[3] Phospho (ST)	0.33	-0.30	-0.32	0.63	0.147	0.192	0.226	0.03	7.80E+03	6.97E+03	1.18E+04	1.30E+04	9.00E+03	1.14E+04	7.64E+03	5.62E+03	8.33E+03	4.53E+03	6.98E+03	9.76E+03	771.35785	2	46.49
YTA7	YGR270W	NTSLLQNFIDYEEYSGEEEEHDK	[14] Phospho (Y)	-0.08	0.21	-0.59	-0.29	0.432	0.359	0.159	0.26	5.94E+04	8.47E+04	2.90E+04	5.83E+04	6.06E+04	4.50E+04	7.42E+04	9.19E+04	3.43E+04	3.10E+04	4.95E+04	3.43E+04	957.06335	3	42.38
SUM1	YDR310C	TPGDEETTTFVPLENSQPSDTIRK	[16] Phospho (ST)	2.74	-1.09	-1.11	3.83	0.000	0.080	0.077	0.00	2.65E+03	8.43E+03	5.79E+03	4.12E+04	3.97E+04	3.23E+04	3.09E+03	1.73E+03	3.10E+03	2.23E+03	3.49E+03	2.07E+03	914.75542	3	37.34
YDR210W-B	R210W-B	HSSTFTAR	[3] Phospho (ST)	-0.69	-0.85	-0.66	0.16	0.067	0.055	0.074	0.32	1.26E+04	6.81E+03	8.14E+03	5.30E+03	4.76E+03	6.97E+03	6.74E+03	3.37E+03	5.12E+03	7.21E+03	5.24E+03	5.00E+03	493.70824	2	36.31
ISW2	YOR304W	TSATREDTPLSQNESTR	[11] Phospho (ST)	2.20	0.20	-0.36	2.00	0.003	0.129	0.128	0.00	3.38E+03	4.53E+03	3.66E+03	2.28E+04	1.51E+04	1.53E+04	4.10E+03	4.92E+03	4.24E+03	3.98E+03	2.91E+03	2.13E+03	658.29171	3	32.65
YPR137C-B	R137C-B	KRSLEDNETEIK	[3] Phospho (ST)	0.16	-0.63	0.24	0.79	0.378	0.254	0.345	0.14	2.91E+03	6.13E+03	1.00E+04	5.67E+03	8.01E+03	7.60E+03	8.68E+03	2.64E+03	9.83E+02	5.13E+03	6.69E+03	1.07E+04	771.36387	2	31.75
WHI5	YOR083W	VYDHNDDGHESESEDDENEEENENQK	[2] Phospho (Y)|[13] Phospho (ST)	-1.62	-2.13	-1.64	0.51	0.089	0.070	0.088	0.18	7.61E+04	2.12E+04	2.84E+04	1.63E+04	1.43E+04	1.03E+04	3.96E+03	1.60E+04	8.72E+03	1.68E+04	9.15E+03	1.42E+04	1089.3678	3	27.78
MSS4	YDR208W	RSESATAEIK	[4] Phospho (ST)	0.12	-0.56	-0.49	0.68	0.299	0.138	0.058	0.09	5.98E+03	5.25E+03	4.08E+03	6.63E+03	4.96E+03	5.05E+03	2.55E+03	2.03E+03	5.80E+03	3.73E+03	2.78E+03	4.42E+03	586.27141	2	26
AIM3	YBR108W	EATGQDEVLNSITNELSHIK	[3] Phospho (ST)	-0.46	0.15	0.47	-0.62	0.129	0.339	0.151	0.05	3.46E+04	5.51E+04	3.05E+04	2.68E+04	3.59E+04	2.43E+04	5.67E+04	4.05E+04	3.62E+04	5.23E+04	7.51E+04	3.90E+04	760.0255	3	47.16
PTA1	YAL043C	RKSDDDDDGNDNEEVGNDGPTANSK	[3] Phospho (ST)	0.07	-0.92	-0.46	0.99	0.419	0.069	0.187	0.00	2.58E+04	1.09E+04	1.86E+04	2.06E+04	1.90E+04	1.85E+04	1.01E+04	6.23E+03	1.28E+04	1.55E+04	8.19E+03	1.65E+04	915.35748	3	45.7
SSB1	YDL229W	IEAALSDALAALQIEDPSADELRK	[18] Phospho (ST)	-0.14	0.29	-0.22	-0.43	0.391	0.254	0.349	0.14	4.33E+04	5.17E+04	1.93E+04	2.75E+04	4.85E+04	2.76E+04	5.99E+04	3.84E+04	4.16E+04	2.42E+04	4.91E+04	2.51E+04	873.76969	3	41.1
MBP1	YDL056W	PLFDFTQTDGSASPPPAPK	[13] Phospho (ST)	-0.89	-0.04	-0.22	-0.85	0.061	0.456	0.302	0.03	2.94E+04	4.59E+04	2.42E+04	2.58E+04	1.69E+04	1.11E+04	3.33E+04	2.68E+04	3.69E+04	1.85E+04	3.61E+04	3.09E+04	1026.9711	2	33.56
YJL070C	YJL070C	RPSLLFDEYQNSVTKPNETK	[3] Phospho (ST)	-0.71	-0.17	-0.10	-0.55	0.031	0.365	0.417	0.18	1.45E+04	2.29E+04	1.66E+04	1.09E+04	1.28E+04	9.18E+03	2.54E+04	1.12E+04	1.13E+04	8.85E+03	2.48E+04	1.67E+04	816.06041	3	38
LCB5	YLR260W	SRSSIDNISR	[3] Phospho (ST)	0.34	0.37	0.31	-0.04	0.094	0.055	0.133	0.42	2.75E+03	2.58E+03	3.63E+03	4.03E+03	3.03E+03	4.26E+03	3.64E+03	4.43E+03	3.54E+03	3.18E+03	3.33E+03	4.57E+03	607.77989	2	17.98
NET1	YJL076W	SSLETIVEK	[2] Phospho (ST)	0.92	0.54	0.23	0.38	0.025	0.087	0.299	0.06	1.06E+03	2.60E+03	2.81E+03	3.24E+03	4.49E+03	4.58E+03	2.77E+03	3.59E+03	3.09E+03	2.44E+03	3.22E+03	1.95E+03	543.26024	2	26.94
RPS7B	YNL096C	TLTAVHDK	[3] Phospho (ST)	2.01	0.21	0.36	1.79	0.002	0.285	0.022	0.00	1.54E+03	1.37E+03	1.62E+03	6.76E+03	4.55E+03	6.99E+03	2.46E+03	1.14E+03	1.66E+03	1.70E+03	2.14E+03	1.97E+03	482.72847	2	21.46
ATP11	YNL315C	SRSPLDPSAPK	[1] Phospho (ST)	0.72	0.36	-0.09	0.36	0.009	0.172	0.414	0.10	1.91E+03	3.19E+03	2.81E+03	4.09E+03	4.15E+03	4.81E+03	4.48E+03	2.50E+03	3.15E+03	1.83E+03	2.00E+03	3.61E+03	617.79497	2	20.77
RPS16B	YDL083C	SATAVAHVK	[1] Phospho (ST)	0.81	-0.34	-0.29	1.15	0.019	0.221	0.204	0.01	6.16E+03	3.26E+03	4.07E+03	7.05E+03	7.31E+03	9.31E+03	4.55E+03	2.16E+03	3.91E+03	4.05E+03	3.70E+03	3.28E+03	482.23641	2	27.77
SUM1	YDR310C	FHQIPSSPSNPVSQPAPVR	[6] Phospho (ST)|[7] Phospho (ST)	2.96	4.39	4.11	-1.43	0.000	0.004	0.000	0.02	1.04E+03	5.37E+02	1.64E+03	7.07E+03	8.81E+03	9.34E+03	1.54E+04	3.06E+04	2.21E+04	1.67E+04	2.00E+04	1.94E+04	735.66877	3	19.22
BAG7	YOR134W	TLSAESLSPR	[3] Phospho (ST)	1.59	2.60	1.64	-1.01	0.030	0.002	0.027	0.02	1.47E+02	1.76E+03	1.90E+03	2.42E+03	3.87E+03	5.25E+03	9.51E+03	6.86E+03	6.82E+03	2.55E+03	5.44E+03	3.97E+03	570.76868	2	31.3
BUL2	YML111W	SVSTEDNIHLLR	[4] Phospho (ST)	0.29	0.56	0.26	-0.26	0.307	0.162	0.355	0.17	2.45E+03	1.19E+04	6.88E+03	6.55E+03	9.70E+03	9.74E+03	1.25E+04	1.03E+04	8.37E+03	4.23E+03	1.06E+04	1.04E+04	732.34852	2	36.28
VPS54	YDR027C	RSSRLSLDSITPR	[3] Phospho (ST)|[6] Phospho (ST)	-0.56	-0.10	-1.09	-0.46	0.065	0.402	0.023	0.14	4.49E+03	8.03E+03	6.50E+03	4.51E+03	3.69E+03	4.70E+03	4.42E+03	8.38E+03	4.92E+03	4.10E+03	2.66E+03	2.18E+03	549.92602	3	17.27
RPP2A	YOL039W	SVDELITEGNEK	[1] Phospho (ST)	0.37	0.45	-0.02	-0.08	0.203	0.174	0.488	0.35	2.64E+03	5.70E+03	8.61E+03	6.46E+03	7.61E+03	7.81E+03	6.10E+03	7.88E+03	9.17E+03	5.98E+03	6.67E+03	4.12E+03	707.31189	2	61.84
ARB1	YER036C	EAAAEESEVDAAAR	[7] Phospho (ST)	-0.64	-0.55	-0.27	-0.08	0.008	0.023	0.047	0.36	9.80E+03	7.95E+03	1.02E+04	6.08E+03	5.16E+03	6.75E+03	6.52E+03	4.95E+03	7.57E+03	8.06E+03	7.78E+03	7.38E+03	749.8075	2	48.72
MLF3	YNL074C	SNSNNSNPSFIFER	[6] Phospho (ST)|[9] Phospho (ST)	-0.70	0.58	0.08	-1.29	0.087	0.230	0.372	0.11	1.59E+04	2.56E+04	1.68E+04	8.10E+03	1.86E+04	9.13E+03	1.67E+04	5.21E+04	1.88E+04	2.31E+04	2.00E+04	1.88E+04	886.83829	2	17.89
MSB1	YOR188W	LNVLQGAVSPSQQVTPK	[9] Phospho (ST)	-0.21	0.55	0.45	-0.77	0.331	0.094	0.115	0.03	7.48E+03	1.71E+04	1.05E+04	6.47E+03	1.08E+04	1.30E+04	1.50E+04	2.12E+04	1.53E+04	1.78E+04	1.57E+04	1.43E+04	923.47743	2	23.33
IGO2	R132W-A	SEDLSPTSSR	[5] Phospho (ST)	0.06	0.49	0.52	-0.44	0.476	0.272	0.293	0.05	1.82E+03	1.24E+03	8.48E+03	3.14E+03	4.86E+03	4.00E+03	6.27E+03	4.65E+03	5.35E+03	7.72E+03	6.46E+03	2.37E+03	579.73865	2	19.05
RDH54	YBR073W	SISAGPTLNLAK	[3] Phospho (ST)	0.40	-1.63	-0.15	2.03	0.082	0.013	0.359	0.00	5.78E+03	7.34E+03	4.50E+03	7.79E+03	9.06E+03	6.45E+03	3.42E+03	1.49E+03	7.58E+02	4.50E+03	7.76E+03	3.60E+03	626.32141	2	40.07
NSG2	YNL156C	ILSASSIHENFPSR	[3] Phospho (ST)	0.05	-0.06	-0.39	0.10	0.453	0.441	0.212	0.33	7.04E+03	1.46E+04	8.62E+03	8.79E+03	1.26E+04	9.88E+03	1.11E+04	7.84E+03	1.02E+04	5.05E+03	9.38E+03	8.73E+03	819.38775	2	25.47
YOL103W-B	L103W-B	AVSPTDSTPPSTHTEDSK	[8] Phospho (ST)	-0.29	-0.04	-0.03	-0.25	0.330	0.479	0.481	0.31	5.04E+03	6.52E+03	1.59E+04	5.77E+03	7.45E+03	9.20E+03	8.85E+03	4.66E+03	1.32E+04	1.09E+04	7.69E+03	8.35E+03	646.27679	3	18.35
SEC16	YPL085W	RESIISTGSEFLPPPK	[3] Phospho (ST)|[6] Phospho (ST)	-0.74	-0.20	-0.39	-0.54	0.045	0.239	0.092	0.09	5.15E+04	6.91E+04	4.60E+04	2.20E+04	4.66E+04	3.09E+04	4.30E+04	6.04E+04	4.16E+04	3.72E+04	5.11E+04	3.84E+04	959.44422	2	25.32
MTC1	YJL123C	SNLSLTDK	[4] Phospho (ST)	0.86	0.56	0.36	0.30	0.016	0.113	0.192	0.15	3.25E+03	1.50E+03	3.24E+03	5.46E+03	4.26E+03	4.82E+03	2.85E+03	3.78E+03	5.20E+03	4.44E+03	2.83E+03	2.99E+03	479.21829	2	15.57
TPS2	YDR074W	SASYTGAKV	[3] Phospho (ST)	-0.94	-0.04	0.30	-0.90	0.011	0.467	0.310	0.09	2.51E+03	2.45E+03	3.34E+03	1.87E+03	1.31E+03	1.13E+03	1.61E+03	4.18E+03	2.30E+03	5.69E+03	2.07E+03	2.45E+03	482.21274	2	19.69
CAF120	YNL278W	LSSSSEQDLNNSDSPSIK	[5] Phospho (ST)	-0.30	-0.89	-0.30	0.59	0.083	0.006	0.083	0.00	1.77E+04	1.25E+04	1.68E+04	1.37E+04	1.31E+04	1.13E+04	8.72E+03	8.68E+03	8.01E+03	1.32E+04	1.13E+04	1.36E+04	994.42936	2	49.85
PIB2	YGL023C	TALHSVSK	[5] Phospho (ST)	1.06	0.59	0.50	0.48	0.024	0.117	0.147	0.14	4.19E+03	2.85E+03	2.54E+03	6.48E+03	4.82E+03	8.74E+03	6.83E+03	3.46E+03	4.11E+03	6.32E+03	4.30E+03	2.95E+03	461.72335	2	26.73
FUN30	YAL019W	VASSSPLKPTSPTVPDASVASLR	[5] Phospho (ST)	-1.61	-1.60	-1.62	-0.02	0.037	0.042	0.042	0.49	1.58E+04	3.70E+04	2.11E+04	4.05E+03	1.31E+04	7.01E+03	1.49E+04	4.60E+03	4.87E+03	1.11E+03	1.20E+04	1.10E+04	1174.0994	2	15.66
ZDS1	YMR273C	SYTEFDDNEDDDNKGDSASETVNK	[1] Phospho (ST)	-0.04	-0.11	0.17	0.07	0.430	0.280	0.305	0.36	2.52E+04	2.14E+04	2.88E+04	2.89E+04	2.42E+04	2.04E+04	2.03E+04	2.31E+04	2.66E+04	3.81E+04	2.60E+04	2.06E+04	925.68837	3	23.22
CUE5	YOR042W	KWQPLPPEPLDTTPTK	[13] Phospho (ST)	-0.60	1.11	0.86	-1.72	0.177	0.029	0.076	0.01	2.20E+04	4.84E+04	2.08E+04	1.34E+04	2.75E+04	1.91E+04	8.50E+04	5.18E+04	6.02E+04	3.37E+04	6.56E+04	6.61E+04	964.48325	2	17.37
SPA2	YLL021W	SEAEVHTSEEDIDESNNVNGK	[7] Phospho (ST)|[8] Phospho (ST)	-0.37	-0.56	-0.54	0.19	0.221	0.221	0.154	0.38	1.57E+04	5.82E+03	1.45E+04	1.07E+04	9.00E+03	8.02E+03	2.16E+03	1.37E+04	8.44E+03	8.80E+03	6.82E+03	9.16E+03	821.64619	3	15.34
ZRT3	YKL175W	SEGECCDLNK	[1] Phospho (ST)	0.99	2.33	1.81	-1.34	0.205	0.090	0.165	0.15	2.55E+03	3.97E+01	1.99E+03	1.18E+03	5.95E+03	2.01E+03	4.99E+02	1.30E+04	9.72E+03	1.19E+04	3.61E+03	5.83E+02	646.22074	2	31.02
MRC1	YCL061C	SNNYEDFETDK	[1] Phospho (ST)	-10.25	-10.66	-1.91	0.27	0.000	0.000	0.003	0.19	1.61E+04	1.35E+04	1.87E+04	0.00E+00	9.66E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.42E+03	2.88E+03	2.50E+03	721.26188	2	47.86
ECM30	YLR436C	GQSSVSLER	[6] Phospho (ST)	0.19	-0.59	-0.27	0.77	0.292	0.119	0.249	0.04	6.25E+03	3.18E+03	5.77E+03	7.03E+03	5.78E+03	4.53E+03	1.91E+03	3.77E+03	4.44E+03	5.46E+03	3.86E+03	3.30E+03	521.73256	2	35.58
GLO3	YER122C	AISSDQLFGR	[3] Phospho (ST)	0.39	0.57	0.35	-0.17	0.167	0.058	0.166	0.18	3.14E+03	7.02E+03	4.28E+03	5.16E+03	7.77E+03	6.05E+03	6.94E+03	7.37E+03	7.08E+03	5.63E+03	6.68E+03	6.07E+03	587.26912	2	42.22
YJL049W	YJL049W	NQDLHEPKESSSEDLLK	[12] Phospho (ST)	0.34	0.07	0.28	0.27	0.163	0.436	0.222	0.27	5.07E+03	8.05E+03	5.89E+03	8.09E+03	1.01E+04	5.88E+03	9.85E+03	5.16E+03	4.94E+03	5.40E+03	7.65E+03	1.01E+04	683.64408	3	16.85
ISA1	YLL027W	FIPKTVPAAADSVSPDSQRPGK	[14] Phospho (ST)|[17] Phospho (ST)	-0.94	-2.19	-0.73	1.25	0.200	0.094	0.249	0.06	2.88E+04	7.74E+03	7.13E+03	5.82E+03	5.05E+03	1.18E+04	1.97E+03	4.77E+03	2.78E+03	9.16E+03	2.99E+03	1.41E+04	607.79104	4	19.19
YMR074C	YMR074C	DFSEDLNSFDK	[3] Phospho (ST)	-0.88	-0.36	-0.09	-0.52	0.109	0.183	0.394	0.19	6.21E+03	1.18E+04	6.95E+03	6.95E+02	6.86E+03	5.99E+03	6.53E+03	5.65E+03	7.25E+03	7.00E+03	8.57E+03	7.83E+03	698.76958	2	41.64
KIN4	YOR233W	HTSVAGLVTIPGSPTTAR	[13] Phospho (ST)	-0.73	0.15	-0.11	-0.88	0.060	0.309	0.376	0.00	3.40E+04	2.24E+04	1.75E+04	1.66E+04	1.39E+04	1.40E+04	2.63E+04	2.72E+04	2.84E+04	2.44E+04	2.61E+04	1.79E+04	922.96809	2	30.18
SPT6	YGR116W	VGDEGNAAESESDNVAASR	[10] Phospho (ST)	0.08	-0.47	-0.63	0.55	0.360	0.094	0.029	0.04	1.22E+04	8.89E+03	1.37E+04	1.06E+04	1.36E+04	1.25E+04	9.03E+03	5.51E+03	1.05E+04	6.14E+03	7.90E+03	8.38E+03	979.39397	2	46.98
ENP2	YGR145W	RHDNSSDEEGIDENGNKK	[5] Phospho (ST)|[6] Phospho (ST)	-0.78	-1.15	-0.90	0.38	0.244	0.181	0.224	0.14	1.13E+05	2.19E+04	2.93E+04	2.87E+04	2.43E+04	4.31E+04	2.13E+04	2.71E+04	2.57E+04	4.31E+04	2.20E+04	2.32E+04	735.28138	3	41.78
ISW2	YOR304W	EDTPLSQNESTR	[3] Phospho (ST)	2.72	0.56	-0.14	2.16	0.001	0.116	0.384	0.00	1.82E+03	2.50E+03	4.37E+03	2.13E+04	1.54E+04	2.07E+04	5.41E+03	3.34E+03	4.06E+03	1.99E+03	2.65E+03	3.25E+03	728.80201	2	18.36
YSP2	YDR326C	SSSFLR	[3] Phospho (ST)	-0.18	0.12	0.05	-0.30	0.307	0.403	0.453	0.22	1.49E+03	3.28E+03	3.11E+03	2.16E+03	2.25E+03	2.52E+03	2.06E+03	4.05E+03	2.42E+03	3.66E+03	2.25E+03	2.24E+03	388.67032	2	32.59
SPC110	YDR356W	NTTQTQVVSPTK	[9] Phospho (ST)	-0.41	-0.20	-0.36	-0.21	0.141	0.316	0.173	0.24	1.07E+04	7.74E+03	1.55E+04	8.36E+03	8.43E+03	8.76E+03	8.10E+03	8.21E+03	1.32E+04	7.89E+03	8.36E+03	1.02E+04	692.32816	2	29.27
MMS1	YPR164W	RPSDFGK	[3] Phospho (ST)	1.17	0.15	-0.03	1.03	0.026	0.380	0.474	0.04	4.52E+03	2.15E+03	3.08E+03	6.71E+03	5.43E+03	9.92E+03	4.78E+03	2.06E+03	3.96E+03	4.08E+03	2.94E+03	2.56E+03	443.69467	2	21.28
SPT20	YOL148C	ENKPNLNSSSSPSNNNSTQDNSK	[11] Phospho (ST)	0.26	-0.25	0.07	0.51	0.287	0.329	0.453	0.01	1.95E+04	6.40E+03	1.02E+04	1.51E+04	1.47E+04	1.35E+04	8.02E+03	1.10E+04	1.13E+04	1.71E+04	9.64E+03	1.11E+04	848.35944	3	25.65
YPI1	YFR003C	RSYSPNAYEIQPDYSEYR	[8] Phospho (Y)	0.01	0.12	-0.57	-0.11	0.486	0.406	0.102	0.39	1.57E+04	2.64E+04	1.35E+04	1.78E+04	1.93E+04	1.90E+04	1.75E+04	2.97E+04	1.33E+04	1.33E+04	1.18E+04	1.24E+04	773.33058	3	26.3
GIN4	YDR507C	HFSESNK	[5] Phospho (ST)	0.47	0.47	0.74	-0.01	0.223	0.067	0.121	0.50	1.29E+04	6.74E+03	9.25E+03	2.00E+04	6.12E+03	1.39E+04	1.51E+04	1.21E+04	1.29E+04	2.47E+04	1.17E+04	1.18E+04	464.68214	2	23.57
NUP100	YKL068W	AHSPQTDLK	[3] Phospho (ST)	0.97	0.39	0.10	0.59	0.031	0.198	0.398	0.08	5.10E+03	2.39E+03	3.47E+03	6.31E+03	5.85E+03	9.42E+03	5.88E+03	3.03E+03	5.43E+03	4.84E+03	3.39E+03	3.49E+03	538.74123	2	28.6
KIN2	YLR096W	GGSLSPTPEAFNDTR	[5] Phospho (ST)	-0.19	-0.08	-0.45	-0.12	0.246	0.377	0.072	0.23	9.78E+03	1.64E+04	1.40E+04	9.66E+03	1.22E+04	1.34E+04	1.18E+04	1.27E+04	1.37E+04	9.00E+03	1.03E+04	1.01E+04	814.85285	2	44.38
HPC2	YBR215W	KENSSLSSIK	[4] Phospho (ST)	-4.20	-1.12	0.23	-3.08	0.023	0.091	0.352	0.00	7.54E+03	1.87E+03	6.81E+03	6.55E+02	4.26E+01	1.56E+02	2.93E+03	2.64E+03	1.88E+03	9.07E+03	5.85E+03	4.12E+03	586.78148	2	27.33
BUD3	YCL014W	DASYAYLK	[3] Phospho (ST)	0.18	1.72	0.79	-1.54	0.403	0.022	0.139	0.01	2.35E+02	3.21E+03	1.70E+03	2.07E+03	1.62E+03	2.13E+03	6.38E+03	7.01E+03	3.59E+03	3.82E+03	3.15E+03	1.98E+03	505.71532	2	26.97
INO80	YGL150C	NANLSDIINEK	[5] Phospho (ST)	-0.22	0.18	0.11	-0.40	0.312	0.191	0.177	0.19	4.62E+03	5.00E+03	5.87E+03	2.43E+03	6.87E+03	4.04E+03	5.12E+03	7.08E+03	5.39E+03	5.86E+03	5.58E+03	5.31E+03	655.80346	2	22.42
IES4	YOR189W	SQESSVLSESQEQLANNPK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.69	-1.04	-2.30	0.36	0.010	0.005	0.000	0.20	4.46E+04	4.83E+04	4.51E+04	2.59E+04	3.74E+04	2.24E+04	1.38E+04	3.08E+04	2.24E+04	8.63E+03	7.84E+03	1.16E+04	1098.9869	2	73.35
GIN4	YDR507C	LYDVGDSTIK	[7] Phospho (ST)	0.85	4.58	3.44	-3.74	0.267	0.001	0.010	0.00	1.16E+03	2.30E+02	3.24E+02	1.63E+02	7.16E+02	2.22E+03	1.72E+04	1.08E+04	1.37E+04	3.76E+03	9.02E+03	6.11E+03	595.77119	2	16.76
NCL1	YBL024W	LSSETPALESEGPQTK	[3] Phospho (ST)	-0.04	-0.13	-0.30	0.09	0.428	0.359	0.116	0.38	1.30E+04	1.85E+04	1.97E+04	1.59E+04	1.68E+04	1.73E+04	1.21E+04	1.28E+04	2.18E+04	1.20E+04	1.44E+04	1.52E+04	877.3961	2	29.35
EAP1	YKL204W	GPSSITDFLNLK	[3] Phospho (ST)	-4.30	-1.95	-0.63	-2.35	0.017	0.035	0.172	0.01	1.66E+04	3.87E+04	1.73E+04	1.34E+03	1.35E+03	9.61E+02	8.43E+03	5.50E+03	4.86E+03	1.31E+04	2.22E+04	1.16E+04	686.33178	2	50.28
YBR235W	YBR235W	RFSTIEPQTIAK	[3] Phospho (ST)	-0.44	0.28	-0.29	-0.72	0.240	0.328	0.348	0.11	3.53E+03	1.35E+04	1.05E+04	5.09E+03	7.91E+03	7.39E+03	1.63E+04	6.37E+03	1.09E+04	2.20E+03	1.07E+04	9.62E+03	735.87173	2	24.05
ETT1	YOR051C	KSDEPSRESTPVR	[6] Phospho (ST)	0.11	0.52	1.02	-0.41	0.442	0.243	0.035	0.27	9.45E+03	1.23E+03	8.76E+03	4.83E+03	4.82E+03	1.14E+04	1.36E+04	4.67E+03	9.62E+03	1.34E+04	1.19E+04	1.41E+04	784.35919	2	21.5
ESC1	YMR219W	VRNSDLEDDESLKK	[4] Phospho (ST)	-0.45	-0.28	-0.09	-0.18	0.013	0.101	0.364	0.26	4.18E+03	4.55E+03	4.57E+03	3.18E+03	2.70E+03	3.82E+03	4.60E+03	2.92E+03	3.43E+03	3.10E+03	3.80E+03	5.57E+03	576.60001	3	21.96
RCN2	YOR220W	GGSSLSPDK	[4] Phospho (ST)	1.79	-1.30	-1.49	3.09	0.022	0.071	0.058	0.01	5.35E+03	1.85E+03	3.07E+03	1.59E+04	6.72E+03	1.28E+04	1.06E+03	8.35E+02	2.25E+03	2.02E+03	8.01E+02	8.11E+02	464.19453	2	21.05

BCY1	YIL033C	TSTPPLPMHFNAQR	[3] Phospho (ST)	-0.03	0.22	0.22	-0.25	0.486	0.363	0.368	0.39	7.67E+03	1.38E+04	8.24E+03	7.55E+03	1.87E+04	2.91E+03	1.92E+04	9.56E+03	5.92E+03	3.87E+03	1.80E+04	1.27E+04	838.88469	2	18.48
MTC1	YJL123C	IFVDEWGHPNNNGITPVEK	[15] Phospho (ST)	0.54	0.39	0.07	0.15	0.089	0.113	0.442	0.28	6.95E+03	1.30E+04	8.48E+03	1.10E+04	1.74E+04	1.28E+04	1.24E+04	1.07E+04	1.40E+04	5.60E+03	1.23E+04	1.18E+04	749.35101	3	23.22
EAP1	YKL204W	SSTPNAESQLLSASDK	[3] Phospho (ST)	0.26	-0.66	-0.22	0.92	0.223	0.033	0.139	0.05	9.92E+03	9.39E+03	7.85E+03	1.48E+04	9.82E+03	7.96E+03	7.26E+03	6.48E+03	3.40E+03	6.31E+03	9.18E+03	7.78E+03	857.88088	2	46.73
RGA2	YDR379W	RPLSPTR	[4] Phospho (ST)	0.89	0.68	0.00	0.21	0.087	0.213	0.495	0.39	3.43E+03	4.10E+03	3.04E+03	4.79E+03	4.68E+03	1.01E+04	1.00E+04	1.89E+03	5.00E+03	3.23E+03	3.83E+03	3.49E+03	453.73136	2	19.32
ENA2	YDR039C	AHNPENDLESNNK	[10] Phospho (ST)	0.17	-1.88	-1.50	2.05	0.256	0.005	0.008	0.00	1.37E+04	7.84E+03	1.09E+04	1.16E+04	1.38E+04	1.10E+04	2.69E+03	2.53E+03	3.56E+03	4.55E+03	2.92E+03	3.99E+03	781.31828	2	31.96
FPK1	YNR047W	NLSNLSLNEIK	[6] Phospho (ST)	1.37	1.92	1.47	-0.55	0.159	0.005	0.026	0.20	4.19E+03	1.81E+03	1.57E+02	3.40E+02	9.31E+03	6.38E+03	6.77E+03	8.19E+03	8.51E+03	4.42E+03	6.46E+03	6.23E+03	662.82948	2	28.74
BUD3	YCL014W	DEPIWVSPSK	[7] Phospho (ST)	-0.16	1.11	0.84	-1.27	0.393	0.014	0.019	0.01	3.96E+03	9.36E+03	5.44E+03	3.49E+03	8.64E+03	4.68E+03	1.22E+04	1.64E+04	1.20E+04	1.13E+04	1.16E+04	1.07E+04	619.27914	2	26.15
DGR2	YKL121W	INNHNNDSILENR	[8] Phospho (ST)	-0.33	-0.42	-0.11	0.10	0.055	0.073	0.212	0.36	1.16E+04	1.06E+04	1.37E+04	1.06E+04	9.98E+03	8.08E+03	8.75E+03	6.58E+03	1.15E+04	1.06E+04	1.06E+04	1.20E+04	816.8601	2	19.71
PAF1	YBR279W	LLVYPESPETNADSSQLINSLYIK	[4] Phospho (Y)	-0.26	-0.17	-0.54	-0.09	0.280	0.346	0.171	0.39	2.85E+04	4.53E+04	2.07E+04	2.13E+04	3.42E+04	2.33E+04	3.56E+04	2.73E+04	2.08E+04	1.79E+04	3.25E+04	1.44E+04	925.45533	3	38.44
YPI1	YFR003C	SYSPNAYEIQPDYSEYR	[3] Phospho (ST)	-0.57	0.18	-0.92	-0.76	0.301	0.430	0.233	0.17	1.09E+04	5.29E+04	9.95E+03	1.42E+04	1.69E+04	1.85E+04	2.30E+04	4.81E+04	1.26E+04	8.91E+03	1.71E+04	1.31E+04	1081.4422	2	53.44
RGP1	YDR137W	RKSSIIDIDSPLEDNEFVK	[3] Phospho (ST)|[4] Phospho (ST)	0.21	-0.56	-0.68	0.77	0.335	0.216	0.173	0.04	7.28E+03	1.70E+04	6.67E+03	1.37E+04	1.18E+04	1.03E+04	5.24E+03	1.05E+04	5.28E+03	9.20E+03	5.78E+03	4.28E+03	789.03067	3	26.91
RXT2	YBR095C	GASDEDDINNK	[3] Phospho (ST)	0.15	-1.91	-0.71	2.06	0.424	0.104	0.257	0.01	1.19E+04	1.62E+03	5.02E+03	9.74E+03	5.54E+03	5.30E+03	1.61E+03	2.05E+03	1.24E+03	6.76E+03	2.65E+03	1.86E+03	629.23689	2	35.1
GAL11	YOL051W	DLSTLVHSSSPSTSSNMDVGNPR	[13] Phospho (ST)	-0.38	0.01	0.02	-0.39	0.282	0.486	0.486	0.27	8.20E+03	1.53E+04	1.07E+04	7.20E+03	1.58E+04	3.27E+03	1.43E+04	1.17E+04	8.42E+03	6.83E+03	1.65E+04	1.13E+04	823.36358	3	32.62
CBF1	YJR060W	DQGLLSQESNDGNIDSALLSEGATLK	[6] Phospho (ST)|[9] Phospho (ST)	0.14	-0.95	-2.11	1.09	0.377	0.057	0.013	0.03	9.11E+04	7.60E+04	3.93E+04	6.27E+04	1.05E+05	5.98E+04	2.70E+04	4.71E+04	3.26E+04	1.64E+04	1.31E+04	1.84E+04	945.75034	3	38.85
VTA1	YLR181C	EIGGESEAEDSDK	[6] Phospho (ST)	1.57	0.90	0.91	0.67	0.009	0.043	0.100	0.03	3.10E+03	1.02E+03	4.25E+03	1.05E+04	7.20E+03	7.27E+03	5.46E+03	4.25E+03	5.90E+03	7.52E+03	3.06E+03	5.13E+03	723.26888	2	40.92
RLF2	YPR018W	RSNSDLQAQTASQSQSPEKK	[16] Phospho (ST)	1.61	2.19	1.65	-0.58	0.001	0.000	0.004	0.00	3.28E+03	2.48E+03	2.19E+03	9.23E+03	6.96E+03	8.12E+03	1.17E+04	1.15E+04	1.31E+04	9.94E+03	6.24E+03	8.90E+03	757.35148	3	29.83
RPH1	YER169W	SSGVSSPLLSR	[6] Phospho (ST)	-0.58	0.03	-0.04	-0.61	0.015	0.434	0.445	0.01	5.54E+03	7.08E+03	5.26E+03	3.61E+03	4.35E+03	3.98E+03	5.43E+03	7.14E+03	5.72E+03	7.40E+03	4.94E+03	5.10E+03	585.28188	2	32.91
JJJ1	YNL227C	FDSADESVK	[3] Phospho (ST)	0.58	0.69	0.69	-0.11	0.043	0.080	0.033	0.36	2.44E+03	2.06E+03	3.94E+03	4.66E+03	4.04E+03	3.94E+03	3.36E+03	4.15E+03	6.16E+03	5.12E+03	4.64E+03	3.84E+03	539.21063	2	30.47
SAS4	YDR181C	NNAASISPTLSEK	[9] Phospho (ST)	-0.08	0.15	0.13	-0.23	0.427	0.358	0.373	0.10	1.52E+04	6.61E+03	8.22E+03	8.48E+03	9.14E+03	1.08E+04	1.09E+04	9.80E+03	1.26E+04	9.76E+03	1.22E+04	1.10E+04	706.32701	2	21.51
KIN2	YLR096W	NESEILER	[3] Phospho (ST)	1.32	0.95	0.72	0.36	0.004	0.031	0.030	0.08	1.26E+03	2.63E+03	3.25E+03	5.38E+03	5.68E+03	6.81E+03	3.65E+03	4.36E+03	5.86E+03	4.06E+03	3.96E+03	3.74E+03	535.23205	2	30.2
SLA1	YBL007C	TGGFVVPQTTFGMQSQVTGGILPVQK	[1] Phospho (ST)|[15] Phospho (ST)	-0.67	0.35	-0.24	-1.02	0.224	0.279	0.368	0.02	2.87E+04	1.05E+05	4.12E+04	2.96E+04	5.73E+04	2.28E+04	7.77E+04	8.51E+04	5.97E+04	4.57E+04	6.59E+04	3.60E+04	946.45129	3	20.12
YBR235W	YBR235W	RISQTYFNYQATPECQK	[3] Phospho (ST)	0.21	-0.12	-0.65	0.32	0.327	0.372	0.124	0.19	1.77E+04	3.73E+04	3.86E+04	2.66E+04	3.11E+04	5.04E+04	2.76E+04	3.11E+04	2.77E+04	1.02E+04	2.18E+04	2.74E+04	1107.491	2	27.93
TIF4632	YGL049C	EATPVLPANEAVK	[3] Phospho (ST)	-1.34	2.07	0.32	-3.40	0.122	0.030	0.362	0.01	7.54E+03	2.65E+03	1.86E+03	1.67E+03	1.26E+03	1.83E+03	2.58E+04	1.04E+04	1.45E+04	2.18E+03	4.10E+03	8.76E+03	709.85116	2	17.25
TGL1	YKL140W	THSADRSPLSVQADEADEVHNADNSR	[3] Phospho (ST)|[7] Phospho (ST)	-0.61	-2.97	-1.33	2.36	0.117	0.007	0.031	0.01	3.33E+04	1.64E+04	2.37E+04	2.31E+04	1.20E+04	1.31E+04	5.81E+03	2.30E+03	1.27E+03	1.58E+04	6.57E+03	6.78E+03	994.41287	3	22.86
PUF4	YGL014W	RQTFHALSPTDLINAANNVTLSK	[10] Phospho (ST)	0.50	0.03	0.13	0.47	0.134	0.487	0.416	0.24	8.51E+03	2.18E+04	1.13E+04	2.04E+04	2.25E+04	1.60E+04	2.71E+04	5.26E+03	1.01E+04	1.24E+04	2.30E+04	1.01E+04	648.58072	4	30.58
ASK10	YGR097W	STSAGNSITANAPVVPK	[2] Phospho (ST)	-0.92	-0.48	-0.34	-0.44	0.002	0.010	0.023	0.04	1.75E+04	2.06E+04	2.07E+04	1.26E+04	8.24E+03	1.02E+04	1.23E+04	1.60E+04	1.37E+04	1.65E+04	1.64E+04	1.35E+04	847.41253	2	54.27
VRP1	YLR337C	SSNISLPSVSAPPLPSASLPTHVSNPPQAPPPPPTPTIGLDSK	[10] Phospho (ST)|[16] Phospho (ST)	0.35	0.46	0.12	-0.11	0.228	0.067	0.374	0.39	4.17E+04	3.68E+04	2.57E+04	4.21E+04	6.39E+04	2.72E+04	5.03E+04	5.53E+04	3.80E+04	4.93E+04	4.11E+04	2.32E+04	1103.2998	4	38.91
SHP1	YBL058W	AINTEHVGGLCPKPGSSQGSNEYLK	[20] Phospho (ST)|[23] Phospho (Y)	1.92	0.31	-0.80	1.60	0.000	0.279	0.011	0.00	6.58E+03	7.95E+03	5.45E+03	2.61E+04	2.78E+04	2.17E+04	7.02E+03	1.30E+04	4.84E+03	4.34E+03	3.46E+03	3.65E+03	935.07739	3	16.89
TAT1	YBR069C	MDDSVSFIAK	[N-term] Acetyl (Protein N-term)|[6] Phospho	-0.14	-0.31	0.06	0.17	0.425	0.223	0.457	0.42	1.49E+04	2.31E+04	1.33E+04	1.23E+04	2.92E+04	5.01E+03	1.65E+04	1.59E+04	8.97E+03	1.11E+04	2.90E+04	1.33E+04	617.75753	2	18.87
CTF4	YPR135W	KNEIGADTEAEEGEEDK	[8] Phospho (ST)	1.93	-0.23	0.48	2.17	0.004	0.208	0.045	0.00	5.37E+03	5.25E+03	7.29E+03	2.20E+04	1.73E+04	2.93E+04	6.06E+03	3.68E+03	5.52E+03	6.80E+03	8.53E+03	9.64E+03	972.39182	2	47.58
PIB2	YGL023C	TLPFTDDQRSNPELDPTNSVVDVSR	[5] Phospho (ST)	0.35	0.44	-0.26	-0.09	0.259	0.209	0.350	0.38	1.18E+04	3.58E+04	1.58E+04	2.33E+04	3.37E+04	2.38E+04	3.60E+04	2.40E+04	2.58E+04	1.26E+04	2.56E+04	1.48E+04	961.4479	3	16.64
VHS2	YIL135C	TVSNNAANSLSR	[3] Phospho (ST)	-0.58	-1.98	-1.21	1.40	0.060	0.006	0.008	0.02	7.98E+03	4.96E+03	7.49E+03	5.66E+03	4.63E+03	3.38E+03	3.16E+03	1.24E+03	7.58E+02	3.27E+03	2.86E+03	2.70E+03	657.29473	2	45.3
TAE2	YPL009C	HCTISSDTDSDSGNAK	[5] Phospho (ST)|[10] Phospho (ST)	0.00	-0.69	-0.13	0.69	0.498	0.240	0.436	0.17	2.26E+04	4.83E+03	1.04E+04	1.25E+04	1.75E+04	7.67E+03	2.54E+03	1.39E+04	6.88E+03	1.93E+04	8.63E+03	6.52E+03	927.81768	2	24.91
IES1	YFL013C	SGSQEEASPSSIQSETETVTTK	[3] Phospho (ST)	0.99	-0.66	-1.04	1.65	0.009	0.109	0.014	0.01	1.24E+04	2.01E+04	1.58E+04	3.20E+04	3.78E+04	2.60E+04	4.24E+03	1.60E+04	1.03E+04	6.68E+03	1.00E+04	6.78E+03	1182.0099	2	78.19
ARG82	YDR173C	LSDSTDNLDSIPVK	[4] Phospho (ST)	0.23	0.49	0.44	-0.25	0.239	0.045	0.056	0.11	5.73E+03	1.01E+04	1.04E+04	8.48E+03	1.27E+04	9.68E+03	1.15E+04	1.24E+04	1.29E+04	1.25E+04	1.19E+04	1.13E+04	792.36399	2	35.25
BUL1	YMR275C	SSSTSNLENLIPLR	[2] Phospho (ST)	-0.38	0.46	-0.19	-0.84	0.191	0.191	0.354	0.07	9.53E+03	1.40E+04	6.85E+03	7.49E+03	9.93E+03	5.96E+03	1.39E+04	1.95E+04	8.36E+03	8.77E+03	1.28E+04	5.13E+03	805.89452	2	45.36
EDE1	YBL047C	ANSNEDGESVSSIQESPK	[16] Phospho (ST)	-0.39	0.53	0.27	-0.92	0.069	0.159	0.085	0.07	9.22E+03	8.17E+03	1.20E+04	8.53E+03	6.89E+03	7.00E+03	7.57E+03	1.47E+04	2.03E+04	1.25E+04	1.10E+04	1.19E+04	979.40729	2	25.09
SKG6	YHR149C	SIYQVYLDR	[1] Phospho (ST)	-0.88	-0.39	-1.18	-0.49	0.173	0.309	0.125	0.15	3.77E+03	1.45E+04	5.75E+03	3.50E+03	6.26E+03	3.27E+03	6.08E+03	8.13E+03	4.12E+03	2.54E+03	4.54E+03	3.46E+03	618.78687	2	34.52
YGL114W	YGL114W	PQSTPSQEVQR	[4] Phospho (ST)	0.19	-0.01	0.27	0.20	0.260	0.486	0.176	0.11	7.10E+03	3.59E+03	5.56E+03	6.82E+03	5.60E+03	6.12E+03	4.66E+03	5.39E+03	6.07E+03	6.74E+03	5.92E+03	6.95E+03	668.79828	2	33.53
MNR2	YKL064W	SLVSDLSPSELESWLK	[7] Phospho (ST)	-0.18	0.31	-0.29	-0.49	0.400	0.324	0.346	0.13	1.00E+04	3.07E+04	9.53E+03	1.39E+04	1.81E+04	1.25E+04	2.82E+04	2.08E+04	1.34E+04	1.29E+04	1.67E+04	1.15E+04	935.44883	2	34.25
SSD1	YDR293C	TSSQSSIYGHSR	[3] Phospho (ST)	0.86	0.30	1.31	0.55	0.143	0.360	0.176	0.21	3.53E+02	2.99E+03	3.87E+03	6.73E+03	3.18E+03	3.17E+03	1.87E+03	4.99E+03	2.05E+03	1.25E+04	3.12E+03	2.39E+03	463.86482	3	15.37
NUP60	YAR002W	GFVFNSVQK	[6] Phospho (ST)	0.15	1.99	1.31	-1.84	0.397	0.001	0.022	0.00	1.60E+03	4.41E+03	1.77E+03	2.45E+03	3.84E+03	2.36E+03	9.76E+03	1.10E+04	1.02E+04	5.62E+03	8.35E+03	5.36E+03	553.25795	2	20.01
NPR1	YNL183C	SQHSSIGDLK	[5] Phospho (ST)	0.47	0.42	0.38	0.04	0.269	0.302	0.308	0.45	9.32E+01	1.77E+03	3.48E+03	2.51E+03	1.95E+03	2.94E+03	1.46E+03	2.69E+03	3.04E+03	2.46E+03	1.95E+03	2.56E+03	576.25823	2	16.45
SEC7	YDR170C	GDGEISSNVETASSVNPSVKPQNAIK	[7] Phospho (ST)	-0.13	-0.05	-0.44	-0.08	0.302	0.419	0.092	0.37	7.38E+03	1.12E+04	1.06E+04	1.07E+04	8.44E+03	7.36E+03	7.49E+03	9.59E+03	1.10E+04	5.23E+03	8.95E+03	7.26E+03	903.43055	3	32.42
KSP1	YHR082C	SPASSEAHLNLSSGPIDPILTGNIGNR	[4] Phospho (ST)	-0.04	0.16	0.22	-0.20	0.467	0.332	0.332	0.27	1.46E+04	2.16E+04	9.18E+03	1.24E+04	2.08E+04	1.10E+04	1.80E+04	1.84E+04	1.44E+04	1.35E+04	2.53E+04	1.41E+04	933.12362	3	23.85
IGO1	YNL157W	YFDSGDYALQK	[4] Phospho (ST)	1.24	0.48	-0.76	0.77	0.012	0.180	0.168	0.00	1.89E+03	8.25E+03	5.07E+03	1.28E+04	1.25E+04	1.07E+04	8.02E+03	7.07E+03	6.07E+03	2.10E+03	3.61E+03	3.28E+03	693.78469	2	45.71
SLK19	YOR195W	NDSFNINTDTLK	[3] Phospho (ST)	-1.17	-0.11	0.68	-1.06	0.053	0.398	0.110	0.00	3.16E+03	8.96E+03	7.67E+03	3.09E+03	2.66E+03	3.01E+03	5.94E+03	6.59E+03	5.79E+03	8.15E+03	1.48E+04	8.81E+03	731.31701	2	38.11
RPC19	YNL113W	TATEVTPQEPK	[6] Phospho (ST)	0.22	-0.89	-0.48	1.11	0.138	0.099	0.054	0.04	5.05E+03	7.62E+03	6.20E+03	7.24E+03	7.94E+03	6.78E+03	6.82E+03	1.30E+03	2.05E+03	5.28E+03	3.70E+03	4.50E+03	640.79221	2	18.56
FLC2	YAL053W	NKNDSELFELR	[5] Phospho (ST)	0.30	0.00	0.24	0.30	0.258	0.498	0.290	0.25	4.96E+03	9.93E+03	7.44E+03	5.87E+03	1.25E+04	9.07E+03	5.73E+03	9.96E+03	6.62E+03	5.29E+03	1.03E+04	1.08E+04	722.82741	2	19.91
GIN4	YDR507C	NRESLISVTSSR	[4] Phospho (ST)	-0.35	-1.01	-0.82	0.66	0.081	0.009	0.024	0.00	4.88E+03	7.62E+03	6.33E+03	4.86E+03	4.87E+03	5.02E+03	3.11E+03	2.78E+03	3.44E+03	2.47E+03	3.97E+03	4.21E+03	714.84606	2	24.95
MSN4	YKL062W	RGSTISPTTTINNSNPNFK	[4] Phospho (ST)|[6] Phospho (ST)	-0.80	-0.33	-0.87	-0.46	0.007	0.203	0.002	0.19	2.35E+04	2.62E+04	3.03E+04	1.48E+04	1.87E+04	1.26E+04	1.04E+04	2.90E+04	2.41E+04	1.34E+04	1.56E+04	1.46E+04	1104.9887	2	22.58
APL1	YJR005W	KPSTLLR	[3] Phospho (ST)	-0.59	0.10	0.17	-0.69	0.260	0.438	0.395	0.15	3.39E+03	1.12E+03	5.88E+03	9.63E+02	1.90E+03	4.03E+03	5.12E+03	2.59E+03	3.46E+03	2.83E+03	4.83E+03	4.00E+03	447.74393	2	28.45
HPC2	YBR215W	SSSASAILPKPTTTK	[2] Phospho (ST)	-3.52	-4.72	-1.80	1.20	0.008	0.006	0.021	0.30	2.36E+04	4.23E+04	2.27E+04	7.50E+03	0.00E+00	2.14E+02	1.56E+03	1.60E+03	1.79E+02	1.49E+04	5.71E+03	4.85E+03	784.90073	2	41.59
IFH1	YLR223C	SVKLSPK	[5] Phospho (ST)	0.78	0.43	0.11	0.35	0.014	0.070	0.344	0.04	8.34E+02	1.43E+03	1.53E+03	2.10E+03	1.94E+03	2.50E+03	1.91E+03	1.53E+03	1.69E+03	1.23E+03	1.41E+03	1.44E+03	419.72506	2	18.05
FAS2	YPL231W	STVQNEILGDLGK	[2] Phospho (ST)	0.22	-0.10	0.71	0.33	0.268	0.415	0.069	0.22	4.72E+03	4.10E+03	7.55E+03	6.07E+03	7.99E+03	5.08E+03	6.20E+03	6.41E+03	2.66E+03	6.34E+03	1.17E+04	8.72E+03	727.35098	2	36.98
SHP1	YBL058W	PGSSQGSNEYLK	[4] Phospho (ST)	3.26	1.15	0.29	2.10	0.000	0.069	0.342	0.00	7.52E+02	7.82E+02	2.72E+03	1.51E+04	1.40E+04	1.19E+04	2.95E+03	2.11E+03	4.44E+03	1.78E+03	2.31E+03	1.13E+03	673.78493	2	33.03
SUP35	YDR172W	GVEEEDISPGFVLTSPK	[15] Phospho (ST)	0.72	0.21	-0.07	0.52	0.028	0.356	0.443	0.15	1.38E+04	2.14E+04	1.76E+04	2.56E+04	3.65E+04	2.52E+04	3.32E+04	1.44E+04	1.34E+04	1.00E+04	2.69E+04	1.33E+04	942.43767	2	22.16
ENP2	YGR145W	RHDNSSDEEGIDENGNK	[5] Phospho (ST)|[6] Phospho (ST)	0.48	-0.65	-0.33	1.13	0.181	0.145	0.256	0.05	1.23E+04	6.48E+03	1.60E+04	1.47E+04	2.27E+04	1.10E+04	3.69E+03	1.08E+04	7.64E+03	1.24E+04	6.00E+03	9.20E+03	692.58257	3	22.57
TAF2	YCR042C	EKEDTPEHDEEEEGKPAR	[5] Phospho (ST)	0.00	0.04	-0.70	-0.04	0.495	0.463	0.114	0.44	1.12E+04	5.89E+03	4.92E+03	6.66E+03	6.46E+03	8.93E+03	8.53E+03	5.78E+03	8.30E+03	3.94E+03	4.50E+03	5.11E+03	735.63329	3	16.58
ABF1	YKL112W	SNSIDYAK	[1] Phospho (ST)	-3.79	-1.13	-2.32	-2.66	0.157	0.276	0.192	0.08	1.60E+04	1.88E+02	2.26E+03	1.00E+03	2.42E+02	6.10E+01	2.21E+02	4.90E+03	3.32E+03	3.04E+03	5.96E+02	3.44E+01	489.20226	2	28.01
BUD2	YKL092C	DLDSPIEVKPEIGELEFEK	[4] Phospho (ST)	0.17	0.08	-0.20	0.10	0.372	0.439	0.381	0.40	7.39E+03	1.87E+04	8.84E+03	9.54E+03	1.77E+04	1.22E+04	1.61E+04	9.91E+03	1.09E+04	5.22E+03	1.53E+04	9.84E+03	756.36479	3	41.61
LTE1	YAL024C	SLLIER	[1] Phospho (ST)	-0.38	0.22	-0.26	-0.60	0.129	0.220	0.205	0.02	4.02E+03	5.75E+03	7.00E+03	3.94E+03	3.77E+03	5.21E+03	6.88E+03	5.25E+03	7.40E+03	3.67E+03	5.26E+03	5.09E+03	405.70962	2	24.49
NTH1	YDR001C	RLSSLSEFNDPFSNAEVYYGPPTDPR	[6] Phospho (ST)	0.44	0.04	0.25	0.40	0.260	0.483	0.395	0.29	5.41E+03	1.98E+04	6.60E+03	8.79E+03	1.71E+04	1.74E+04	2.07E+04	6.67E+03	5.33E+03	7.17E+03	2.32E+04	7.49E+03	760.34563	4	17.89
SIP1	YDR422C	GNAGGSNDDFTAPISATAK	[6] Phospho (ST)	-0.48	-0.81	-0.18	0.33	0.083	0.003	0.091	0.20	2.62E+04	2.50E+04	2.08E+04	1.90E+04	2.25E+04	1.02E+04	1.32E+04	1.57E+04	1.21E+04	2.24E+04	2.09E+04	1.99E+04	937.40485	2	50.1
SDA1	YGR245C	EENFEENSEDEDGFDLDALR	[8] Phospho (ST)	-1.01	-0.76	-0.30	-0.25	0.041	0.065	0.285	0.19	3.42E+04	3.94E+04	1.84E+04	1.21E+04	1.94E+04	1.41E+04	1.78E+04	2.17E+04	1.47E+04	1.09E+04	3.07E+04	3.29E+04	818.31618	3	24.92
PIN2	YOR104W	VAPLVYEEENFEGSSPQPQYDAR	[15] Phospho (ST)	0.24	0.44	-0.32	-0.20	0.299	0.146	0.213	0.31	4.55E+03	9.57E+03	8.02E+03	5.87E+03	1.22E+04	8.12E+03	8.04E+03	1.32E+04	8.84E+03	4.56E+03	7.29E+03	5.82E+03	677.05061	4	20.02
IGD1	YFR017C	STNYMDALNSR	[2] Phospho (ST)	0.46	1.30	0.91	-0.83	0.303	0.049	0.077	0.16	3.32E+03	4.42E+03	2.93E+03	3.37E+03	9.61E+03	1.76E+03	6.19E+03	1.35E+04	6.56E+03	4.38E+03	1.01E+04	5.64E+03	676.2723	2	34.97
NET1	YJL076W	VRPSLSSLSDLVSR	[7] Phospho (ST)	-0.03	0.61	0.91	-0.64	0.486	0.242	0.154	0.18	8.84E+02	7.68E+03	3.07E+03	2.25E+03	5.98E+03	3.14E+03	9.39E+03	3.85E+03	4.53E+03	3.35E+03	1.06E+04	7.88E+03	532.61051	3	44.91
RGA2	YDR379W	ENEIIVNTPR	[8] Phospho (ST)	0.63	0.80	0.24	-0.17	0.066	0.058	0.376	0.26	1.89E+03	5.10E+03	5.26E+03	5.86E+03	5.88E+03	7.17E+03	8.51E+03	5.06E+03	7.77E+03	9.63E+02	7.06E+03	6.48E+03	632.8008	2	16.76
MAP2	YBL091C	TDAEIENSPASDLK	[N-term] Acetyl (Protein N-term)|[1] Phospho	-0.03	-1.08	-0.15	1.05	0.455	0.022	0.271	0.04	1.02E+04	1.30E+04	1.10E+04	1.03E+04	1.41E+04	9.23E+03	4.84E+03	8.94E+03	2.43E+03	1.08E+04	1.25E+04	7.53E+03	806.34346	2	19.28
DNF2	YDR093W	DQLSPVTTTNNLPR	[4] Phospho (ST)	-0.49	-0.61	-0.24	0.12	0.030	0.020	0.185	0.19	1.07E+04	1.53E+04	1.24E+04	8.56E+03	1.00E+04	8.67E+03	8.10E+03	9.49E+03	7.47E+03	9.38E+03	1.37E+04	9.37E+03	818.3907	2	52.41
BUL2	YML111W	ASDSQDDDIRSASTTNLDR	[13] Phospho (ST)	-0.34	-0.77	-0.07	0.43	0.120	0.024	0.429	0.07	1.68E+04	1.12E+04	1.21E+04	1.09E+04	8.55E+03	1.23E+04	8.18E+03	6.09E+03	9.33E+03	1.31E+04	7.88E+03	1.74E+04	1073.9472	2	26.31
BOP3	YNL042W	NLSLPIGK	[3] Phospho (ST)	-0.49	-0.04	-0.05	-0.45	0.136	0.429	0.438	0.10	3.81E+03	6.05E+03	4.15E+03	2.45E+03	4.91E+03	2.61E+03	4.58E+03	4.61E+03	4.41E+03	3.95E+03	5.97E+03	3.58E+03	461.24388	2	21
RLM1	YPL089C	SSKISPLSASASGPLTLQK	[8] Phospho (ST)|[10] Phospho (ST)	-0.48	-0.49	-0.45	0.01	0.126	0.265	0.147	0.49	9.83E+03	1.81E+04	1.06E+04	8.06E+03	9.16E+03	1.04E+04	4.23E+03	1.86E+04	4.56E+03	1.15E+04	8.79E+03	8.02E+03	677.99708	3	18.9
SET2	YJL168C	SNTQVNSPSSSGIPK	[7] Phospho (ST)	-0.62	-0.10	-0.45	-0.52	0.011	0.396	0.148	0.13	4.75E+03	6.33E+03	6.43E+03	4.09E+03	3.70E+03	3.62E+03	4.01E+03	7.97E+03	4.37E+03	6.55E+03	3.69E+03	2.58E+03	791.85912	2	25.65
TPK1	YJL164C	SLDDRQGEESQK	[1] Phospho (ST)	1.16	-0.18	0.31	1.34	0.022	0.374	0.323	0.01	5.60E+03	2.35E+03	2.87E+03	8.95E+03	5.77E+03	9.57E+03	4.50E+03	2.10E+03	2.94E+03	7.31E+03	2.95E+03	3.15E+03	736.30615	2	26.28
SPE4	YLR146C	VNNSQHPYIK	[4] Phospho (ST)	2.20	2.32	0.15	-0.12	0.075	0.005	0.436	0.43	1.73E+03	5.09E+01	1.14E+03	2.47E+03	2.68E+03	8.33E+03	4.10E+03	4.31E+03	6.27E+03	1.50E+03	1.42E+03	3.16E+02	640.29565	2	17.85
ALE1	YOR175C	KMSFSGYSPK	[3] Phospho (ST)	0.06	4.30	5.24	-4.25	0.468	0.002	0.002	0.00	0.00E+00	5.05E+02	5.03E+02	4.40E+02	2.64E+02	3.49E+02	7.56E+03	8.09E+03	4.86E+03	9.20E+03	1.65E+04	1.36E+04	606.26275	2	46.47
NTH1	YDR001C	RGSEDDTYSSSQGNR	[8] Phospho (Y)	0.86	-1.38	-0.71	2.24	0.085	0.143	0.228	0.00	6.34E+03	2.15E+03	1.50E+03	6.85E+03	4.84E+03	6.51E+03	5.74E+02	5.69E+02	2.68E+03	2.59E+03	1.26E+03	2.27E+03	580.22692	3	26.23
BNI1	YNL271C	SLPENSTASAASAFDK	[1] Phospho (ST)	-0.53	-0.51	-0.43	-0.02	0.016	0.010	0.051	0.46	1.17E+04	1.38E+04	1.25E+04	9.21E+03	1.03E+04	6.74E+03	9.68E+03	9.71E+03	7.28E+03	9.09E+03	1.20E+04	7.14E+03	838.36485	2	95.28
YPR089W	YPR089W	TNSGTSDFTGDEDK	[3] Phospho (ST)|[6] Phospho (ST)	-0.40	-0.21	-0.29	-0.19	0.204	0.378	0.288	0.38	8.71E+03	3.73E+03	9.58E+03	6.50E+03	5.80E+03	4.38E+03	3.75E+03	1.11E+04	4.21E+03	8.37E+03	4.81E+03	4.88E+03	817.26933	2	23.39
SSN2	YDR443C	SVFAPLNFNPIIENNVDNK	[1] Phospho (ST)	-0.23	0.54	0.30	-0.77	0.320	0.074	0.235	0.05	1.09E+04	1.85E+04	1.06E+04	1.01E+04	1.70E+04	7.03E+03	2.31E+04	1.96E+04	1.55E+04	1.38E+04	2.24E+04	1.32E+04	742.36046	3	34.65
YMR124W	YMR124W	RGDITSAGSTSGEDSSQPK	[9] Phospho (ST)	0.43	-0.17	0.07	0.60	0.002	0.323	0.410	0.06	7.33E+03	7.61E+03	6.65E+03	9.31E+03	1.02E+04	9.55E+03	5.57E+03	4.09E+03	9.49E+03	1.05E+04	6.05E+03	6.11E+03	980.41939	2	16.33
HXT5	YHR096C	PVSSYISHEGPPKDELEELQK	[7] Phospho (ST)	-0.61	0.11	0.67	-0.71	0.072	0.397	0.159	0.09	9.97E+03	1.38E+04	8.26E+03	6.77E+03	9.18E+03	5.06E+03	1.61E+04	7.89E+03	1.05E+04	6.87E+03	2.47E+04	1.94E+04	821.38888	3	36.7

SFL1	YOR140W	RKGSGVYSLLNQEDSSTSSADPK	[7] Phospho (Y)	0.55	-0.50	-0.77	1.06	0.082	0.180	0.051	0.03	1.00E+04	1.85E+04	1.16E+04	2.44E+04	1.90E+04	1.54E+04	1.38E+04	1.03E+04	4.21E+03	8.58E+03	6.87E+03	7.99E+03	836.05442	3	45.61
RPL22A	YLR061W	LAFYQVTPEEDEEEDEE	[4] Phospho (Y)	2.29	1.74	0.57	0.55	0.012	0.000	0.053	0.11	1.11E+04	1.81E+04	8.69E+03	5.05E+04	8.92E+04	4.58E+04	4.29E+04	4.35E+04	4.04E+04	1.93E+04	1.95E+04	1.72E+04	1076.4141	2	16.75
ACC1	YNR016C	AVSVSDLSYVANSQSSPLR	[8] Phospho (ST)	-0.26	0.04	-0.65	-0.30	0.323	0.467	0.154	0.23	1.08E+04	1.96E+04	2.86E+04	9.90E+03	2.40E+04	1.53E+04	1.96E+04	1.65E+04	2.44E+04	8.53E+03	1.89E+04	1.03E+04	1030.4906	2	61.09
AGP1	YCL025C	SLYELK	[1] Phospho (ST)	-1.01	-0.64	-1.21	-0.37	0.025	0.062	0.019	0.06	4.08E+03	7.29E+03	7.45E+03	2.95E+03	2.74E+03	3.66E+03	4.49E+03	4.31E+03	3.27E+03	2.73E+03	3.41E+03	2.00E+03	416.69615	2	21.22
SNC1	YAL030W	LTSIEDK	[3] Phospho (ST)	0.37	0.19	0.34	0.18	0.321	0.415	0.344	0.26	4.29E+02	1.24E+03	4.31E+03	2.62E+03	2.41E+03	2.75E+03	1.72E+03	2.02E+03	3.11E+03	3.34E+03	2.24E+03	2.03E+03	443.20181	2	22
YPL260W	YPL260W	NSSPAYDEDGNDDRLR	[3] Phospho (ST)	1.15	0.60	0.43	0.55	0.003	0.049	0.214	0.00	2.63E+03	2.02E+03	4.33E+03	6.79E+03	6.55E+03	6.61E+03	4.44E+03	4.93E+03	4.25E+03	5.93E+03	2.87E+03	3.31E+03	635.25381	3	25.81
YPK1	YKL126W	GTINPSNSSVVPVR	[6] Phospho (ST)	-0.21	0.11	0.30	-0.32	0.173	0.253	0.058	0.01	8.89E+03	1.23E+04	1.27E+04	9.50E+03	1.12E+04	8.69E+03	1.22E+04	1.21E+04	1.22E+04	1.44E+04	1.41E+04	1.31E+04	753.87025	2	24.48
HYP2	YEL034W	MSDEEHTFETADAGSSATYPMQCSALRK	[7] Phospho (ST)	-3.39	-2.01	-0.59	-1.37	0.029	0.050	0.212	0.09	4.53E+04	1.86E+04	1.69E+04	4.10E+03	3.04E+03	5.56E+02	8.67E+03	9.35E+03	1.98E+03	1.48E+04	2.64E+04	1.24E+04	800.83045	4	24.22
PHO4	YFR034C	SSGALVDDDKR	[1] Phospho (ST)	-2.33	0.23	-1.09	-2.56	0.102	0.396	0.194	0.02	1.04E+04	1.63E+03	3.34E+03	1.56E+03	5.27E+02	9.49E+02	3.41E+03	5.95E+03	8.69E+03	3.54E+03	2.81E+03	8.81E+02	621.77205	2	32.81
TFG1	YGR186W	DEEAPSENEEDELFGEK	[6] Phospho (ST)	0.09	0.27	-0.27	-0.18	0.392	0.073	0.286	0.26	1.81E+04	2.27E+04	1.73E+04	1.62E+04	2.78E+04	1.76E+04	2.34E+04	2.58E+04	2.08E+04	6.65E+03	2.42E+04	1.72E+04	1023.8899	2	39.9
VPS27	YNR006W	LTLSNSPTAMFDSK	[6] Phospho (ST)	-0.03	0.59	0.43	-0.62	0.487	0.079	0.230	0.19	6.35E+03	1.08E+04	7.77E+03	7.38E+03	1.52E+04	1.91E+03	1.64E+04	1.18E+04	9.38E+03	6.24E+03	1.74E+04	9.90E+03	796.35825	2	39.3
SCS2	YER120W	AVADVWSDLEAEFK	[7] Phospho (ST)	-0.19	0.05	-0.62	-0.24	0.371	0.463	0.163	0.31	8.86E+03	1.56E+04	5.54E+03	6.95E+03	1.24E+04	6.92E+03	1.51E+04	7.88E+03	8.13E+03	4.76E+03	8.33E+03	6.36E+03	830.37073	2	48.11
NET1	YJL076W	EGPSSPASILPAK	[5] Phospho (ST)	0.41	0.88	0.68	-0.47	0.254	0.060	0.071	0.14	2.23E+03	8.30E+03	5.51E+03	3.75E+03	9.06E+03	8.54E+03	1.25E+04	9.58E+03	7.47E+03	8.58E+03	8.06E+03	9.12E+03	667.32292	2	16.7
IGD1	YFR017C	TDPHLNTPQVSTSPTFER	[N-term] Acetyl (Protein N-term)|[12] Phosph	2.10	1.66	1.14	0.44	0.000	0.002	0.051	0.00	4.43E+03	8.31E+03	2.93E+03	2.19E+04	2.23E+04	2.31E+04	1.80E+04	1.70E+04	1.48E+04	7.43E+03	1.60E+04	1.11E+04	1074.9833	2	18.47
AFR1	YDR085C	RNSLPDSSFDK	[3] Phospho (ST)	-0.10	0.36	-0.17	-0.46	0.387	0.056	0.295	0.11	3.84E+03	4.61E+03	4.83E+03	2.42E+03	4.38E+03	5.58E+03	5.90E+03	4.65E+03	6.49E+03	2.71E+03	3.78E+03	5.34E+03	673.29327	2	17.95
RPS11A	YDR025W	STELTVQSER	[N-term] Acetyl (Protein N-term)|[2] Phospho	0.03	-0.63	0.14	0.66	0.457	0.105	0.325	0.05	5.10E+03	6.16E+03	9.28E+03	8.10E+03	6.15E+03	6.77E+03	5.27E+03	5.64E+03	2.37E+03	8.34E+03	8.07E+03	6.21E+03	636.27974	2	25.71
SFK1	YKL051W	SFNQDYNTVDELPWYK	[1] Phospho (ST)	0.38	0.63	-0.28	-0.24	0.252	0.108	0.294	0.30	5.20E+03	1.03E+04	4.74E+03	7.41E+03	1.31E+04	5.94E+03	1.11E+04	1.31E+04	7.09E+03	3.84E+03	7.13E+03	5.72E+03	700.29871	3	18.87
GPR1	YDL035C	TNTGSDENVSASGGVR	[5] Phospho (ST)	-0.15	0.04	-0.27	-0.19	0.358	0.461	0.290	0.23	8.29E+03	3.44E+03	7.24E+03	6.11E+03	4.47E+03	6.50E+03	5.32E+03	6.23E+03	7.93E+03	7.29E+03	4.12E+03	4.31E+03	815.83952	2	58.15
ALF1	YNL148C	DEESAEVEDVHDDVESDDEI	[16] Phospho (ST)	-0.88	-0.08	-0.60	-0.80	0.129	0.439	0.083	0.19	2.38E+04	3.36E+04	1.77E+04	3.27E+03	2.78E+04	9.92E+03	1.61E+04	3.74E+04	1.76E+04	1.71E+04	1.27E+04	1.97E+04	1178.4298	2	26.05
KCC4	YCL024W	NASGLGLYQR	[3] Phospho (ST)	-0.28	-0.08	-0.60	-0.20	0.079	0.427	0.011	0.32	4.42E+03	6.15E+03	5.35E+03	4.35E+03	4.74E+03	4.06E+03	2.89E+03	4.88E+03	7.35E+03	3.54E+03	3.41E+03	3.57E+03	579.76945	2	32.94
AHP1	YLR109W	VIITGAPAAFSPTCTVSHIPGYINYLDELVK	[22] Phospho (Y)	-0.34	-1.26	-0.93	0.92	0.314	0.123	0.156	0.10	4.50E+04	9.36E+04	2.42E+04	3.68E+04	5.64E+04	3.56E+04	4.33E+04	1.89E+04	5.96E+03	2.27E+04	4.56E+04	1.70E+04	1142.906	3	17.73
BAP2	YBR068C	SFSAGNNFQSSSSEK	[3] Phospho (ST)	0.06	-0.29	0.00	0.34	0.416	0.119	0.496	0.13	8.49E+03	1.02E+04	1.20E+04	1.01E+04	8.30E+03	1.35E+04	6.98E+03	9.99E+03	8.10E+03	1.03E+04	1.06E+04	9.80E+03	828.83143	2	42.46
NUP145	YGL092W	STSPNEIFSPSYSK	[2] Phospho (ST)	-0.29	0.26	-0.74	-0.55	0.296	0.321	0.135	0.12	5.85E+03	1.51E+04	7.68E+03	6.27E+03	9.60E+03	7.57E+03	1.15E+04	1.56E+04	7.24E+03	4.37E+03	7.57E+03	5.25E+03	812.35076	2	27.98
SHP1	YBL058W	LGSPIPGESSPAEVPK	[3] Phospho (ST)	1.08	1.21	0.54	-0.13	0.027	0.023	0.155	0.33	9.47E+02	4.05E+03	3.39E+03	5.01E+03	7.26E+03	5.50E+03	7.55E+03	4.71E+03	7.14E+03	3.07E+03	4.08E+03	5.08E+03	548.93476	3	26.12
PGK1	YCR012W	ISHVSTGGGASLELLEGK	[6] Phospho (ST)	-0.22	0.36	0.32	-0.58	0.229	0.209	0.169	0.11	3.72E+03	6.15E+03	5.18E+03	3.67E+03	5.33E+03	3.89E+03	9.10E+03	5.88E+03	4.33E+03	5.94E+03	7.95E+03	4.89E+03	612.30391	3	18.34
ITC1	YGL133W	RKPTEVNDSENNSSEEDK	[13] Phospho (ST)	1.09	0.42	0.05	0.67	0.009	0.119	0.438	0.05	4.37E+03	5.52E+03	6.17E+03	8.43E+03	1.30E+04	1.29E+04	7.51E+03	4.94E+03	9.11E+03	7.57E+03	3.82E+03	5.28E+03	719.96946	3	36.67
RPT5	YOR117W	ATLEELDAQTLPGDDELDQEILNLSTQELQTR	[N-term] Acetyl (Protein N-term)|[10] Phosph	-0.31	0.22	-0.09	-0.53	0.273	0.307	0.424	0.08	2.21E+04	3.00E+04	1.11E+04	1.31E+04	2.27E+04	1.51E+04	3.13E+04	2.18E+04	2.06E+04	1.62E+04	2.62E+04	1.70E+04	930.94005	4	45.42
FKS1	YLR342W	TLSQIGGK	[3] Phospho (ST)	-0.50	-0.80	0.27	0.30	0.114	0.055	0.270	0.13	2.59E+03	4.99E+03	3.40E+03	2.65E+03	2.11E+03	3.00E+03	2.66E+03	1.83E+03	1.82E+03	6.07E+03	3.93E+03	3.20E+03	442.22053	2	22.62
MSH6	YDR097C	STTTDEDLSSSQSR	[11] Phospho (ST)	0.05	-1.32	-1.34	1.37	0.457	0.066	0.064	0.01	1.02E+04	3.20E+03	6.44E+03	8.41E+03	7.05E+03	5.19E+03	1.59E+03	3.26E+03	3.10E+03	3.63E+03	2.18E+03	2.03E+03	797.31846	2	25.65
YNL115C	YNL115C	DIESDGFIK	[4] Phospho (ST)	3.30	4.23	3.77	-0.93	0.076	0.000	0.008	0.08	0.00E+00	7.18E+02	1.53E+02	2.71E+02	5.44E+03	3.18E+03	5.39E+03	6.53E+03	5.07E+03	3.07E+03	5.95E+03	3.27E+03	552.23684	2	22.7
REG1	YDR028C	SDSGVHSPITDNSSVASSTTSR	[3] Phospho (ST)	-0.06	0.72	0.14	-0.78	0.399	0.008	0.245	0.00	1.42E+04	2.22E+04	2.04E+04	1.62E+04	1.98E+04	1.85E+04	3.39E+04	3.22E+04	2.75E+04	2.00E+04	1.99E+04	2.29E+04	1136.4925	2	20.09
NET1	YJL076W	ISSGIDAGKK	[3] Phospho (ST)	0.00	-1.07	-0.12	1.07	0.498	0.103	0.417	0.03	7.03E+03	2.00E+03	3.94E+03	3.89E+03	3.11E+03	6.00E+03	2.54E+03	1.44E+03	2.21E+03	4.63E+03	3.94E+03	3.40E+03	528.25988	2	29.21
SKY1	YMR216C	HVSRSSDITANDSSDEK	[5] Phospho (ST)|[6] Phospho (ST)	-0.94	-1.64	-0.68	0.71	0.046	0.014	0.124	0.07	9.40E+03	5.19E+03	5.73E+03	4.43E+03	3.87E+03	2.31E+03	1.50E+03	2.25E+03	2.73E+03	6.83E+03	3.54E+03	2.33E+03	669.92837	3	33.94
NOP53	YPL146C	DLEEVINSEETEILSAIESDSNK	[15] Phospho (ST)	0.01	-0.27	0.01	0.28	0.484	0.213	0.492	0.17	1.93E+04	2.86E+04	1.92E+04	2.02E+04	2.70E+04	2.04E+04	2.39E+04	1.80E+04	1.39E+04	2.24E+04	2.86E+04	1.64E+04	882.06334	3	70.27
STU1	YBL034C	LKDDNEPTVK	[8] Phospho (ST)	-0.87	0.68	0.27	-1.56	0.225	0.160	0.374	0.01	7.53E+03	1.05E+03	3.10E+03	1.42E+03	1.03E+03	3.92E+03	7.66E+03	4.79E+03	6.33E+03	7.10E+03	4.34E+03	2.63E+03	619.7869	2	36.54
SBE22	YHR103W	SQTCSSTGYNNSSILK	[1] Phospho (ST)	-1.06	-0.31	-0.26	-0.76	0.002	0.088	0.255	0.02	1.31E+04	1.13E+04	1.05E+04	4.64E+03	7.02E+03	5.06E+03	8.74E+03	1.16E+04	7.91E+03	1.48E+04	6.94E+03	7.45E+03	913.88561	2	68.32
SHE3	YBR130C	SFYTASPLLSSGSIPK	[3] Phospho (Y)	0.51	1.23	0.79	-0.72	0.238	0.079	0.133	0.10	1.93E+03	2.15E+04	9.47E+03	1.62E+04	1.76E+04	1.28E+04	3.07E+04	3.33E+04	1.31E+04	2.01E+04	2.22E+04	1.44E+04	867.92255	2	33.87
GRX2	YDR513W	ALVLELDEMSNGSEIQDALEEISGQK	[13] Phospho (ST)	0.08	0.00	0.01	0.08	0.458	0.498	0.492	0.46	1.69E+04	2.68E+04	1.26E+04	1.62E+04	3.59E+04	7.39E+03	2.28E+04	2.03E+04	1.33E+04	1.35E+04	3.16E+04	1.17E+04	966.782	3	34.83
BEM2	YER155C	ASFSTNR	[2] Phospho (ST)	0.50	0.09	0.03	0.41	0.173	0.446	0.483	0.16	2.21E+03	5.02E+02	1.69E+03	2.60E+03	1.73E+03	1.90E+03	8.14E+02	1.79E+03	2.08E+03	2.37E+03	1.33E+03	7.96E+02	431.6764	2	15.61
ALY2	YJL084C	SLSTPQREESK	[4] Phospho (ST)	0.75	0.71	1.16	0.04	0.037	0.301	0.005	0.49	3.54E+03	2.52E+03	2.16E+03	4.67E+03	3.45E+03	5.72E+03	1.06E+04	2.50E+03	4.28E+02	7.23E+03	5.12E+03	6.01E+03	671.30546	2	16.57
YLR345W	YLR345W	PNVLSDDEELLNGLGSEIMK	[5] Phospho (ST)	-0.85	0.11	0.24	-0.96	0.135	0.424	0.381	0.09	1.24E+04	1.74E+04	5.71E+03	6.58E+03	1.06E+04	2.47E+03	1.82E+04	1.18E+04	8.26E+03	7.41E+03	2.51E+04	9.38E+03	751.68316	3	19.46
SPC29	YPL124W	FQDDTLNR	[5] Phospho (ST)	0.16	-0.14	0.15	0.30	0.192	0.284	0.243	0.06	2.97E+03	2.36E+03	3.52E+03	3.41E+03	3.47E+03	3.04E+03	2.12E+03	2.95E+03	2.97E+03	3.79E+03	2.95E+03	3.09E+03	544.72425	2	19.54
AIM21	YIR003W	AISEESLSPSEAIANR	[8] Phospho (ST)	-0.14	-0.06	-0.19	-0.08	0.320	0.406	0.302	0.34	1.24E+04	2.15E+04	1.61E+04	1.26E+04	1.84E+04	1.42E+04	1.60E+04	1.75E+04	1.43E+04	9.97E+03	1.82E+04	1.56E+04	877.399	2	25.41
BCP1	YDR361C	KYEVNFDTDDDTDSGK	[8] Phospho (ST)	-0.35	-0.92	-0.02	0.57	0.141	0.046	0.477	0.07	1.02E+04	1.32E+04	7.23E+03	7.59E+03	8.74E+03	7.77E+03	6.58E+03	6.90E+03	2.68E+03	8.29E+03	1.44E+04	7.50E+03	964.87601	2	49.53
POL1	YNL102W	YANDVQDLLDDVENSPVVATK	[15] Phospho (ST)	0.08	1.61	1.07	-1.53	0.420	0.016	0.014	0.02	8.31E+03	8.05E+03	5.90E+03	7.09E+03	1.12E+04	5.22E+03	3.07E+04	2.28E+04	1.46E+04	1.33E+04	2.02E+04	1.32E+04	795.70269	3	52.15
YSC84	YHR016C	GYGDFDSEDEDYDYGR	[7] Phospho (ST)	-0.71	-0.10	-1.93	-0.61	0.267	0.462	0.118	0.28	7.02E+03	3.72E+04	1.02E+04	4.06E+03	1.80E+04	1.13E+04	9.12E+03	3.32E+04	8.43E+03	4.32E+03	5.93E+03	4.04E+03	991.83452	2	51.22
BBC1	YJL020C	RSTTHDVGEISNNVK	[3] Phospho (ST)|[4] Phospho (ST)	0.62	0.27	-0.25	0.35	0.011	0.092	0.037	0.07	7.03E+03	8.50E+03	8.24E+03	1.06E+04	1.42E+04	1.18E+04	7.81E+03	9.97E+03	1.09E+04	6.47E+03	6.35E+03	7.18E+03	908.88526	2	28.77
REG1	YDR028C	SDSGVHSPITDNSSVASSTTSR	[1] Phospho (ST)	0.26	-0.24	-0.30	0.50	0.200	0.325	0.220	0.12	7.97E+03	1.61E+04	1.16E+04	1.60E+04	1.35E+04	1.34E+04	1.57E+04	6.32E+03	8.29E+03	8.38E+03	8.55E+03	1.20E+04	1136.4901	2	40.69
BUL2	YML111W	IDDTASQSPSYDSK	[11] Phospho (Y)	0.74	0.29	0.17	0.44	0.039	0.278	0.344	0.14	5.28E+03	2.62E+03	5.25E+03	8.92E+03	5.94E+03	7.08E+03	2.87E+03	6.21E+03	7.07E+03	6.22E+03	3.26E+03	5.29E+03	797.32085	2	23.75
BUD4	YJR092W	VNSELEESPAAVHQER	[3] Phospho (ST)	-0.92	0.20	0.54	-1.11	0.025	0.371	0.097	0.09	5.66E+03	9.08E+03	1.05E+04	4.48E+03	4.49E+03	4.38E+03	1.11E+04	3.55E+03	1.42E+04	1.11E+04	9.48E+03	1.61E+04	937.91856	2	42.67
CUE4	YML101C	PAPSVATNDPSPEPVPSAPEER	[11] Phospho (ST)	1.73	1.74	0.24	-0.01	0.005	0.001	0.244	0.49	3.11E+03	5.99E+03	4.50E+03	1.88E+04	1.52E+04	1.12E+04	1.57E+04	1.30E+04	1.66E+04	6.73E+03	4.28E+03	5.09E+03	775.35311	3	22.57
YBT1	YLL048C	ANSSANLAAK	[3] Phospho (ST)	0.95	1.62	1.95	-0.67	0.224	0.000	0.059	0.18	1.38E+03	6.49E+02	1.30E+03	1.44E+03	4.91E+02	4.55E+03	3.57E+03	3.24E+03	3.52E+03	7.51E+03	2.70E+03	2.74E+03	513.73372	2	40.57
NTH2	YBR001C	RGSEDDSFLSSQGNR	[3] Phospho (ST)	-0.29	-0.63	-0.57	0.34	0.078	0.012	0.009	0.05	8.75E+03	1.17E+04	1.08E+04	7.43E+03	8.66E+03	9.58E+03	5.78E+03	6.78E+03	7.71E+03	6.69E+03	7.19E+03	7.19E+03	867.85908	2	28.74
SNC1	YAL030W	SSSTPFDPYALSEHDEERPQNVQSK	[N-term] Acetyl (Protein N-term)|[4] Phospho	0.04	-0.18	-0.08	0.22	0.459	0.211	0.428	0.27	2.23E+04	2.82E+04	1.82E+04	3.33E+04	1.80E+04	1.93E+04	2.15E+04	2.08E+04	1.83E+04	3.23E+04	1.77E+04	1.52E+04	990.76809	3	21.49
OAF1	YAL051W	RSASPINTNNASGDSPDTKK	[15] Phospho (ST)	-0.25	-0.44	-0.19	0.19	0.337	0.230	0.368	0.33	2.45E+03	6.71E+03	8.34E+03	6.55E+03	5.25E+03	2.90E+03	5.22E+03	2.96E+03	4.68E+03	3.94E+03	4.72E+03	6.72E+03	713.99333	3	26.44
DCP2	YNL118C	SINETVGLSSTTNTVK	[1] Phospho (ST)	-0.48	-0.47	-0.33	-0.01	0.009	0.006	0.034	0.48	2.03E+04	2.31E+04	2.28E+04	1.45E+04	1.45E+04	1.84E+04	1.37E+04	1.74E+04	1.66E+04	1.43E+04	1.90E+04	1.93E+04	865.91839	2	51.89
RBS1	YDL189W	RASVEGSPSSR	[3] Phospho (ST)	1.53	0.54	0.33	0.98	0.085	0.162	0.200	0.15	2.01E+03	3.29E+03	2.04E+03	6.14E+03	2.87E+03	1.22E+04	5.34E+03	2.29E+03	3.09E+03	3.97E+03	2.20E+03	3.04E+03	606.7714	2	38.71
SEC16	YPL085W	LGTVPSNYVSSPDLVR	[11] Phospho (ST)	-0.36	-0.46	-0.88	0.10	0.229	0.195	0.056	0.42	2.16E+04	3.03E+04	1.35E+04	1.11E+04	2.29E+04	1.69E+04	2.13E+04	8.42E+03	1.78E+04	1.07E+04	1.35E+04	1.13E+04	892.43487	2	37.97
SUI3	YPL237W	TKDSSVDAFEK	[5] Phospho (ST)	0.14	0.36	-0.26	-0.22	0.337	0.120	0.245	0.19	2.64E+03	4.53E+03	4.71E+03	4.13E+03	3.49E+03	5.44E+03	5.85E+03	5.09E+03	4.26E+03	4.28E+03	2.42E+03	3.23E+03	653.78166	2	25.05
GIS4	YML006C	SLPLPTLLK	[1] Phospho (ST)	-0.53	-0.35	-1.01	-0.18	0.248	0.246	0.089	0.40	6.95E+03	1.08E+04	4.35E+03	3.28E+03	9.83E+03	2.20E+03	7.35E+03	5.96E+03	4.04E+03	1.49E+03	5.91E+03	3.56E+03	531.30444	2	15.29
EIS1	YMR031C	IASGLISPVLGEVSER	[7] Phospho (ST)	0.14	0.04	0.52	0.11	0.327	0.456	0.167	0.36	2.41E+04	1.53E+04	1.50E+04	2.38E+04	2.11E+04	1.51E+04	2.38E+04	1.73E+04	1.46E+04	2.47E+04	3.79E+04	1.54E+04	853.94107	2	39.82
SHS1	YDL225W	KNDTYTDLASIASGRD	[4] Phospho (ST)	0.80	0.65	0.49	0.15	0.060	0.141	0.195	0.33	3.57E+03	1.49E+04	1.26E+04	1.94E+04	2.02E+04	1.45E+04	2.08E+04	1.81E+04	9.93E+03	1.08E+04	1.99E+04	1.31E+04	903.8996	2	64.55
IOC2	YLR095C	SPQHTLSQR	[7] Phospho (ST)	2.39	-1.62	-2.92	4.00	0.004	0.120	0.072	0.00	2.66E+03	7.72E+02	6.39E+02	7.31E+03	5.38E+03	8.74E+03	4.83E+02	1.80E+02	6.44E+02	2.22E+02	1.69E+02	1.21E+02	567.25831	2	25.02
EFG1	R271C-A	DHEDGSQVSPTQDRK	[9] Phospho (ST)	1.26	-0.56	-0.79	1.82	0.045	0.269	0.143	0.03	5.85E+03	5.13E+03	1.69E+03	1.25E+04	5.46E+03	1.24E+04	1.72E+03	9.00E+02	5.96E+03	1.60E+03	1.94E+03	3.78E+03	593.58262	3	23.07
SSN2	YDR443C	DFSPNFTGIDK	[3] Phospho (ST)	-0.06	0.88	0.36	-0.95	0.469	0.036	0.241	0.06	5.05E+03	8.71E+03	2.82E+03	1.26E+03	9.38E+03	5.22E+03	1.09E+04	1.12E+04	8.48E+03	6.05E+03	9.20E+03	6.01E+03	660.7807	2	22.43
NET1	YJL076W	VRPSLSSLSDLVSR	[4] Phospho (ST)	0.13	0.83	0.89	-0.71	0.419	0.160	0.130	0.16	2.20E+03	8.85E+03	4.33E+03	4.24E+03	7.18E+03	5.37E+03	1.49E+04	5.22E+03	7.31E+03	4.61E+03	1.39E+04	1.00E+04	798.41203	2	29.65
SPA2	YLL021W	ITAQESIKSPEAAR	[9] Phospho (ST)	0.89	2.52	1.72	-1.63	0.021	0.011	0.032	0.02	8.53E+02	1.73E+03	1.53E+03	1.96E+03	2.80E+03	2.91E+03	9.77E+03	4.40E+03	9.58E+03	2.35E+03	4.70E+03	6.58E+03	790.88728	2	20.44
BMS1	YPL217C	WRGEDDDSKDESDIEEDVDDDFFR	[12] Phospho (ST)	-0.05	-0.28	-0.32	0.23	0.453	0.212	0.207	0.26	6.58E+04	9.18E+04	4.80E+04	7.82E+04	8.07E+04	3.97E+04	5.88E+04	6.27E+04	4.83E+04	5.80E+04	6.69E+04	3.95E+04	1005.3889	3	31.05
SPA2	YLL021W	HYSDDDDSSYQFVPMK	[3] Phospho (ST)	-0.23	-0.27	-0.03	0.04	0.408	0.320	0.472	0.49	1.25E+04	1.86E+04	8.98E+03	5.44E+03	2.62E+04	2.34E+03	1.47E+04	1.45E+04	3.97E+03	9.88E+03	1.91E+04	1.01E+04	1007.3829	2	31.93
SEC2	YNL272C	IGPLVEDDSDEDQNDAISVR	[9] Phospho (ST)	1.77	3.06	2.52	-1.29	0.117	0.009	0.011	0.06	4.01E+02	3.59E+03	1.47E+03	2.28E+02	8.89E+03	9.57E+03	8.80E+03	1.72E+04	1.97E+04	6.12E+03	1.21E+04	1.33E+04	756.32884	3	22.19
PEX30	YLR324W	NEAESGVSEDNDNGSLEK	[15] Phospho (ST)	0.82	0.03	0.43	0.78	0.010	0.474	0.154	0.03	6.78E+03	3.92E+03	7.12E+03	1.06E+04	9.26E+03	1.16E+04	3.29E+03	6.05E+03	8.87E+03	1.08E+04	6.01E+03	7.18E+03	987.38469	2	37.13
YLR257W	YLR257W	SNSLITSTDPVEDHISK	[3] Phospho (ST)	-4.94	-3.06	-2.41	-1.88	0.006	0.008	0.011	0.01	2.32E+04	4.57E+04	2.70E+04	0.00E+00	1.43E+03	1.66E+03	5.16E+03	3.22E+03	3.12E+03	3.77E+03	8.52E+03	5.74E+03	961.94264	2	64.81
ENT2	YLR206W	TRSNPHDSSPSYQDDLEK	[3] Phospho (ST)	0.14	-0.13	-0.79	0.27	0.315	0.387	0.084	0.20	9.39E+03	1.77E+04	1.14E+04	1.46E+04	1.52E+04	1.28E+04	1.60E+04	1.18E+04	7.52E+03	4.69E+03	6.17E+03	1.14E+04	1078.4497	2	28.29
PDS1	YDR113C	SFIFPETSNQSK	[1] Phospho (ST)	0.25	-0.14	-1.17	0.40	0.290	0.383	0.054	0.14	6.38E+03	1.53E+04	8.81E+03	1.07E+04	1.58E+04	9.83E+03	9.27E+03	1.15E+04	6.87E+03	5.42E+03	4.83E+03	3.28E+03	732.82447	2	19.63
BEM3	YPL115C	SPLQER	[1] Phospho (ST)	0.36	0.05	-0.04	0.31	0.268	0.460	0.477	0.25	3.50E+03	1.26E+03	2.20E+03	2.80E+03	1.82E+03	4.32E+03	2.24E+03	1.97E+03	2.98E+03	3.71E+03	1.83E+03	1.24E+03	405.18109	2	20.12
PRB1	YEL060C	DDDEEPSDSEDK	[7] Phospho (ST)	1.11	0.51	0.98	0.60	0.106	0.243	0.258	0.15	4.52E+03	8.07E+02	1.39E+03	7.33E+03	2.90E+03	4.26E+03	2.64E+03	4.07E+03	2.85E+03	1.01E+04	1.95E+03	1.23E+03	730.73299	2	15.33
STU2	YLR045C	VASSPLRNDNK	[4] Phospho (ST)	-0.20	0.09	0.02	-0.29	0.337	0.430	0.484	0.23	5.43E+03	2.12E+03	3.34E+03	3.06E+03	2.62E+03	3.81E+03	5.32E+03	2.58E+03	3.70E+03	4.85E+03	2.75E+03	3.43E+03	640.80257	2	15.55
SEC7	YDR170C	VSYESSR	[2] Phospho (ST)	-0.32	-0.32	-0.18	0.00	0.357	0.360	0.428	0.49	4.32E+03	6.40E+02	1.57E+03	1.65E+03	1.55E+03	2.01E+03	1.48E+03	1.52E+03	2.22E+03	3.38E+03	1.28E+03	1.09E+03	454.18129	2	17.83
RSP5	YER125W	LPSSSPHSQAPSGHTASSSTNTSSTTR	[5] Phospho (ST)	-0.05	-0.39	0.07	0.34	0.408	0.195	0.441	0.22	8.66E+03	1.03E+04	7.31E+03	9.91E+03	7.91E+03	7.59E+03	9.58E+03	2.95E+03	7.53E+03	1.40E+04	7.97E+03	5.55E+03	917.40274	3	23.01
BNI5	YNL166C	SGGSTPLDSQTK	[1] Phospho (ST)	0.49	1.20	0.76	-0.71	0.298	0.113	0.180	0.14	7.52E+02	9.63E+02	5.33E+03	2.81E+03	2.33E+03	4.78E+03	2.40E+03	6.30E+03	7.56E+03	4.99E+03	3.07E+03	3.93E+03	629.27161	2	22.19
BUD3	YCL014W	LGDDYSDKETAK	[6] Phospho (ST)	-0.25	-0.71	-0.54	0.45	0.265	0.107	0.126	0.08	5.03E+03	2.54E+03	2.78E+03	3.15E+03	2.61E+03	2.93E+03	1.51E+03	1.85E+03	2.97E+03	2.67E+03	2.32E+03	2.10E+03	711.29528	2	23.17
NTC20	YBR188C	VLQEPDRDNDDSG	[12] Phospho (ST)	-0.44	-0.50	-0.21	0.06	0.224	0.226	0.340	0.45	8.44E+03	2.50E+03	7.73E+03	5.62E+03	4.32E+03	3.80E+03	2.22E+03	4.98E+03	6.00E+03	5.78E+03	4.96E+03	5.41E+03	770.30184	2	17.45
GAT1	YFL021W	RNPSPSIVKPGSR	[12] Phospho (ST)	-0.56	-0.47	-0.45	-0.09	0.138	0.196	0.186	0.39	6.23E+03	7.31E+03	1.35E+04	5.69E+03	6.65E+03	6.08E+03	7.24E+03	4.10E+03	8.25E+03	5.17E+03	6.53E+03	8.07E+03	737.88044	2	18.7
CDC55	YGL190C	AVLSLQSLK	[4] Phospho (ST)	-0.18	0.47	0.25	-0.66	0.411	0.243	0.373	0.06	6.45E+02	4.86E+03	2.32E+03	1.82E+03	3.07E+03	2.01E+03	4.59E+03	2.80E+03	3.50E+03	2.02E+03	4.59E+03	2.73E+03	519.78401	2	47.02

PSH1	YOL054W	NYAGGRDEFDEEEYSEGELDEIR	[14] Phospho (Y)	0.48	-0.06	-0.93	0.54	0.268	0.469	0.179	0.20	1.57E+04	1.31E+04	1.62E+03	2.24E+04	1.11E+04	9.04E+03	1.13E+04	5.38E+03	1.26E+04	6.28E+03	2.08E+03	7.65E+03	934.70853	3	31.08
SEC16	YPL085W	GHTSSISSYTPNQNEHASR	[5] Phospho (ST)	-0.19	0.24	-0.08	-0.43	0.319	0.266	0.435	0.06	1.01E+04	2.06E+04	1.19E+04	1.14E+04	1.50E+04	1.09E+04	2.01E+04	1.58E+04	1.42E+04	9.88E+03	1.21E+04	1.85E+04	1076.9555	2	29.1
NMD5	YJR132W	NRADSLDFVDGYDAK	[5] Phospho (ST)	-0.67	-0.28	-0.19	-0.39	0.036	0.181	0.222	0.08	8.10E+03	1.31E+04	1.00E+04	5.36E+03	6.75E+03	7.53E+03	1.03E+04	8.68E+03	6.82E+03	8.33E+03	9.90E+03	9.10E+03	883.37733	2	23.07
YMR124W	YMR124W	ASSFTQSSFSNFFK	[2] Phospho (ST)	-0.48	0.54	0.02	-1.02	0.195	0.155	0.478	0.04	6.78E+03	1.38E+04	6.52E+03	5.69E+03	8.70E+03	5.09E+03	1.65E+04	1.52E+04	7.95E+03	8.07E+03	1.08E+04	8.74E+03	832.85482	2	51.88
CNM67	YNL225C	NTSYQESPGLQERPK	[7] Phospho (ST)	0.12	-0.36	-0.07	0.48	0.290	0.097	0.401	0.04	4.74E+03	6.99E+03	5.89E+03	6.08E+03	5.60E+03	7.49E+03	4.63E+03	3.60E+03	5.46E+03	4.50E+03	4.89E+03	7.35E+03	907.40916	2	16.49
TAE2	YPL009C	HCTISSDTDSDSGNAK	[6] Phospho (ST)	1.20	0.83	1.35	0.38	0.038	0.143	0.057	0.21	1.59E+03	2.04E+03	5.69E+03	5.75E+03	9.33E+03	6.43E+03	2.79E+03	5.95E+03	7.82E+03	1.20E+04	5.80E+03	6.04E+03	887.83334	2	36.04
MLF3	YNL074C	TTELPATSPYVSPQQSAR	[10] Phospho (Y)	-0.50	1.56	0.10	-2.05	0.134	0.018	0.385	0.01	4.09E+03	9.01E+03	6.76E+03	3.85E+03	4.73E+03	5.48E+03	1.90E+04	2.65E+04	1.30E+04	6.09E+03	8.44E+03	6.82E+03	1006.9706	2	35.7
PFK1	YGR240C	ASSDASDLLR	[2] Phospho (ST)	0.27	0.68	0.20	-0.41	0.240	0.047	0.393	0.01	1.08E+03	2.75E+03	2.97E+03	2.60E+03	2.87E+03	2.75E+03	3.59E+03	3.35E+03	3.99E+03	1.47E+03	4.60E+03	1.75E+03	557.74304	2	21
HOS4	YIL112W	NTTEPENVEK	[3] Phospho (ST)	-1.69	-2.99	-3.03	1.29	0.234	0.179	0.177	0.22	2.12E+04	1.64E+03	9.10E+02	5.53E+03	1.02E+03	7.80E+02	8.67E+01	4.95E+02	2.39E+03	1.44E+03	5.14E+02	9.35E+02	620.75748	2	26.42
BOI1	YBL085W	SSFDEEETK	[2] Phospho (ST)	0.61	0.84	1.05	-0.23	0.253	0.180	0.138	0.28	0.00E+00	7.32E+02	2.54E+03	2.13E+03	1.62E+03	1.26E+03	1.26E+03	2.09E+03	2.53E+03	3.34E+03	1.93E+03	1.52E+03	576.21066	2	16.79
IKS1	YJL057C	RASAGVESESSR	[3] Phospho (ST)	0.67	0.43	0.02	0.24	0.076	0.245	0.482	0.32	4.04E+03	2.57E+03	2.21E+03	4.96E+03	3.16E+03	5.97E+03	6.03E+03	1.76E+03	4.11E+03	4.07E+03	2.62E+03	2.24E+03	658.28496	2	47.05
ENA2	YDR039C	STNQSNENDQSSLSQHNEK	[12] Phospho (ST)	-0.22	0.44	0.00	-0.66	0.425	0.302	0.499	0.09	1.58E+04	8.25E+02	4.81E+03	4.55E+03	3.60E+03	1.03E+04	8.40E+03	1.05E+04	1.02E+04	1.35E+04	4.49E+03	3.46E+03	742.96796	3	15
RPS21A	YKR057W	SRGESDDSLNR	[5] Phospho (ST)	2.03	-0.09	-0.22	2.12	0.004	0.416	0.338	0.00	2.53E+03	1.32E+03	1.21E+03	8.59E+03	5.23E+03	6.97E+03	1.81E+03	1.52E+03	1.44E+03	2.11E+03	9.96E+02	1.24E+03	658.26753	2	21
AAD4	YDL243C	TVSGTSKQTDK	[9] Phospho (ST)	2.70	3.65	3.67	-0.95	0.159	0.021	0.000	0.19	3.69E+02	8.54E+02	5.43E+02	5.63E+02	9.66E+03	1.44E+03	1.22E+04	5.16E+03	5.22E+03	6.62E+03	8.43E+03	7.78E+03	616.28563	2	17.46
MDS3	YGL197W	SSISEAEHQR	[2] Phospho (ST)	-1.79	0.50	-0.56	-2.29	0.119	0.254	0.306	0.01	5.26E+03	1.14E+03	1.39E+03	9.46E+02	7.57E+02	5.28E+02	2.44E+03	3.96E+03	4.62E+03	3.21E+03	1.37E+03	6.98E+02	612.25482	2	21.49
SUB2	YDL084W	SHEGEEDLLEYSDNEQEIQIDASK	[N-term] Acetyl (Protein N-term)|[11] Phosph	0.25	0.52	-0.25	-0.27	0.244	0.105	0.206	0.26	1.09E+04	1.63E+04	1.47E+04	1.43E+04	2.28E+04	1.28E+04	2.13E+04	2.59E+04	1.30E+04	8.68E+03	1.14E+04	1.51E+04	725.80618	4	20.65
HOG1	YLR113W	IQDPQMTGYVSTR	[7] Phospho (ST)|[9] Phospho (Y)	-0.97	-0.31	0.57	-0.67	0.029	0.249	0.027	0.18	9.00E+03	7.53E+03	1.05E+04	4.25E+03	7.24E+03	2.26E+03	3.82E+03	1.12E+04	6.78E+03	1.46E+04	1.50E+04	1.06E+04	828.33164	2	16.09
SSK1	YLR006C	SPQKPIAPSNPHSFK	[1] Phospho (ST)	0.01	0.20	-0.17	-0.19	0.490	0.289	0.359	0.05	3.08E+03	7.77E+03	6.14E+03	5.04E+03	6.11E+03	5.97E+03	6.31E+03	6.46E+03	6.74E+03	3.43E+03	6.21E+03	5.49E+03	857.91926	2	23.52
RPL7A	YGL076C	INSGTFVK	[3] Phospho (ST)	-1.69	-0.49	-0.21	-1.20	0.001	0.063	0.069	0.03	3.69E+03	4.54E+03	4.36E+03	1.08E+03	9.84E+02	1.81E+03	3.04E+03	1.96E+03	3.94E+03	3.42E+03	3.94E+03	3.54E+03	473.22611	2	20.96
IVY1	YDR229W	PDNNTEQLQGSPSSDQR	[11] Phospho (ST)	-0.28	-0.13	-0.17	-0.14	0.273	0.365	0.317	0.33	1.29E+04	5.86E+03	1.19E+04	1.14E+04	8.04E+03	5.89E+03	7.96E+03	8.61E+03	1.14E+04	9.37E+03	8.70E+03	9.19E+03	976.90396	2	37.17
YEL043W	YEL043W	ISSDFNLLVPNLSPR	[13] Phospho (ST)	0.01	-0.11	-0.04	0.12	0.482	0.382	0.442	0.36	1.35E+04	1.99E+04	1.39E+04	1.28E+04	1.91E+04	1.58E+04	1.94E+04	1.49E+04	9.70E+03	1.74E+04	1.77E+04	1.08E+04	876.43982	2	29.5
PIF1	YML061C	KESSFDELQNNSISQER	[4] Phospho (ST)	-3.37	-1.35	-0.46	-2.02	0.000	0.001	0.022	0.00	1.61E+04	1.83E+04	1.44E+04	1.99E+03	3.96E+02	2.30E+03	7.70E+03	5.07E+03	6.38E+03	9.89E+03	1.19E+04	1.36E+04	1045.9575	2	19.11
ENP2	YGR145W	HDNSSDEEGIDENGNKK	[4] Phospho (ST)|[5] Phospho (ST)	-1.74	-0.91	-1.12	-0.82	0.194	0.283	0.251	0.18	3.64E+04	1.22E+03	7.49E+03	3.04E+03	3.92E+03	6.53E+03	2.51E+03	1.36E+04	7.78E+03	1.04E+04	6.41E+03	3.94E+03	1024.3683	2	26.92
RPL13A	YDL082W	APEAEQVLSAAATFPIAQPATDVEAR	[9] Phospho (ST)	-0.74	-0.38	-0.76	-0.37	0.193	0.280	0.173	0.24	1.73E+04	3.73E+04	1.14E+04	6.23E+03	2.19E+04	1.14E+04	1.94E+04	1.42E+04	1.72E+04	7.20E+03	1.82E+04	1.36E+04	911.77661	3	16.4
GAL11	YOL051W	VPVSAAATPSLNK	[10] Phospho (ST)	-6.27	-6.45	-4.15	0.17	0.000	0.000	0.000	0.45	1.32E+04	1.38E+04	1.37E+04	9.57E+00	2.89E+02	2.00E+02	0.00E+00	4.37E+02	2.54E-01	1.38E+03	8.02E+02	8.43E+01	667.83969	2	21.14
TOA2	YKL058W	DASQNGSGDSQSVISVDK	[3] Phospho (ST)	1.88	-0.16	0.24	2.04	0.001	0.389	0.301	0.00	5.66E+03	4.31E+03	8.40E+03	2.40E+04	2.43E+04	1.94E+04	9.11E+03	3.75E+03	3.52E+03	4.78E+03	9.97E+03	6.89E+03	937.39446	2	24.05
SKG6	YHR149C	SHGSPIHNNQLSR	[4] Phospho (ST)	0.19	-0.42	0.02	0.61	0.314	0.195	0.477	0.01	2.77E+03	7.35E+03	6.95E+03	6.10E+03	7.39E+03	5.98E+03	4.91E+03	4.13E+03	3.67E+03	5.00E+03	5.47E+03	6.89E+03	763.84461	2	26.58
SEC21	YNL287W	RADANSFAGPNLDDHQEDLLATK	[6] Phospho (ST)	0.31	0.24	-0.28	0.08	0.353	0.365	0.387	0.44	8.06E+02	1.02E+04	6.38E+03	3.97E+03	1.13E+04	6.32E+03	5.84E+03	6.67E+03	7.95E+03	1.69E+03	8.00E+03	4.67E+03	860.05838	3	19.89
TSC11	YER093C	SVTNTTPLLTPR	[1] Phospho (ST)	-0.62	-0.57	-0.73	-0.06	0.059	0.072	0.049	0.25	9.18E+03	1.25E+04	6.77E+03	5.83E+03	6.42E+03	6.22E+03	6.67E+03	6.77E+03	5.80E+03	4.70E+03	6.23E+03	6.28E+03	690.34951	2	34.42
NUM1	YDR150W	GLAEAAATTAYEDSESHPQIEEQSHR	[11] Phospho (Y)	0.77	0.75	0.03	0.02	0.155	0.144	0.485	0.47	3.08E+02	1.44E+04	8.94E+03	9.26E+03	1.33E+04	1.78E+04	1.19E+04	1.62E+04	1.15E+04	6.60E+03	6.50E+03	1.11E+04	969.75571	3	20.9
CAF20	YOR276W	PILGFNAFAALESEDEDDEA	[13] Phospho (ST)	0.90	1.04	0.17	-0.14	0.047	0.062	0.394	0.37	1.05E+04	2.43E+04	1.25E+04	2.45E+04	3.84E+04	2.51E+04	4.67E+04	2.19E+04	2.86E+04	1.20E+04	2.84E+04	1.28E+04	744.97864	3	21.67
SUB2	YDL084W	SHEGEEDLLEYSDNEQEIQIDASK	[N-term] Acetyl (Protein N-term)|[12] Phosph	-0.18	0.03	-1.39	-0.20	0.401	0.484	0.114	0.24	1.39E+04	3.04E+04	6.52E+04	2.84E+04	4.00E+04	2.86E+04	3.11E+04	3.38E+04	4.67E+04	9.36E+03	2.35E+04	8.76E+03	967.41087	3	18.96
RSC4	YKR008W	INQALLGASSPK	[10] Phospho (ST)	0.79	0.76	0.08	0.03	0.138	0.138	0.462	0.46	4.68E+01	4.24E+03	2.67E+03	2.91E+03	4.47E+03	4.63E+03	4.67E+03	3.80E+03	3.33E+03	1.67E+03	3.31E+03	2.38E+03	639.82668	2	33.65
CYC8	YBR112C	SNGAPTNASPAPPPVILQPTLQPNDQGNPLNTR	[1] Phospho (ST)	0.10	0.00	-0.05	0.10	0.377	0.495	0.408	0.38	2.13E+04	1.53E+04	2.21E+04	1.59E+04	2.74E+04	1.95E+04	1.58E+04	2.38E+04	1.89E+04	2.25E+04	1.74E+04	1.68E+04	1152.9059	3	16.12
SWI4	YER111C	DNTNHQNITPISK	[9] Phospho (ST)	0.27	1.13	1.31	-0.87	0.271	0.020	0.006	0.03	2.96E+03	1.19E+03	2.64E+03	2.86E+03	1.93E+03	3.39E+03	5.74E+03	3.53E+03	5.68E+03	6.63E+03	4.74E+03	5.50E+03	781.35362	2	22.11
MRC1	YCL061C	IPIIPTELIGTSPLFQSIQNR	[11] Phospho (ST)	-1.26	-2.22	-1.99	0.96	0.049	0.022	0.024	0.03	1.70E+04	2.88E+04	1.16E+04	6.22E+03	1.01E+04	7.62E+03	5.04E+03	5.26E+03	1.99E+03	5.15E+03	5.45E+03	3.86E+03	806.43244	3	34.37
MET30	YIL046W	SPSSSPDLATNDSGTR	[3] Phospho (ST)	-2.03	-2.42	-1.01	0.39	0.004	0.003	0.029	0.11	9.64E+03	8.84E+03	1.42E+04	2.43E+03	2.35E+03	3.19E+03	1.38E+03	2.24E+03	2.47E+03	7.86E+03	4.43E+03	3.88E+03	836.3454	2	62.04
CBF1	YJR060W	DQGLLSQESNDGNIDSALLSEGATLK	[16] Phospho (ST)	-1.42	-1.06	-1.52	-0.36	0.021	0.018	0.009	0.25	3.45E+04	4.72E+04	2.71E+04	7.21E+03	2.35E+04	9.94E+03	1.89E+04	1.88E+04	1.44E+04	9.26E+03	1.61E+04	1.24E+04	919.09422	3	26.59
CHS2	YBR038W	EGYTLR	[3] Phospho (Y)	4.08	4.38	3.79	-0.30	0.002	0.001	0.000	0.17	1.86E+02	1.36E+00	1.28E+02	1.98E+03	1.39E+03	2.48E+03	1.86E+03	2.62E+03	2.72E+03	1.48E+03	1.49E+03	1.82E+03	409.67577	2	16.79
TAT1	YBR069C	EYENSESSENPNSSR	[5] Phospho (ST)	0.06	-1.10	-0.50	1.16	0.458	0.103	0.233	0.00	8.91E+03	2.25E+03	5.52E+03	6.77E+03	5.55E+03	5.03E+03	1.83E+03	2.64E+03	3.30E+03	5.26E+03	3.12E+03	3.39E+03	904.83508	2	20.87
YMR086W	YMR086W	KVSQESLHSQPK	[3] Phospho (ST)	-1.36	0.02	-0.34	-1.38	0.046	0.485	0.242	0.05	6.55E+03	5.00E+03	2.85E+03	1.20E+03	9.60E+02	3.43E+03	6.82E+03	2.72E+03	5.05E+03	4.85E+03	4.14E+03	2.43E+03	724.35094	2	39.07
SPT5	YML010W	DGGASAWGNQDDGNR	[5] Phospho (ST)	-0.21	-0.50	1.10	0.29	0.333	0.281	0.054	0.37	4.87E+03	2.09E+03	3.04E+03	1.81E+03	3.47E+03	3.36E+03	2.63E+02	4.77E+03	2.04E+03	1.05E+04	5.14E+03	5.88E+03	800.29511	2	28.17
SER33	YIL074C	AMNFSGSPGAVSTSPTQSFMNTLPR	[7] Phospho (ST)	-1.11	0.33	0.26	-1.44	0.124	0.285	0.359	0.07	2.11E+04	1.55E+04	7.47E+03	3.77E+03	1.53E+04	1.36E+03	2.34E+04	2.26E+04	9.29E+03	8.34E+03	3.01E+04	1.45E+04	889.06595	3	31.52
STM1	YLR150W	SNPFDLLGNDVEDADVVVLPPK	[N-term] Acetyl (Protein N-term)|[1] Phospho	1.09	0.92	0.75	0.17	0.001	0.088	0.148	0.33	5.34E+03	9.31E+03	6.77E+03	1.48E+04	1.61E+04	1.48E+04	2.05E+04	8.00E+03	1.20E+04	1.07E+04	1.94E+04	6.04E+03	825.72803	3	19.66
SAK1	YER129W	SSATNLAGMAEGAR	[4] Phospho (ST)	-0.59	-0.31	0.04	-0.28	0.218	0.273	0.453	0.37	3.47E+03	6.13E+03	3.94E+03	2.21E+03	5.99E+03	7.59E+02	3.38E+03	5.56E+03	1.98E+03	3.40E+03	5.89E+03	4.67E+03	708.30414	2	39.55
HEK2	YBL032W	SSGEPTSPSTSSNTR	[7] Phospho (ST)	1.00	1.48	1.23	-0.48	0.142	0.005	0.072	0.18	4.40E+03	1.68E+03	7.00E+03	6.93E+03	4.33E+03	1.49E+04	1.14E+04	1.36E+04	1.15E+04	1.58E+04	8.65E+03	6.31E+03	787.8207	2	32.36
REF2	YDR195W	KLSFSK	[5] Phospho (ST)	-2.55	-1.52	-3.16	-1.04	0.050	0.094	0.041	0.18	4.57E+03	5.36E+03	8.85E+02	1.20E+03	2.99E+02	3.19E+02	2.76E+02	1.31E+03	2.17E+03	2.54E+02	2.37E+02	6.94E+02	395.19874	2	23.34
GIN4	YDR507C	ESFTNLVDILK	[2] Phospho (ST)	-0.35	0.50	-0.27	-0.84	0.329	0.221	0.369	0.08	2.81E+03	9.87E+03	4.22E+03	2.63E+03	6.96E+03	3.68E+03	1.12E+04	6.17E+03	6.43E+03	2.18E+03	7.52E+03	4.34E+03	679.83457	2	43.01
RLM1	YPL089C	SSKISPLSASASGPLTLQK	[5] Phospho (ST)|[8] Phospho (ST)	-1.17	-0.65	-0.66	-0.52	0.047	0.182	0.114	0.28	1.32E+04	2.36E+04	1.24E+04	4.06E+03	1.12E+04	6.54E+03	4.30E+03	1.94E+04	7.71E+03	1.48E+04	7.79E+03	8.49E+03	1016.4915	2	25.59
RAD16	YBR114W	DVSDDDEPLTK	[3] Phospho (ST)	-0.12	0.08	0.05	-0.20	0.383	0.406	0.446	0.30	4.73E+03	3.35E+03	6.14E+03	3.12E+03	3.86E+03	6.10E+03	4.29E+03	4.37E+03	6.37E+03	3.59E+03	5.88E+03	5.21E+03	657.26112	2	32.22
IMH1	YLR309C	IRSSSSLELDSEK	[3] Phospho (ST)	-0.07	-0.47	-1.24	0.41	0.432	0.187	0.051	0.20	5.39E+03	6.18E+03	3.07E+03	5.43E+03	3.18E+03	5.37E+03	4.94E+03	1.58E+03	4.02E+03	4.10E+02	2.08E+03	3.70E+03	765.85671	2	28.11
ESC1	YMR219W	VRNSDLEDDESLK	[4] Phospho (ST)	0.46	0.80	0.49	-0.34	0.135	0.161	0.142	0.30	1.25E+03	2.88E+03	2.96E+03	2.67E+03	3.02E+03	4.09E+03	6.81E+03	1.83E+03	3.71E+03	2.34E+03	3.42E+03	4.16E+03	800.34923	2	25.92
KCS1	YDR017C	DDFLSDLDQENNGK	[5] Phospho (ST)	-0.44	-0.34	0.01	-0.10	0.290	0.226	0.482	0.46	1.14E+04	1.04E+04	7.45E+03	1.53E+03	1.52E+04	4.86E+03	4.43E+03	1.18E+04	6.95E+03	7.11E+03	1.32E+04	9.22E+03	845.33708	2	35.4
PTK2	YJR059W	VEDNLSEDDSTMK	[6] Phospho (ST)	0.70	-1.09	0.39	1.80	0.274	0.015	0.097	0.15	3.04E+03	2.88E+03	2.65E+03	1.51E+03	1.01E+04	2.34E+03	7.62E+02	2.22E+03	1.02E+03	2.67E+03	4.54E+03	4.00E+03	781.79964	2	34.15
KIN2	YLR096W	RISQSGQSQHPTR	[3] Phospho (ST)	1.35	-0.65	-0.13	2.00	0.075	0.310	0.438	0.04	1.32E+03	5.49E+03	1.36E+03	6.96E+03	3.59E+03	1.03E+04	4.20E+03	5.53E+02	4.26E+02	2.64E+03	1.70E+03	3.11E+03	781.36544	2	36.37
YFL042C	YFL042C	RISNATIAEIGSPLQQVEKPDEVK	[3] Phospho (ST)	-1.06	-0.04	-0.35	-1.03	0.163	0.481	0.338	0.04	2.55E+03	1.84E+04	8.86E+03	4.57E+03	5.41E+03	4.29E+03	1.37E+04	6.48E+03	8.93E+03	5.68E+03	7.94E+03	9.79E+03	901.46417	3	23.01
SDS23	YGL056C	NTEANKSDTESLHK	[11] Phospho (ST)	1.02	-1.12	-0.35	2.14	0.023	0.065	0.223	0.01	4.73E+03	3.21E+03	2.51E+03	6.31E+03	5.74E+03	9.22E+03	1.52E+03	3.51E+02	2.92E+03	1.98E+03	2.24E+03	3.95E+03	827.3598	2	15.87
TAO3	YIL129C	SSSHFAADR	[3] Phospho (ST)	0.86	-0.04	-0.02	0.90	0.050	0.460	0.485	0.02	2.88E+03	1.29E+03	1.50E+03	3.12E+03	2.73E+03	4.47E+03	2.06E+03	1.76E+03	1.68E+03	2.89E+03	1.49E+03	1.21E+03	529.20885	2	26
ESF1	YDR365C	AYLASDSDESDGQVDEEAK	[2] Phospho (Y)|[5] Phospho (ST)|[7] Phospho	-0.25	-1.60	-1.84	1.35	0.408	0.052	0.027	0.23	2.03E+04	4.95E+04	4.86E+04	1.53E+02	7.91E+04	2.00E+04	6.19E+02	2.85E+04	9.83E+03	2.56E+03	1.67E+04	1.36E+04	1134.8805	2	17.91
STU2	YLR045C	SILSNDEGEYQIDK	[1] Phospho (ST)	0.38	0.55	0.47	-0.18	0.185	0.016	0.071	0.28	4.41E+03	6.74E+03	4.87E+03	9.74E+03	5.25E+03	5.82E+03	7.40E+03	8.39E+03	7.72E+03	9.15E+03	6.23E+03	6.89E+03	845.86489	2	55
SSK1	YLR006C	RASQELKDEEK	[3] Phospho (ST)	-0.22	-0.94	0.01	0.72	0.359	0.216	0.485	0.30	3.75E+03	1.93E+03	3.41E+03	1.52E+03	1.77E+03	4.51E+03	4.72E+03	0.00E+00	0.00E+00	2.68E+03	2.93E+03	3.55E+03	471.55148	3	15.21
LDB19	YOR322C	STFGSALSSR	[2] Phospho (ST)	0.61	0.90	0.39	-0.29	0.059	0.050	0.245	0.19	7.30E+02	1.83E+03	1.27E+03	1.72E+03	1.99E+03	2.18E+03	1.66E+03	3.11E+03	2.41E+03	1.05E+03	2.50E+03	1.50E+03	546.73982	2	40
YTA7	YGR270W	NRRGSDVEDASNAK	[5] Phospho (ST)	0.67	-0.41	0.03	1.08	0.293	0.250	0.468	0.22	5.12E+03	3.16E+03	2.26E+03	3.01E+03	1.43E+03	1.23E+04	3.55E+03	9.82E+02	3.38E+03	4.36E+03	2.47E+03	3.97E+03	533.56721	3	60.37
MOT1	YPL082C	MTSRVSR	[6] Phospho (ST)	0.26	-0.30	-0.10	0.56	0.200	0.124	0.277	0.07	3.45E+03	2.63E+03	3.57E+03	2.81E+03	3.84E+03	4.92E+03	3.26E+03	2.20E+03	2.39E+03	3.22E+03	3.06E+03	2.75E+03	458.7052	2	17.97
TAF2	YCR042C	EKEDTPEHDEEEEGKPAR	[5] Phospho (ST)	0.40	-0.40	-0.81	0.80	0.163	0.269	0.068	0.08	5.74E+03	3.36E+03	2.80E+03	5.61E+03	3.91E+03	6.18E+03	5.13E+03	1.39E+03	2.50E+03	2.22E+03	1.99E+03	2.56E+03	551.97944	4	18.03
BRE2	YLR015W	ENADDSVDEVQSGIYEK	[6] Phospho (ST)	0.96	1.80	1.94	-0.84	0.033	0.010	0.001	0.04	2.24E+03	4.31E+03	6.64E+03	9.28E+03	6.44E+03	1.00E+04	1.86E+04	1.74E+04	1.02E+04	1.77E+04	1.47E+04	1.83E+04	989.40425	2	29.66
HOF1	YMR032W	SSPVQLQSNVDDSVLR	[2] Phospho (ST)	0.20	2.20	1.20	-2.00	0.331	0.003	0.026	0.00	1.61E+03	3.41E+03	2.31E+03	2.27E+03	3.90E+03	2.24E+03	1.30E+04	1.27E+04	8.07E+03	7.23E+03	5.97E+03	3.69E+03	912.43042	2	43.62
FLC2	YAL053W	NDSELFELR	[3] Phospho (ST)	1.99	1.89	1.58	0.10	0.112	0.012	0.032	0.45	0.00E+00	1.39E+03	1.33E+03	6.60E+02	7.02E+03	3.26E+03	2.43E+03	3.48E+03	4.27E+03	1.61E+03	3.34E+03	3.22E+03	601.75862	2	50.05
RAD53	YPL153C	SIEAETR	[1] Phospho (ST)	-3.81	-4.89	-3.92	1.07	0.037	0.033	0.036	0.06	6.34E+03	1.40E+03	3.39E+03	3.94E+02	2.00E+02	1.74E+02	1.20E+02	1.31E+02	9.47E+01	2.08E+02	2.18E+02	2.80E+02	443.18917	2	15.12
NOP6	YDL213C	RPNSAAGNDGEEPVK	[4] Phospho (ST)	2.42	1.54	1.89	0.88	0.009	0.039	0.009	0.04	0.00E+00	8.49E+02	2.25E+03	4.33E+03	4.92E+03	7.48E+03	3.20E+03	2.02E+03	3.86E+03	4.08E+03	3.27E+03	4.23E+03	810.85446	2	31.78
CMP2	YML057W	TERPQSSTTPIDSK	[6] Phospho (ST)	-0.17	0.03	-0.68	-0.20	0.156	0.412	0.019	0.05	3.27E+03	2.46E+03	3.22E+03	2.85E+03	2.50E+03	2.62E+03	3.09E+03	2.77E+03	3.30E+03	2.37E+03	1.55E+03	1.66E+03	813.87226	2	19.85
YDR365W-B	R365W-B	AHNVSTSNNSPSTDNDSISK	[19] Phospho (ST)	0.21	0.15	-0.09	0.07	0.352	0.419	0.448	0.44	7.18E+03	6.19E+03	1.90E+04	1.11E+04	1.45E+04	1.20E+04	7.41E+03	1.03E+04	1.82E+04	1.38E+04	1.00E+04	6.63E+03	718.9693	3	18.48
NUP60	YAR002W	SRSNLSQENDNEGK	[3] Phospho (ST)	-3.10	-2.15	-0.32	-0.95	0.021	0.033	0.331	0.08	1.08E+04	4.61E+03	4.77E+03	9.27E+02	7.47E+02	6.43E+02	1.89E+03	1.96E+03	6.61E+02	9.29E+03	3.28E+03	3.61E+03	829.34446	2	49.89
DUN1	YDL101C	REHSGDVTDSSFK	[4] Phospho (ST)|[11] Phospho (ST)	-7.08	-6.35	-3.14	-0.74	0.011	0.011	0.016	0.19	1.71E+04	6.80E+03	9.82E+03	1.49E+02	2.12E+01	4.92E+01	8.07E+01	9.37E+01	2.09E+02	1.86E+03	7.61E+02	1.18E+03	812.80615	2	16.06
LCP5	YER127W	VTSFEEDNFTR	[3] Phospho (ST)	-3.75	-2.80	-1.16	-0.94	0.000	0.000	0.001	0.22	9.66E+03	1.03E+04	1.00E+04	0.00E+00	1.35E+03	8.59E+02	2.79E+03	5.42E+02	9.39E+02	2.87E+03	5.59E+03	4.98E+03	712.79092	2	36.88
BNI4	YNL233W	DSEVQTVNMTTSPSLSALADILNER	[14] Phospho (ST)	-0.47	0.12	0.29	-0.59	0.206	0.394	0.284	0.12	1.36E+04	2.40E+04	1.16E+04	1.09E+04	1.78E+04	6.77E+03	2.37E+04	1.60E+04	1.37E+04	1.67E+04	2.90E+04	1.45E+04	924.43278	3	45.93
KCC4	YCL024W	FLGSLLNVR	[4] Phospho (ST)	-0.64	-0.22	-0.67	-0.42	0.313	0.422	0.303	0.28	0.00E+00	1.28E+04	4.80E+03	1.12E+03	5.87E+03	4.29E+03	7.53E+03	2.81E+03	4.75E+03	2.36E+03	5.95E+03	2.73E+03	549.78952	2	47.24
MON2	YNL297C	NISTSSVTTSPVESTK	[3] Phospho (ST)	1.59	3.56	2.93	-1.97	0.196	0.001	0.000	0.01	0.00E+00	8.66E+02	2.14E+03	7.00E+02	1.34E+03	7.11E+03	9.37E+03	1.39E+04	1.27E+04	7.07E+03	8.46E+03	7.57E+03	859.39788	2	48.59
DIG1	YPL049C	SEEGSRNSSVGSSANAGPTQQR	[5] Phospho (ST)	-0.85	-0.58	-0.57	-0.27	0.016	0.066	0.123	0.22	4.85E+03	3.57E+03	3.25E+03	2.02E+03	1.86E+03	2.58E+03	1.73E+03	2.70E+03	3.38E+03	4.18E+03	1.55E+03	2.14E+03	762.66338	3	16.23
MCM3	YEL032W	VRQPASNSGSPIK	[8] Phospho (ST)	0.36	0.68	1.01	-0.32	0.274	0.117	0.026	0.18	7.73E+02	1.53E+03	3.00E+03	1.61E+03	2.23E+03	2.97E+03	3.48E+03	2.12E+03	2.93E+03	3.69E+03	3.37E+03	3.65E+03	710.8507	2	26.01
SSB2	YNL209W	RFDDESVQK	[6] Phospho (ST)	0.33	0.18	0.14	0.15	0.260	0.374	0.400	0.30	4.61E+02	2.14E+03	2.02E+03	1.90E+03	2.24E+03	1.67E+03	1.62E+03	2.29E+03	1.35E+03	1.36E+03	1.61E+03	2.14E+03	602.25548	2	15.6
TGL4	YKR089C	NPENSTLLTRTPTK	[11] Phospho (ST)	0.25	-0.09	0.08	0.34	0.326	0.469	0.452	0.36	1.08E+03	4.96E+03	4.47E+03	2.86E+03	4.76E+03	4.93E+03	7.73E+03	1.69E+03	4.69E+02	1.73E+03	4.16E+03	5.25E+03	826.40604	2	17.79
ECM30	YLR436C	SRGQSSVSLER	[5] Phospho (ST)	0.28	0.76	-0.37	-0.48	0.221	0.017	0.230	0.04	1.49E+03	2.93E+03	2.07E+03	3.36E+03	2.15E+03	2.40E+03	3.93E+03	3.22E+03	3.85E+03	2.41E+03	9.38E+02	1.68E+03	643.29961	2	21.75
IDS2	YJL146W	ESVSDILNDLTLGSPEPSER	[2] Phospho (ST)	0.06	0.06	-0.26	0.00	0.462	0.465	0.314	0.50	5.50E+03	1.09E+04	3.85E+03	4.85E+03	1.09E+04	5.33E+03	1.10E+04	2.62E+03	7.56E+03	5.49E+03	5.74E+03	5.67E+03	746.67855	3	29.1

YPT31	YER031C	SSEDYGYDYDLLFK	[N-term] Acetyl (Protein N-term)|[5] Phospho	-0.25	0.53	-0.59	-0.77	0.372	0.245	0.232	0.14	1.08E+04	2.41E+04	5.94E+03	9.87E+03	1.72E+04	7.36E+03	2.43E+04	2.64E+04	8.22E+03	6.83E+03	1.22E+04	8.13E+03	918.86692	2	23.94
HTS1	YPR033C	SSSIIR	[3] Phospho (ST)	6.26	5.85	5.88	0.41	0.000	0.001	0.000	0.06	0.00E+00	4.43E+01	0.00E+00	2.01E+03	1.64E+03	2.24E+03	1.20E+03	1.42E+03	1.80E+03	1.37E+03	1.48E+03	1.67E+03	371.67847	2	15.02
BUD3	YCL014W	RAVVSSPK	[6] Phospho (ST)	1.10	1.80	1.23	-0.70	0.084	0.031	0.001	0.16	1.15E+03	1.63E+03	1.39E+03	3.25E+03	1.24E+03	4.46E+03	7.38E+03	2.79E+03	4.39E+03	3.55E+03	2.83E+03	3.48E+03	462.23902	2	20.19
TAH11	YJR046W	TVLSSK	[5] Phospho (ST)	0.35	0.37	0.16	-0.02	0.206	0.161	0.371	0.48	1.34E+03	1.34E+03	1.79E+03	2.75E+03	1.34E+03	1.64E+03	1.23E+03	2.46E+03	2.13E+03	2.63E+03	1.24E+03	1.15E+03	357.67516	2	18.28
SHS1	YDL225W	KNDTYTDLASIASGRD	[13] Phospho (ST)	0.08	-0.16	-0.39	0.24	0.460	0.439	0.340	0.37	5.82E+02	1.01E+04	5.75E+03	7.59E+03	6.23E+03	3.60E+03	7.65E+03	6.68E+03	3.83E+02	2.87E+03	6.06E+03	3.63E+03	903.89817	2	19.96
IMH1	YLR309C	GGITTGDISEEETVDNSINTEEYDK	[9] Phospho (ST)	0.36	1.11	-0.12	-0.75	0.287	0.004	0.379	0.05	5.07E+03	7.60E+03	3.44E+03	3.05E+03	1.05E+04	7.12E+03	1.21E+04	1.18E+04	1.09E+04	4.40E+03	5.83E+03	4.59E+03	932.72542	3	28.13
BEM3	YPL115C	GSKSPLQER	[2] Phospho (ST)	0.10	-0.66	-0.26	0.77	0.439	0.218	0.355	0.09	3.91E+03	9.94E+02	1.67E+03	2.85E+03	1.35E+03	2.87E+03	1.99E+03	9.41E+02	1.22E+03	2.25E+03	1.68E+03	1.55E+03	541.25322	2	17.55
ETT1	YOR051C	SDEPSRESTPVR	[1] Phospho (ST)	0.07	0.39	0.81	-0.32	0.425	0.206	0.013	0.25	1.23E+03	2.16E+03	2.20E+03	1.54E+03	1.69E+03	2.65E+03	3.43E+03	1.51E+03	2.42E+03	3.45E+03	2.77E+03	3.60E+03	720.31189	2	17.73
DCS2	YOR173W	RPSQSGRSTPIFFHR	[3] Phospho (ST)|[5] Phospho (ST)	2.07	-0.72	0.65	2.79	0.013	0.285	0.217	0.01	0.00E+00	2.40E+03	3.67E+03	1.16E+04	7.60E+03	6.44E+03	2.63E+03	6.66E+02	3.78E+02	4.31E+03	1.69E+03	3.52E+03	483.97136	4	17.21
GLN1	YPR035W	GSSIRIPR	[3] Phospho (ST)	0.04	0.58	-0.26	-0.54	0.444	0.230	0.221	0.25	2.38E+03	1.65E+03	1.73E+03	1.53E+03	1.83E+03	2.57E+03	5.14E+03	1.28E+03	2.23E+03	1.00E+03	1.88E+03	1.91E+03	483.24916	2	15.97
STH1	YIL126W	TISIVTAEDK	[3] Phospho (ST)	0.04	1.79	0.72	-1.74	0.459	0.016	0.050	0.02	2.56E+03	1.84E+03	1.05E+03	2.38E+03	1.66E+03	1.58E+03	8.38E+03	3.84E+03	6.66E+03	2.32E+03	3.48E+03	3.21E+03	578.77808	2	31.51
LCB4	YOR171C	APVSESQSFPK	[8] Phospho (ST)	1.81	1.15	0.59	0.66	0.004	0.038	0.256	0.01	2.36E+02	2.15E+03	2.88E+03	6.31E+03	6.90E+03	5.27E+03	4.04E+03	3.10E+03	4.58E+03	4.49E+03	1.39E+03	2.04E+03	628.78236	2	20.96
MTR4	YJL050W	VVVPVLADSFEQEASR	[9] Phospho (ST)	1.58	-1.90	-0.94	3.48	0.016	0.103	0.197	0.00	1.69E+03	1.20E+04	5.06E+03	1.60E+04	2.35E+04	1.66E+04	1.27E+03	2.08E+03	1.65E+03	1.57E+03	4.62E+03	3.52E+03	913.44127	2	40.47
BEM3	YPL115C	RPHASSVSTVK	[6] Phospho (ST)	-0.29	-0.93	-0.81	0.64	0.342	0.216	0.070	0.33	7.19E+03	4.41E+03	3.51E+03	2.07E+03	2.65E+03	7.64E+03	7.67E+03	1.70E+02	8.63E+01	2.32E+03	2.64E+03	3.66E+03	624.80828	2	21.71
BFR2	YDR299W	LPELISPVVK	[6] Phospho (ST)	0.63	0.48	0.08	0.15	0.213	0.302	0.466	0.42	1.52E+03	6.92E+03	2.62E+03	3.56E+03	8.77E+03	4.79E+03	9.04E+03	2.24E+03	4.18E+03	8.50E+02	6.17E+03	4.67E+03	587.82861	2	28.64
MCM3	YEL032W	VRQPASNSGSPIK	[6] Phospho (ST)	-0.11	-0.64	0.08	0.53	0.378	0.089	0.407	0.10	1.94E+03	3.53E+03	3.60E+03	2.46E+03	2.28E+03	3.64E+03	1.49E+03	1.62E+03	2.71E+03	3.57E+03	2.27E+03	3.76E+03	710.85111	2	26.11
TAP42	YMR028W	ELYLMR	[3] Phospho (Y)	0.83	0.44	0.55	0.38	0.040	0.277	0.140	0.23	5.68E+02	3.91E+02	1.08E+03	1.42E+03	1.11E+03	1.12E+03	1.46E+03	3.29E+02	1.00E+03	1.28E+03	9.71E+02	7.52E+02	452.70397	2	19.67
TIF4631	YGR162W	STVSPQPESK	[4] Phospho (ST)	1.62	0.57	0.34	1.04	0.056	0.069	0.098	0.10	2.01E+03	1.70E+03	1.64E+03	5.12E+03	2.54E+03	8.84E+03	3.34E+03	1.79E+03	2.85E+03	2.79E+03	1.80E+03	2.20E+03	570.2518	2	32.86
RHO4	YKR055W	LPTPFAR	[3] Phospho (ST)	1.48	0.88	0.19	0.60	0.013	0.107	0.386	0.11	5.26E+02	1.81E+03	1.64E+03	2.73E+03	4.66E+03	3.80E+03	3.23E+03	1.16E+03	2.98E+03	5.78E+02	1.92E+03	2.06E+03	441.21773	2	21.05
SSK1	YLR006C	SSVSPTAGSFGLSK	[4] Phospho (ST)	0.19	0.39	-0.27	-0.20	0.386	0.280	0.370	0.25	1.07E+03	6.40E+03	2.89E+03	4.44E+03	4.27E+03	3.15E+03	4.45E+03	5.74E+03	3.40E+03	3.10E+03	3.69E+03	1.80E+03	702.82417	2	36.09
GLC8	YMR311C	SREALKDEDEDEDDSTTK	[1] Phospho (ST)	-0.06	0.04	0.39	-0.10	0.353	0.431	0.130	0.32	3.53E+03	3.14E+03	4.23E+03	3.72E+03	3.24E+03	3.51E+03	4.65E+03	3.10E+03	3.46E+03	6.00E+03	3.26E+03	5.02E+03	721.62511	3	23.06
TIF4632	YGL049C	ANMFDALMNNDGDSD	[14] Phospho (ST)	-0.16	0.56	0.40	-0.72	0.455	0.311	0.264	0.33	8.31E+03	1.48E+04	7.34E+03	4.57E+02	2.63E+04	3.55E+02	1.04E+03	3.06E+04	1.30E+04	9.20E+03	9.42E+03	2.14E+04	855.29599	2	16.42
VTC3	YPL019C	LSHFSNLEDASFK	[5] Phospho (ST)	-0.70	0.41	0.72	-1.11	0.133	0.306	0.160	0.13	2.88E+03	6.48E+03	3.09E+03	3.13E+03	2.77E+03	1.75E+03	9.84E+03	3.71E+03	2.96E+03	2.87E+03	9.71E+03	7.89E+03	787.84868	2	37.81
YBL086C	YBL086C	DNNSVEDNNPTDFLTDR	[4] Phospho (ST)	-0.11	-0.45	0.16	0.35	0.334	0.036	0.269	0.10	1.23E+04	1.61E+04	1.21E+04	1.26E+04	1.53E+04	9.73E+03	8.37E+03	1.07E+04	1.05E+04	1.26E+04	1.89E+04	1.36E+04	1023.4084	2	61.82
MPT5	YGL178W	RSNSSVTNNFSNQYAQDQK	[4] Phospho (ST)	-0.26	-0.84	-0.25	0.59	0.093	0.019	0.128	0.05	1.15E+04	1.52E+04	1.28E+04	1.12E+04	1.23E+04	9.51E+03	6.75E+03	1.03E+04	4.94E+03	1.22E+04	8.77E+03	1.23E+04	1134.4886	2	26.06
SPN1	YPR133C	VVEATPEDGTASSQK	[5] Phospho (ST)	0.00	0.76	0.15	-0.76	0.495	0.101	0.341	0.08	1.65E+03	3.75E+03	4.14E+03	3.42E+03	2.69E+03	3.46E+03	6.35E+03	2.95E+03	6.87E+03	3.19E+03	3.36E+03	4.06E+03	799.85166	2	24.93
COX20	YDR231C	SFQIAQLAK	[1] Phospho (ST)	0.77	0.40	-0.16	0.37	0.070	0.123	0.352	0.14	1.04E+03	2.07E+03	1.14E+03	2.07E+03	3.31E+03	1.91E+03	1.82E+03	1.79E+03	2.01E+03	9.94E+02	1.45E+03	1.37E+03	543.27402	2	21.99
RPS12	YOR369C	SDVEEVVEVQEETVVEQTAEVTIEDALK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.72	-0.18	-0.82	0.90	0.067	0.369	0.076	0.06	1.76E+05	1.14E+05	8.82E+04	2.28E+05	2.54E+05	1.39E+05	5.16E+04	1.65E+05	1.16E+05	4.60E+04	1.03E+05	6.38E+04	1080.5049	3	19.07
ARE1	YCR048W	RLNSAEANK	[4] Phospho (ST)	1.42	-0.05	-0.86	1.47	0.080	0.473	0.163	0.09	2.38E+03	2.71E+03	1.58E+03	7.91E+03	1.67E+03	8.32E+03	3.65E+02	2.33E+03	3.74E+03	7.56E+02	2.83E+03	7.25E+01	541.75357	2	28.55
PIB2	YGL023C	KNSAEENVR	[3] Phospho (ST)	2.35	1.46	1.15	0.89	0.043	0.022	0.119	0.14	1.18E+03	1.98E+03	8.95E+02	1.01E+04	2.12E+03	8.50E+03	5.22E+03	2.82E+03	3.16E+03	5.32E+03	1.96E+03	1.76E+03	563.74845	2	46.55
SKO1	YNL167C	NNSTSTITQHSQR	[3] Phospho (ST)	-0.59	0.51	0.64	-1.10	0.294	0.254	0.248	0.01	1.47E+03	4.68E+02	4.47E+03	1.16E+03	1.25E+03	1.84E+03	2.37E+03	3.23E+03	3.54E+03	5.45E+03	2.03E+03	2.53E+03	777.33895	2	23.75
SLI15	YBR156C	TVKESPIAFK	[5] Phospho (ST)	-0.12	0.58	0.12	-0.70	0.447	0.250	0.445	0.12	6.21E+02	3.22E+03	7.74E+02	8.49E+02	1.75E+03	1.64E+03	3.46E+03	1.83E+03	1.60E+03	1.66E+03	2.07E+03	1.28E+03	600.30739	2	17.53
SEC16	YPL085W	TGLGTPNQQVSVPNIVSPKPPVVK	[17] Phospho (ST)	-0.32	0.52	-1.43	-0.84	0.383	0.271	0.178	0.05	1.05E+03	1.29E+04	3.84E+03	3.55E+03	6.62E+03	4.10E+03	5.71E+03	9.92E+03	9.90E+03	1.95E+03	2.23E+03	2.43E+03	846.12367	3	25.18
SPT2	YER161C	KASPGATLR	[3] Phospho (ST)	0.29	-0.06	-0.81	0.34	0.235	0.452	0.046	0.22	2.13E+03	1.09E+03	1.55E+03	1.56E+03	1.67E+03	2.61E+03	2.11E+03	9.17E+02	1.57E+03	7.34E+02	9.64E+02	1.01E+03	490.7496	2	21.29
CRP1	YHR146W	KQTASPLSSSTEEPK	[5] Phospho (ST)	0.56	-0.17	-0.13	0.72	0.006	0.384	0.268	0.09	3.32E+03	3.04E+03	3.19E+03	5.28E+03	4.71E+03	4.11E+03	4.99E+03	1.57E+03	1.95E+03	2.16E+03	3.13E+03	3.45E+03	835.38884	2	21.47
TGL4	YKR089C	RHSIDGRPPSQATK	[3] Phospho (ST)	0.04	-0.47	-0.32	0.52	0.399	0.214	0.039	0.20	3.97E+03	3.77E+03	3.53E+03	4.59E+03	3.23E+03	3.79E+03	5.03E+03	1.12E+03	1.96E+03	2.64E+03	2.79E+03	3.58E+03	408.20174	4	19.24
ENP2	YGR145W	RHDNSSDEEGIDENGNK	[5] Phospho (ST)|[6] Phospho (ST)	0.67	-0.60	-0.28	1.27	0.150	0.187	0.285	0.06	7.26E+03	5.64E+03	1.34E+04	1.12E+04	2.12E+04	9.42E+03	2.83E+03	9.10E+03	5.41E+03	8.74E+03	5.75E+03	7.12E+03	1038.3713	2	20.44
RAD23	YEL037C	TESASTPGFVVGTER	[6] Phospho (ST)	0.41	0.42	-0.34	0.00	0.160	0.192	0.262	0.50	7.35E+03	1.34E+04	5.17E+03	1.04E+04	1.24E+04	1.18E+04	1.46E+04	1.10E+04	9.01E+03	5.22E+03	8.30E+03	6.93E+03	809.36186	2	15.87
PPS1	YBR276C	NRADTVVSDK	[5] Phospho (ST)	0.49	0.04	0.23	0.45	0.318	0.489	0.388	0.38	1.30E+03	1.83E+03	5.61E+02	1.25E+03	3.48E+03	4.57E+02	3.48E+03	1.51E+02	1.62E+02	2.36E+03	3.31E+02	1.63E+03	592.76801	2	24.15
SAR1	YPL218W	SALGLLNTTGSQR	[11] Phospho (ST)	1.47	-0.72	-1.36	2.19	0.053	0.279	0.163	0.02	0.00E+00	3.38E+03	2.10E+03	2.69E+03	6.60E+03	5.94E+03	2.06E+02	1.01E+03	2.10E+03	6.18E+02	1.08E+03	4.11E+02	699.34289	2	15.62
STE20	YHL007C	SPVMNSAANVSPLK	[11] Phospho (ST)	-0.88	-0.55	0.61	-0.34	0.008	0.027	0.069	0.14	7.57E+03	8.59E+03	1.00E+04	5.06E+03	5.68E+03	3.44E+03	6.14E+03	7.13E+03	4.65E+03	8.62E+03	1.63E+04	1.51E+04	747.85785	2	21.81
PHO4	YFR034C	RSSGALVDDDK	[3] Phospho (ST)	0.54	0.06	-0.01	0.48	0.075	0.443	0.492	0.12	3.93E+03	2.06E+03	3.36E+03	3.64E+03	4.37E+03	5.61E+03	3.51E+03	1.89E+03	4.37E+03	2.76E+03	3.25E+03	3.30E+03	621.77082	2	28.34
THS1	YIL078W	DISESPER	[3] Phospho (ST)	-1.10	-2.81	-2.14	1.70	0.287	0.179	0.200	0.18	9.68E+03	3.04E+02	1.03E+03	3.89E+03	7.57E+02	4.83E+02	1.25E+03	1.18E+02	1.81E+02	1.23E+03	1.07E+03	1.81E+02	506.70287	2	17.18
TCB3	YML072C	SFDRR	[1] Phospho (ST)	1.20	0.69	0.84	0.51	0.120	0.059	0.143	0.26	1.97E+03	1.48E+03	1.24E+03	5.01E+03	6.72E+02	5.17E+03	3.22E+03	1.72E+03	2.66E+03	4.77E+03	1.83E+03	1.80E+03	380.66104	2	16.28
PCL6	YER059W	HESPSNESSLDK	[3] Phospho (ST)	0.28	-2.07	-1.06	2.35	0.303	0.045	0.100	0.01	6.95E+03	2.54E+03	3.23E+03	6.73E+03	3.61E+03	5.12E+03	1.55E+03	4.38E+01	1.42E+03	1.71E+03	1.45E+03	2.93E+03	705.28199	2	40.69
DIG1	YPL049C	NSSVGSSANAGPTQQR	[3] Phospho (ST)	-0.14	-0.60	-0.46	0.46	0.389	0.178	0.200	0.12	7.83E+03	2.75E+03	4.84E+03	5.41E+03	3.86E+03	4.75E+03	1.99E+03	3.39E+03	4.79E+03	3.70E+03	3.25E+03	4.23E+03	820.85716	2	52.58
FBA1	YKL060C	FAIPAINVTSSSTAVAALEAAR	[13] Phospho (ST)	-0.90	0.51	0.17	-1.40	0.222	0.308	0.417	0.10	5.74E+03	1.50E+04	1.58E+03	2.93E+03	5.79E+03	3.24E+03	1.89E+04	5.66E+03	7.19E+03	8.37E+03	1.12E+04	5.62E+03	747.38292	3	16.59
YDR239C	YDR239C	SLQQVSK	[1] Phospho (ST)	0.50	-0.40	-0.01	0.89	0.197	0.299	0.496	0.04	2.56E+03	5.69E+02	1.45E+03	2.49E+03	1.50E+03	2.48E+03	6.42E+02	1.20E+03	1.63E+03	2.91E+03	9.93E+02	6.48E+02	435.20972	2	28.13
BUL2	YML111W	SASTTNLDR	[3] Phospho (ST)	0.26	-0.35	0.05	0.61	0.320	0.293	0.475	0.04	3.79E+03	9.22E+02	2.18E+03	2.98E+03	2.01E+03	3.29E+03	1.66E+03	2.09E+03	1.64E+03	4.08E+03	1.94E+03	1.11E+03	522.72152	2	38.32
RPS24B	YIL069C	VISNPLLAR	[3] Phospho (ST)	0.15	0.08	0.07	0.07	0.426	0.462	0.467	0.44	8.91E+02	4.80E+03	1.47E+03	1.70E+03	3.71E+03	2.56E+03	3.63E+03	1.57E+03	2.38E+03	1.18E+03	3.40E+03	2.96E+03	531.78927	2	36.86
ECM30	YLR436C	GQSSVSLER	[3] Phospho (ST)	1.03	1.19	0.61	-0.16	0.020	0.056	0.094	0.37	5.57E+02	9.53E+02	1.19E+03	2.27E+03	1.91E+03	1.38E+03	1.07E+03	2.93E+03	2.20E+03	1.15E+03	1.86E+03	1.12E+03	521.73157	2	38.75
YDR186C	YDR186C	SLSLMDPALQK	[3] Phospho (ST)	-0.22	-0.12	0.10	-0.10	0.420	0.455	0.455	0.46	5.35E+02	4.81E+03	2.16E+03	2.34E+03	3.85E+03	2.56E+02	3.97E+03	2.60E+03	3.34E+02	1.74E+03	4.26E+03	2.03E+03	641.81003	2	39.96
ITC1	YGL133W	SNSANVSSPESEK	[3] Phospho (ST)	-1.59	-1.93	-0.01	0.34	0.034	0.023	0.496	0.25	3.57E+03	3.19E+03	6.87E+03	2.28E+03	1.17E+03	1.06E+03	1.02E+03	9.84E+02	1.56E+03	7.59E+03	3.72E+03	2.26E+03	708.28926	2	39.42
CDC48	YDL126C	GGSLGDAGGASDR	[3] Phospho (ST)	-0.76	0.27	0.11	-1.03	0.135	0.282	0.436	0.00	2.78E+03	8.18E+02	1.82E+03	1.18E+03	1.18E+03	8.29E+02	1.90E+03	2.11E+03	2.53E+03	3.27E+03	1.59E+03	1.02E+03	600.23811	2	35.18
STE11	YLR362W	LSIAQR	[2] Phospho (ST)	1.46	0.97	0.74	0.49	0.012	0.125	0.089	0.16	1.30E+02	7.15E+02	5.34E+02	1.22E+03	1.06E+03	1.57E+03	3.44E+02	1.11E+03	1.28E+03	6.35E+02	9.44E+02	7.53E+02	384.19402	2	26.1
HAL5	YJL165C	NSLSTPR	[2] Phospho (ST)	1.42	-1.07	-0.02	2.49	0.017	0.099	0.492	0.01	6.67E+02	6.02E+02	1.22E+03	2.70E+03	2.60E+03	1.44E+03	7.48E+02	3.55E+01	3.89E+02	1.53E+03	6.08E+02	3.27E+02	427.69214	2	22.14
BIK1	YCL029C	NRSIVR	[3] Phospho (ST)	0.80	0.81	0.82	-0.01	0.127	0.019	0.075	0.49	9.93E+02	8.07E+02	9.10E+02	1.64E+03	6.77E+02	2.44E+03	2.04E+03	1.34E+03	1.41E+03	2.39E+03	1.19E+03	1.25E+03	412.71041	2	15.93
XRN1	YGL173C	KGEIKPSSGTNSTECQSPK	[12] Phospho (ST)	-1.32	-1.19	-0.97	-0.13	0.110	0.125	0.160	0.42	1.03E+04	3.42E+03	3.48E+03	1.72E+03	1.65E+03	3.51E+03	1.51E+03	2.12E+03	3.90E+03	4.79E+03	1.50E+03	2.45E+03	705.65252	3	15.96
POL12	YBL035C	SLNSSPLFGLSIPK	[4] Phospho (ST)|[5] Phospho (ST)	2.04	4.83	3.58	-2.79	0.024	0.036	0.002	0.05	3.38E+02	1.99E+03	4.01E+02	3.99E+03	5.13E+03	2.18E+03	1.39E+04	4.67E+04	1.78E+04	1.29E+04	1.20E+04	8.07E+03	810.37907	2	30.53
MAP2	YBL091C	ADESDPVESKK	[4] Phospho (ST)	1.76	0.64	0.30	1.11	0.004	0.094	0.264	0.01	1.44E+03	5.76E+02	9.23E+02	3.75E+03	2.50E+03	3.76E+03	1.97E+03	1.12E+03	1.51E+03	1.67E+03	9.95E+02	9.77E+02	642.77128	2	43.52
IRC8	YJL051W	NQSIDFSYVR	[3] Phospho (ST)	-0.84	2.07	1.18	-2.91	0.142	0.006	0.044	0.00	7.00E+02	1.76E+03	6.83E+02	7.95E+02	5.75E+02	3.74E+02	3.99E+03	5.74E+03	3.56E+03	1.56E+03	3.22E+03	2.40E+03	654.78508	2	23.28
YOX1	YML027W	RPVSNPSGSPK	[9] Phospho (ST)	1.90	0.36	-0.40	1.54	0.074	0.324	0.311	0.09	6.59E+02	2.61E+03	8.42E+02	5.17E+03	1.66E+03	8.63E+03	2.64E+03	9.17E+02	1.74E+03	1.07E+03	9.18E+02	1.13E+03	603.28706	2	18.41
ZRG8	YER033C	RNNSDDETEHTSAIK	[4] Phospho (ST)	-1.29	-0.05	0.53	-1.24	0.161	0.477	0.310	0.02	7.18E+03	1.74E+03	1.88E+03	9.50E+02	7.53E+02	2.70E+03	4.05E+03	2.80E+03	3.61E+03	9.99E+03	3.22E+03	2.42E+03	898.87551	2	30.46
SPT7	YBR081C	SRSDLEAATDEQDRENTNDEPDTNQK	[1] Phospho (ST)	-2.61	-2.17	-0.77	-0.44	0.000	0.000	0.003	0.21	1.75E+04	1.86E+04	1.60E+04	3.83E+03	2.07E+03	2.61E+03	2.00E+03	5.34E+03	4.22E+03	1.10E+04	7.92E+03	1.16E+04	1020.0894	3	17.84
LHP1	YDL051W	SRSFNGHK	[3] Phospho (ST)	1.61	0.06	0.84	1.55	0.259	0.471	0.153	0.27	2.24E+03	3.42E+03	1.24E+03	2.04E+04	3.28E+00	7.72E+02	3.86E+03	3.29E+03	5.95E+01	6.95E+03	2.92E+03	2.49E+03	506.72179	2	16.57
SKY1	YMR216C	SSDITANDSSDEK	[9] Phospho (ST)	1.69	0.56	1.86	1.12	0.027	0.232	0.159	0.05	1.79E+03	6.21E+02	4.87E+02	4.47E+03	2.13E+03	2.83E+03	1.65E+03	2.01E+03	6.50E+02	8.00E+03	1.57E+03	1.08E+03	724.77472	2	39.09
HSL1	YKL101W	ISEESSQLVLPVVEK	[6] Phospho (ST)	-0.80	-0.19	-0.23	-0.61	0.095	0.322	0.303	0.04	5.86E+03	1.32E+04	8.18E+03	5.46E+03	7.04E+03	3.16E+03	8.85E+03	7.61E+03	7.44E+03	5.70E+03	9.09E+03	8.41E+03	868.93969	2	18.51
SAP190	YKR028W	ISEHRDGNSLYNEDNDENGSDK	[9] Phospho (ST)	-0.86	-1.28	-0.48	0.41	0.006	0.018	0.032	0.22	3.70E+03	2.71E+03	2.79E+03	1.61E+03	1.63E+03	1.80E+03	8.15E+02	7.15E+02	2.24E+03	2.37E+03	1.93E+03	2.29E+03	863.34542	3	15.07
NSR1	YGR159C	RKSEDAEEEEDEESSNK	[3] Phospho (ST)	1.91	1.40	1.24	0.50	0.002	0.043	0.045	0.09	2.05E+03	4.38E+02	1.39E+03	4.43E+03	4.58E+03	5.62E+03	4.88E+03	2.03E+03	3.40E+03	4.38E+03	2.56E+03	2.30E+03	697.60596	3	51.81
MDR1	YGR100W	RVDSVATR	[4] Phospho (ST)	0.38	0.19	-0.59	0.19	0.277	0.383	0.124	0.39	1.72E+03	1.04E+03	7.37E+02	9.97E+02	1.10E+03	2.47E+03	2.12E+03	5.67E+02	1.31E+03	7.78E+02	7.07E+02	8.20E+02	492.23701	2	23.94
PIG2	YIL045W	LNSLEFLHK	[3] Phospho (ST)	-0.72	0.47	0.26	-1.19	0.165	0.295	0.343	0.13	9.21E+02	2.25E+03	9.36E+02	7.43E+02	1.23E+03	5.08E+02	3.49E+03	9.98E+02	1.21E+03	8.22E+02	2.42E+03	1.70E+03	590.7917	2	23.57
AVT4	YNL101W	RSSVSHGNEAIPR	[3] Phospho (ST)	-0.75	-1.13	-0.26	0.38	0.125	0.123	0.218	0.38	3.47E+03	3.14E+03	1.84E+03	3.20E+02	2.60E+03	2.09E+03	3.30E+03	9.92E+01	4.35E+02	1.95E+03	2.66E+03	2.43E+03	745.34901	2	30.96
NUP100	YKL068W	SPNGSTSIPMIENEK	[1] Phospho (ST)	0.20	0.09	1.00	0.11	0.391	0.412	0.032	0.45	2.80E+03	2.06E+03	1.93E+03	2.55E+03	4.58E+03	6.94E+02	1.27E+03	3.21E+03	2.78E+03	2.93E+03	5.81E+03	4.86E+03	842.37338	2	59.53
SUI3	YPL237W	SSDLAAELGFDPALK	[N-term] Acetyl (Protein N-term)|[2] Phospho	-0.59	-0.46	-0.34	-0.13	0.194	0.271	0.257	0.44	4.27E+03	8.54E+03	4.15E+03	1.22E+03	5.73E+03	4.31E+03	7.03E+03	8.24E+02	4.50E+03	4.43E+03	5.92E+03	3.03E+03	828.38322	2	44.82
MTC5	YDR128W	NIHGGDNSSIRSDDHHAR	[9] Phospho (ST)|[12] Phospho (ST)	-0.18	-0.74	-0.43	0.55	0.226	0.046	0.166	0.07	3.38E+03	3.43E+03	4.87E+03	3.92E+03	3.41E+03	2.95E+03	3.35E+03	1.70E+03	1.93E+03	4.43E+03	2.03E+03	2.18E+03	537.71533	4	15.3
SSK1	YLR006C	RASQELKDEEK	[3] Phospho (ST)	0.08	-0.85	0.33	0.93	0.449	0.241	0.201	0.25	3.18E+03	1.64E+03	2.58E+03	2.03E+03	1.32E+03	4.48E+03	4.05E+03	2.61E+01	2.31E+01	2.20E+03	3.14E+03	3.97E+03	706.82398	2	20.79
AKL1	YBR059C	NEALLIELSPLK	[9] Phospho (ST)	1.00	2.83	2.00	-1.84	0.068	0.056	0.040	0.08	4.88E+02	2.07E+03	1.18E+03	1.82E+03	2.21E+03	3.45E+03	1.63E+04	3.82E+03	6.75E+03	4.79E+03	7.79E+03	2.45E+03	710.37811	2	41.8
TPO4	YOR273C	NEPISNSLYSAIK	[9] Phospho (Y)|[10] Phospho (ST)	0.54	-1.05	0.40	1.60	0.359	0.195	0.318	0.21	7.09E+02	6.33E+03	2.52E+03	3.11E+02	1.13E+04	2.30E+03	2.32E+03	1.54E+03	7.34E+02	3.04E+03	6.40E+03	3.17E+03	798.34275	2	18.75
RTT107	YHR154W	LTFGSFSSSSTNK	[5] Phospho (ST)	-5.03	-3.30	-4.14	-1.74	0.006	0.007	0.006	0.05	3.74E+03	7.22E+03	4.17E+03	2.00E+02	2.27E+02	6.11E+00	7.48E+02	5.55E+02	2.12E+02	2.45E+02	2.93E+02	2.95E+02	721.81415	2	33.06
NAB6	YML117W	RGSFAR	[3] Phospho (ST)	1.11	0.86	0.00	0.25	0.028	0.052	0.498	0.26	1.31E+03	7.10E+02	7.14E+02	1.60E+03	1.69E+03	2.68E+03	1.97E+03	1.06E+03	1.98E+03	1.37E+03	6.95E+02	6.72E+02	387.17639	2	17.45
HXT1	YHR094C	SNSSNSYELESGR	[4] Phospho (ST)	-0.31	-0.30	-0.48	-0.01	0.243	0.332	0.190	0.50	3.91E+03	2.34E+03	3.92E+03	4.06E+03	2.16E+03	2.01E+03	8.12E+02	5.09E+03	2.38E+03	3.63E+03	8.76E+02	2.80E+03	755.29758	2	44.44
ABP140	YOR239W	SDFEKSDTEGSR	[6] Phospho (ST)	-2.67	-0.34	-2.01	-2.33	0.136	0.387	0.160	0.03	7.67E+03	1.86E+03	5.05E+02	1.18E+03	1.55E+02	2.08E+02	1.24E+03	3.15E+03	3.52E+03	1.55E+03	6.66E+02	2.43E+02	719.28039	2	22.96
DPS1	YLL018C	RASLFPR	[3] Phospho (ST)	0.06	0.74	0.21	-0.68	0.469	0.176	0.413	0.14	5.21E+02	2.86E+03	1.12E+03	7.91E+02	1.84E+03	2.06E+03	3.51E+03	1.26E+03	2.77E+03	4.26E+02	1.94E+03	2.83E+03	463.73383	2	19.04
SEC16	YPL085W	TNSAISQSPVNYAFPNPYK	[8] Phospho (ST)	-1.53	-0.44	-1.23	-1.09	0.128	0.346	0.154	0.18	4.97E+03	1.82E+04	4.38E+03	3.11E+03	4.00E+03	2.40E+03	2.79E+03	1.35E+04	3.99E+03	4.62E+03	3.46E+03	3.62E+03	1089.4983	2	35.38

CIC1	YHR052W	KSTPVSTPSK	[2] Phospho (ST)	2.03	1.53	1.22	0.50	0.062	0.118	0.048	0.29	3.41E+02	1.76E+03	5.20E+02	4.71E+03	9.50E+02	5.12E+03	4.74E+03	1.25E+03	1.63E+03	1.78E+03	1.71E+03	2.64E+03	556.27314	2	22.39
LHP1	YDL051W	SEKPQQEEQEKPQSR	[14] Phospho (ST)	0.35	-0.22	-1.63	0.57	0.169	0.370	0.022	0.15	5.93E+03	2.46E+03	4.84E+03	4.78E+03	5.95E+03	6.12E+03	1.56E+03	3.21E+03	6.55E+03	1.49E+03	1.34E+03	1.41E+03	954.4287	2	27.77
RIM15	YFL033C	SDSFSTR	[3] Phospho (ST)	-0.37	-0.69	-0.34	0.32	0.335	0.238	0.376	0.27	1.73E+03	2.20E+02	8.96E+02	1.03E+03	7.17E+02	4.50E+02	3.59E+02	8.60E+02	5.38E+02	1.53E+03	4.76E+02	2.43E+02	440.16576	2	19.1
GIP4	YAL031C	SSSLQSYTNK	[7] Phospho (Y)	1.80	0.93	0.77	0.87	0.050	0.152	0.092	0.16	9.66E+02	7.62E+02	7.59E+02	2.48E+03	1.48E+03	4.77E+03	2.76E+03	5.65E+02	1.43E+03	2.10E+03	1.30E+03	8.60E+02	597.75569	2	17.32
TGL4	YKR089C	RKSDTISTSR	[3] Phospho (ST)	1.92	0.66	0.73	1.27	0.017	0.122	0.051	0.04	7.37E+02	1.12E+03	6.39E+02	4.36E+03	1.87E+03	3.34E+03	1.87E+03	1.34E+03	7.46E+02	1.81E+03	1.07E+03	1.30E+03	615.79548	2	19.67
ESC1	YMR219W	VVDVAESFVK	[7] Phospho (ST)	-1.54	-1.60	-0.30	0.05	0.003	0.003	0.190	0.41	2.26E+03	3.17E+03	2.27E+03	9.89E+02	9.41E+02	6.99E+02	1.07E+03	6.87E+02	7.66E+02	2.10E+03	2.75E+03	1.41E+03	586.78369	2	18.72
YNL234W	YNL234W	SEGSVYQVK	[4] Phospho (ST)	0.79	-0.06	-0.59	0.85	0.105	0.473	0.248	0.08	1.88E+02	1.47E+03	9.75E+02	1.98E+03	1.34E+03	1.27E+03	2.72E+02	1.43E+03	8.19E+02	8.47E+02	5.08E+02	3.81E+02	538.73677	2	21.21
DIG1	YPL049C	STQDPIGDTEISVANAK	[2] Phospho (ST)	3.09	-0.66	-0.22	3.74	0.096	0.221	0.402	0.09	5.22E+02	1.13E+03	4.39E+02	0.00E+00	1.16E+04	6.34E+03	7.07E+01	8.05E+02	4.37E+02	0.00E+00	7.35E+02	1.05E+03	913.41597	2	64.02
ULP1	YPL020C	SASFSGIYK	[3] Phospho (ST)	-1.06	0.90	-0.11	-1.97	0.216	0.190	0.456	0.06	2.18E+02	2.50E+03	8.09E+02	2.24E+02	5.89E+02	8.60E+02	1.44E+03	3.81E+03	1.39E+03	1.62E+03	1.16E+03	4.78E+02	520.22859	2	22.65
TOF2	YKR010C	KSSLEIK	[3] Phospho (ST)	-0.13	-1.05	-0.25	0.92	0.343	0.037	0.239	0.03	1.73E+03	9.12E+02	1.49E+03	1.49E+03	1.24E+03	1.04E+03	1.00E+03	5.37E+02	4.41E+02	1.31E+03	1.27E+03	8.94E+02	442.72795	2	15.3
YML119W	YML119W	SPSPSVSPR	[3] Phospho (ST)	0.22	4.08	3.06	-3.86	0.438	0.007	0.023	0.01	0.00E+00	4.10E+01	1.52E+02	2.12E+00	2.12E+01	2.09E+02	1.04E+03	9.12E+02	1.84E+03	9.41E+02	6.33E+02	2.83E+02	497.22441	2	19.19
YCR016W	YCR016W	RQTISSGDESK	[6] Phospho (ST)	1.42	-0.69	1.12	2.10	0.056	0.287	0.053	0.06	1.09E+03	9.41E+02	6.26E+02	3.72E+03	1.23E+03	2.22E+03	1.62E+03	3.24E+00	1.76E+01	2.92E+03	1.41E+03	1.50E+03	644.28254	2	17.97
REG1	YDR028C	YPASQSEDDESDDENK	[11] Phospho (ST)	0.01	-0.96	-0.40	0.98	0.490	0.114	0.322	0.08	5.31E+03	2.25E+03	2.42E+03	4.76E+03	3.18E+03	2.15E+03	7.50E+02	2.69E+03	1.68E+03	5.05E+03	1.71E+03	7.84E+02	954.83716	2	28.87
CRZ1	YNL027W	RSSQTSNNSFTSR	[3] Phospho (ST)	-0.34	-0.97	-2.51	0.63	0.385	0.249	0.121	0.26	3.89E+03	1.29E+03	2.48E+02	2.48E+03	1.07E+03	7.40E+02	2.15E+01	9.19E+02	1.81E+03	2.04E+02	9.66E+01	6.27E+02	776.33122	2	15.82
BBC1	YJL020C	NEPYTETEEAEENEK	[4] Phospho (Y)	-0.73	-0.27	0.39	-0.46	0.108	0.307	0.275	0.12	3.68E+03	1.32E+03	2.65E+03	1.54E+03	1.70E+03	1.37E+03	1.34E+03	2.74E+03	2.26E+03	4.37E+03	4.33E+03	1.33E+03	946.3596	2	23.23
SRO9	YCL037C	DATSQENGQSTQQQQPPHHR	[4] Phospho (ST)	0.82	-1.09	-0.49	1.91	0.093	0.044	0.125	0.02	4.20E+03	2.89E+03	2.23E+03	5.59E+03	3.05E+03	7.78E+03	2.29E+03	7.31E+02	1.33E+03	2.42E+03	1.54E+03	2.65E+03	785.3351	3	30.45
EFG1	R271C-A	DHEDGSQVSPTQDRK	[9] Phospho (ST)	1.46	-0.18	-0.14	1.64	0.014	0.384	0.352	0.02	2.77E+03	3.47E+03	1.69E+03	8.10E+03	4.82E+03	8.97E+03	1.88E+03	1.15E+03	3.96E+03	1.92E+03	2.42E+03	2.87E+03	889.87542	2	32.51
AIM21	YIR003W	SPTSVEEGK	[3] Phospho (ST)	1.64	0.72	0.34	0.92	0.030	0.088	0.326	0.08	1.57E+03	7.64E+02	7.70E+02	3.81E+03	1.67E+03	4.30E+03	2.26E+03	1.16E+03	1.73E+03	2.32E+03	8.69E+02	7.49E+02	507.21554	2	16.94
KRE29	YER038C	AESGDDFDPILK	[3] Phospho (ST)	2.25	2.25	2.29	-0.01	0.124	0.002	0.019	0.50	1.35E+02	9.29E+02	2.41E+02	1.76E+01	4.23E+03	2.08E+03	2.34E+03	1.81E+03	2.19E+03	1.27E+03	3.03E+03	2.22E+03	693.79572	2	36.04
PBP1	YGR178C	SGSNISQGQSSTGHTTR	[3] Phospho (ST)	-1.08	-1.68	-3.68	0.60	0.204	0.137	0.077	0.29	7.31E+03	3.67E+03	3.94E+02	3.47E+03	7.40E+02	1.15E+03	2.87E+02	1.12E+03	2.13E+03	4.71E+02	8.66E+01	3.01E+02	892.88228	2	41.1
SYP1	YCR030C	NNENSSHLEEAR	[6] Phospho (ST)	-0.63	0.62	0.43	-1.25	0.132	0.108	0.258	0.02	1.52E+03	5.97E+02	1.07E+03	8.63E+02	4.72E+02	7.20E+02	1.19E+03	2.17E+03	1.56E+03	2.22E+03	1.43E+03	6.59E+02	740.29674	2	25.43
HSL1	YKL101W	AIHASPSTK	[7] Phospho (ST)	1.40	0.42	-0.14	0.97	0.108	0.072	0.345	0.16	6.72E+02	9.13E+02	7.14E+02	1.87E+03	6.35E+02	3.60E+03	1.09E+03	7.91E+02	1.22E+03	4.64E+02	9.86E+02	6.29E+02	496.23114	2	27.46
TSR3	YOR006C	SREAQSEESEDEESGSK	[9] Phospho (ST)	1.68	0.09	0.91	1.60	0.057	0.461	0.191	0.07	1.56E+03	1.53E+03	6.23E+02	5.99E+03	1.47E+03	4.55E+03	2.45E+03	1.39E+03	1.06E+02	4.44E+03	9.62E+02	1.59E+03	982.37461	2	39.93
PAN6	YIL145C	NNNGLALSSR	[9] Phospho (ST)	1.17	0.43	-0.03	0.74	0.040	0.160	0.480	0.08	4.79E+02	1.21E+03	1.12E+03	1.90E+03	1.47E+03	2.99E+03	1.51E+03	9.21E+02	1.37E+03	1.07E+03	4.66E+02	1.22E+03	563.25372	2	15.4
MCD1	YDL003W	NDQNNDDDDNSVEQGRR	[11] Phospho (ST)	-1.63	-0.87	-2.82	-0.76	0.233	0.307	0.173	0.27	1.10E+04	1.44E+03	2.54E+02	3.48E+03	4.41E+02	1.51E+02	5.41E+02	2.61E+03	3.75E+03	1.23E+03	4.58E+02	7.16E+01	1035.8918	2	21.48
YFL002W-B	L002W-B	NVSRTSPNTTNTK	[6] Phospho (ST)	0.09	0.26	0.63	-0.17	0.455	0.334	0.197	0.40	1.93E+03	2.60E+03	8.38E+02	3.00E+03	4.67E+02	2.23E+03	3.15E+03	1.18E+03	2.09E+03	4.45E+03	1.45E+03	2.40E+03	750.34641	2	25.68
ERG6	YML008C	KPENAETPSQTSQEATQ	[16] Phospho (ST)	3.33	0.08	-0.64	3.25	0.001	0.460	0.262	0.00	4.46E+02	1.60E+02	8.33E+02	6.09E+03	4.23E+03	4.50E+03	6.47E+02	1.72E+02	7.04E+02	0.00E+00	3.91E+02	5.24E+02	963.41098	2	38.02
SHP1	YBL058W	GSTSPEPTK	[4] Phospho (ST)	1.98	1.17	1.12	0.80	0.090	0.014	0.107	0.21	1.11E+03	7.77E+02	6.01E+02	5.29E+03	3.25E+02	4.27E+03	2.29E+03	1.36E+03	2.01E+03	3.05E+03	1.53E+03	8.58E+02	492.20878	2	18.05
SKO1	YNL167C	KNSAVTTAPAQK	[3] Phospho (ST)	2.00	1.15	0.34	0.85	0.031	0.119	0.238	0.13	5.25E+02	1.12E+03	3.79E+02	2.81E+03	1.37E+03	4.03E+03	2.57E+03	6.50E+02	1.33E+03	9.59E+02	7.68E+02	8.51E+02	648.32114	2	40.77
HAL5	YJL165C	SVFSLSGLFK	[6] Phospho (ST)	-0.28	-0.21	-2.73	-0.08	0.393	0.421	0.114	0.44	4.80E+02	1.74E+03	1.81E+02	8.94E+02	6.63E+02	4.09E+02	1.04E+03	5.91E+02	4.38E+02	0.00E+00	2.56E+02	7.94E+01	582.78935	2	38.36
UTP23	YOR004W	KVNSPSDEVK	[4] Phospho (ST)	1.51	0.09	0.04	1.41	0.010	0.407	0.452	0.01	7.96E+02	4.94E+02	6.23E+02	1.60E+03	1.46E+03	2.45E+03	9.25E+02	4.02E+02	7.19E+02	8.68E+02	5.75E+02	5.24E+02	591.7737	2	22.55
BBC1	YJL020C	EAESSPNTGSTEQR	[5] Phospho (ST)	2.55	1.14	1.21	1.41	0.018	0.065	0.118	0.05	3.51E+02	4.16E+02	2.48E+02	2.76E+03	9.75E+02	2.37E+03	1.18E+03	6.32E+02	4.66E+02	1.45E+03	4.64E+02	4.78E+02	786.81248	2	25.41
MLH1	YMR167W	VTNVSHSQEAEK	[7] Phospho (ST)	3.38	0.69	-1.19	2.68	0.029	0.043	0.033	0.03	1.35E+02	2.79E+02	1.75E+02	2.31E+03	7.89E+02	3.33E+03	3.86E+02	2.58E+02	3.31E+02	6.55E+01	1.14E+02	6.28E+01	704.8087	2	21.95
LCP5	YER127W	GGIKSLR	[5] Phospho (ST)	-0.33	-0.32	0.30	-0.01	0.206	0.202	0.152	0.49	5.56E+02	3.18E+02	4.35E+02	3.64E+02	2.15E+02	4.59E+02	4.59E+02	2.36E+02	3.51E+02	6.43E+02	5.22E+02	4.55E+02	405.71509	2	25.35
OSH2	YDL019C	TRTAASAGNGPTDDGTK	[3] Phospho (ST)|[6] Phospho (ST)	-0.11	-4.10	-1.53	3.98	0.451	0.053	0.124	0.03	5.06E+03	1.83E+03	1.13E+03	3.63E+03	7.34E+02	3.06E+03	2.03E+02	7.86E+01	1.58E+02	1.79E+03	1.90E+02	7.77E+02	890.35186	2	28.57
REG1	YDR028C	SDVKPQENGNDSS	[13] Phospho (ST)	1.55	0.38	1.02	1.16	0.138	0.292	0.172	0.17	1.43E+03	3.46E+02	7.32E+02	4.88E+03	6.94E+02	1.82E+03	7.62E+02	1.67E+03	8.44E+02	3.18E+03	1.08E+03	8.51E+02	728.78306	2	20.32
RBS1	YDL189W	LNKSEDDVK	[4] Phospho (ST)	1.27	0.68	0.58	0.58	0.021	0.088	0.143	0.12	4.72E+02	2.76E+02	3.74E+02	9.13E+02	6.15E+02	1.22E+03	8.36E+02	3.83E+02	6.06E+02	8.57E+02	4.21E+02	4.19E+02	564.25177	2	25.17
IST2	YBR086C	KPLATESTEK	[7] Phospho (ST)	1.24	-0.05	0.96	1.28	0.018	0.472	0.070	0.03	5.79E+02	5.52E+02	9.92E+02	1.54E+03	1.29E+03	2.23E+03	1.12E+03	2.76E+02	6.66E+02	9.72E+02	1.13E+03	2.07E+03	592.28348	2	27.57
SKG1	YKR100C	NSSITSVNK	[3] Phospho (ST)	2.46	-0.58	-2.06	2.99	0.076	0.350	0.180	0.06	0.00E+00	8.81E+00	1.21E+02	4.74E+02	3.60E+02	2.97E+01	3.66E+00	4.39E+01	3.16E+01	6.73E+00	0.00E+00	2.43E+00	515.23519	2	15.35
NSR1	YGR159C	RKSEDAEEEEDEESSNK	[15] Phospho (ST)	2.51	1.80	1.49	0.72	0.001	0.019	0.007	0.03	5.29E+02	8.50E+01	5.63E+02	2.00E+03	2.56E+03	2.31E+03	1.87E+03	8.66E+02	1.44E+03	1.26E+03	1.11E+03	9.95E+02	1045.9065	2	18.15
HST2	YPL015C	LNGHDSDEDGASNSSSSQK	[6] Phospho (ST)	2.02	0.76	1.01	1.26	0.031	0.036	0.106	0.06	4.75E+02	6.76E+02	3.55E+02	2.55E+03	8.78E+02	2.79E+03	1.03E+03	8.93E+02	6.48E+02	1.70E+03	6.18E+02	7.58E+02	1007.8851	2	28.21
PUF4	YGL014W	KPSVGANNTAK	[3] Phospho (ST)	2.90	1.44	1.43	1.46	0.036	0.141	0.024	0.09	8.33E+01	4.19E+02	1.79E+02	2.43E+03	5.18E+02	2.35E+03	1.26E+03	2.96E+02	3.50E+02	8.15E+02	4.65E+02	6.13E+02	583.7819	2	24.84
PBS2	YJL128C	RSASVGSNQSEQDK	[4] Phospho (ST)	1.77	-0.24	1.16	2.00	0.057	0.442	0.149	0.06	1.48E+02	4.95E+02	7.54E+01	1.17E+03	3.08E+02	1.06E+03	5.98E+02	7.49E+00	1.45E+00	9.91E+02	2.56E+02	4.01E+02	786.83643	2	28.89
RPS10B	YMR230W	NPSQRPQR	[3] Phospho (ST)	5.60	1.54	3.12	4.05	0.191	0.146	0.170	0.20	5.95E+00	1.01E+00	1.78E+02	1.05E+04	5.36E+00	0.00E+00	2.68E+02	3.32E+02	5.08E+00	1.00E+01	1.64E+03	2.13E+02	531.74579	2	15.71
STE20	YHL007C	HQQPVASSTVNSNK	[12] Phospho (ST)	-0.63	0.00	-2.27	-0.63	0.305	0.498	0.097	0.25	1.69E+03	9.62E+02	8.12E+01	1.30E+03	3.08E+02	1.48E+02	6.92E+02	6.35E+02	1.42E+03	2.82E+02	1.56E+02	1.04E+02	788.85996	2	16.28
TAF4	YMR005W	ASELSHSLPSPSQIK	[10] Phospho (ST)	-0.71	-0.11	-0.50	-0.60	0.072	0.398	0.164	0.09	9.41E+03	1.89E+04	1.74E+04	8.87E+03	1.20E+04	7.20E+03	1.57E+04	9.20E+03	1.76E+04	5.38E+03	1.46E+04	1.23E+04	830.89878	2	16.58
YMR086W	YMR086W	VVTPIK	[3] Phospho (ST)	-0.69	-0.67	-0.11	-0.02	0.161	0.298	0.440	0.50	1.28E+03	1.54E+03	4.10E+02	7.11E+02	4.31E+02	8.58E+02	1.90E+03	9.09E+01	3.19E+01	3.97E+02	9.21E+02	1.68E+03	368.70342	2	21.43
YGR130C	YGR130C	VVSNEPK	[3] Phospho (ST)	1.84	0.72	0.54	1.13	0.046	0.131	0.189	0.09	2.62E+03	1.43E+03	8.93E+02	6.60E+03	2.40E+03	8.80E+03	3.89E+03	1.72E+03	2.52E+03	3.53E+03	1.72E+03	1.95E+03	426.69621	2	19.92
RPL16B	YNL069C	VSSASAAASESDVAK	[3] Phospho (ST)	-0.17	-0.27	-0.06	0.11	0.245	0.194	0.389	0.34	2.47E+04	1.83E+04	2.86E+04	2.33E+04	1.78E+04	2.27E+04	1.94E+04	1.47E+04	2.51E+04	2.43E+04	2.10E+04	2.34E+04	730.31931	2	39.03
SYP1	YCR030C	VGSIFGR	[3] Phospho (ST)	-0.34	-0.36	-0.54	0.02	0.234	0.215	0.141	0.47	2.89E+03	7.05E+03	6.17E+03	3.03E+03	4.81E+03	4.90E+03	4.67E+03	3.16E+03	4.69E+03	2.80E+03	4.01E+03	4.29E+03	408.19415	2	40.32
EDE1	YBL047C	TTPLSANSTGVSSLTR	[5] Phospho (ST)	-0.16	0.51	0.05	-0.66	0.363	0.131	0.455	0.03	7.64E+04	1.59E+05	7.80E+04	8.60E+04	1.10E+05	8.56E+04	1.77E+05	1.59E+05	1.10E+05	9.14E+04	1.34E+05	9.89E+04	836.40106	2	80.57
ABP1	YCR088W	TPSPAPAAK	[3] Phospho (ST)	2.03	1.72	0.74	0.31	0.061	0.042	0.071	0.34	2.17E+03	4.38E+03	1.75E+03	1.08E+04	4.14E+03	1.90E+04	1.41E+04	5.05E+03	8.21E+03	5.60E+03	3.55E+03	4.68E+03	460.2178	2	29
PDC1	YLR044C	TPANAAVPASTPLK	[10] Phospho (ST)	-0.22	0.30	-0.06	-0.51	0.198	0.244	0.463	0.13	9.04E+03	8.56E+03	5.90E+03	6.03E+03	6.28E+03	7.93E+03	1.38E+04	6.79E+03	8.29E+03	2.99E+03	6.96E+03	1.27E+04	709.35743	2	38.25
RPG1	YBR079C	TAGGSSPATPATPATPATPTPSSGPK	[6] Phospho (ST)	0.22	0.57	-0.33	-0.34	0.280	0.141	0.237	0.17	4.43E+04	8.47E+04	3.92E+04	5.95E+04	6.73E+04	6.94E+04	9.81E+04	1.00E+05	5.05E+04	4.56E+04	4.05E+04	4.77E+04	1194.0598	2	41.11
NSG2	YNL156C	SVSIDSTK	[3] Phospho (ST)	0.12	-0.17	-0.19	0.29	0.426	0.397	0.405	0.31	2.07E+03	5.19E+02	1.97E+03	2.47E+03	1.07E+03	1.40E+03	6.65E+02	1.72E+03	1.66E+03	2.28E+03	1.24E+03	4.68E+02	458.70481	2	26.76
GPD1	YDL022W	SSSSVSLK	[3] Phospho (ST)	-0.53	-0.33	-0.23	-0.20	0.195	0.290	0.369	0.32	5.13E+04	1.58E+04	3.58E+04	3.10E+04	2.17E+04	1.87E+04	1.95E+04	3.82E+04	2.41E+04	4.81E+04	2.22E+04	1.75E+04	437.69951	2	48.53
AVT3	YKL146W	SSGTTGGLLK	[2] Phospho (ST)	0.59	0.57	0.14	0.02	0.051	0.035	0.309	0.46	4.34E+03	6.06E+03	7.76E+03	1.11E+04	7.43E+03	8.81E+03	8.00E+03	1.03E+04	8.69E+03	7.60E+03	6.91E+03	5.53E+03	500.73938	2	18.9
YDR186C	YDR186C	NLSSATLIK	[3] Phospho (ST)	-0.65	-0.35	-0.51	-0.30	0.025	0.088	0.057	0.01	5.75E+03	8.54E+03	6.05E+03	4.42E+03	4.49E+03	4.02E+03	5.03E+03	5.59E+03	5.30E+03	4.73E+03	5.61E+03	3.97E+03	513.76533	2	17.43
HHF1	YBR009C	SFLESVIR	[1] Phospho (ST)	-1.93	-1.30	-1.42	-0.63	0.017	0.027	0.033	0.06	1.13E+04	2.36E+04	1.48E+04	2.72E+03	6.73E+03	3.56E+03	6.90E+03	6.56E+03	6.70E+03	4.17E+03	9.97E+03	4.43E+03	515.75145	2	41.98
SOK2	YMR016C	TSTSDEATQPNEPSEAEPVK	[8] Phospho (ST)	3.31	-1.61	-1.48	4.92	0.001	0.079	0.098	0.00	2.03E+03	1.26E+03	4.29E+02	1.50E+04	1.17E+04	1.06E+04	6.83E+02	3.45E+02	1.71E+02	7.95E+02	0.00E+00	5.19E+02	1098.9623	2	30.68
VMA2	YBR127C	DASQEESLI	[7] Phospho (ST)	0.09	0.25	0.16	-0.16	0.341	0.220	0.260	0.31	3.29E+04	4.48E+04	4.21E+04	3.71E+04	5.20E+04	3.86E+04	3.27E+04	6.02E+04	4.94E+04	5.09E+04	4.93E+04	3.36E+04	536.21604	2	26.47
DUN1	YDL101C	YASSSSTDIENDDEK	[3] Phospho (ST)	-3.34	-0.92	0.01	-2.43	0.000	0.007	0.490	0.00	6.75E+04	4.87E+04	6.72E+04	5.84E+03	6.13E+03	6.06E+03	2.73E+04	3.25E+04	3.73E+04	7.34E+04	4.96E+04	6.12E+04	870.8279	2	86.72
TIF5	YPR041W	SQNAPSDGTGSSTPQHHDEDEDELSR	[13] Phospho (ST)	0.91	0.36	0.19	0.55	0.001	0.025	0.134	0.01	2.57E+05	2.63E+05	2.55E+05	5.49E+05	4.47E+05	4.65E+05	3.84E+05	3.11E+05	3.00E+05	3.25E+05	2.38E+05	3.22E+05	959.37979	3	33.81
VHS2	YIL135C	SLSSQSFDNETSPAHPR	[1] Phospho (ST)	-0.37	-0.67	-0.43	0.30	0.023	0.003	0.023	0.03	4.71E+04	5.56E+04	4.54E+04	3.87E+04	4.21E+04	3.41E+04	3.38E+04	2.78E+04	3.14E+04	3.04E+04	3.92E+04	4.05E+04	970.41381	2	74.47
MKS1	YNL076W	KSSFPQK	[3] Phospho (ST)	1.60	0.98	0.86	0.61	0.004	0.030	0.042	0.06	1.07E+03	7.63E+02	9.58E+02	2.66E+03	2.30E+03	3.56E+03	2.46E+03	1.28E+03	1.80E+03	2.25E+03	1.70E+03	1.13E+03	451.21246	2	20.91
RPL18A	YOL120C	ILSTGR	[4] Phospho (ST)	-3.59	0.44	-0.57	-4.03	0.066	0.307	0.282	0.02	4.32E+02	0.00E+00	4.34E+02	0.00E+00	4.48E+01	0.00E+00	1.96E+02	3.45E+02	6.45E+02	2.71E+02	2.11E+02	9.52E+01	363.68075	2	16.09
YMR086W	YMR086W	FSSNPENGESR	[3] Phospho (ST)	-3.30	-3.95	-1.67	0.63	0.057	0.052	0.123	0.32	1.61E+03	5.72E+02	3.77E+02	0.00E+00	1.51E+02	8.32E+01	0.00E+00	0.00E+00	1.38E+02	6.66E+02	1.21E+02	0.00E+00	652.24994	2	19.98
SPT21	YMR179W	TQSLPIWNLK	[3] Phospho (ST)	-4.18	-4.13	-4.13	-0.06	0.078	0.079	0.079	0.48	2.52E+02	4.18E+03	1.85E+03	2.08E+02	8.27E+01	2.81E+01	1.57E+02	1.74E+02	0.00E+00	0.00E+00	3.31E+02	0.00E+00	640.32644	2	28.77
PLM2	YDR501W	PLLIASPALVK	[6] Phospho (ST)	-8.10	-7.10	-2.37	-1.01	0.014	0.014	0.030	0.24	1.35E+04	2.79E+04	1.15E+04	0.00E+00	6.06E+01	1.02E+02	2.65E+02	0.00E+00	8.92E+01	8.40E+02	6.47E+03	2.90E+03	601.35205	2	20.27
DEP1	YAL013W	SLANLPELK	[1] Phospho (ST)	2.44	4.26	3.30	-1.82	0.027	0.000	0.006	0.00	0.00E+00	2.42E+02	1.26E+02	5.87E+02	1.13E+03	4.41E+02	2.85E+03	2.51E+03	2.33E+03	8.25E+02	1.70E+03	1.41E+03	532.77324	2	36.52
INP52	YNL106C	LLSPTK	[3] Phospho (ST)	-1.21	1.93	0.12	-3.14	0.148	0.016	0.440	0.01	1.20E+03	3.28E+02	2.47E+03	3.62E+02	5.59E+02	7.92E+02	4.56E+03	3.71E+03	7.03E+03	1.53E+03	1.97E+03	8.37E+02	369.69346	2	27.86
RPN13	YLR421C	MIGVLNNSSESDEEESNDEK	[11] Phospho (ST)|[16] Phospho (ST)	-0.09	0.83	0.60	-0.92	0.470	0.216	0.069	0.25	4.72E+04	2.91E+04	3.28E+04	8.98E+02	8.68E+04	1.49E+04	2.82E+04	1.28E+05	3.73E+04	4.50E+04	7.23E+04	4.83E+04	1193.4375	2	22.11
PET127	YOR017W	DESLLK	[3] Phospho (ST)	-8.72	-4.82	-1.30	-3.90	0.068	0.074	0.168	0.05	2.72E+04	7.20E+03	4.99E+03	5.29E+01	0.00E+00	1.09E+01	8.50E+02	1.80E+02	3.35E+02	5.97E+03	3.36E+03	6.67E+03	392.67774	2	22.54
MYO3	YKL129C	KVFILTK	[6] Phospho (ST)	-0.16	-0.18	-0.30	0.02	0.200	0.361	0.159	0.49	2.19E+04	1.51E+04	1.86E+04	1.52E+04	1.66E+04	1.79E+04	2.52E+04	6.55E+03	1.73E+04	1.19E+04	1.35E+04	1.97E+04	464.76396	2	17.39
YMR144W	YMR144W	SFSTIDGSIK	[1] Phospho (ST)	-8.37	-3.11	-1.25	-5.26	0.003	0.005	0.021	0.00	1.16E+04	2.29E+04	1.65E+04	1.14E+02	1.09E+00	8.96E+00	2.10E+03	1.91E+03	1.85E+03	6.90E+03	8.01E+03	6.45E+03	567.7581	2	27.05
ALK2	YBL009W	LLSPSK	[3] Phospho (ST)	0.37	0.64	1.35	-0.27	0.128	0.120	0.003	0.28	4.36E+02	6.87E+02	6.70E+02	8.64E+02	5.63E+02	8.98E+02	1.39E+03	7.88E+02	6.31E+02	1.30E+03	1.50E+03	1.82E+03	362.6853	2	25.53
GLN3	YER040W	KNSLIK	[3] Phospho (ST)	0.10	-1.08	-1.54	1.18	0.409	0.073	0.040	0.01	1.77E+03	9.43E+02	7.39E+02	1.01E+03	1.52E+03	1.18E+03	3.87E+02	4.44E+02	7.88E+02	2.19E+02	4.99E+02	4.53E+02	391.71196	2	19.4
YRB2	YIL063C	SETNGGNAARENSEVK	[N-term] Acetyl (Protein N-term)|[13] Phosph	-4.24	-4.32	-2.64	0.08	0.048	0.048	0.066	0.47	9.20E+03	2.21E+03	3.42E+03	7.20E+01	3.25E+02	3.61E+02	5.50E+02	9.57E+01	6.77E+01	1.63E+03	2.51E+02	4.74E+02	892.87635	2	40.49
SRC1	YML034W	VSASFADKLPQK	[4] Phospho (ST)	-6.80	-3.84	-1.42	-2.96	0.003	0.004	0.015	0.03	8.19E+03	1.56E+04	1.48E+04	0.00E+00	1.27E+02	1.89E+02	1.43E+03	8.42E+02	3.95E+02	3.51E+03	5.24E+03	5.66E+03	685.83976	2	47.56
NOP13	YNL175C	GSAAIVPSQGK	[8] Phospho (ST)	-0.15	-1.34	-0.91	1.19	0.425	0.152	0.213	0.02	5.91E+03	1.59E+03	1.47E+03	2.45E+03	2.85E+03	2.78E+03	4.66E+02	9.41E+02	2.12E+03	6.57E+02	1.34E+03	2.77E+03	547.76293	2	19.47
ACC1	YNR016C	SEESLFESSPQK	[N-term] Acetyl (Protein N-term)|[1] Phospho	0.62	2.01	0.43	-1.39	0.229	0.061	0.300	0.09	0.00E+00	2.24E+03	3.33E+03	2.04E+03	4.28E+03	2.24E+03	2.09E+03	1.03E+04	1.01E+04	2.84E+03	3.24E+03	1.41E+03	745.31004	2	18.36
RLF2	YPR018W	RSNSDLQAQTASQSQSPEK	[4] Phospho (ST)	-5.09	-3.37	-2.24	-1.72	0.001	0.002	0.004	0.01	2.24E+04	1.37E+04	2.23E+04	3.65E+02	5.63E+02	7.56E+02	1.15E+03	2.17E+03	2.29E+03	5.69E+03	2.34E+03	4.27E+03	714.65343	3	24.63
SGV1	YPR161C	GESPVVK	[3] Phospho (ST)	0.57	-0.89	-0.27	1.45	0.134	0.157	0.326	0.02	6.95E+03	1.97E+03	4.29E+03	6.24E+03	5.28E+03	8.04E+03	5.75E+02	2.44E+03	4.11E+03	4.53E+03	3.70E+03	2.75E+03	398.1859	2	27.19
SWI4	YER111C	DPLNSVK	[5] Phospho (ST)	0.73	0.51	1.20	0.22	0.183	0.280	0.099	0.20	7.94E+01	4.26E+02	1.51E+03	9.92E+02	1.08E+03	1.30E+03	1.13E+03	6.76E+02	1.07E+03	2.16E+03	1.67E+03	8.54E+02	426.69662	2	18.07

UBP3	YER151C	SSSPLLSK	[3] Phospho (ST)	0.48	-0.73	0.01	1.21	0.122	0.018	0.421	0.03	4.60E+03	4.32E+03	4.74E+03	8.26E+03	3.83E+03	6.97E+03	3.26E+03	3.36E+03	1.62E+03	4.67E+03	4.29E+03	4.82E+03	449.71784	2	26.42
NDD1	YOR372C	ILNDVGTPYAK	[9] Phospho (Y)	0.94	3.27	1.98	-2.33	0.003	0.012	0.062	0.02	3.15E+02	3.48E+02	2.27E+02	5.03E+02	6.44E+02	5.93E+02	2.79E+03	1.75E+03	4.34E+03	5.56E+02	2.11E+03	9.42E+02	635.80784	2	32.38
RPA43	YOR340C	SQAESLPIVSNK	[1] Phospho (ST)	2.41	1.43	-0.88	0.98	0.003	0.119	0.089	0.07	6.36E+02	1.38E+03	1.76E+03	7.19E+03	8.18E+03	4.81E+03	5.96E+02	5.80E+03	3.84E+03	8.88E+02	7.03E+02	4.49E+02	676.8267	2	54.78
RPG1	YBR079C	DPFDIFASTASK	[11] Phospho (ST)	4.04	3.01	1.03	1.03	0.051	0.006	0.184	0.16	1.57E+02	5.52E+02	3.87E+02	2.16E+03	1.14E+04	4.94E+03	4.09E+03	2.84E+03	2.10E+03	1.73E+02	1.45E+03	6.56E+02	689.80063	2	44.36
NUP2	YLR335W	SSFTFGSTTIEK	[2] Phospho (ST)	-3.41	-4.53	-2.69	1.12	0.026	0.021	0.030	0.18	6.32E+03	1.98E+04	1.05E+04	4.79E+02	2.32E+03	6.27E+02	5.01E+02	4.81E+02	5.76E+02	2.16E+03	1.88E+03	1.61E+03	692.80585	2	39.06
LCB3	YJL134W	TLSNPNDFQEPNYLLDPGNHPSDHFR	[3] Phospho (ST)	-0.44	-0.15	-0.44	-0.29	0.183	0.360	0.191	0.05	3.13E+04	6.76E+04	3.62E+04	3.01E+04	3.13E+04	3.81E+04	4.48E+04	4.00E+04	3.68E+04	2.75E+04	4.16E+04	3.02E+04	776.84431	4	28.5
YEL043W	YEL043W	TGSIDLISNNNK	[1] Phospho (ST)	-0.77	-0.54	-0.67	-0.23	0.004	0.113	0.009	0.33	1.30E+04	1.05E+04	1.18E+04	8.26E+03	6.31E+03	6.09E+03	4.39E+03	1.28E+04	7.15E+03	9.11E+03	6.38E+03	6.75E+03	678.31787	2	30.6
HSP42	YDR171W	SSSFAHLQAPSPIPDPLQVSKPETR	[11] Phospho (ST)	3.36	2.30	-0.16	1.07	0.000	0.035	0.390	0.01	2.00E+03	3.83E+03	1.70E+03	2.42E+04	2.76E+04	2.58E+04	2.02E+04	7.22E+03	9.69E+03	3.05E+03	1.19E+03	2.50E+03	923.79195	3	23.21
ARP8	YOR141C	SVTGLSVDPR	[1] Phospho (ST)	-0.44	-0.49	-0.64	0.05	0.068	0.143	0.036	0.45	8.24E+03	6.78E+03	5.03E+03	4.52E+03	4.94E+03	5.27E+03	7.29E+03	3.35E+03	3.61E+03	4.00E+03	4.96E+03	3.89E+03	555.76066	2	29.57
HSP104	YLL026W	ALERDEDADSTTK	[10] Phospho (ST)	0.79	-2.78	-1.75	3.57	0.210	0.076	0.110	0.04	5.90E+03	2.63E+03	8.01E+02	9.06E+03	1.95E+03	5.17E+03	8.42E+02	1.05E+02	3.88E+02	5.89E+02	7.27E+02	1.43E+03	765.82332	2	48.1
STB1	YNL309W	FSHIKPSASSPQSTFK	[10] Phospho (ST)	-1.99	-1.90	-0.41	-0.09	0.023	0.058	0.262	0.48	4.63E+03	9.54E+03	4.73E+03	1.74E+03	8.68E+02	2.11E+03	4.98E+03	1.05E+01	4.60E+01	1.89E+03	4.98E+03	7.30E+03	914.93497	2	15.29
SEC3	YER008C	AVITNRPGSVSPIK	[11] Phospho (ST)	0.36	0.94	0.21	-0.57	0.067	0.035	0.314	0.08	1.06E+04	1.61E+04	1.42E+04	1.50E+04	1.80E+04	1.96E+04	3.54E+04	1.91E+04	2.39E+04	8.37E+03	2.11E+04	1.80E+04	759.90657	2	26.55
PUP2	YGR253C	ATSPLLESDSIEK	[3] Phospho (ST)	0.62	-0.10	-0.47	0.72	0.152	0.435	0.269	0.04	4.76E+02	2.81E+03	2.38E+03	2.00E+03	3.09E+03	3.64E+03	1.47E+03	1.85E+03	1.96E+03	8.79E+02	1.94E+03	1.27E+03	735.34251	2	36.33
YMR086W	YMR086W	PSSLNIEK	[3] Phospho (ST)	4.01	3.64	3.23	0.37	0.000	0.001	0.000	0.03	2.80E+01	2.40E+01	1.88E+02	1.57E+03	1.41E+03	1.39E+03	1.05E+03	9.76E+02	1.34E+03	9.07E+02	8.75E+02	7.48E+02	484.22851	2	28.59
MEC1	YBR136W	KVPTDPSSSQEYAK	[9] Phospho (ST)	3.82	2.79	1.28	1.03	0.001	0.014	0.121	0.02	5.27E+00	7.15E+02	3.46E+02	4.77E+03	6.26E+03	4.48E+03	3.21E+03	1.32E+03	3.07E+03	4.39E+02	6.92E+02	1.51E+03	808.86342	2	26.89
STU1	YBL034C	RTSSTDSVVIHDDNDK	[4] Phospho (ST)|[7] Phospho (ST)	-2.22	-1.85	-0.68	-0.37	0.003	0.007	0.054	0.27	1.52E+04	9.58E+03	1.59E+04	3.59E+03	3.02E+03	2.13E+03	1.52E+03	4.16E+03	5.61E+03	1.10E+04	5.96E+03	8.39E+03	650.26274	3	20.46
FUN30	YAL019W	LSSIHGNINNK	[3] Phospho (ST)	-3.63	-3.64	-1.55	0.01	0.013	0.013	0.036	0.49	1.48E+04	1.15E+04	2.68E+04	1.55E+03	1.21E+03	1.50E+03	9.05E+02	6.15E+02	2.70E+03	5.68E+03	4.36E+03	8.02E+03	638.80592	2	25
SWI3	YJL176C	LDSQETPSTEESR	[3] Phospho (ST)	3.31	-2.95	-2.50	6.25	0.000	0.036	0.040	0.00	5.35E+02	7.03E+02	1.61E+03	9.19E+03	1.04E+04	9.01E+03	2.67E+02	0.00E+00	7.53E+01	2.35E+02	8.82E+01	1.55E+02	779.81767	2	40.95
YOR052C	YOR052C	SDSGTVLGAIPLNSR	[5] Phospho (ST)	-0.66	0.54	0.46	-1.20	0.084	0.118	0.081	0.02	2.53E+04	4.03E+04	2.01E+04	1.51E+04	1.93E+04	2.00E+04	4.16E+04	5.38E+04	2.93E+04	3.91E+04	4.24E+04	3.65E+04	783.87958	2	45.21
PFK2	YMR205C	PTPPPAPEASAESGLSSK	[13] Phospho (ST)	0.89	0.34	0.26	0.56	0.003	0.033	0.094	0.02	2.63E+04	2.79E+04	2.84E+04	5.45E+04	5.66E+04	4.23E+04	3.68E+04	2.92E+04	3.83E+04	2.63E+04	3.54E+04	3.71E+04	901.91437	2	20.89
PFK2	YMR205C	PTPPPAPEASAESGLSSK	[17] Phospho (ST)	0.90	0.55	0.31	0.34	0.007	0.011	0.105	0.04	1.13E+04	1.60E+04	1.76E+04	2.91E+04	3.14E+04	2.33E+04	2.23E+04	2.11E+04	2.26E+04	1.57E+04	1.96E+04	2.05E+04	601.61231	3	51.75
NSP1	YJL041W	PAFSFGAK	[4] Phospho (ST)	-7.25	-5.47	-5.50	-1.82	0.004	0.004	0.004	0.19	1.09E+03	2.08E+03	1.36E+03	0.00E+00	0.00E+00	0.00E+00	7.29E+01	0.00E+00	0.00E+00	0.00E+00	7.10E+01	0.00E+00	452.70205	2	22.56
RPL3	YOR063W	KYEAPR	[2] Phospho (Y)	-0.82	0.87	-0.45	-1.69	0.215	0.241	0.202	0.16	1.17E+03	9.91E+02	4.21E+02	1.21E+03	6.65E+01	1.70E+02	1.17E+03	3.32E+03	2.70E+02	7.17E+02	7.45E+02	4.29E+02	422.19184	2	18.39
DSL1	YNL258C	LLPYILK	[4] Phospho (Y)	-6.93	-5.78	-0.72	-1.18	0.122	0.124	0.319	0.16	7.12E+03	1.08E+03	5.00E+02	0.00E+00	0.00E+00	4.15E+01	6.29E+01	6.63E+01	0.00E+00	4.25E+02	1.75E+03	3.10E+03	470.26611	2	17.06
MCR1	YKL150W	MFSRLSR	[N-term] Acetyl (Protein N-term)|[6] Phospho	-0.44	1.61	0.90	-2.05	0.358	0.101	0.226	0.08	1.55E+02	4.80E+02	6.75E+01	0.00E+00	3.49E+02	1.65E+02	1.35E+03	4.23E+02	4.42E+02	6.49E+02	6.95E+02	0.00E+00	509.73394	2	16.92
HSP12	YFL014W	ASEALKPDSQKSYAEQGK	[12] Phospho (ST)|[13] Phospho (Y)	4.05	-1.36	-1.40	5.40	0.003	0.148	0.152	0.00	7.43E+02	0.00E+00	5.88E+02	5.71E+03	6.84E+03	9.97E+03	2.54E+02	1.19E+02	1.29E+02	1.79E+01	1.86E+02	2.82E+02	1048.9504	2	20.23
ESF1	YDR365C	KGRYQK	[4] Phospho (Y)	0.17	-0.99	-0.63	1.15	0.425	0.201	0.272	0.07	1.98E+03	5.89E+02	3.28E+02	9.12E+02	6.52E+02	1.70E+03	4.92E+02	3.59E+02	5.95E+02	5.48E+02	4.85E+02	8.26E+02	430.21116	2	15.45
IQG1	YPL242C	FTPIEPSLLGPTPSLEYSPIK	[17] Phospho (Y)	1.70	5.04	3.36	-3.34	0.106	0.026	0.015	0.03	3.50E+02	1.51E+02	3.59E+02	1.81E+02	1.73E+03	9.64E+02	1.63E+04	4.49E+03	8.49E+03	1.85E+03	4.68E+03	2.63E+03	789.40291	3	27.86
YOX1	YML027W	SVESALR	[1] Phospho (ST)	0.17	-1.44	-1.32	1.60	0.333	0.010	0.012	0.01	8.57E+02	8.57E+02	1.37E+03	1.60E+03	8.38E+02	1.05E+03	3.12E+02	3.82E+02	4.30E+02	4.39E+02	3.66E+02	4.19E+02	421.1942	2	16.89
YHL009W-B	L009W-B	KSNKVYNSK	[6] Phospho (Y)	-0.74	-2.67	-1.60	1.92	0.297	0.145	0.195	0.04	3.99E+03	7.01E+02	3.77E+02	5.57E+02	1.04E+03	1.43E+03	7.02E+02	4.36E+01	2.95E+01	1.33E+02	5.26E+02	9.97E+02	574.27715	2	23.06
HSP12	YFL014W	ASEALKPDSQKSYAEQGK	[9] Phospho (ST)|[13] Phospho (Y)	4.55	-1.74	-0.46	6.28	0.000	0.173	0.357	0.00	1.64E+03	3.94E+02	1.18E+02	1.58E+04	1.85E+04	1.68E+04	2.33E+02	3.43E+02	4.74E+01	3.36E+02	3.26E+02	8.92E+02	699.63603	3	16.24
YDR186C	YDR186C	SGSSTDVLSSGIDSMAK	[3] Phospho (ST)	-1.27	-1.13	-0.63	-0.14	0.083	0.039	0.100	0.45	5.49E+03	6.87E+03	3.31E+03	4.04E+02	5.09E+03	1.00E+03	2.59E+03	3.34E+03	1.23E+03	3.26E+03	4.49E+03	2.39E+03	861.3704	2	70.52
RPH1	YER169W	SPNIVTLNISR	[1] Phospho (ST)	1.85	1.10	0.53	0.75	0.009	0.000	0.037	0.05	1.56E+03	1.46E+03	1.52E+03	3.97E+03	7.43E+03	5.07E+03	3.55E+03	3.17E+03	3.09E+03	1.84E+03	2.74E+03	1.99E+03	647.33315	2	26.9
ABF1	YKL112W	NDTEDDSINK	[7] Phospho (ST)	4.92	-1.94	-0.50	6.81	0.019	0.031	0.290	0.02	1.22E+02	4.41E+01	6.17E+01	4.05E+03	1.16E+03	2.67E+03	0.00E+00	1.40E+01	2.37E+01	1.17E+02	2.67E+01	1.14E+01	615.73051	2	15.88
MSC3	YLR219W	ANSITVK	[3] Phospho (ST)	0.87	0.76	0.74	0.11	0.058	0.063	0.159	0.29	2.17E+03	5.43E+02	1.24E+03	2.98E+03	2.05E+03	2.23E+03	2.22E+03	2.10E+03	2.41E+03	3.38E+03	1.94E+03	1.29E+03	406.69894	2	29.19
YCL019W	YCL019W	VNNDHINESTVSSQYLSDDNELSLGQQQK	[17] Phospho (ST)	-1.97	-0.94	-0.89	-1.03	0.001	0.002	0.004	0.01	3.91E+04	3.05E+04	3.52E+04	1.19E+04	6.05E+03	8.75E+03	1.61E+04	1.82E+04	2.04E+04	2.09E+04	2.11E+04	1.44E+04	1114.8303	3	21.44
PRM5	YIL117C	LLNSPESDGSVNR	[7] Phospho (ST)	0.80	-0.29	0.09	1.09	0.007	0.301	0.338	0.03	1.17E+04	1.59E+04	1.48E+04	2.18E+04	2.30E+04	2.89E+04	7.67E+03	6.67E+03	2.03E+04	1.48E+04	1.23E+04	1.81E+04	734.32852	2	42.64
RAD9	YDR217C	INFEPILEVPETSSPSK	[16] Phospho (ST)	-0.96	-0.44	-0.07	-0.52	0.017	0.109	0.413	0.07	3.96E+04	3.97E+04	2.47E+04	1.73E+04	1.50E+04	2.13E+04	2.26E+04	3.30E+04	2.12E+04	4.07E+04	3.46E+04	2.38E+04	983.97546	2	16.45
HSP60	YLR259C	RGSQVAVEK	[3] Phospho (ST)	0.70	-0.40	-0.56	1.09	0.155	0.314	0.185	0.10	1.83E+03	9.45E+02	6.62E+02	1.55E+03	1.18E+03	2.86E+03	1.62E+03	2.60E+02	7.20E+02	9.76E+02	5.77E+02	7.66E+02	527.25677	2	28.31
ENT2	YLR206W	IPAQHTK	[6] Phospho (ST)	2.49	1.06	-0.16	1.42	0.069	0.171	0.418	0.12	9.52E+02	3.15E+03	8.38E+02	1.26E+04	1.22E+03	1.41E+04	6.37E+03	1.39E+03	2.61E+03	1.00E+03	1.86E+03	1.55E+03	437.71242	2	16.16
EFM1	YHL039W	YFPNLSER	[1] Phospho (Y)	1.94	2.66	2.22	-0.73	0.001	0.000	0.023	0.00	6.79E+02	1.30E+03	2.65E+03	6.64E+03	5.58E+03	5.62E+03	9.12E+03	1.11E+04	9.33E+03	1.09E+04	6.40E+03	4.42E+03	553.23661	2	15.23
MDG1	YNL173C	DTSTSADAEASEDQNK	[3] Phospho (ST)	0.74	-0.25	-0.25	0.99	0.045	0.324	0.353	0.00	7.18E+03	2.53E+03	3.96E+03	7.78E+03	7.53E+03	7.57E+03	3.00E+03	3.65E+03	4.85E+03	6.07E+03	2.73E+03	2.72E+03	874.82865	2	73.7
TIF4631	YGR162W	FGNNSSR	[5] Phospho (ST)	0.01	-0.16	0.13	0.17	0.495	0.410	0.436	0.39	5.42E+03	1.14E+03	2.42E+03	4.70E+03	8.35E+02	3.51E+03	2.90E+03	2.24E+03	2.90E+03	5.30E+03	2.00E+03	2.52E+03	431.16647	2	15.74
MED1	YPR070W	HGSVVEASR	[3] Phospho (ST)	1.40	1.09	0.62	0.32	0.140	0.072	0.023	0.37	3.43E+03	3.60E+03	3.50E+03	5.85E+03	3.55E+03	1.85E+04	1.17E+04	4.26E+03	6.50E+03	6.46E+03	4.19E+03	5.61E+03	511.22709	2	58.75
NOT3	YIL038C	IGSALNTPK	[3] Phospho (ST)	-0.26	-0.10	0.26	-0.16	0.159	0.308	0.216	0.28	1.54E+04	1.84E+04	2.00E+04	1.22E+04	1.36E+04	1.93E+04	1.89E+04	1.34E+04	1.79E+04	1.51E+04	2.11E+04	2.84E+04	490.74464	2	55.87
NOT3	YIL038C	IGSALNTPK	[7] Phospho (ST)	-0.20	0.53	0.25	-0.73	0.333	0.204	0.326	0.14	1.27E+03	2.79E+03	2.57E+03	1.21E+03	2.08E+03	2.49E+03	3.90E+03	1.30E+03	4.40E+03	1.68E+03	2.16E+03	4.05E+03	490.74427	2	17.6
RGA2	YDR379W	KGSISNASPK	[3] Phospho (ST)	1.20	0.74	0.65	0.46	0.095	0.077	0.131	0.23	1.73E+02	5.00E+02	2.00E+02	6.90E+02	2.87E+02	1.07E+03	5.46E+02	3.97E+02	5.35E+02	6.16E+02	3.47E+02	4.24E+02	534.75766	2	22.1
HRK1	YOR267C	KQSNDSLR	[3] Phospho (ST)	2.48	1.72	1.65	0.76	0.229	0.031	0.101	0.35	1.54E+03	8.00E+02	5.77E+02	1.64E+04	3.42E+00	9.56E+00	4.47E+03	3.54E+03	1.66E+03	5.68E+03	2.38E+03	1.16E+03	514.23215	2	25.79
BOI1	YBL085W	TSLSPINSK	[4] Phospho (ST)	0.18	0.32	0.38	-0.14	0.163	0.090	0.045	0.27	2.71E+04	2.18E+04	2.74E+04	3.06E+04	2.40E+04	3.21E+04	2.51E+04	3.66E+04	3.36E+04	3.53E+04	2.73E+04	3.65E+04	513.74687	2	32.66
APL5	YPL195W	FVDDSDTSYEEK	[8] Phospho (ST)|[9] Phospho (Y)	0.57	0.24	0.00	0.32	0.020	0.326	0.497	0.23	5.49E+03	6.80E+03	8.73E+03	1.14E+04	1.04E+04	9.31E+03	4.26E+03	1.28E+04	7.82E+03	1.01E+04	7.06E+03	3.91E+03	797.76573	2	33.13
JSN1	YJR091C	GLSVSSVK	[3] Phospho (ST)	1.32	1.75	0.66	-0.43	0.006	0.002	0.172	0.02	1.11E+02	3.88E+02	4.96E+02	8.06E+02	9.01E+02	8.37E+02	1.31E+03	1.06E+03	1.05E+03	2.52E+02	7.47E+02	5.94E+02	428.71249	2	19.1
LHP1	YDL051W	PQQEEQEKPQSR	[11] Phospho (ST)	1.94	0.97	0.85	0.98	0.042	0.055	0.040	0.11	7.19E+03	1.54E+04	7.35E+03	5.21E+04	1.43E+04	4.88E+04	2.23E+04	1.20E+04	2.42E+04	1.93E+04	1.39E+04	2.08E+04	782.344	2	40.29
LHP1	YDL051W	PQQEEQEKPQSR	[11] Phospho (ST)	1.81	1.13	0.87	0.67	0.047	0.039	0.045	0.17	2.40E+03	5.81E+03	3.25E+03	1.80E+04	4.90E+03	1.72E+04	9.56E+03	5.15E+03	1.04E+04	7.98E+03	5.03E+03	7.89E+03	521.89808	3	19.34
PWP1	YLR196W	ATLEEAEGESGVEDDAATGSSNK	[10] Phospho (ST)	0.50	0.14	0.48	0.36	0.009	0.211	0.019	0.02	7.69E+05	5.93E+05	8.01E+05	1.10E+06	9.92E+05	9.65E+05	6.91E+05	8.29E+05	8.71E+05	1.12E+06	8.88E+05	1.01E+06	782.98769	3	47.43
YCF1	YDR135C	LNDLDFGNSDAISLR	[13] Phospho (ST)	-0.18	0.27	0.10	-0.45	0.303	0.164	0.379	0.05	2.75E+05	3.89E+05	2.20E+05	2.24E+05	3.33E+05	2.24E+05	3.94E+05	3.59E+05	3.15E+05	2.56E+05	4.06E+05	2.88E+05	865.39481	2	79.92
CKI1	YLR133W	QRSSQR	[4] Phospho (ST)	0.25	0.07	0.17	0.17	0.161	0.399	0.262	0.21	6.61E+04	4.08E+04	4.76E+04	6.68E+04	5.36E+04	6.29E+04	5.30E+04	4.36E+04	6.61E+04	6.82E+04	5.42E+04	5.13E+04	421.18581	2	25.36
RPL3	YOR063W	RAASIR	[4] Phospho (ST)	1.71	1.18	0.43	0.53	0.077	0.176	0.160	0.30	6.89E+03	1.03E+04	3.94E+03	3.65E+04	6.16E+03	2.63E+04	3.23E+04	6.13E+03	9.31E+03	1.18E+04	8.67E+03	8.01E+03	377.19246	2	21.05
CKI1	YLR133W	RHSLTR	[3] Phospho (ST)	1.69	0.96	0.38	0.73	0.029	0.168	0.304	0.14	2.76E+03	6.68E+03	1.49E+03	1.65E+04	7.35E+03	1.15E+04	1.25E+04	3.60E+03	5.16E+03	6.92E+03	4.68E+03	2.65E+03	425.20826	2	24.29
DIG1	YPL049C	RSEEGSR	[6] Phospho (ST)	0.65	0.53	0.81	0.12	0.106	0.070	0.038	0.38	5.47E+04	3.81E+04	7.06E+04	1.20E+05	8.02E+04	5.61E+04	7.25E+04	6.65E+04	9.66E+04	1.22E+05	9.14E+04	7.26E+04	450.68003	2	15.89
SCH9	YHR205W	SSSQLDQLNSCSSVTDPSK	[3] Phospho (ST)	-1.02	-0.42	-0.24	-0.60	0.002	0.043	0.104	0.03	2.23E+05	1.75E+05	2.07E+05	1.03E+05	7.85E+04	1.17E+05	1.26E+05	1.84E+05	1.43E+05	1.99E+05	1.49E+05	1.64E+05	1060.4469	2	76.15
CDC1	YDR182W	SVLSTHSK	[5] Phospho (ST)	0.54	-0.07	-0.19	0.61	0.114	0.443	0.338	0.06	3.75E+04	1.79E+04	2.02E+04	3.43E+04	2.92E+04	4.65E+04	3.07E+04	1.64E+04	2.51E+04	2.88E+04	1.92E+04	1.81E+04	469.72083	2	22.88
ASG1	YIL130W	YLPLNYPSE	[8] Phospho (ST)	-0.25	-0.13	-1.07	-0.12	0.292	0.376	0.054	0.37	5.36E+03	1.12E+04	6.88E+03	6.97E+03	8.27E+03	4.49E+03	5.27E+03	8.79E+03	7.31E+03	4.16E+03	5.06E+03	1.91E+03	588.25555	2	16.24
TAO3	YIL129C	RHVSSSFNNK	[4] Phospho (ST)	-1.17	-1.67	-0.61	0.50	0.181	0.151	0.298	0.31	2.87E+03	8.61E+02	4.50E+02	7.06E+02	3.77E+02	7.64E+02	1.06E+03	1.76E+02	5.38E+01	1.65E+03	6.32E+02	4.48E+02	628.28135	2	18.53
BCK1	YJL095W	SFISLR	[1] Phospho (ST)	0.50	-0.05	0.17	0.55	0.254	0.480	0.420	0.02	1.29E+02	1.05E+03	2.93E+02	6.21E+02	8.20E+02	6.60E+02	4.56E+02	4.24E+02	5.45E+02	5.91E+02	6.77E+02	3.92E+02	401.69619	2	18.25
LAA1	YJL207C	QTNFIR	[2] Phospho (ST)	0.47	-0.01	-0.02	0.48	0.135	0.495	0.480	0.13	1.74E+05	9.86E+04	8.10E+04	2.04E+05	1.58E+05	1.30E+05	1.72E+05	8.25E+04	9.73E+04	1.19E+05	1.54E+05	7.52E+04	429.69839	2	19.6
SRO9	YCL037C	NRTPTPK	[5] Phospho (ST)	3.88	-0.34	-0.14	4.21	0.074	0.410	0.461	0.07	6.17E+01	8.66E+02	9.62E+01	8.97E+03	2.61E+00	6.51E+03	5.64E+01	1.91E+02	5.57E+02	1.85E+01	5.17E+02	3.94E+02	447.21531	2	15.7
TOD6	YBL054W	RASLVVSPYMSPR	[3] Phospho (ST)|[9] Phospho (Y)	-0.83	-0.07	0.36	-0.77	0.134	0.458	0.344	0.21	2.73E+03	1.32E+03	1.68E+03	5.63E+02	2.07E+03	5.64E+02	2.22E+03	2.75E+03	5.01E+02	2.31E+03	4.62E+03	4.52E+02	811.86274	2	15.95
CDC28	YBR160W	AYTHEIVTLWYR	[2] Phospho (Y)	0.09	1.25	-0.81	-1.17	0.452	0.214	0.218	0.22	5.63E+02	1.27E+03	3.65E+02	5.31E+02	5.61E+02	1.25E+03	4.04E+03	5.54E+02	7.02E+02	1.86E+01	8.65E+02	3.60E+02	816.88743	2	15.65
STP4	YDL048C	SNSLHANFTSPVPR	[1] Phospho (ST)	-1.29	-1.19	-1.29	-0.10	0.059	0.062	0.081	0.39	1.94E+03	4.98E+03	2.69E+03	1.20E+03	1.83E+03	8.90E+02	1.59E+03	1.52E+03	1.09E+03	3.89E+02	1.02E+03	2.50E+03	803.87253	2	32.53
MYO1	YHR023W	STSYSDDPLDK	[2] Phospho (ST)	0.66	0.24	0.39	0.42	0.042	0.322	0.239	0.10	1.11E+03	5.30E+02	1.38E+03	1.70E+03	1.60E+03	1.50E+03	6.54E+02	1.46E+03	1.46E+03	1.85E+03	1.37E+03	7.52E+02	654.25669	2	15.86
HIF1	YLL022C	PLGDFNDLSQLVK	[9] Phospho (ST)	4.47	1.20	0.90	3.26	0.024	0.132	0.255	0.03	1.33E+02	2.62E+02	0.00E+00	2.47E+03	5.27E+03	1.74E+03	5.41E+02	1.16E+02	2.99E+02	5.37E+02	2.32E+02	0.00E+00	763.36977	2	23.07
RUD3	YOR216C	MSTDPEADGIVASPDDEGK	[13] Phospho (ST)	0.79	0.98	1.20	-0.18	0.199	0.022	0.009	0.39	2.40E+03	2.05E+03	1.45E+03	2.33E+03	6.40E+03	1.52E+03	3.25E+03	3.32E+03	5.08E+03	4.02E+03	5.71E+03	3.84E+03	1007.4019	2	34.72
ROM2	YLR371W	SPLQGFGFFSR	[1] Phospho (ST)	0.08	-0.36	-0.52	0.44	0.452	0.321	0.260	0.17	1.27E+03	6.57E+03	3.43E+03	3.77E+03	5.45E+03	2.73E+03	4.00E+03	2.65E+03	2.15E+03	2.38E+03	3.57E+03	1.91E+03	661.80103	2	34.98
AKL1	YBR059C	LSDSEENLLNDMFLSSFEISSK	[4] Phospho (ST)	-0.47	0.30	-0.85	-0.77	0.187	0.303	0.067	0.13	4.52E+03	4.26E+03	2.07E+03	2.19E+03	3.86E+03	1.77E+03	7.02E+03	2.95E+03	3.41E+03	1.31E+03	2.54E+03	2.16E+03	862.38565	3	21.97
PIL1	YGR086C	SAAGAFGPELSR	[1] Phospho (ST)	0.36	0.74	0.14	-0.39	0.232	0.061	0.405	0.05	6.07E+02	1.78E+03	8.84E+02	1.64E+03	1.41E+03	1.15E+03	2.06E+03	1.60E+03	1.83E+03	1.06E+03	1.69E+03	8.59E+02	621.78034	2	16.71
ENT2	YLR206W	SNPHDSSPSYQDDLEK	[1] Phospho (ST)	-0.07	0.11	-0.14	-0.18	0.456	0.401	0.325	0.39	2.16E+03	3.91E+03	3.05E+03	1.09E+03	3.04E+03	4.59E+03	4.62E+03	3.30E+03	1.94E+03	2.52E+03	2.41E+03	3.32E+03	949.87602	2	30.76
YFR016C	YFR016C	KASADDIFK	[3] Phospho (ST)	0.57	0.59	0.44	-0.02	0.264	0.217	0.297	0.49	3.17E+02	1.58E+03	6.21E+02	4.13E+02	1.33E+03	2.02E+03	1.75E+03	6.53E+02	1.42E+03	4.26E+02	1.61E+03	1.40E+03	537.74661	2	18.17
SCD5	YOR329C	SHSDTTLSYR	[3] Phospho (ST)	-0.73	-0.56	-0.25	-0.18	0.041	0.036	0.305	0.27	7.30E+02	1.05E+03	7.24E+02	3.06E+02	6.25E+02	5.67E+02	5.54E+02	6.05E+02	5.39E+02	1.06E+03	7.30E+02	3.09E+02	623.75906	2	16.74
AKL1	YBR059C	QSSDPTISEQSPR	[3] Phospho (ST)	0.13	-0.09	0.35	0.22	0.390	0.414	0.223	0.28	1.75E+03	9.07E+02	9.33E+02	1.65E+03	1.51E+03	7.82E+02	1.04E+03	1.35E+03	1.00E+03	2.08E+03	1.34E+03	1.17E+03	756.32334	2	17.54
KSP1	YHR082C	SSFVGFPK	[2] Phospho (ST)	1.13	1.39	0.06	-0.27	0.043	0.053	0.471	0.25	0.00E+00	1.10E+03	8.41E+02	1.26E+03	1.48E+03	1.53E+03	2.11E+03	2.11E+03	9.27E+02	4.93E+02	1.00E+03	5.27E+02	474.71505	2	17.24
YSP2	YDR326C	SFSDGHFFK	[3] Phospho (ST)	-1.51	-1.07	-1.96	-0.44	0.062	0.106	0.058	0.19	2.65E+03	6.35E+03	2.46E+03	1.37E+03	1.57E+03	1.06E+03	2.48E+03	2.03E+03	9.27E+02	2.15E+02	2.26E+03	4.60E+02	576.23214	2	17
PFK26	YIL107C	SSFASDFLSR	[2] Phospho (ST)	0.81	1.92	0.90	-1.11	0.213	0.036	0.211	0.06	1.86E+02	1.58E+03	1.91E+02	8.37E+02	1.80E+03	8.17E+02	3.27E+03	2.89E+03	1.31E+03	6.71E+02	2.11E+03	8.93E+02	598.75337	2	25.57
YCG1	YDR325W	NVSFVLPDEK	[3] Phospho (ST)	-2.16	-0.46	-0.42	-1.70	0.080	0.296	0.318	0.02	5.95E+02	3.93E+03	1.98E+03	2.67E+02	8.09E+02	3.51E+02	2.19E+03	1.51E+03	1.01E+03	1.28E+03	2.55E+03	1.01E+03	614.28779	2	22.8
RBG2	YGR173W	IDDEDVVSLFAK	[8] Phospho (ST)	1.14	1.18	0.71	-0.04	0.189	0.097	0.215	0.48	3.24E+02	3.04E+03	9.97E+02	1.00E+03	6.30E+03	2.37E+03	4.92E+03	3.13E+03	1.90E+03	1.04E+03	3.05E+03	3.05E+03	715.82708	2	56.42

HSP26	YBR072W	SFNSPFFDFFDNINNEVDAFNR	[N-term] Acetyl (Protein N-term) [4] Phospho	0.37	-0.20	-0.82	0.57	0.278	0.381	0.174	0.14	6.61E+04	2.84E+04	2.24E+04	3.72E+04	7.33E+04	4.08E+04	2.64E+04	4.80E+04	2.77E+04	9.77E+03	3.75E+04	1.91E+04	926.72532	3	49.63
UBP3	YER151C	SHSIPK	[1] Phospho (ST)	1.59	1.01	0.46	0.57	0.028	0.007	0.144	0.14	1.28E+02	1.31E+02	1.24E+02	3.42E+02	2.66E+02	6.09E+02	3.24E+02	2.06E+02	2.78E+02	2.62E+02	1.64E+02	1.15E+02	374.67281	2	18.41
RTG3	YBL103C	AGSFLSSSFR	[3] Phospho (ST)	-0.37	0.49	-0.68	-0.86	0.358	0.223	0.233	0.09	4.01E+02	2.12E+03	8.60E+02	4.07E+02	1.69E+03	5.17E+02	1.86E+03	1.26E+03	1.63E+03	4.73E+02	7.76E+02	8.57E+02	569.75095	2	19.61
BOI1	YBL085W	SSSVTTELQRPSSVVVNPNFK	[13] Phospho (ST)	-1.07	0.07	-1.25	-1.13	0.153	0.460	0.135	0.01	4.53E+03	1.24E+04	2.95E+03	3.26E+03	3.93E+03	2.27E+03	6.73E+03	8.47E+03	5.61E+03	1.46E+03	2.89E+03	3.96E+03	1178.5795	2	18.81
FAA3	YIL009W	QATGGHLK	[3] Phospho (ST)	1.76	1.57	0.63	0.18	0.039	0.224	0.162	0.44	6.86E+01	5.16E+01	1.65E+02	3.83E+02	1.59E+02	5.05E+02	8.01E+02	5.84E+01	5.70E+01	1.24E+02	2.31E+02	1.07E+02	446.21586	2	17.42
ATG13	YPR185W	SIDSISSSFIK	[1] Phospho (ST)	-0.56	-0.03	-0.59	-0.53	0.185	0.469	0.141	0.15	3.10E+03	6.01E+03	3.20E+03	2.34E+03	4.51E+03	1.49E+03	4.79E+03	4.15E+03	3.11E+03	1.65E+03	3.58E+03	2.95E+03	632.29786	2	29.54
TCB3	YML072C	SPSNLNSTSVTPR	[1] Phospho (ST)	-0.74	-0.31	-1.06	-0.43	0.223	0.350	0.159	0.17	2.81E+04	5.31E+03	1.16E+04	8.14E+03	5.66E+03	1.31E+04	9.10E+03	1.16E+04	1.56E+04	7.03E+03	6.13E+03	8.42E+03	720.3299	2	29.7
TDH3	YGR192C	YAGEVSHDDK	[6] Phospho (ST)	0.45	-0.78	-0.25	1.21	0.255	0.155	0.379	0.09	2.17E+02	1.29E+02	7.47E+01	1.20E+02	1.42E+02	3.26E+02	1.25E+02	1.10E+01	9.70E+01	2.24E+02	9.51E+01	3.13E+01	600.73221	2	17.44
SIS2	YKR072C	QSISPTLSNATTTTTK	[4] Phospho (ST)	-0.97	-0.85	-1.06	-0.12	0.098	0.111	0.087	0.40	4.15E+03	6.12E+03	1.99E+03	2.31E+03	1.10E+03	2.83E+03	2.74E+03	1.40E+03	2.63E+03	2.45E+03	9.77E+02	2.45E+03	865.91454	2	39.5
SEC16	YPL085W	RESIISTGSEFLPPPK	[3] Phospho (ST)	-0.88	-0.18	-0.31	-0.70	0.186	0.417	0.345	0.17	3.63E+03	1.29E+04	3.96E+03	2.39E+03	4.10E+03	4.63E+03	9.82E+03	2.86E+03	5.38E+03	4.56E+03	5.56E+03	6.43E+03	919.45987	2	23.63
SYH1	YPL105C	TVSNITNEEESIVK	[6] Phospho (ST)	-0.02	-0.35	-1.30	0.32	0.487	0.327	0.136	0.21	6.90E+02	5.97E+03	4.28E+03	2.67E+03	5.00E+03	3.10E+03	2.37E+03	3.63E+03	2.60E+03	6.60E+02	2.89E+03	8.67E+02	821.88256	2	29.97
STE12	YHR084W	YPYQLSVAPTFPVPPSSSR	[18] Phospho (ST)	-1.21	-0.46	-0.14	-0.74	0.191	0.334	0.443	0.07	2.01E+03	2.78E+04	9.93E+03	5.47E+03	7.19E+03	4.53E+03	1.34E+04	8.67E+03	6.78E+03	7.98E+03	1.65E+04	1.16E+04	1087.0216	2	16.22
AAC3	YBR085W	QFNGLTDVYKK	[9] Phospho (Y)	-0.84	-1.35	-0.20	0.51	0.220	0.147	0.419	0.15	1.12E+04	1.61E+03	4.29E+03	2.12E+03	2.84E+03	4.58E+03	2.64E+03	1.66E+03	2.41E+03	2.88E+03	3.87E+03	8.22E+03	696.82994	2	19.17
AZF1	YOR113W	LNSLSVNNK	[3] Phospho (ST)	-0.59	-0.45	-0.55	-0.14	0.098	0.189	0.126	0.38	2.95E+03	1.44E+03	2.02E+03	1.22E+03	1.33E+03	1.70E+03	7.91E+02	1.88E+03	2.00E+03	1.67E+03	9.66E+02	1.74E+03	534.7587	2	30.32
DYS1	YHR068W	SDINEKLPELLQDAVLK	[N-term] Acetyl (Protein N-term) [1] Phospho	-1.71	-1.64	-0.90	-0.07	0.009	0.010	0.033	0.39	1.31E+04	1.37E+04	7.39E+03	3.06E+03	3.54E+03	3.85E+03	4.60E+03	3.49E+03	2.87E+03	6.28E+03	7.15E+03	4.88E+03	683.01723	3	25.99
AKL1	YBR059C	RHSTGHELSTR	[3] Phospho (ST)	-1.53	-3.30	-1.80	1.76	0.090	0.042	0.075	0.10	2.92E+03	6.48E+02	1.59E+03	1.00E+03	5.39E+02	2.26E+02	4.97E+02	0.00E+00	0.00E+00	2.20E+02	3.27E+02	9.14E+02	680.80922	2	17.15
MCM3	YEL032W	FALLGEDIGNDIDEEESEYEEALSK	[19] Phospho (Y)	-0.86	0.24	-0.92	-1.10	0.080	0.263	0.062	0.03	1.71E+04	2.40E+04	1.17E+04	5.62E+03	1.53E+04	8.04E+03	2.23E+04	2.45E+04	1.54E+04	4.70E+03	1.20E+04	1.13E+04	965.75107	3	17.31
SWA2	YDR320C	VEDYDLPQVNDSPNR	[12] Phospho (ST)	0.26	0.56	-0.43	-0.30	0.361	0.157	0.260	0.29	2.33E+03	6.93E+03	2.97E+03	1.90E+03	7.39E+03	5.40E+03	4.31E+03	6.49E+03	7.29E+03	2.29E+03	3.15E+03	3.65E+03	920.89174	2	18.22
FUN30	YAL019W	SNSFNLQSAR	[3] Phospho (ST)	-4.12	-4.63	-1.80	0.51	0.000	0.000	0.000	0.17	1.04E+04	8.45E+03	8.51E+03	5.40E+02	6.14E+02	3.94E+02	1.11E+02	5.32E+02	4.35E+02	2.60E+03	2.66E+03	2.56E+03	602.26178	2	38.31
YDL180W	YDL180W	SSSSTYGSIR	[2] Phospho (ST)	0.32	0.91	0.10	-0.59	0.223	0.216	0.412	0.29	5.44E+02	7.99E+02	5.81E+02	9.84E+02	9.85E+02	4.49E+02	5.29E+02	2.53E+03	5.97E+02	1.03E+03	4.70E+02	5.58E+02	562.73511	2	20.1
RAD9	YDR217C	GNSLQLHDDNK	[3] Phospho (ST)	1.54	0.40	0.52	1.14	0.009	0.277	0.209	0.00	2.41E+03	7.60E+02	4.96E+03	8.88E+03	6.85E+03	7.96E+03	3.70E+03	2.52E+03	4.53E+03	3.01E+03	4.56E+03	4.10E+03	660.77987	2	41.6
GDS1	YOR355W	SSSELAAIHK	[3] Phospho (ST)	-2.35	-1.88	-1.19	-0.47	0.000	0.000	0.002	0.06	4.19E+03	5.52E+03	5.10E+03	1.26E+03	6.03E+02	1.01E+03	1.38E+03	1.27E+03	1.34E+03	2.45E+03	1.74E+03	2.27E+03	561.76332	2	37.18
BEM3	YPL115C	SPSSLLEVK	[1] Phospho (ST)	-0.64	-0.57	-0.35	-0.07	0.137	0.147	0.231	0.43	1.57E+03	3.19E+03	1.61E+03	9.89E+02	1.91E+03	1.19E+03	1.66E+03	1.63E+03	1.00E+03	1.78E+03	1.94E+03	1.27E+03	520.25736	2	19.31
RFX1	YLR176C	SNSSAYPLSFK	[3] Phospho (ST)	-6.58	-1.97	-1.46	-4.61	0.034	0.078	0.094	0.09	6.43E+03	2.00E+04	7.01E+03	9.04E+01	1.20E+02	1.10E+02	1.30E+03	6.26E+03	9.72E+02	4.54E+03	4.71E+03	2.92E+03	640.78202	2	43.75
HAL5	YJL165C	SVFSLSGLFK	[1] Phospho (ST)	-3.11	-1.04	-1.91	-2.07	0.018	0.096	0.048	0.05	8.39E+02	2.32E+03	1.38E+03	6.74E+01	2.34E+02	1.98E+02	1.17E+03	7.19E+02	3.05E+02	9.67E+01	9.57E+02	1.37E+02	582.79024	2	31.03

Table 2.3: Mec1-100 dependent phosphopeptides

red: S/TQ phosphopeptides

Protein				log2 Ratio mutant vs WT				T-test mutant vs WT				Normalized abundance wt			rad53			mec1-100-tel1			mec1-100-tel1-pph3					
SwissProt	SGD	Sequence	Variable modifications ([position] description)	rad53 vs. WT	tel1 mec1-100 vs. WT	pph3 vs. WT	rad53 vs. tel1 mec1-100	rad53 vs. WT	tel1 mec1-100 vs. WT	pph3 vs. WT	rad53 vs. tel1 mec1-100	131114_198 1-1_3uL	131114_198 1-2_3uL	131114_198 1-3_3uL	131115_737 3-1_3uL	131115_737 3-2_3uL	131115_737 3-3_3uL	131116_691 3-1_3uL	131116_691 3-2_3uL	131116_691 3-3_3uL	131115_773 4-1_3uL	131115_773 4-2_3uL	131115_773 4-3_3uL	m/z	Charge	Best peptide match/ Score
FEN1	YCR034W	NVPTPSPSPKPQHR	[4] Phospho (ST)|[6] Phospho (ST)	-0.68	-1.42	-0.95	0.74	0.009	0.001	0.003	0.02	1.40E+06	1.16E+06	1.16E+06	9.46E+05	7.13E+05	6.69E+05	5.04E+05	3.53E+05	5.39E+05	7.78E+05	5.40E+05	6.08E+05	851.379786	2	17.01
NOG2	YNR053C	AASFQDSTIPDAR	[3] Phospho (ST)	-0.85	-1.65	-0.59	0.80	0.002	0.000	0.005	0.00	2.74E+05	2.97E+05	3.44E+05	1.61E+05	1.61E+05	1.85E+05	9.05E+04	9.14E+04	1.09E+05	2.00E+05	1.88E+05	2.20E+05	729.81741	2	58.35
RPL36B	L249C-A	RLGSFTR	[4] Phospho (ST)	1.50	-1.01	-0.33	2.50	0.002	0.016	0.132	0.00	9.30E+03	1.44E+04	1.12E+04	3.77E+04	2.70E+04	3.37E+04	7.27E+03	3.84E+03	6.26E+03	7.26E+03	9.65E+03	1.09E+04	458.723614	2	23.79
SRP40	YKR092C	AEETPASSNESTPSASSSSSANK	[8] Phospho (ST)	-0.54	-1.56	-1.05	1.02	0.119	0.015	0.032	0.02	8.91E+04	4.45E+04	6.37E+04	5.99E+04	3.83E+04	3.73E+04	2.04E+04	1.83E+04	2.82E+04	3.91E+04	2.76E+04	2.86E+04	769.314777	3	22.17
MSB1	YOR188W	RDSAPDNQGIYHTVISK	[3] Phospho (ST)	-0.52	-1.14	0.10	0.62	0.147	0.040	0.401	0.04	1.87E+05	8.62E+04	1.15E+05	1.14E+05	7.29E+04	8.32E+04	4.86E+04	6.47E+04	6.24E+04	1.69E+05	1.06E+05	1.42E+05	990.956842	2	23.18
PAH1	YMR165C	RASSAAATSIDK	[3] Phospho (ST)	-0.10	-1.26	-0.66	1.17	0.382	0.038	0.105	0.02	3.91E+04	2.69E+04	2.08E+04	2.72E+04	2.33E+04	3.07E+04	1.53E+04	2.96E+03	1.79E+04	1.33E+04	1.42E+04	2.75E+04	629.295134	2	51.99
PDS1	YDR113C	KLSQISR	[3] Phospho (ST)	0.47	-1.17	-0.79	1.63	0.127	0.026	0.112	0.02	1.28E+04	9.90E+03	8.37E+03	1.96E+04	1.10E+04	1.23E+04	2.72E+03	3.16E+03	7.93E+03	2.41E+03	4.05E+03	1.14E+04	456.238946	2	21.02
PIG2	YIL045W	SVHFDR	[1] Phospho (ST)	-0.87	-1.26	-0.63	0.40	0.056	0.032	0.134	0.28	1.46E+04	1.20E+04	7.88E+03	9.55E+03	4.20E+03	5.16E+03	3.46E+03	2.60E+03	8.27E+03	4.64E+03	5.35E+03	1.24E+04	420.673591	2	19.33
KEL1	YHR158C	NNSPILETLPSNEIK	[3] Phospho (ST)	-0.51	-2.24	-0.48	1.73	0.011	0.000	0.000	0.00	8.19E+04	8.64E+04	7.93E+04	6.65E+04	6.18E+04	4.53E+04	1.78E+04	1.30E+04	2.15E+04	6.04E+04	5.95E+04	5.81E+04	874.928252	2	24.33
TSL1	YML100W	IASPIQHEHDSGSR	[3] Phospho (ST)	0.34	-1.22	-0.24	1.55	0.010	0.004	0.035	0.00	2.31E+04	2.80E+04	2.44E+04	3.15E+04	3.35E+04	3.02E+04	1.52E+04	6.89E+03	1.03E+04	2.12E+04	2.23E+04	2.04E+04	807.356619	2	33.97
BCD1	YHR040W	FIDNAREEEDAEEDSQPTEEPVQK	[15] Phospho (ST)	1.01	-1.44	-1.16	2.45	0.001	0.004	0.006	0.00	6.13E+04	4.76E+04	7.41E+04	1.29E+05	1.22E+05	1.17E+05	2.30E+04	2.10E+04	2.34E+04	2.56E+04	2.55E+04	3.05E+04	962.407596	3	53.88
STB1	YNL309W	FSHIKPSASSPQSTFK	[10] Phospho (ST)	-0.72	-1.70	-0.09	0.99	0.012	0.032	0.367	0.16	3.41E+04	4.77E+04	4.23E+04	2.71E+04	2.06E+04	2.78E+04	3.38E+04	1.62E+03	2.65E+03	3.30E+04	3.41E+04	4.96E+04	610.292842	3	19.02
GNP1	YDR508C	RAEGSHANSPDSSNSNGTTPISTKDSSSQLDNELNR	[22] Phospho (ST)|[23] Phospho (ST)	-0.69	-1.13	-0.11	0.45	0.038	0.012	0.350	0.07	1.44E+05	8.64E+04	1.22E+05	8.82E+04	6.94E+04	6.20E+04	4.43E+04	6.72E+04	4.94E+04	1.29E+05	8.26E+04	1.15E+05	984.16876	4	36.86
RPC31	YNL151C	ELAEDVDDASTGDGAAK	[10] Phospho (ST)	-0.53	-1.76	-0.04	1.23	0.010	0.000	0.427	0.00	3.14E+04	2.78E+04	3.52E+04	1.96E+04	2.42E+04	2.16E+04	1.15E+04	8.10E+03	8.25E+03	3.50E+04	2.29E+04	3.38E+04	872.352227	2	54.54
MSH6	YDR097C	STTTDEDLSSQSRR	[11] Phospho (ST)	0.49	-1.11	-0.85	1.60	0.055	0.019	0.053	0.00	2.82E+04	1.61E+04	1.90E+04	3.27E+04	2.59E+04	3.02E+04	9.84E+03	8.37E+03	1.10E+04	1.67E+04	7.41E+03	1.09E+04	875.368281	2	26.73
HXT1	YHR094C	NESFHDNLSESQVQPAVAPPNTGK	[11] Phospho (ST)	-0.23	-1.10	-0.44	0.88	0.295	0.013	0.081	0.07	3.87E+04	2.38E+04	3.56E+04	3.38E+04	1.47E+04	3.54E+04	1.21E+04	1.92E+04	1.43E+04	2.57E+04	2.02E+04	2.66E+04	662.301924	4	22.72
BEM3	YPL115C	ITIKSPNK	[2] Phospho (ST)	-0.78	-2.33	-1.01	1.55	0.056	0.006	0.032	0.03	1.54E+04	1.13E+04	8.70E+03	9.58E+03	4.78E+03	6.34E+03	2.59E+03	6.60E+02	3.80E+03	4.15E+03	5.12E+03	8.38E+03	490.762501	2	16.51
ESBP6	YNL125C	KLSISR	[3] Phospho (ST)	-0.27	-1.09	-0.22	0.82	0.079	0.033	0.135	0.07	8.11E+03	6.12E+03	7.93E+03	5.73E+03	5.82E+03	6.84E+03	6.32E+03	1.95E+03	2.12E+03	5.69E+03	5.89E+03	7.39E+03	392.208485	2	22.36
ENT2	YLR206W	TRSNPHDSSPSYQDDLEK	[1] Phospho (ST)|[3] Phospho (ST)	-0.03	-1.00	-0.60	0.97	0.441	0.014	0.027	0.01	6.70E+04	4.95E+04	4.90E+04	5.48E+04	5.87E+04	4.89E+04	2.17E+04	3.91E+04	2.19E+04	3.89E+04	2.93E+04	4.13E+04	1118.43448	2	16.55
NDD1	YOR372C	RSQSLLSDSGSK	[4] Phospho (ST)	0.53	-1.19	-1.64	1.72	0.057	0.017	0.009	0.00	9.47E+03	6.46E+03	1.19E+04	1.51E+04	1.08E+04	1.43E+04	3.68E+03	3.33E+03	5.13E+03	2.48E+03	2.65E+03	3.79E+03	672.811105	2	24.97
YDR348C	YDR348C	NLSLSRDNYDVGHSNEGVR	[3] Phospho (ST)	-0.41	-1.94	-0.10	1.53	0.031	0.009	0.313	0.03	2.20E+04	2.16E+04	2.58E+04	2.04E+04	1.42E+04	1.77E+04	1.45E+04	1.58E+03	1.95E+03	2.46E+04	1.67E+04	2.35E+04	737.997775	3	31.47
RLF2	YPR018W	SNSDLQAQTASQSQSPEK	[3] Phospho (ST)	-0.51	-1.05	-0.21	0.54	0.056	0.004	0.209	0.07	2.68E+04	2.07E+04	2.87E+04	2.03E+04	1.22E+04	2.10E+04	1.03E+04	1.29E+04	1.37E+04	2.49E+04	1.59E+04	2.50E+04	993.426172	2	73.98
HXT1	YHR094C	NSTPDLISPQK	[2] Phospho (ST)	-0.05	-1.20	-0.47	1.15	0.464	0.049	0.226	0.06	1.16E+04	1.11E+04	2.27E+04	1.00E+04	1.14E+04	2.24E+04	9.13E+03	5.83E+03	4.76E+03	1.74E+04	6.05E+03	9.35E+03	640.300373	2	30.3
YSH1	YLR277C	IEPIKEENEDNLDSQAEK	[14] Phospho (ST)	2.54	-1.10	-1.77	3.64	0.000	0.006	0.003	0.00	9.71E+03	1.46E+04	1.43E+04	7.44E+04	7.11E+04	7.93E+04	6.21E+03	5.81E+03	6.03E+03	2.51E+03	4.04E+03	4.75E+03	1090.98296	2	38.79
MHP1	YJL042W	RASFSLHNDKPQPAK	[3] Phospho (ST)	-0.10	-1.41	-0.83	1.31	0.131	0.003	0.021	0.00	2.07E+04	2.25E+04	1.93E+04	2.05E+04	1.91E+04	1.88E+04	1.24E+04	5.33E+03	5.68E+03	7.47E+03	1.03E+04	1.74E+04	592.62361	3	21.16
FBA1	YKL060C	GISNEGQNASIK	[10] Phospho (ST)	-0.40	-1.51	-0.62	1.11	0.103	0.005	0.041	0.01	2.98E+04	1.94E+04	2.23E+04	2.24E+04	1.67E+04	1.51E+04	6.28E+03	7.98E+03	1.09E+04	1.89E+04	1.26E+04	1.51E+04	649.292144	2	23.98
TIF4631	YGR162W	SPVPTK	[5] Phospho (ST)	1.31	-1.44	-0.98	2.75	0.016	0.029	0.069	0.00	4.50E+03	2.26E+03	5.47E+03	1.00E+04	7.36E+03	1.30E+04	1.54E+03	1.06E+03	1.90E+03	2.91E+03	2.22E+03	1.05E+03	354.669978	2	19.02
LEO1	YOR123C	KQSQILR	[3] Phospho (ST)	1.40	-1.15	-0.69	2.55	0.002	0.007	0.013	0.00	3.37E+03	2.32E+03	3.05E+03	7.47E+03	6.59E+03	9.06E+03	1.69E+03	1.35E+03	8.74E+02	1.96E+03	1.65E+03	1.80E+03	476.751944	2	41.17
PIB2	YGL023C	KLSSFK	[4] Phospho (ST)	0.64	-1.05	-0.18	1.70	0.016	0.042	0.254	0.01	2.53E+03	2.78E+03	2.94E+03	4.15E+03	3.58E+03	5.18E+03	2.36E+03	2.32E+02	1.36E+03	1.74E+03	2.31E+03	3.23E+03	395.198768	2	22.17
HRK1	YOR267C	KLSMSQLR	[3] Phospho (ST)	-0.08	-1.10	0.51	1.02	0.464	0.020	0.212	0.20	2.94E+03	4.52E+03	2.78E+03	1.95E+03	6.73E+03	1.03E+03	1.77E+03	1.91E+03	1.07E+03	2.26E+03	7.58E+03	4.76E+03	521.759493	2	32.75
ZRT2	YLR130C	DHYSHENDHQDVSQLATR	[3] Phospho (Y)	-0.53	-2.26	-0.79	1.73	0.085	0.002	0.014	0.04	2.51E+04	2.42E+04	2.95E+04	2.70E+04	1.22E+04	1.54E+04	1.17E+04	3.08E+03	1.65E+03	1.64E+04	9.67E+03	1.94E+04	558.733253	4	17.67
RDH54	YBR073W	SISAGPTLNLAK	[3] Phospho (ST)	0.40	-1.63	-0.15	2.03	0.082	0.013	0.359	0.00	5.78E+03	7.34E+03	4.50E+03	7.79E+03	9.06E+03	6.45E+03	3.42E+03	1.49E+03	7.58E+02	4.50E+03	7.76E+03	3.60E+03	626.321411	2	40.07
IES4	YOR189W	SQESSVLSESQEQLANNPK	[N-term] Acetyl (Protein N-term)|[1] Phospho (ST)	-0.69	-1.04	-2.30	0.36	0.010	0.005	0.000	0.20	4.46E+04	4.83E+04	4.51E+04	2.59E+04	3.74E+04	2.24E+04	1.38E+04	3.08E+04	2.24E+04	8.63E+03	7.84E+03	1.16E+04	1098.98687	2	73.35
ENA2	YDR039C	AHNPENDLESNNK	[10] Phospho (ST)	0.17	-1.88	-1.50	2.05	0.256	0.005	0.008	0.00	1.37E+04	7.84E+03	1.09E+04	1.16E+04	1.38E+04	1.10E+04	2.69E+03	2.53E+03	3.56E+03	4.55E+03	2.92E+03	3.99E+03	781.318283	2	31.96
TGL1	YKL140W	THSADRSPLSVQADEADEVHNADNSR	[3] Phospho (ST)|[7] Phospho (ST)	-0.61	-2.97	-1.33	2.36	0.117	0.007	0.031	0.01	3.33E+04	1.64E+04	2.37E+04	2.31E+04	1.20E+04	1.31E+04	5.81E+03	2.30E+03	1.27E+03	1.58E+04	6.57E+03	6.78E+03	994.412865	3	22.86
VHS2	YIL135C	TVSNNAANSLSR	[3] Phospho (ST)	-0.58	-1.98	-1.21	1.40	0.060	0.006	0.008	0.02	7.98E+03	4.96E+03	7.49E+03	5.66E+03	4.63E+03	3.38E+03	3.16E+03	1.24E+03	7.58E+02	3.27E+03	2.86E+03	2.70E+03	657.294732	2	45.3
GIN4	YDR507C	NRESLISVTSSR	[4] Phospho (ST)	-0.35	-1.01	-0.82	0.66	0.081	0.009	0.024	0.00	4.88E+03	7.62E+03	6.33E+03	4.86E+03	4.87E+03	5.02E+03	3.11E+03	2.78E+03	3.44E+03	2.47E+03	3.97E+03	4.21E+03	714.846058	2	24.95
MAP2	YBL091C	TDAEIENSPASDLK	[N-term] Acetyl (Protein N-term)|[1] Phospho (ST)	-0.03	-1.08	-0.15	1.05	0.455	0.022	0.271	0.04	1.02E+04	1.30E+04	1.10E+04	1.03E+04	1.41E+04	9.23E+03	4.84E+03	8.94E+03	2.43E+03	1.08E+04	1.25E+04	7.53E+03	806.343456	2	19.28
SKY1	YMR216C	HVSRSSDITANDSSDEK	[5] Phospho (ST)|[6] Phospho (ST)	-0.94	-1.64	-0.68	0.71	0.046	0.014	0.124	0.07	9.40E+03	5.19E+03	5.73E+03	4.43E+03	3.87E+03	2.31E+03	1.50E+03	2.25E+03	2.73E+03	6.88E+03	3.54E+03	2.33E+03	669.928375	3	33.94
PTK2	YJR059W	VEDNLSEDDSTMK	[6] Phospho (ST)	0.70	-1.09	0.39	1.80	0.274	0.015	0.097	0.15	3.04E+03	2.88E+03	2.65E+03	1.51E+03	1.01E+04	2.34E+03	7.62E+02	2.22E+03	1.02E+03	2.67E+03	4.54E+03	4.00E+03	781.799636	2	34.15
PCL6	YER059W	HESPSNESSLDK	[3] Phospho (ST)	0.28	-2.07	-1.06	2.35	0.303	0.045	0.100	0.01	6.95E+03	2.54E+03	3.23E+03	6.73E+03	3.61E+03	5.12E+03	1.55E+03	4.38E+01	1.42E+03	1.71E+03	1.45E+03	2.93E+03	705.281985	2	40.69
SAP190	YKR028W	ISEHRDGNSLYNEDNDENGSDK	[9] Phospho (ST)	-0.86	-1.28	-0.48	0.41	0.006	0.018	0.032	0.22	3.70E+03	2.71E+03	2.79E+03	1.61E+03	1.63E+03	1.80E+03	8.15E+02	7.15E+02	2.24E+03	2.37E+03	1.93E+03	2.29E+03	863.345424	3	15.07
TOF2	YKR010C	KSSLEIK	[3] Phospho (ST)	-0.13	-1.05	-0.25	0.92	0.343	0.037	0.239	0.03	1.73E+03	9.12E+02	1.49E+03	1.49E+03	1.24E+03	1.04E+03	1.00E+03	5.37E+02	4.41E+02	1.31E+03	1.27E+03	8.94E+02	442.727948	2	15.3
SRO9	YCL037C	DATSQENGQSTQQQQPPHHR	[4] Phospho (ST)	0.82	-1.09	-0.49	1.91	0.093	0.044	0.125	0.02	4.20E+03	2.89E+03	2.23E+03	5.59E+03	3.05E+03	7.78E+03	2.29E+03	7.31E+02	1.33E+03	2.42E+03	1.54E+03	2.65E+03	785.335099	3	30.45
SWI3	YJL176C	LDSQLETPSTEESR	[3] Phospho (ST)	3.31	-2.95	-2.50	6.25	0.000	0.036	0.040	0.00	5.35E+02	7.03E+02	1.61E+03	9.19E+03	1.04E+04	9.01E+03	2.67E+02	0.00E+00	7.53E+01	2.35E+02	8.82E+01	1.55E+02	779.817667	2	40.95
YOX1	YML027W	SVESALR	[1] Phospho (ST)	0.17	-1.44	-1.32	1.60	0.333	0.010	0.012	0.01	8.57E+02	8.57E+02	1.37E+03	1.60E+03	8.38E+02	1.05E+03	3.12E+02	3.82E+02	4.30E+02	4.39E+02	3.66E+02	4.19E+02	421.194205	2	16.89
ABF1	YKL112W	NDTEDDSINK	[7] Phospho (ST)	4.92	-1.94	-0.50	6.81	0.019	0.031	0.290	0.02	1.22E+02	4.41E+01	6.17E+01	4.05E+03	1.16E+03	2.67E+03	0.00E+00	1.40E+01	2.37E+01	1.17E+02	2.67E+01	1.14E+01	615.730514	2	15.88

Table 2.4: Selected SQ/TQ phosphopeptides

red: S/TQ phosphopeptides

Protein					log2 Ratio				T-test				Normalized abundance															
					mutant vs WT				mutant vs WT				wt			rad53			mec1-100-tel1			mec1-100-tel1-pph3						
SwissProt	SGD	Sequence	Variable modifications ([position] description)	found by Chen et al., 2010	rad53 vs. WT	tel1 mec1-100 vs. WT	pph3 vs. WT	rad53 vs. tel1 mec1-100	rad53 vs. WT	tel1 mec1-100 vs. WT	pph3 vs. WT	rad53 vs. tel1 mec1-100	131114_198 1-1_3uL	131114_198 1-2_3uL	131114_198 1-3_3uL	131115_737 3-1_3uL	131115_737 3-2_3uL	131115_737 3-3_3uL	131116_691 3-1_3uL	131116_691 3-2_3uL	131116_691 3-3_3uL	131115_773 4-1_3uL	131115_773 4-2_3uL	131115_773 4-3_3uL	m/z	Charge	Best peptide match/ Score
BCD1	YHR040W	FIDNAREEEDAEEDSQPTEEPVQK	[15] Phospho (ST)	+	1.01	-1.44	-1.16	2.45	0.001	0.004	0.006	0.00	6.13E+04	4.76E+04	7.41E+04	1.29E+05	1.22E+05	1.17E+05	2.30E+04	2.10E+04	2.34E+04	2.56E+04	2.55E+04	3.05E+04	962.407596	3	53.88
BDF1	YLR399C	ALSQEEQSR	[3] Phospho (ST)	+	0.83	-0.72	-1.79	1.55	0.107	0.225	0.109	0.01	5.56E+03	5.32E+02	7.50E+03	8.33E+03	5.86E+03	1.01E+04	1.79E+03	3.21E+03	3.23E+03	2.81E+03	8.02E+02	2.92E+02	564.24118	2	31.66
CBF1	YJR060W	DQGLLSQESNDGNIDSALLSEGATLK	[6] Phospho (ST)|[9] Phospho (ST)	+	0.14	-0.95	-2.11	1.09	0.377	0.057	0.013	0.03	9.11E+04	7.60E+04	3.93E+04	6.27E+04	1.05E+05	5.98E+04	2.70E+04	4.71E+04	3.26E+04	1.64E+04	1.31E+04	1.84E+04	945.750341	3	38.85
CBF5	YLR175W	EYVPLDNAEQSTSSSQETK	[18] Phospho (ST)	+	2.19	0.04	-0.62	2.16	0.001	0.413	0.003	0.00	2.68E+05	2.18E+05	2.52E+05	1.36E+06	1.11E+06	9.00E+05	2.14E+05	2.91E+05	2.52E+05	1.68E+05	1.45E+05	1.67E+05	1096.96527	2	38.96
CBF5	YLR175W	EYVPLDNAEQSTSSSQETKETEEEPKK	[11] Phospho (ST)	+	1.46	-0.89	-1.48	2.35	0.002	0.000	0.000	0.00	8.26E+04	7.74E+04	7.92E+04	2.64E+05	1.91E+05	2.03E+05	4.39E+04	4.32E+04	4.19E+04	2.34E+04	2.54E+04	3.68E+04	1055.13369	3	29.23
CBF5	YLR175W	EYVPLDNAEQSTSSSQETKETEEEPK	[14] Phospho (ST)	+	2.18	-0.73	-1.71	2.91	0.001	0.009	0.000	0.00	1.87E+04	1.92E+04	1.97E+04	1.07E+05	7.33E+04	8.04E+04	8.49E+03	1.10E+04	1.51E+04	5.73E+03	5.87E+03	5.91E+03	1012.43508	3	16.01
CCT3	YJL014W	KGESQTNIEIEK	[4] Phospho (ST)	-	1.84	0.45	0.72	1.39	0.005	0.071	0.084	0.01	2.18E+03	1.98E+03	3.55E+03	6.78E+03	9.49E+03	1.14E+04	3.28E+03	3.47E+03	3.78E+03	5.94E+03	3.04E+03	3.77E+03	728.339427	2	34.55
CDC3	YLR314C	DYEEELANDQEEEEGQGEGHENQSQEQR	[24] Phospho (ST)	-	1.05	-0.25	-0.40	1.30	0.015	0.254	0.108	0.01	1.11E+05	6.65E+04	8.54E+04	2.27E+05	1.77E+05	1.39E+05	4.82E+04	9.70E+04	7.61E+04	7.77E+04	5.51E+04	6.64E+04	1129.43366	3	20.36
DCS2	YOR173W	RPSQSGRSTPIFFHR	[3] Phospho (ST)|[5] Phospho (ST)	-	2.07	-0.72	0.65	2.79	0.013	0.285	0.217	0.01	0.00E+00	2.40E+03	3.67E+03	1.16E+04	7.60E+03	6.44E+03	2.63E+03	6.66E+02	3.78E+02	4.31E+03	1.69E+03	3.52E+03	483.971357	4	17.21
DEP1	YAL013W	SQQTPQESEQTTAK	[N-term] Acetyl (Protein N-term)|[1] Phospho (ST)	-	0.45	-0.82	-1.32	1.27	0.167	0.111	0.053	0.02	2.01E+04	7.81E+03	2.15E+04	2.91E+04	2.04E+04	1.81E+04	4.56E+03	1.19E+04	1.15E+04	1.01E+04	3.58E+03	6.07E+03	842.856673	2	18.28
ERG6	YML008C	KPENAETPSQTSQEATQ	[16] Phospho (ST)	-	3.33	0.08	-0.64	3.25	0.001	0.460	0.262	0.00	4.46E+02	1.60E+02	8.33E+02	6.09E+03	4.23E+03	4.50E+03	6.47E+02	1.72E+02	7.04E+02	0.00E+00	3.91E+02	5.24E+02	963.410982	2	38.02
GOS1	YHL031C	SQFHSQSNVLNTANNK	[1] Phospho (ST)	-	0.37	-0.75	-0.07	1.12	0.101	0.111	0.386	0.04	1.48E+04	1.59E+04	2.08E+04	1.74E+04	2.24E+04	2.70E+04	1.45E+04	1.49E+04	1.35E+03	1.53E+04	1.43E+04	1.97E+04	934.918784	2	62.36
HIF1	YLL022C	PLGDFNDLSQLVK	[9] Phospho (ST)	-	4.47	1.20	0.90	3.26	0.024	0.132	0.255	0.03	1.33E+02	2.62E+02	0.00E+00	2.47E+03	5.27E+03	1.74E+03	5.41E+02	1.16E+02	2.99E+02	5.37E+02	2.32E+02	0.00E+00	763.369769	2	23.07
HPR1	YDR138W	INSASQTEGDELK	[5] Phospho (ST)	+	2.78	-0.11	-1.04	2.89	0.000	0.332	0.042	0.00	6.93E+03	7.24E+03	1.04E+04	6.08E+04	4.88E+04	6.00E+04	6.85E+03	7.39E+03	8.60E+03	6.87E+03	2.25E+03	2.83E+03	736.319049	2	66.79
HSP12	YFL014W	ASEALKPDSQKSYAEQGK	[9] Phospho (ST)|[13] Phospho (Y)	+	4.55	-1.74	-0.46	6.28	0.000	0.173	0.357	0.00	1.64E+03	3.94E+02	1.18E+02	1.58E+04	1.85E+04	1.68E+04	2.33E+02	3.43E+02	4.74E+01	3.36E+02	3.26E+02	8.92E+02	699.636034	3	16.24
HSP12	YFL014W	ASEALKPDSQK	[9] Phospho (ST)	+	4.92	-0.36	-1.40	5.29	0.002	0.224	0.031	0.00	1.10E+04	5.62E+03	5.96E+03	2.41E+05	1.60E+05	2.85E+05	7.01E+03	3.90E+03	6.65E+03	3.85E+03	2.53E+03	2.19E+03	627.292143	2	42.09
HTA2	YBL003C	TAKASQEL	[5] Phospho (ST)	-	3.34	-0.63	1.29	3.97	0.002	0.153	0.050	0.00	7.89E+04	2.49E+04	5.56E+04	6.85E+05	4.65E+05	4.61E+05	2.68E+04	3.95E+04	3.63E+04	1.95E+05	9.44E+04	1.00E+05	464.212801	2	28.54
HXT1	YHR094C	NESFHDNLSESQVQPAVAPPNTGK	[11] Phospho (ST)	-	-0.23	-1.10	-0.44	0.88	0.295	0.013	0.081	0.07	3.87E+04	2.38E+04	3.56E+04	3.38E+04	1.47E+04	3.54E+04	1.21E+04	1.92E+04	1.43E+04	2.57E+04	2.02E+04	2.66E+04	662.301924	4	22.72
IES1	YFL013C	SGSQEEASPSSIQSETETVTTK	[3] Phospho (ST)	-	0.99	-0.66	-1.04	1.65	0.009	0.109	0.014	0.01	1.24E+04	2.01E+04	1.58E+04	3.20E+04	3.78E+04	2.60E+04	4.24E+03	1.60E+04	1.03E+04	6.68E+03	1.00E+04	6.78E+03	1182.00988	2	78.19
IES4	YOR189W	SQESSVLSESQEQLANNPK	[N-term] Acetyl (Protein N-term)|[1] Phospho (ST)	(+) different resdiue	-0.69	-1.04	-2.30	0.36	0.010	0.005	0.000	0.20	4.46E+04	4.83E+04	4.51E+04	2.59E+04	3.74E+04	2.24E+04	1.38E+04	3.08E+04	2.24E+04	8.63E+03	7.84E+03	1.16E+04	1098.98587	2	73.35
IOC2	YLR095C	SPQHTLSQLR	[7] Phospho (ST)	+	2.39	-1.62	-2.92	4.00	0.004	0.120	0.072	0.00	2.66E+03	7.72E+02	6.39E+02	7.31E+03	5.38E+03	8.74E+03	4.83E+02	1.80E+02	6.44E+02	2.22E+02	1.69E+02	1.21E+02	567.258309	2	25.02
ISW2	YOR304W	TSATREDTPLSQNESTR	[11] Phospho (ST)	+	2.20	0.20	-0.36	2.00	0.003	0.129	0.128	0.00	3.38E+03	4.53E+03	3.66E+03	2.28E+04	1.51E+04	1.53E+04	4.10E+03	4.92E+03	4.24E+03	3.98E+03	2.91E+03	2.13E+03	658.291707	3	32.65
ISW2	YOR304W	EDTPLSQNESTR	[3] Phospho (ST)	+	2.72	0.56	-0.14	2.16	0.001	0.116	0.384	0.00	1.82E+03	2.50E+03	4.37E+03	2.13E+04	1.54E+04	2.07E+04	5.41E+03	3.34E+03	4.06E+03	1.99E+03	2.65E+03	3.25E+03	728.802009	2	18.36
KIN2	YLR096W	RISQSGQSQLHPTR	[3] Phospho (ST)	-	1.35	-0.65	-0.13	2.00	0.075	0.310	0.438	0.04	1.32E+03	5.49E+03	1.36E+03	6.96E+03	3.59E+03	1.03E+04	4.20E+03	5.53E+02	4.26E+02	2.64E+03	1.70E+03	3.11E+03	781.365439	2	36.37
LEO1	YOR123C	KQSQILR	[3] Phospho (ST)	-	1.40	-1.15	-0.69	2.55	0.002	0.007	0.013	0.00	3.37E+03	2.32E+03	3.05E+03	7.47E+03	6.59E+03	9.06E+03	1.69E+03	1.35E+03	8.74E+02	1.96E+03	1.65E+03	1.80E+03	476.751944	2	41.17
MEC1	YBR136W	KVPTDPSSSQEYAK	[9] Phospho (ST)	+	3.82	2.79	1.28	1.03	0.001	0.014	0.121	0.02	5.27E+00	7.15E+02	3.46E+02	4.77E+03	6.26E+03	4.48E+03	3.21E+03	1.32E+03	3.07E+03	4.39E+02	6.92E+02	1.51E+03	808.863415	2	26.89
MLH1	YMR167W	VTNVSHSQEAEK	[7] Phospho (ST)	-	3.38	0.69	-1.19	2.68	0.029	0.043	0.033	0.03	1.35E+02	2.79E+02	1.75E+02	2.31E+03	7.89E+02	3.33E+03	3.86E+02	2.58E+02	3.31E+02	6.55E+01	1.14E+02	6.28E+01	704.8087	2	21.95
MSH6	YDR097C	STTTDEDLSSSQSRR	[11] Phospho (ST)	+	0.49	-1.11	-0.85	1.60	0.055	0.019	0.053	0.00	2.82E+04	1.61E+04	1.90E+04	3.27E+04	2.59E+04	3.02E+04	9.84E+03	8.37E+03	1.10E+04	1.67E+04	7.41E+03	1.09E+04	875.368281	2	26.73
MSH6	YDR097C	STTTDEDLSSSQSR	[11] Phospho (ST)	+	0.05	-1.32	-1.34	1.37	0.457	0.066	0.064	0.01	1.02E+04	3.20E+03	6.44E+03	8.41E+03	7.05E+03	5.19E+03	1.59E+03	3.26E+03	3.10E+03	3.63E+03	2.18E+03	2.03E+03	797.318456	2	25.65
NOP13	YNL175C	GSAAIVPSQGK	[8] Phospho (ST)	-	-0.15	-1.34	-0.91	1.19	0.425	0.152	0.213	0.02	5.91E+03	1.59E+03	1.47E+03	2.45E+03	2.85E+03	2.78E+03	4.66E+02	9.41E+02	2.12E+03	6.57E+02	1.34E+03	2.77E+03	547.762929	2	19.47
NUP2	YLR335W	EESTTEATGNESQDATK	[4] Phospho (ST)	-	2.21	-0.18	0.29	2.39	0.001	0.375	0.345	0.00	8.98E+03	2.56E+03	5.28E+03	2.74E+04	2.82E+04	2.24E+04	4.11E+03	4.75E+03	5.98E+03	1.13E+04	4.54E+03	4.73E+03	939.368346	2	27.74
PDS1	YDR113C	KLSQISR	[3] Phospho (ST)	-	0.47	-1.17	-0.79	1.63	0.127	0.026	0.112	0.02	1.28E+04	9.90E+03	8.37E+03	1.96E+04	1.10E+04	1.23E+04	2.72E+03	3.16E+03	7.93E+03	2.41E+03	4.05E+03	1.14E+04	456.238946	2	21.02
PRP19	YLL036C	SSQQAVAITR	[2] Phospho (ST)	+	0.95	-0.15	-0.34	1.09	0.001	0.280	0.086	0.00	8.58E+04	7.19E+04	9.84E+04	1.78E+05	1.52E+05	1.63E+05	9.77E+04	7.02E+04	6.35E+04	7.31E+04	5.28E+04	7.70E+04	570.77413	2	49.98
RFA1	YAR007C	FANENPNSQK	[8] Phospho (ST)	+	2.79	-0.08	1.41	2.87	0.010	0.468	0.049	0.01	4.03E+04	1.12E+04	9.94E+03	1.99E+05	9.25E+04	1.33E+05	3.49E+04	1.20E+04	1.13E+04	7.20E+04	3.10E+04	6.03E+04	614.753219	2	25.38
RFA2	YNL312W	GYGSQVAQQFEIGGYVK	[4] Phospho (ST)	+	0.99	1.54	0.90	-0.55	0.056	0.017	0.075	0.11	3.02E+04	7.24E+04	2.94E+04	1.07E+05	9.84E+04	5.59E+04	1.56E+05	1.43E+05	8.34E+04	8.26E+04	1.09E+05	5.41E+04	955.938702	2	90.45
RHO1	YPR165W	SQQVGNSIR	[N-term] Acetyl (Protein N-term)|[1] Phospho (ST)	-	1.28	-0.33	-0.47	1.61	0.001	0.237	0.060	0.00	2.20E+04	2.22E+04	2.72E+04	6.22E+04	5.00E+04	6.14E+04	7.99E+03	2.11E+04	2.78E+04	2.29E+04	1.42E+04	1.44E+04	555.750289	2	15.71
RPL1B	YGL135W	ITSSQIVR	[4] Phospho (ST)	-	2.55	0.05	-0.20	2.50	0.003	0.461	0.388	0.00	1.92E+04	5.54E+03	1.15E+04	8.78E+04	5.40E+04	7.05E+04	1.04E+04	1.18E+04	1.53E+04	1.68E+04	7.98E+03	6.75E+03	435.707543	2	29.38
SAR1	YPL218W	SALGLLNTTGSQR	[11] Phospho (ST)	-	1.47	-0.72	-1.36	2.19	0.053	0.279	0.163	0.02	0.00E+00	3.38E+03	2.10E+03	2.69E+03	6.60E+03	5.94E+03	2.06E+02	1.01E+03	2.10E+03	6.18E+02	1.08E+03	4.11E+02	699.342888	2	15.62
SHP1	YBL058W	AINTEHVGGLCPKPGSSQGSNEYLK	[20] Phospho (ST)|[23] Phospho (Y)	-	1.92	0.31	-0.80	1.60	0.000	0.279	0.011	0.00	6.58E+03	7.95E+03	5.45E+03	2.61E+04	2.78E+04	2.17E+04	7.02E+03	1.30E+04	4.84E+03	4.34E+03	3.46E+03	3.65E+03	935.077389	3	16.89
SHP1	YBL058W	PGSSQGSNEYLK	[4] Phospho (ST)	-	3.26	1.15	0.29	2.10	0.000	0.069	0.342	0.00	7.52E+02	7.82E+02	2.72E+03	1.51E+04	1.40E+04	1.19E+04	2.95E+03	2.11E+03	4.44E+03	1.78E+03	2.31E+03	1.13E+03	673.784935	2	33.03
SIR4	YDR227W	VSLSQPVSASK	[2] Phospho (ST)	+	0.90	0.26	-0.34	0.64	0.001	0.056	0.015	0.00	1.38E+04	1.46E+04	1.33E+04	2.48E+04	2.87E+04	2.40E+04	1.92E+04	1.53E+04	1.54E+04	9.38E+03	1.19E+04	1.16E+04	591.79175	2	39.5
SOK2	YMR016C	TSTSDEATQPNEPSEAEPVK	[8] Phospho (ST)	-	3.31	-1.61	-1.48	4.92	0.001	0.079	0.098	0.00	2.03E+03	1.26E+03	4.29E+02	1.50E+04	1.17E+04	1.06E+04	6.83E+02	3.45E+02	1.71E+02	7.95E+02	0.00E+00	5.19E+02	1098.96225	2	30.68
SPE4	YLR146C	VNNSQHPYIK	[4] Phospho (ST)	+	2.20	2.32	0.15	-0.12	0.075	0.005	0.436	0.43	1.73E+03	5.09E+01	1.14E+03	2.47E+03	2.68E+03	8.33E+03	4.10E+03	4.31E+03	6.27E+03	1.50E+03	1.42E+03	3.16E+02	640.295655	2	17.85
SPN1	YPR133C	VVEATPEDGTASSQKSTINAENENTK	[12] Phospho (ST)|[13] Phospho (ST)	+	0.25	-0.40	-0.07	0.64	0.168	0.087	0.394	0.01	1.43E+06	8.81E+05	1.34E+06	1.48E+06	1.22E+06	1.62E+06	9.13E+05	8.30E+05	1.02E+06	1.17E+06	9.47E+05	1.35E+06	960.745431	3	20.06
SPN1	YPR133C	VVEATPEDGTASSQK	[13] Phospho (ST)	+	0.87	-0.35	-0.96	1.22	0.012	0.124	0.019	0.00	2.69E+05	1.64E+05	2.62E+05	4.93E+05	3.50E+05	4.27E+05	1.68E+05	1.67E+05	2.11E+05	1.27E+05	8.92E+04	1.40E+05	799.851834	2	30.47
SPT7	YBR081C	SDDVSSQTIK	[6] Phospho (ST)	+	1.52	-0.23	-0.52	1.75	0.027	0.305	0.176	0.02	1.81E+04	8.52E+03	1.59E+04	5.73E+04	3.98E+04	2.49E+04	7.60E+03	1.55E+04	1.32E+04	1.56E+04	7.73E+03	6.34E+03	580.247982	2	25.72
SRO9	YCL037C	DATSQENGQSTQQQQPPHHR	[4] Phospho (ST)	-	0.82	-1.09	-0.49	1.91	0.093	0.044	0.125	0.02	4.20E+03	2.89E+03	2.23E+03	5.59E+03	3.05E+03	7.78E+03	2.29E+03	7.31E+02	1.33E+03	2.42E+03	1.54E+03	2.65E+03	785.335099	3	30.45
SUM1	YDR310C	TPGDEETTTFVPLENSQPSDTIRK	[16] Phospho (ST)	+	2.74	-1.09	-1.11	3.83	0.000	0.080	0.077	0.00	2.65E+03	8.43E+03	5.79E+03	4.12E+04	3.97E+04	3.23E+04	3.09E+03	1.73E+03	3.10E+03	2.23E+03	3.49E+03	2.07E+03	914.75542	3	37.34
SWI3	YJL176C	LDSQLETPSTEESR	[3] Phospho (ST)	+	3.31	-2.95	-2.50	6.25	0.000	0.036	0.040	0.00	5.35E+02	7.03E+02	1.61E+03	9.19E+03	1.04E+04	9.01E+03	2.67E+02	0.00E+00	7.53E+01	2.35E+02	8.82E+01	1.55E+02	779.817667	2	40.95
TAT1	YBR069C	NSELESQLEK	[6] Phospho (ST)	-	0.18	-1.19	-0.59	1.37	0.407	0.160	0.287	0.01	6.63E+04	9.50E+03	2.66E+04	4.75E+04	3.06E+04	3.74E+04	1.18E+04	1.58E+04	1.72E+04	3.93E+04	1.61E+04	1.25E+04	572.233296	2	22.34
TFG1	YGR186W	DGSQTPTVDSVTK	[3] Phospho (ST)	-	3.37	0.39	-0.88	2.98	0.000	0.047	0.017	0.00	3.00E+03	2.88E+03	3.74E+03	3.60E+04	2.66E+04	3.74E+04	3.49E+03	4.39E+03	4.77E+03	1.87E+03	1.03E+03	2.32E+03	707.808695	2	43.85
TOA2	YKL058W	DASQNGSGDSQSVISVDK	[3] Phospho (ST)	+	1.88	-0.16	0.24	2.04	0.001	0.389	0.301	0.00	5.66E+03	4.31E+03	8.40E+03	2.40E+04	2.43E+04	1.94E+04	9.11E+03	3.75E+03	3.52E+03	4.78E+03	9.97E+03	6.89E+03	937.394465	2	24.05
YSH1	YLR277C	IEPIKEENEDNLDSQLAEK	[14] Phospho (ST)	+	2.54	-1.10	-1.77	3.64	0.000	0.006	0.003	0.00	9.71E+03	1.46E+04	1.43E+04	7.44E+04	7.11E+04	7.93E+04	6.21E+03	5.81E+03	6.03E+03	2.51E+03	4.04E+03	4.75E+03	1090.98296	2	38.79

Table 2.5: Query strains and library used for EMAP

NOTE: Gene description taken from the SGD Database (March 17th, 2007). Essentiality status taken from Saccharomyces Genome Deletion Project
NOTE: The Primary Functional category was defined by the the top ranked GO term in the list of the 25 most frequently found GO slim terms (taken from SGD) for all array and query genes.

Gene	ORF	Essential?	Description	Primary Functional Category
PEX22	YAL055W	No	Putative Peroxisomal Membrane Protein	Signaling
CBP4	YGR174C	No	Mitochondrial Protein Required For Assembly Of Cytochrome Bc1 Complex	Protein Complex Biogenesis
ERG2	YMR202W	No	C-8 Sterol Isomerase	Lipid Metabolic Process
	YLR224W	No	F-Box Protein And Component Of Scf Ubiquitin Ligase Complexes	Response To Chemical
FLC2	YAL053W	No	Putative Fad Transporter	Miscellaneous
PBP1	YGR178C	No	Component Of Glucose Deprivation Induced Stress Granules	Miscellaneous
PFK2	YMR205C	No	Beta Subunit Of Heterooctameric Phosphofructokinase	Carbohydrate Metabolic Process
CAP1	YKL007W	No	Alpha Subunit Of The Capping Protein Heterodimer (Cap1P And Cap2P)	Protein Complex Biogenesis
GEM1	YAL048C	No	Outer Mitochondrial Membrane Gtpase, Subunit Of The Ermes Complex	Regulation Of Organelle Organization
UBR1	YGR184C	No	E3 Ubiquitin Ligase (N-Recognin)	Response To Chemical
SKY1	YMR216C	No	Sr Protein Kinase (Srpk)	Response To Chemical
SPT23	YKL020C	No	Er Membrane Protein Involved In Regulation Of Ole1 Transcription	Transcription From Rna Polymerase Ii Promoter
SAW1	YAL027W	No	5'- And 3'-Flap DNA Binding Protein	Cellular Response To DNA Damage Stimulus
ELP2	YGR200C	No	Subunit Of Elongator Complex	Transcription From Rna Polymerase Ii Promoter
MRE11	YMR224C	No	Nuclease Subunit Of The Mrx Complex With Rad50P And Xrs2P	Cellular Response To DNA Damage Stimulus
IXR1	YKL032C	No	Transcriptional Repressor That Regulates Hypoxic Genes During Normoxia	Transcription From Rna Polymerase Ii Promoter
CCR4	YAL021C	No	Component Of The Ccr4-Not Transcriptional Complex	Transcription From Rna Polymerase Ii Promoter
RPS0A	YGR214W	No	Ribosomal 40S Subunit Protein S0A	Miscellaneous
GFD1	YMR255W	No	Coiled-Coiled Protein Of Unknown Function	Miscellaneous
TMA19	YKL056C	No	Protein That Associates With Ribosomes	Response To Chemical
MDM10	YAL010C	No	Subunit Of Both The Ermes And The Sam Complex	Protein Complex Biogenesis
WSC4	YHL028W	No	Endoplasmic Reticulum (Er) Membrane Protein	Protein Targeting
RCE1	YMR274C	No	Type Ii Caax Prenyl Protease	Miscellaneous
TEF4	YKL081W	No	Gamma Subunit Of Translational Elongation Factor Eef1B	Miscellaneous
KIN3	YAR018C	No	Nonessential Serine/Threonine Protein Kinase	Protein Phosphorylation
VPS29	YHR012W	No	Subunit Of The Membrane-Associated Retromer Complex	Miscellaneous
NGL2	YMR285C	No	Protein Involved In 5.8S Rrna Processing	Miscellaneous
RAD27	YKL113C	No	5' To 3' Exonuclease, 5' Flap Endonuclease	Cellular Response To DNA Damage Stimulus
UBI4	YLL039C	No	Ubiquitin	Meiotic Cell Cycle
	YHR078W	No	High Osmolarity-Regulated Gene Of Unknown Function	Biological_Process
PEX6	YNL329C	No	Aaa-Peroxin	Signaling
LST4	YKL176C	No	Protein Possibly Involved In A Post-Golgi Secretory Pathway	Golgi Vesicle Transport
SPT8	YLR055C	No	Subunit Of The Saga Transcriptional Regulatory Complex	Transcription From Rna Polymerase Ii Promoter
DMA1	YHR115C	No	Ubiquitin-Protein Ligase (E3)	Mitotic Cell Cycle
TRF5	YNL299W	No	Non-Canonical Poly(A) Polymerase	Miscellaneous
ENV11	YGR071C	No	Protein Proposed To Be Involved In Vacuolar Functions	Miscellaneous
GEP5	YLR091W	No	Protein Of Unknown Function	Miscellaneous
REC104	YHR157W	No	Protein Involved In Early Stages Of Meiotic Recombination	Organelle Fission
TOF1	YNL273W	No	Subunit Of A Replication-Pausing Checkpoint Complex	Mitotic Cell Cycle
UFO1	YML088W	No	F-Box Receptor Protein	Cellular Response To DNA Damage Stimulus
MNL1	YHR204W	No	Alpha-1,2-Specific Exomannosidase Of The Endoplasmic Reticulum	Proteolysis Involved In Cellular Protein Catabolic Process
TSR3	YOR006C	No	Protein Required For 20S Pre-Rrna Processing	Miscellaneous
VAM3	YOR106W	No	Syntaxin-Like Vacuolar T-Snare	Miscellaneous
GSF2	YML048W	No	Endoplasmic Reticulum (Er) Localized Integral Membrane Protein	Miscellaneous
BIK1	YCL029C	No	Microtubule-Associated Protein	Mitotic Cell Cycle
DFG16	YOR030W	No	Probable Multiple Transmembrane Protein	Miscellaneous
VPS17	YOR132W	No	Subunit Of The Membrane-Associated Retromer Complex	Miscellaneous
MAD1	YGL086W	No	Coiled-Coil Protein Involved In Spindle-Assembly Checkpoint	Mitotic Cell Cycle
DMA2	YNL116W	No	Ubiquitin-Protein Ligase (E3)	Mitotic Cell Cycle
RPO41	YFL036W	No	Mitochondrial Rna Polymerase	Miscellaneous
DAL81	YIR023W	No	Positive Regulator Of Genes In Multiple Nitrogen Degradation Pathways	Transcription From Rna Polymerase Ii Promoter
MMS2	YGL087C	No	Ubiquitin-Conjugating Enzyme Variant	Cellular Response To DNA Damage Stimulus
RAS2	YNL098C	No	Gtp-Binding Protein	Response To Chemical
SWP82	YFL049W	No	Member Of The Swi/Snf Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
MDM35	YKL053C-A	No	Mitochondrial Intermembrane Space Protein	Protein Complex Biogenesis
KEX2	YNL238W	No	Subtilisin-Like Protease (Proprotein Convertase)	Miscellaneous
YDJ1	YNL064C	No	Type I Hsp40 Co-Chaperone	Protein Targeting
UBP6	YFR010W	No	Ubiquitin-Specific Protease	Protein Modification By Small Protein Conjugation Or Removal
RBL2	YOR265W	No	Protein Involved In Microtubule Morphogenesis	Protein Complex Biogenesis
PDR16	YNL231C	No	Phosphatidylinositol Transfer Protein (Pitp)	Response To Chemical
HPM1	YIL110W	No	Adomet-Dependent Methyltransferase	Miscellaneous
YTA7	YGR270W	No	Protein That Localizes To Chromatin	Transcription From Rna Polymerase Ii Promoter
RIM20	YOR275C	No	Protein Involved In Proteolytic Activation Of Rim101P	Miscellaneous
SQS1	YNL224C	No	Protein That Stimulates The Atpase And Helicase Activities Of Prp43P	Miscellaneous
MET18	YIL128W	No	Component Of Cytosolic Iron-Sulfur Protein Assembly (Cia) Machinery	Miscellaneous
MGA2	YIR033W	No	Er Membrane Protein Involved In Regulation Of Ole1 Transcription	Transcription From Rna Polymerase Ii Promoter
IWR1	YDL115C	No	Rna Polymerase Ii Transport Factor, Conserved From Yeast To Humans	Miscellaneous
RTT106	YNL206C	No	Histone Chaperone	Transcription From Rna Polymerase Ii Promoter
MLP2	YIL149C	No	Myosin-Like Protein Associated With The Nuclear Envelope	Mitotic Cell Cycle
NUP133	YKR082W	No	Subunit Of Nup84P Subcomplex Of Nuclear Pore Complex (Npc)	Transcription From Rna Polymerase Ii Promoter
ESL2	YKR096W	No	Protein Of Unknown Function	Biological_Process
SKO1	YNL167C	No	Basic Leucine Zipper Transcription Factor Of The Atf/Creb Family	Transcription From Rna Polymerase Ii Promoter
MPH1	YIR002C	No	3'-5' DNA Helicase Involved In Error-Free Bypass Of DNA Lesions	Cellular Response To DNA Damage Stimulus
RCO1	YMR075W	No	Essential Component Of The Rpd3S Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
EAF3	YPR023C	No	Component Of The Rpd3S Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
CBT1	YKL208W	No	Protein Involved In 5' Rna End Processing	Protein Complex Biogenesis
FKH2	YNL068C	No	Forkhead Family Transcription Factor	Transcription From Rna Polymerase Ii Promoter
INO4	YOL108C	No	Transcription Factor Involved In Phospholipid Synthesis	Transcription From Rna Polymerase Ii Promoter
PBY1	YBR094W	No	Putative Tubulin Tyrosine Ligase Associated With P-Bodies	Biological_Process
GMH1	YKR030W	No	Golgi Membrane Protein Of Unknown Function	Miscellaneous
TCB2	YNL087W	No	Er Protein Involved In Er-Plasma Membrane Tethering	Lipid Metabolic Process
IES5	YER092W	No	Protein That Associates With The Ino80 Chromatin Remodeling Complex	Biological_Process
TPS1	YBR126C	No	Synthase Subunit Of Trehalose-6-P Synthase/Phosphatase Complex	Response To Chemical
PAM17	YKR065C	No	Constituent Of The Tim23 Complex	Protein Targeting
RAV2	YDR202C	No	Subunit Of Rave Complex (Rav1P, Rav2P, Skp1P)	Protein Complex Biogenesis
	YMR209C	No	Putative S-Adenosylmethionine-Dependent Methyltransferase	Biological_Process
TYR1	YBR166C	No	Prephenate Dehydrogenase Involved In Tyrosine Biosynthesis	Miscellaneous
PMP3	YDR276C	No	Small Plasma Membrane Protein	Response To Chemical
CTK1	YKL139W	No	Catalytic (Alpha) Subunit Of C-Terminal Domain Kinase I (Ctdk-I)	Transcription From Rna Polymerase Ii Promoter
CAC2	YML102W	No	Subunit Of Chromatin Assembly Factor I (Caf-1), With Rlf2P And Msi1P	Chromatin Organization
SLM3	YDL033C	No	Trna-Specific 2-Thiouridylase	Miscellaneous
SUM1	YDR310C	No	Transcriptional Repressor That Regulates Middle-Sporulation Genes	Transcription From Rna Polymerase Ii Promoter
BIT2	YBR270C	No	Subunit Of Torc2 Membrane-Associated Complex	Biological_Process
TUB3	YML124C	No	Alpha-Tubulin	Mitotic Cell Cycle
BDF2	YDL070W	No	Protein Involved In Transcription Initiation	Chromatin Organization
	YOR342C	No	Protein Of Unknown Function	Biological_Process
FAR1	YJL157C	No	Cdk Inhibitor And Nuclear Anchor	Response To Chemical
SWC5	YBR231C	No	Component Of The Swr1 Complex	Chromatin Organization

UGA1	YGR019W	No	Gamma-Aminobutyrate (Gaba) Transaminase	Miscellaneous
TYE7	YOR344C	No	Serine-Rich Protein That Contains A Bhlh DNA Binding Motif	Carbohydrate Metabolic Process
VPS35	YJL154C	No	Endosomal Subunit Of Membrane-Associated Retromer Complex	Miscellaneous
	YBR238C	No	Mitochondrial Membrane Protein	Miscellaneous
RPS6A	YPL090C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
CIN1	YOR349W	No	Tubulin Folding Factor D Involved In Beta-Tubulin (Tub2P) Folding	Protein Complex Biogenesis
RPA34	YJL148W	No	Rna Polymerase I Subunit A34.5	Miscellaneous
MTC4	YBR255W	No	Protein Of Unknown Function	Biological_Process
ELP3	YPL086C	No	Subunit Of Elongator Complex	Transcription From Rna Polymerase Ii Promoter
PDE2	YOR360C	No	High-Affinity Cyclic Amp Phosphodiesterase	Signaling
TIF2	YJL138C	No	Translation Initiation Factor Eif4A	Miscellaneous
VMS1	YDR049W	No	Component Of A Cdc48P-Complex Involved In Protein Quality Control	Response To Chemical
BTS1	YPL069C	No	Geranylgeranyl Diphosphate Synthase	Lipid Metabolic Process
PFA4	YOL003C	No	Palmitoyltransferase With Autoacylation Activity	Miscellaneous
NUP2	YLR335W	No	Nucleoporin Involved In Nucleocytoplasmic Transport	Protein Targeting
DOA4	YDR069C	No	Ubiquitin Hydrolase That Deubiquitinates Ilv Cargo Proteins	Proteolysis Involved In Cellular Protein Catabolic Process
ARL3	YPL051W	No	Arf-Like Small Gtpase Of The Ras Superfamily	Golgi Vesicle Transport
HTZ1	YOL012C	No	Histone Variant H2Az	Transcription From Rna Polymerase Ii Promoter
VPS38	YLR360W	No	Part Of A Vps34P Phosphatidylinositol 3-Kinase Complex	Miscellaneous
VPS41	YDR080W	No	Vacuolar Membrane Protein That Is A Subunit Of The Hops Complex	Protein Complex Biogenesis
EGD1	YPL037C	No	Subunit Beta1 Of The Nascent Polypeptide-Associated Complex (Nac)	Protein Targeting
SIL1	YOL031C	No	Nucleotide Exchange Factor For The Er Lumenal Hsp70 Chaperone Kar2P	Protein Targeting
PSY3	YLR376C	No	Component Of The Shu Complex, Which Promotes Error-Free DNA Repair	Cellular Response To DNA Damage Stimulus
ARX1	YDR101C	No	Nuclear Export Factor For The Ribosomal Pre-60S Subunit	Miscellaneous
CLB2	YPR119W	No	B-Type Cyclin Involved In Cell Cycle Progression	Mitotic Cell Cycle
PSH1	YOL054W	No	E3 Ubiquitin Ligase Targeting Centromere-Binding Protein Cse4P	Protein Modification By Small Protein Conjugation Or Removal
DUS3	YLR401C	No	Dihydrouridine Synthase	Miscellaneous
ARO1	YDR127W	No	Pentafunctional Arom Protein	Miscellaneous
URN1	YPR152C	No	Putative Protein Of Unknown Function Containing Ww And Ff Domains	Biological_Process
IRA2	YOL081W	No	Gtpase-Activating Protein	Response To Chemical
LIP2	YLR239C	No	Lipoyl Ligase	Miscellaneous
XRS2	YDR369C	No	Protein Required For DNA Repair	Cellular Response To DNA Damage Stimulus
CDC26	YFR036W	No	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Chromatin Organization
YAR1	YPL239W	No	Ankyrin-Repeat Containing, Nucleocytoplasmic Shuttling Chaperone	Response To Chemical
PIG1	YLR273C	No	Putative Targeting Subunit For Type-1 Protein Phosphatase Glc7P	Carbohydrate Metabolic Process
SAC7	YDR389W	No	Gtpase Activating Protein (Gap) For Rho1P	Regulation Of Organelle Organization
	YGR237C	No	Putative Protein Of Unknown Function	Biological_Process
DDC1	YPL194W	No	DNA Damage Checkpoint Protein	Mitotic Cell Cycle
NKP2	YLR315W	No	Central Kinetochore Protein And Subunit Of The Ctf19 Complex	Miscellaneous
SIP1	YDR422C	No	Alternate Beta-Subunit Of The Snf1P Kinase Complex	Protein Complex Biogenesis
RPL19B	YBL027W	No	Ribosomal 60S Subunit Protein L19B	Miscellaneous
NIP100	YPL174C	No	Large Subunit Of The Dynactin Complex	Mitotic Cell Cycle
SAC3	YDR159W	No	Nuclear Pore-Associated Protein	Mitotic Cell Cycle
MTC7	YEL033W	No	Protein Of Unknown Function	Biological_Process
SKT5	YBL061C	No	Activator Of Chs3P (Chitin Synthase Iii) During Vegetative Growth	Carbohydrate Metabolic Process
PHO86	YJL117W	No	Endoplasmic Reticulum (Er) Resident Protein	Golgi Vesicle Transport
ITC1	YGL133W	No	Subunit Of Atp-Dependent Isw2P-Itc1P Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
APE3	YBR286W	No	Vacuolar Aminopeptidase Y	Miscellaneous
VAM6	YDL077C	No	Vacuolar Protein Involved In Vacuolar Membrane Fusion Tethering	Protein Complex Biogenesis
ASF1	YJL115W	No	Nucleosome Assembly Factor	Transcription From Rna Polymerase Ii Promoter
MRM2	YGL136C	No	Mitochondrial 2' O-Ribose Methyltransferase	Miscellaneous
BSD2	YBR290W	No	Heavy Metal Ion Homeostasis Protein	Protein Targeting
VPS72	YDR485C	No	Htz1P-Binding Component Of The Swr1 Complex	Chromatin Organization
SAP185	YJL098W	No	Protein That Forms A Complex With The Sit4P Protein Phosphatase	Mitotic Cell Cycle
RPL9A	YGL147C	No	Ribosomal 60S Subunit Protein L9A	Miscellaneous
PCA1	YBR295W	No	Cadmium Transporting P-Type Atpase	Miscellaneous
HAP2	YGL237C	No	Subunit Of The Hap2P/3P/4P/5P Ccaat-Binding Complex	Transcription From Rna Polymerase Ii Promoter
IML2	YJL082W	No	Protein Of Unknown Function	Biological_Process
YIP5	YGL161C	No	Protein That Interacts With Rab Gtpases	Biological_Process
PMP1	YCR024C-A	No	Regulatory Subunit For The Plasma Membrane H(+)-Atpase Pma1P	Miscellaneous
CCW12	YLR110C	No	Cell Wall Mannoprotein	Response To Chemical
UBX6	YJL048C	No	Ubx (Ubiquitin Regulatory X) Domain-Containing Protein	Proteolysis Involved In Cellular Protein Catabolic Process
XRN1	YGL173C	No	Evolutionarily-Conserved 5'-3' Exonuclease	Transcription From Rna Polymerase Ii Promoter
ELO2	YCR034W	No	Fatty Acid Elongase, Involved In Sphingolipid Biosynthesis	Lipid Metabolic Process
	YIL029C	No	Putative Protein Of Unknown Function	Biological_Process
UBC8	YEL012W	No	Ubiquitin-Conjugating Enzyme That Regulates Gluconeogenesis	Protein Modification By Small Protein Conjugation Or Removal
SLX8	YER116C	No	Subunit Of Slx5-Slx8 Sumo-Targeted Ubiquitin Ligase (Stubl) Complex	Cellular Response To DNA Damage Stimulus
RAD18	YCR066W	No	E3 Ubiquitin Ligase	Cellular Response To DNA Damage Stimulus
CDC53	YDL132W	Yes	Cullin	Mitotic Cell Cycle
TDA3	YHR009C	No	Putative Oxidoreductase Involved In Late Endosome To Golgi Transport	Miscellaneous
UBP3	YER151C	No	Ubiquitin-Specific Protease Involved In Transport And Osmotic Response	Protein Modification By Small Protein Conjugation Or Removal
	YCR087C-A	No	Putative Protein Of Unknown Function	Biological_Process
UBC1	YDR177W	Yes	Ubiquitin-Conjugating Enzyme	Protein Modification By Small Protein Conjugation Or Removal
OPI3	YJR073C	No	Methylene-Fatty-Acyl-Phospholipid Synthase	Lipid Metabolic Process
BCK2	YER167W	No	Serine/Threonine-Rich Protein Involved In Pkc1 Signaling Pathway	Mitotic Cell Cycle
RAD26	YJR035W	No	Protein Involved In Transcription-Coupled Nucleotide Excision Repair	Chromatin Organization
POL3	YDL102W	Yes	Catalytic Subunit Of DNA Polymerase Delta	Miscellaneous
BAS1	YKR099W	No	Myb-Related Transcription Factor	Transcription From Rna Polymerase Ii Promoter
FET3	YMR058W	No	Ferro-O2-Oxidoreductase	Response To Chemical
BUG1	YDL099W	No	Cis-Golgi Localized Protein Involved In Er To Golgi Transport	Golgi Vesicle Transport
RPB5	YBR154C	Yes	Rna Polymerase Subunit Abc27	Transcription From Rna Polymerase Ii Promoter
TSR2	YLR435W	No	Protein With A Potential Role In Pre-Rrna Processing	Miscellaneous
BIM1	YER016W	No	Microtubule Plus End-Tracking Protein	Mitotic Cell Cycle
RPL35B	YDL136W	No	Ribosomal 60S Subunit Protein L35B	Miscellaneous
APC2	YLR127C	Yes	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Mitotic Cell Cycle
	YNR065C	No	Protein Of Unknown Function	Biological_Process
SPT20	YOL148C	No	Subunit Of The Saga Transcriptional Regulatory Complex	Chromatin Organization
DOM34	YNL001W	No	Protein That Facilitates Ribosomal Subunit Dissociation	Miscellaneous
SMT3	YDR510W	Yes	Ubiquitin-Like Protein Of The Sumo Family	Protein Modification By Small Protein Conjugation Or Removal
JHD2	YJR119C	No	Jmjc Domain Family Histone Demethylase	Chromatin Organization
RRN10	YBL025W	No	Protein Involved In Promoting High Level Transcription Of RDNA	Miscellaneous
SIW14	YNL032W	No	Tyrosine Phosphatase Involved In Actin Organization And Endocytosis	Cytoskeleton Organization
RSC4	YKR008W	Yes	Component Of The Rsc Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
OAF1	YAL051W	No	Oleate-Activated Transcription Factor	Transcription From Rna Polymerase Ii Promoter
TIM13	YGR181W	No	Mitochondrial Intermembrane Space Protein	Protein Targeting
SCJ1	YMR214W	No	One Of Several Homologs Of Bacterial Chaperone DNAj	Response To Chemical
MRT4	YKL009W	No	Protein Involved In Mrna Turnover And Ribosome Assembly	Miscellaneous
ERV46	YAL042W	No	Protein Localized To Copii-Coated Vesicles	Golgi Vesicle Transport
FYV8	YGR196C	No	Protein Of Unknown Function	Biological_Process
ESC1	YMR219W	No	Protein Localized To The Nuclear Periphery	Miscellaneous
	YKL023W	No	Putative Protein Of Unknown Function	Biological_Process
DRS2	YAL026C	No	Trans-Golgi Network Aminophospholipid Translocase (Flippase)	Golgi Vesicle Transport
PCT1	YGR202C	No	Cholinephosphate Cytidylyltransferase	Lipid Metabolic Process
RPS10B	YMR230W	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
AIM26	YKL037W	No	Putative Protein Of Unknown Function	Miscellaneous

ATS1	YAL020C	No	Protein Required For Modification Of Wobble Nucleosides In Trna	Cytoskeleton Organization
CCH1	YGR217W	No	Voltage-Gated High-Affinity Calcium Channel	Miscellaneous
CUE1	YMR264W	No	Ubiquitin-Binding Protein	Proteolysis Involved In Cellular Protein Catabolic Process
NUP100	YKL068W	No	Fg-Nucleoporin Component Of Central Core Of The Nuclear Pore Complex	Protein Targeting
ERP2	YAL007C	No	Member Of The P24 Family Involved In Er To Golgi Transport	Golgi Vesicle Transport
RIM101	YHL027W	No	Cys2His2 Zinc-Finger Transcriptional Repressor	Transcription From Rna Polymerase Ii Promoter
BUL1	YMR275C	No	Ubiquitin-Binding Component Of The Rsp5P E3-Ubiquitin Ligase Complex	Protein Modification By Small Protein Conjugation Or Removal
CUE2	YKL090W	No	Protein Of Unknown Function	Biological_Process
DNM1	YLL001W	No	Dynamin-Related Gtpase Involved In Mitochondrial Organization	Organelle Fission
SLT2	YHR030C	No	Serine/Threonine Map Kinase	Response To Chemical
GOT1	YMR292W	No	Homodimeric Protein That Is Packaged Into Copii Vesicles	Golgi Vesicle Transport
OAC1	YKL120W	No	Mitochondrial Inner Membrane Transporter	Miscellaneous
VPS13	YLL040C	No	Protein Of Unknown Function	Meiotic Cell Cycle
IRE1	YHR079C	No	Serine-Threonine Kinase And Endoribonuclease	Response To Chemical
FIG4	YNL325C	No	Phosphatidylinositol 3,5-Bisphosphate (Ptdins[3,5]P) Phosphatase	Lipid Metabolic Process
COY1	YKL179C	No	Golgi Membrane Protein With Similarity To Mammalian Casp	Golgi Vesicle Transport
ERG3	YLR056W	No	C-5 Sterol Desaturase	Lipid Metabolic Process
ARP1	YHR129C	No	Actin-Related Protein Of The Dynactin Complex	Mitotic Cell Cycle
CLA4	YNL298W	No	Cdc42P-Activated Signal Transducing Kinase	Mitotic Cell Cycle
UPF3	YGR072W	No	Component Of The Nonsense-Mediated Mrna Decay (Nmd) Pathway	Protein Modification By Small Protein Conjugation Or Removal
IOC2	YLR095C	No	Subunit Of The Isw1B Complex	Chromatin Organization
KEL1	YHR158C	No	Protein Required For Proper Cell Fusion And Cell Morphology	Mitotic Cell Cycle
BNI1	YNL271C	No	Formin	Mitotic Cell Cycle
SRB5	YGR104C	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
RPS1B	YML063W	No	Ribosomal Protein 10 (Rp10) Of The Small (40S) Subunit	Miscellaneous
SKN7	YHR206W	No	Nuclear Response Regulator And Transcription Factor	Transcription From Rna Polymerase Ii Promoter
SLG1	YOR008C	No	Sensor-Transducer Of The Stress-Activated Pkc1-Mpk1 Kinase Pathway	Signaling
INP53	YOR109W	No	Polyphosphatidylinositol Phosphatase	Lipid Metabolic Process
AMD1	YML035C	No	Amp Deaminase	Miscellaneous
STE50	YCL032W	No	Protein Involved In Mating Response	Response To Chemical
EXO1	YOR033C	No	5'-3' Exonuclease And Flap-Endonuclease	Cellular Response To DNA Damage Stimulus
SFL1	YOR140W	No	Transcriptional Repressor And Activator	Transcription From Rna Polymerase Ii Promoter
PPZ1	YML016C	No	Serine/Threonine Protein Phosphatase Z, Isoform Of Ppz2P	Miscellaneous
MRC1	YCL061C	No	S-Phase Checkpoint Protein Required For DNA Replication	Mitotic Cell Cycle
STD1	YOR047C	No	Protein Involved In Control Of Glucose-Regulated Gene Expression	Transcription From Rna Polymerase Ii Promoter
GAC1	YOR178C	No	Regulatory Subunit For Glc7P Type-1 Protein Phosphatase (Pp1)	Transcription From Rna Polymerase Ii Promoter
LIF1	YGL090W	No	Component Of The DNA Ligase Iv Complex	Cellular Response To DNA Damage Stimulus
RPL16B	YNL069C	No	Ribosomal 60S Subunit Protein L16B	Miscellaneous
GCN20	YFR009W	No	Positive Regulator Of The Gcn2P Kinase Activity	Miscellaneous
ATP11	YNL315C	No	Molecular Chaperone	Protein Complex Biogenesis
SIN4	YNL236W	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
VAC7	YNL054W	No	Integral Vacuolar Membrane Protein	Lipid Metabolic Process
RPL2A	YFR031C-A	No	Ribosomal 60S Subunit Protein L2A	Miscellaneous
PNT1	YOR266W	No	Mitochondrial Integral Inner Membrane Protein	Miscellaneous
ELA1	YNL230C	No	Elongin A	Protein Modification By Small Protein Conjugation Or Removal
HOS4	YIL112W	No	Subunit Of The Set3 Complex	Chromatin Organization
RTT102	YGR275W	No	Component Of Both The Swi/Snf And Rsc Chromatin Remodeling Complexes	Transcription From Rna Polymerase Ii Promoter
IRC15	YPL017C	No	Microtubule Associated Protein	Mitotic Cell Cycle
ALG9	YNL219C	No	Mannosyltransferase, Involved In N-Linked Glycosylation	Carbohydrate Metabolic Process
RPL16A	YIL133C	No	Ribosomal 60S Subunit Protein L16A	Miscellaneous
GPT2	YKR067W	No	Glycerol-3-Phosphate/Dihydroxyacetone Phosphate Sn-1 Acyltransferase	Lipid Metabolic Process
FAB1	YFR019W	No	1-Phosphatidylinositol-3-Phosphate 5-Kinase	Lipid Metabolic Process
PSY2	YNL201C	No	Subunit Of Protein Phosphatase Pp4 Complex	Cellular Response To DNA Damage Stimulus
RRD1	YIL153W	No	Peptidyl-Prolyl Cis/Trans-Isomerase	Transcription From Rna Polymerase Ii Promoter
KAR5	YMR065W	No	Protein Required For Nuclear Membrane Fusion During Karyogamy	Miscellaneous
BNI5	YNL166C	No	Protein Involved In Organization Of Septins At The Mother-Bud Neck	Protein Complex Biogenesis
AIM21	YIR003W	No	Protein Of Unknown Function	Miscellaneous
CTF18	YMR078C	No	Subunit Of A Complex With Ctf8P	Mitotic Cell Cycle
YME1	YPR024W	No	Catalytic Subunit Of The I-Aaa Protease Complex	Protein Targeting
TRP3	YKL211C	No	Indole-3-Glycerol-Phosphate Synthase	Miscellaneous
TOM7	YNL070W	No	Component Of The Tom (Translocase Of Outer Membrane) Complex	Protein Targeting
MDY2	YOL111C	No	Protein Involved In Inserting Tail-Anchored Proteins Into Er Membranes	Response To Chemical
RXT2	YBR095C	No	Component Of The Histone Deacetylase Rpd3L Complex	Transcription From Rna Polymerase Ii Promoter
UTH1	YKR042W	No	Mitochondrial Inner Membrane Protein	Chromatin Organization
PHO23	YNL097C	No	Component Of The Rpd3L Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
RAD51	YER095W	No	Strand Exchange Protein	Organelle Fission
AGP2	YBR132C	No	Plasma Membrane Regulator Of Polyamine And Carnitine Transport	Miscellaneous
PEX5	YDR244W	No	Peroxisomal Membrane Signal Receptor For Peroxisomal Matrix Proteins	Protein Complex Biogenesis
MDM34	YGL219C	No	Mitochondrial Component Of The Ermes Complex	Miscellaneous
ELP6	YMR312W	No	Subunit Of Hexameric Reca-Like Atpase Elp456 Elongator Subcomplex	Transcription From Rna Polymerase Ii Promoter
NPL4	YBR170C	No	Substrate-Recruiting Cofactor Of The Cdc48P-Npl4P-Ufd1P Segregase	Mitotic Cell Cycle
RNH202	YDR279W	No	Ribonuclease H2 Subunit	Miscellaneous
MNN4	YKL201C	No	Putative Positive Regulator Of Mannosylphosphate Transferase Mnn6P	Carbohydrate Metabolic Process
NUP188	YML103C	No	Subunit Of The Inner Ring Of The Nuclear Pore Complex (Npc)	Protein Targeting
STP4	YDL048C	No	Protein Containing A Kruppel-Type Zinc-Finger Domain	Biological_Process
SSF2	YDR312W	No	Protein Required For Ribosomal Large Subunit Maturation	Miscellaneous
RPL19A	YBR084C-A	No	Ribosomal 60S Subunit Protein L19A	Miscellaneous
MSC1	YML128C	No	Protein Of Unknown Function	Organelle Fission
RXT3	YDL076C	No	Component Of The Rpd3L Histone Deacetylase Complex	Miscellaneous
IRC3	YDR332W	No	Putative Rna Helicase Of The Deah/D-Box Family	Biological_Process
HSM3	YBR272C	No	Proteasome-Interacting Protein	Cellular Response To DNA Damage Stimulus
ASC1	YMR116C	No	G-Protein Beta Subunit And Guanine Dissociation Inhibitor For Gpa2P	Response To Chemical
PMT5	YDL093W	No	Protein O-Mannosyltransferase	Carbohydrate Metabolic Process
REV1	YOR346W	No	Deoxycytidyl Transferase	Cellular Response To DNA Damage Stimulus
DAS1	YJL149W	No	Putative Scf Ubiquitin Ligase F-Box Protein	Proteolysis Involved In Cellular Protein Catabolic Process
ISW1	YBR245C	No	Atpase Subunit Of Imitation-Switch (Iswi) Class Chromatin Remodelers	Transcription From Rna Polymerase Ii Promoter
RLM1	YPL089C	No	Mads-Box Transcription Factor	Transcription From Rna Polymerase Ii Promoter
GDS1	YOR355W	No	Protein Of Unknown Function	Miscellaneous
RPB4	YJL140W	No	Rna Polymerase Ii Subunit B32	Transcription From Rna Polymerase Ii Promoter
RGD1	YBR260C	No	Gtpase-Activating Protein (Rhogap) For Rho3P And Rho4P	Response To Chemical
RPL21B	YPL079W	No	Ribosomal 60S Subunit Protein L21B	Miscellaneous
RAD17	YOR368W	No	Checkpoint Protein	Cellular Response To DNA Damage Stimulus
LCB3	YJL134W	No	Long-Chain Base-1-Phosphate Phosphatase	Signaling
YOS9	YDR057W	No	Er Quality-Control Lectin	Response To Chemical
	YPL068C	No	Protein Of Unknown Function	Biological_Process
SIN3	YOL004W	No	Component Of Both The Rpd3S And Rpd3L Histone Deacetylase Complexes	Transcription From Rna Polymerase Ii Promoter
FKS1	YLR342W	No	Catalytic Subunit Of 1,3-Beta-D-Glucan Synthase	Carbohydrate Metabolic Process
IPT1	YDR072C	No	Inositolphosphotransferase	Lipid Metabolic Process
SGF11	YPL047W	No	Integral Subunit Of Saga Histone Acetyltransferase Complex	Transcription From Rna Polymerase Ii Promoter
HRD1	YOL013C	No	Ubiquitin-Protein Ligase	Response To Chemical
NMD4	YLR363C	No	Protein That May Be Involved In Nonsense-Mediated Mrna Decay	Miscellaneous
RRP8	YDR083W	No	Nucleolar S-Adenosylmethionine-Dependent Rrna Methyltransferase	Miscellaneous
RAD1	YPL022W	No	Single-Stranded DNA Endonuclease (With Rad10P)	Cellular Response To DNA Damage Stimulus
OPI10	YOL032W	No	Protein With A Possible Role In Phospholipid Biosynthesis	Carbohydrate Metabolic Process
CTF3	YLR381W	No	Outer Kinetochore Protein That Forms A Complex With Mcm16P And Mcm22P	Mitotic Cell Cycle

TRS85	YDR108W	No	Subunit Of Trappiii (Transport Protein Particle)	Organelle Fission
CLB5	YPR120C	No	B-Type Cyclin Involved In DNA Replication During S Phase	Mitotic Cell Cycle
PRS5	YOL061W	No	5-Phospho-Ribosyl-1(Alpha)-Pyrophosphate Synthetase	Miscellaneous
VIP1	YLR410W	No	Inositol Hexakisphosphate And Inositol Heptakisphosphate Kinase	Miscellaneous
MTC5	YDR128W	No	Subunit Of The Sea (Seh1-Associated) Complex	Biological_Process
MMS1	YPR164W	No	Subunit Of E3 Ubiquitin Ligase Complex Involved In Replication Repair	Cellular Response To DNA Damage Stimulus
KAR9	YPL269W	No	Karyogamy Protein	Cytoskeleton Organization
ARV1	YLR242C	No	Cortical Er Protein	Lipid Metabolic Process
VPS74	YDR372C	No	Golgi Phosphatidylinositol-4-Kinase Effector And Ptdins4P Sensor	Response To Chemical
SAP155	YFR040W	No	Protein Required For Function Of The Sit4P Protein Phosphatase	Mitotic Cell Cycle
ALG5	YPL227C	No	Udp-Glucose:Dolichyl-Phosphate Glucosyltransferase	Carbohydrate Metabolic Process
	YLR278C	No	Zinc-Cluster Protein	Biological_Process
SPT3	YDR392W	No	Subunit Of The Saga And Saga-Like Transcriptional Regulatory Complexes	Transcription From Rna Polymerase Ii Promoter
SLA1	YBL007C	No	Cytoskeletal Protein Binding Protein	Protein Complex Biogenesis
PRM3	YPL192C	No	Protein Required For Nuclear Envelope Fusion During Karyogamy	Miscellaneous
EST2	YLR318W	No	Reverse Transcriptase Subunit Of The Telomerase Holoenzyme	Miscellaneous
CAD1	YDR423C	No	Ap-1-Like Basic Leucine Zipper (Bzip) Transcriptional Activator	Transcription From Rna Polymerase Ii Promoter
HEK2	YBL032W	No	Rna Binding Protein Involved In Asymmetric Localization Of Ash1 Mrna	Miscellaneous
COX10	YPL172C	No	Heme A:Farnesyltransferase	Miscellaneous
	YDR161W	No	Putative Protein Of Unknown Function	Proteolysis Involved In Cellular Protein Catabolic Process
RAD23	YEL037C	No	Protein With Ubiquitin-Like N Terminus	Proteolysis Involved In Cellular Protein Catabolic Process
SEF1	YBL066C	No	Putative Transcription Factor	Biological_Process
	YPL150W	No	Protein Kinase Of Unknown Cellular Role	Protein Phosphorylation
PLP1	YDR183W	No	Protein That Interacts With Cct (Chaperonin Containing Tcp-1) Complex	Transcription From Rna Polymerase Ii Promoter
HAT2	YEL056W	No	Subunit Of The Hat1P-Hat2P Histone Acetyltransferase Complex	Chromatin Organization
ALG3	YBL082C	No	Dolichol-P-Man Dependent Alpha(1-3) Mannosyltransferase	Lipid Metabolic Process
CHS6	YJL099W	No	Member Of The Chaps (Chs5P-Arf1P-Binding Proteins) Family	Carbohydrate Metabolic Process
HUL5	YGL141W	No	Multiubiquitin Chain Assembly Factor (E4)	Protein Complex Biogenesis
CTP1	YBR291C	No	Mitochondrial Inner Membrane Citrate Transporter	Miscellaneous
NCS6	YGL211W	No	Protein Required For Uridine Thiolation Of Gln, Lys, And Glu Trnas	Protein Modification By Small Protein Conjugation Or Removal
BCK1	YJL095W	No	Mapkkk Acting In The Protein Kinase C Signaling Pathway	Response To Chemical
NUT1	YGL151W	No	Component Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
MAL31	YBR298C	No	Maltose Permease	Miscellaneous
YNG2	YHR090C	No	Subunit Of Nua4, An Essential Histone Acetyltransferase Complex	Chromatin Organization
JEM1	YJL073W	No	DNAj-Like Chaperone Required For Nuclear Membrane Fusion During Mating	Proteolysis Involved In Cellular Protein Catabolic Process
RAD54	YGL163C	No	DNA-Dependent Atpase That Stimulates Strand Exchange	Chromatin Organization
NPP1	YCR026C	No	Nucleotide Pyrophosphatase/Phosphodiesterase	Miscellaneous
SPP1	YPL138C	No	Subunit Of Compass (Set1C)	Chromatin Organization
RTT101	YJL047C	No	Cullin Subunit Of A Roc1P-Dependent E3 Ubiquitin Ligase Complex	Mitotic Cell Cycle
BUD13	YGL174W	No	Subunit Of The Res Complex	Mitotic Cell Cycle
RBK1	YCR036W	No	Putative Ribokinase	Carbohydrate Metabolic Process
PEX2	YJL210W	No	Ring-Finger Peroxin And E3 Ubiquitin Ligase	Protein Targeting
YPT31	YER031C	No	Rab Family Gtpase	Golgi Vesicle Transport
SCS2	YER120W	No	Integral Er Membrane Protein, Regulates Phospholipid Metabolism	Protein Targeting
IMG2	YCR071C	No	Mitochondrial Ribosomal Protein Of The Large Subunit	Miscellaneous
RPO21	YDL140C	Yes	Rna Polymerase Ii Largest Subunit B220	Transcription From Rna Polymerase Ii Promoter
THR1	YHR025W	No	Homoserine Kinase	Miscellaneous
BEM2	YER155C	No	Rho Gtpase Activating Protein (Rhogap)	Signaling
BBC1	YJL020C	No	Protein Possibly Involved In Assembly Of Actin Patches	Cytoskeleton Organization
ABF1	YKL112W	Yes	DNA Binding Protein With Possible Chromatin-Reorganizing Activity	Transcription From Rna Polymerase Ii Promoter
HOC1	YJR075W	No	Alpha-1,6-Mannosyltransferase	Carbohydrate Metabolic Process
RAD24	YER173W	No	Checkpoint Protein	Cellular Response To DNA Damage Stimulus
HUL4	YJR036C	No	Protein With Similarity To Hect Domain E3 Ubiquitin-Protein Ligases	Protein Modification By Small Protein Conjugation Or Removal
TFA2	YKR062W	Yes	Tfiie Small Subunit	Transcription From Rna Polymerase Ii Promoter
SKG1	YKR100C	No	Transmembrane Protein With A Role In Cell Wall Polymer Composition	Miscellaneous
TOR1	YJR066W	No	Pik-Related Protein Kinase And Rapamycin Target	Cellular Response To DNA Damage Stimulus
GET3	YDL100C	No	Guanine Nucleotide Exchange Factor For Gpa1P	Response To Chemical
CDC28	YBR160W	Yes	Cyclin-Dependent Kinase (Cdk) Catalytic Subunit	Transcription From Rna Polymerase Ii Promoter
ECM30	YLR436C	No	Putative Protein Of Unknown Function	Biological_Process
LTE1	YAL024C	No	Protein Similar To Gdp/Gtp Exchange Factors	Mitotic Cell Cycle
CRD1	YDL142C	No	Cardiolipin Synthase	Lipid Metabolic Process
TAF11	YML015C	Yes	Tfiid Subunit (40 Kda)	Transcription From Rna Polymerase Ii Promoter
HAM1	YJR069C	No	Nucleoside Triphosphate Pyrophosphohydrolase	Miscellaneous
GSM1	YJL103C	No	Putative Zinc Cluster Protein Of Unknown Function	Transcription From Rna Polymerase Ii Promoter
ASI3	YNL008C	No	Putative Integral Membrane E3 Ubiquitin Ligase	Proteolysis Involved In Cellular Protein Catabolic Process
RBA50	YDR527W	Yes	Protein Involved In Transcription	Transcription From Rna Polymerase Ii Promoter
ENT3	YJR125C	No	Protein Containing An N-Terminal Epsin-Like Domain	Cytoskeleton Organization
GET1	YGL020C	No	Subunit Of The Get Complex	Golgi Vesicle Transport
IDH1	YNL037C	No	Subunit Of Mitochondrial Nad(+)-Dependent Isocitrate Dehydrogenase	Miscellaneous
RSP5	YER125W	Yes	E3 Ubiquitin Ligase Of The Nedd4 Family	Transcription From Rna Polymerase Ii Promoter
RPS4A	YJR145C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
GRR1	YJR090C	No	F-Box Protein Component Of An Scf Ubiquitin-Ligase Complex	Mitotic Cell Cycle
ATP23	YNR020C	No	Putative Metalloprotease Of The Mitochondrial Inner Membrane	Protein Complex Biogenesis
CDC36	YDL165W	Yes	Component Of The Kinetochore-Associated Ndc80 Complex	Transcription From Rna Polymerase Ii Promoter
CLN3	YAL040C	No	G1 Cyclin Involved In Cell Cycle Progression	Transcription From Rna Polymerase Ii Promoter
SNG1	YGR197C	No	Protein Involved In Resistance To Nitrosoguanidine And 6-Azauracil	Miscellaneous
UBP8	YMR223W	No	Ubiquitin-Specific Protease Component Of The Saga Acetylation Complex	Chromatin Organization
PAN3	YKL025C	No	Essential Subunit Of The Pan2P-Pan3P Poly(A)-Ribonuclease Complex	Cellular Response To DNA Damage Stimulus
YCH1	YGR203W	No	Phosphatase With Sequence Similarity To Cdc25P	Miscellaneous
PEP5	YMR231W	No	Histone E3 Ligase, Component Of Corvet Tethering Complex	Chromatin Organization
VPS24	YKL041W	No	One Of Four Subunits Of The Escrt-Iii Complex	Proteolysis Involved In Cellular Protein Catabolic Process
FUN30	YAL019W	No	Snf2P Family Member With Atp-Dependent Chromatin Remodeling Activity	Chromatin Organization
RPL8A	YHL033C	No	Ribosomal 60S Subunit Protein L8A	Miscellaneous
RSN1	YMR266W	No	Membrane Protein Of Unknown Function	Golgi Vesicle Transport
LHS1	YKL073W	No	Molecular Chaperone Of The Endoplasmic Reticulum Lumen	Response To Chemical
VPS8	YAL002W	No	Membrane-Binding Component Of The Corvet Complex	Protein Targeting
NPR3	YHL023C	No	Subunit Of Sea (Seh1-Associated), Npr2/3, And Iml1P Complexes	Organelle Fission
CAT8	YMR280C	No	Zinc Cluster Transcriptional Activator	Transcription From Rna Polymerase Ii Promoter
BUD2	YKL092C	No	Gtpase Activating Factor For Rsr1P/Bud1P	Mitotic Cell Cycle
RTT109	YLL002W	No	Histone Acetyltransferase	Transcription From Rna Polymerase Ii Promoter
RRM3	YHR031C	No	DNA Helicase Involved In RDNA Replication And Ty1 Transposition	Miscellaneous
JNM1	YMR294W	No	Component Of The Yeast Dynactin Complex	Mitotic Cell Cycle
DGR2	YKL121W	No	Protein Of Unknown Function	Biological_Process
FPS1	YLL043W	No	Aquaglyceroporin, Plasma Membrane Channel	Response To Chemical
LRP1	YHR081W	No	Nuclear Exosome-Associated Nucleic Acid Binding Protein	Miscellaneous
LEM3	YNL323W	No	Membrane Protein Of The Plasma Membrane And Er	Signaling
ASH1	YKL185W	No	Component Of The Rpd3L Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
SIC1	YLR079W	No	Cyclin-Dependent Kinase Inhibitor (Cki)	Mitotic Cell Cycle
WSS1	YHR134W	No	Sumoylated Protein Localizing To The Nuclear Periphery Of Mother Cells	Cellular Response To DNA Damage Stimulus
SNN1	YNL086W	No	Subunit Of The Bloc-1 Complex Involved In Endosomal Maturation	Miscellaneous
PEX8	YGR077C	No	Intraperoxisomal Organizer Of The Peroxisomal Import Machinery	Protein Targeting
KIN2	YLR096W	No	Serine/Threonine Protein Kinase Involved In Regulation Of Exocytosis	Protein Phosphorylation
THP2	YHR167W	No	Subunit Of The Tho And Trex Complexes	Transcription From Rna Polymerase Ii Promoter
ALP1	YNL270C	No	Arginine Transporter	Miscellaneous
VMA21	YGR105W	No	Integral Membrane Protein Required For V-Atpase Function	Protein Complex Biogenesis

MFT1	YML062C	No	Subunit Of The Tho Complex	Transcription From Rna Polymerase Ii Promoter
SET5	YHR207C	No	Methyltransferase Involved In Methylation Of Histone H4 Lys5, -8, -12	Chromatin Organization
RTS1	YOR014W	No	B-Type Regulatory Subunit Of Protein Phosphatase 2A (Pp2A)	Mitotic Cell Cycle
CEX1	YOR112W	No	Component Of The Nuclear Aminoacylation-Dependent Trna Export Pathway	Miscellaneous
SRC1	YML034W	No	Inner Nuclear Membrane Protein	Mitotic Cell Cycle
MXR2	YCL033C	No	Methionine-R-Sulfoxide Reductase	Response To Chemical
AKR2	YOR034C	No	Ankyrin Repeat-Containing Protein	Miscellaneous
ARP8	YOR141C	No	Nuclear Actin-Related Protein Involved In Chromatin Remodeling	Chromatin Organization
UBX2	YML013W	No	Bridging Factor Involved In Er-Associated Protein Degradation (Erad)	Proteolysis Involved In Cellular Protein Catabolic Process
SAT4	YCR008W	No	Ser/Thr Protein Kinase Involved In Salt Tolerance	Mitotic Cell Cycle
ASE1	YOR058C	No	Mitotic Spindle Midzone-Localized Microtubule Bundling Protein	Mitotic Cell Cycle
SER1	YOR184W	No	3-Phosphoserine Aminotransferase	Miscellaneous
	YMR010W	No	Putative Protein Of Unknown Function	Biological_Process
MAK31	YCR020C-A	No	Non-Catalytic Subunit Of N-Terminal Acetyltransferase Of The Natc Type	Miscellaneous
VPS5	YOR069W	No	Nexin-1 Homolog	Miscellaneous
SAS5	YOR213C	No	Subunit Of The Sas Complex (Sas2P, Sas4P, Sas5P)	Miscellaneous
BNI4	YNL233W	No	Targeting Subunit For Glc7P Protein Phosphatase	Miscellaneous
SLM1	YIL105C	No	Phosphoinositide Pi4,5P(2) Binding Protein, Forms A Complex With Slm2P	Signaling
APL6	YGR261C	No	Beta3-Like Subunit Of The Yeast Ap-3 Complex	Protein Targeting
PAC1	YOR269W	No	Involved In Nuclear Migration, Part Of The Dynein/Dynactin Pathway	Miscellaneous
URE2	YNL229C	No	Nitrogen Catabolite Repression Transcriptional Regulator	Response To Chemical
RPI1	YIL119C	No	Transcription Factor, Allelic Differences Between S288C And Sigma1278B	Transcription From Rna Polymerase Ii Promoter
ERV29	YGR284C	No	Protein Localized To Copii-Coated Vesicles	Golgi Vesicle Transport
GPA1	YHR005C	Yes	Subunit Of The G Protein Involved In Pheromone Response	Response To Chemical
MGS1	YNL218W	No	Protein With DNA-Dependent Atpase And SsDNA Annealing Activities	Cellular Response To DNA Damage Stimulus
FLX1	YIL134W	No	Protein Required For Transport Of Flavin Adenine Dinucleotide (Fad)	Miscellaneous
SIS2	YKR072C	No	Negative Regulatory Subunit Of Protein Phosphatase 1 (Ppz1P)	Mitotic Cell Cycle
SET4	YJL105W	No	Protein Of Unknown Function, Contains A Set Domain	Biological_Process
GCR2	YNL199C	No	Transcriptional Activator Of Genes Involved In Glycolysis	Transcription From Rna Polymerase Ii Promoter
IMP2'	YIL154C	No	Transcriptional Activator Involved In Maintenance Of Ion Homeostasis	Transcription From Rna Polymerase Ii Promoter
UBX4	YMR067C	No	Ubx Domain-Containing Protein That Interacts With Cdc48P	Proteolysis Involved In Cellular Protein Catabolic Process
SIR3	YLR442C	No	Silencing Protein	Chromatin Organization
YCK2	YNL154C	No	Palmitoylated Plasma Membrane-Bound Casein Kinase I Isoform	Response To Chemical
IST3	YIR005W	No	Component Of The U2 Snrnp	Miscellaneous
NAM7	YMR080C	No	Atp-Dependent Rna Helicase Of The Sfi Superfamily	Protein Modification By Small Protein Conjugation Or Removal
NTO1	YPR031W	No	Subunit Of The Nua3 Histone Acetyltransferase Complex	Chromatin Organization
SAC1	YKL212W	No	Phosphatidylinositol Phosphate (Ptdinsp) Phosphatase	Lipid Metabolic Process
LAT1	YNL071W	No	Dihydrolipoamide Acetyltransferase Component (E2) Of The Pdc	Miscellaneous
PAP2	YOL115W	No	Non-Canonical Poly(A) Polymerase	Cellular Response To DNA Damage Stimulus
SIF2	YBR103W	No	Wd40 Repeat-Containing Subunit Of Set3C Histone Deacetylase Complex	Chromatin Organization
SHB17	YKR043C	No	Sedoheptulose Bisphosphatase Involved In Riboneogenesis	Miscellaneous
OCA1	YNL099C	No	Putative Protein Tyrosine Phosphatase	Response To Chemical
UBP9	YER098W	No	Ubiquitin-Specific Protease That Cleaves Ubiquitin-Protein Fusions	Protein Modification By Small Protein Conjugation Or Removal
BMT2	YBR141C	No	Nucleolar S-Adenosylmethionine-Dependent Rrna Methyltransferase	Biological_Process
CHL4	YDR254W	No	Outer Kinetochore Protein Required For Chromosome Stability	Mitotic Cell Cycle
ORM1	YGR038W	No	Protein Of Unknown Function	Response To Chemical
COG8	YML071C	No	Component Of The Conserved Oligomeric Golgi Complex	Protein Targeting
SEC66	YBR171W	No	Non-Essential Subunit Of Sec63 Complex	Protein Targeting
RTT103	YDR289C	No	Protein Involved In Transcription Termination By Rna Polymerase Ii	Cellular Response To DNA Damage Stimulus
EAP1	YKL204W	No	Eif4E-Associated Protein, Competes With Eif4G For Binding To Eif4E	Miscellaneous
PML39	YML107C	No	Protein Required For Nuclear Retention Of Unspliced Pre-Mrnas	Miscellaneous
LHP1	YDL051W	No	Rna Binding Protein Required For Maturation Of Trna And U6 Snrna	Miscellaneous
PIB1	YDR313C	No	Ring-Type Ubiquitin Ligase Of The Endosomal And Vacuolar Membranes	Protein Modification By Small Protein Conjugation Or Removal
ASI1	YMR119W	No	Putative Integral Membrane E3 Ubiquitin Ligase	Proteolysis Involved In Cellular Protein Catabolic Process
MVP1	YMR004W	No	Protein Required For Sorting Proteins To The Vacuole	Protein Targeting
THI3	YDL080C	No	Regulatory Protein That Binds Pdc2P And Thi2P Transcription Factors	Transcription From Rna Polymerase Ii Promoter
SWR1	YDR334W	No	Swi2/Snf2-Related Atpase	Chromatin Organization
RIF1	YBR275C	No	Protein That Binds To The Rap1P C-Terminus	Cellular Response To DNA Damage Stimulus
RPL15B	YMR121C	No	Ribosomal 60S Subunit Protein L15B	Miscellaneous
PMT1	YDL095W	No	Protein O-Mannosyltransferase Of The Er Membrane	Response To Chemical
CKA1	YIL035C	No	Alpha Catalytic Subunit Of Casein Kinase 2 (Ck2)	Cellular Response To DNA Damage Stimulus
THR4	YCR053W	No	Threonine Synthase	Miscellaneous
DSS4	YPR017C	No	Guanine Nucleotide Dissociation Stimulator For Sec4P	Golgi Vesicle Transport
STP1	YDR463W	No	Transcription Factor	Transcription From Rna Polymerase Ii Promoter
HAP5	YOR358W	No	Subunit Of The Hap2P/3P/4P/5P Ccaat-Binding Complex	Transcription From Rna Polymerase Ii Promoter
YUR1	YJL139C	No	Mannosyltransferase Involved In Protein N-Glycosylation	Carbohydrate Metabolic Process
SLM6	YBR266C	No	Protein With A Potential Role In Actin Cytoskeleton Organization	Miscellaneous
UBP16	YPL072W	No	Deubiquitinating Enzyme Anchored To The Outer Mitochondrial Membrane	Protein Modification By Small Protein Conjugation Or Removal
GPB1	YOR371C	No	Multistep Regulator Of Camp-Pka Signaling	Response To Chemical
PEX30	YLR324W	No	Peroxisomal Integral Membrane Protein	Miscellaneous
UBC5	YDR059C	No	Ubiquitin-Conjugating Enzyme	Protein Modification By Small Protein Conjugation Or Removal
SUR1	YPL057C	No	Mannosylinositol Phosphorylceramide (Mipc) Synthase Catalytic Subunit	Lipid Metabolic Process
TOP1	YOL006C	No	Topoisomerase I	Transcription From Rna Polymerase Ii Promoter
ORM2	YLR350W	No	Protein Of Unknown Function	Response To Chemical
SNF11	YDR073W	No	Subunit Of The Swi/Snf Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
ELC1	YPL046C	No	Elongin C, Conserved Among Eukaryotes	Cellular Response To DNA Damage Stimulus
ESC8	YOL017W	No	Protein Involved In Telomeric And Mating-Type Locus Silencing	Miscellaneous
MDM30	YLR368W	No	F-Box Component Of An Scf Ubiquitin Protein Ligase Complex	Protein Modification By Small Protein Conjugation Or Removal
UBC13	YDR092W	No	E2 Ubiquitin-Conjugating Enzyme	Cellular Response To DNA Damage Stimulus
CTF19	YPL018W	No	Outer Kinetochore Protein, Needed For Accurate Chromosome Segregation	Mitotic Cell Cycle
NOP12	YOL041C	No	Nucleolar Protein Involved In Pre-25S Rrna Processing	Miscellaneous
IKI3	YLR384C	No	Subunit Of Elongator Complex	Transcription From Rna Polymerase Ii Promoter
TRM1	YDR120C	No	Trna Methyltransferase	Miscellaneous
SCD6	YPR129W	No	Repressor Of Translation Initiation	Miscellaneous
APM4	YOL062C	No	Mu2-Like Subunit Of The Clathrin Associated Protein Complex (Ap-2)	Miscellaneous
CDC73	YLR418C	No	Component Of The Paf1P Complex	Transcription From Rna Polymerase Ii Promoter
	YDR131C	No	F-Box Protein Subunit Of Scf Ubiquitin Ligase Complex	Proteolysis Involved In Cellular Protein Catabolic Process
MET16	YPR167C	No	3'-Phosphoadenylsulfate Reductase	Miscellaneous
CLN2	YPL256C	No	G1 Cyclin Involved In Regulation Of The Cell Cycle	Response To Chemical
YPT6	YLR262C	No	Rab Family Gtpase	Miscellaneous
LSM6	YDR378C	No	Lsm (Like Sm) Protein	Miscellaneous
ERJ5	YFR041C	No	Type I Membrane Protein With A J Domain	Miscellaneous
NEW1	YPL226W	No	Atp Binding Cassette Protein	Miscellaneous
	YLR287C	No	Putative Protein Of Unknown Function	Biological_Process
SHE9	YDR393W	No	Protein Required For Normal Mitochondrial Morphology	Miscellaneous
HIR1	YBL008W	No	Subunit Of The Hir Complex	Transcription From Rna Polymerase Ii Promoter
GUP2	YPL189W	No	Probable Membrane Protein	Miscellaneous
BUD6	YLR319C	No	Actin- And Formin-Interacting Protein	Mitotic Cell Cycle
PPM1	YDR435C	No	Carboxyl Methyltransferase	Protein Complex Biogenesis
	YBL036C	No	Putative Non-Specific Single-Domain Racemase	Biological_Process
REV3	YPL167C	No	Catalytic Subunit Of DNA Polymerase Zeta	Cellular Response To DNA Damage Stimulus
NBP2	YDR162C	No	Protein Involved In The Hog (High Osmolarity Glycerol) Pathway	Signaling
YEF1	YEL041W	No	Atp-Nadh Kinase	Miscellaneous
UBP13	YBL067C	No	Ubiquitin-Specific Protease That Cleaves Ub-Protein Fusions	Miscellaneous
POC4	YPL144W	No	Component Of A Heterodimeric Poc4P-Irc25P Chaperone	Protein Complex Biogenesis

HST4	YDR191W	No	Member Of The Sir2 Family Of Nad(+)-Dependent Protein Deacetylases	Chromatin Organization
PRB1	YEL060C	No	Vacuolar Proteinase B (Yscb)	Miscellaneous
BOI1	YBL085W	No	Protein Implicated In Polar Growth	Miscellaneous
KAP120	YPL125W	No	Karyopherin Responsible For The Nuclear Import Of Rfp1P	Protein Targeting
HTA1	YDR225W	No	Histone H2A	Transcription From Rna Polymerase Ii Promoter
PAC2	YER007W	No	Microtubule Effector Required For Tubulin Heterodimer Formation	Protein Complex Biogenesis
COG7	YGL005C	No	Component Of The Conserved Oligomeric Golgi Complex	Protein Targeting
SRS2	YJL092W	No	DNA Helicase And DNA-Dependent Atpase	Cellular Response To DNA Damage Stimulus
PEX14	YGL153W	No	Central Component Of The Peroxisomal Protein Import Machinery	Protein Complex Biogenesis
	YCL001W-A	No	Putative Protein Of Unknown Function	Biological_Process
IKI1	YHR187W	No	Subunit Of Hexameric Reca-Like Atpase Elp456 Elongator Subcomplex	Miscellaneous
LAS21	YJL062W	No	Integral Plasma Membrane Protein	Lipid Metabolic Process
PMR1	YGL167C	No	High Affinity Ca2+/Mn2+ P-Type Atpase	Miscellaneous
RHB1	YCR027C	No	Putative Rheb-Related Gtpase	Miscellaneous
HUT1	YPL244C	No	Protein With A Role In Udp-Galactose Transport To The Golgi Lumen	Miscellaneous
AIM22	YJL046W	No	Putative Lipoate-Protein Ligase	Miscellaneous
SAE2	YGL175C	No	Endonuclease Involved In Processesing Hairpin DNA Structures	Cellular Response To DNA Damage Stimulus
	YCR050C	No	Non-Essential Protein Of Unknown Function	Biological_Process
NUC1	YJL208C	No	Major Mitochondrial Nuclease	DNA Recombination
BUB1	YGR188C	No	Protein Kinase Involved In The Cell Cycle Checkpoint Into Anaphase	Mitotic Cell Cycle
YCK3	YER123W	No	Palmitoylated Vacuolar Membrane-Localized Casein Kinase I Isoform	Protein Phosphorylation
PAT1	YCR077C	No	Deadenylation-Dependent Mrna-Decapping Factor	Miscellaneous
SRB4	YER022W	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
SRB2	YHR041C	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
	YER156C	No	Putative Protein Of Unknown Function	Biological_Process
PET130	YJL023C	No	Protein Required For Respiratory Growth	Biological_Process
ESS1	YJR017C	Yes	Peptidylprolyl-Cis/Trans-Isomerase (Ppiase)	Transcription From Rna Polymerase Ii Promoter
EAF6	YJR082C	No	Subunit Of The Nua4 Acetyltransferase Complex	Chromatin Organization
GRX4	YER174C	No	Glutathione-Dependent Oxidoreductase	Response To Chemical
POL32	YJR043C	No	Third Subunit Of DNA Polymerase Delta	Cellular Response To DNA Damage Stimulus
POL30	YBR088C	Yes	Proliferating Cell Nuclear Antigen (Pcna)	Mitotic Cell Cycle
SIR1	YKR101W	No	Protein Involved In Silencing At Mating-Type Loci Hml And Hmr	Chromatin Organization
FKH1	YIL131C	No	Forkhead Family Transcription Factor	Transcription From Rna Polymerase Ii Promoter
CYK3	YDL117W	No	Sh3-Domain Protein Located In The Bud Neck And Cytokinetic Actin Ring	Miscellaneous
MED8	YBR193C	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
HMG2	YLR450W	No	Hmg-Coa Reductase	Lipid Metabolic Process
PTC2	YER089C	No	Type 2C Protein Phosphatase (Pp2C)	Cellular Response To DNA Damage Stimulus
CLB3	YDL155W	No	B-Type Cyclin Involved In Cell Cycle Progression	Mitotic Cell Cycle
TAF13	YML098W	Yes	Tfiid Subunit (19 Kda)	Transcription From Rna Polymerase Ii Promoter
LIA1	YJR070C	No	Deoxyhypusine Hydroxylase	Cytoskeleton Organization
PET123	YOR158W	No	Mitochondrial Ribosomal Protein Of The Small Subunit	Miscellaneous
PUB1	YNL016W	No	Poly (A)+ Rna-Binding Protein	Miscellaneous
RPB7	YDR404C	Yes	Rna Polymerase Ii Subunit B16	Transcription From Rna Polymerase Ii Promoter
VPS70	YJR126C	No	Protein Of Unknown Function Involved In Vacuolar Protein Sorting	Protein Targeting
RPB9	YGL070C	No	Rna Polymerase Ii Subunit B12.6	Transcription From Rna Polymerase Ii Promoter
COG6	YNL041C	No	Component Of The Conserved Oligomeric Golgi Complex	Protein Targeting
ARP4	YJL081C	Yes	Nuclear Actin-Related Protein Involved In Chromatin Remodeling	Transcription From Rna Polymerase Ii Promoter
BYE1	YKL005C	No	Negative Regulator Of Transcription Elongation	Transcription From Rna Polymerase Ii Promoter
PER1	YCR044C	No	Protein Of The Endoplasmic Reticulum	Lipid Metabolic Process
ALG12	YNR030W	No	Alpha-1,6-Mannosyltransferase Localized To The Er	Carbohydrate Metabolic Process
TAF8	YML114C	Yes	Tfiid Subunit (65 Kda)	Transcription From Rna Polymerase Ii Promoter
ARF1	YDL192W	No	Adp-Ribosylation Factor	Golgi Vesicle Transport
NRP1	YDL167C	No	Putative Rna Binding Protein Of Unknown Function	Biological_Process
HHF1	YBR009C	No	Histone H4	Transcription From Rna Polymerase Ii Promoter
EPL1	YFL024C	Yes	Subunit Of Nua4, An Essential Histone H4/H2A Acetyltransferase Complex	Transcription From Rna Polymerase Ii Promoter
PMT2	YAL023C	No	Protein O-Mannosyltransferase Of The Er Membrane	Response To Chemical
SER2	YGR208W	No	Phosphoserine Phosphatase Of The Phosphoglycerate Pathway	Miscellaneous
RKR1	YMR247C	No	Ring Domain E3 Ubiquitin Ligase	Chromatin Organization
ELM1	YKL048C	No	Serine/Threonine Protein Kinase That Regulates Cellular Morphogenesis	Mitotic Cell Cycle
DEP1	YAL013W	No	Component Of The Rpd3L Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
GOS1	YHL031C	No	V-Snare Protein Involved In Golgi Transport	Golgi Vesicle Transport
SCS7	YMR272C	No	Sphingolipid Alpha-Hydroxylase	Lipid Metabolic Process
MUD2	YKL074C	No	Protein Involved In Early Pre-Mrna Splicing	Miscellaneous
NUP60	YAR002W	No	Fg-Nucleoporin Component Of Central Core Of The Nuclear Pore Complex	Cellular Response To DNA Damage Stimulus
OPI1	YHL020C	No	Transcriptional Regulator Of A Variety Of Genes	Transcription From Rna Polymerase Ii Promoter
AEP2	YMR282C	No	Mitochondrial Protein	Miscellaneous
HSL1	YKL101W	No	Nim1P-Related Protein Kinase	Mitotic Cell Cycle
KNS1	YLL019C	No	Protein Kinase Involved In Negative Regulation Of Poliii Transcription	Protein Phosphorylation
PIH1	YHR034C	No	Component Of The Conserved R2Tp Complex (Rvb1-Rvb2-Tah1-Pih1)	Miscellaneous
DYN3	YMR299C	No	Dynein Light Intermediate Chain (Lic)	Miscellaneous
TGL1	YKL140W	No	Steryl Ester Hydrolase	Lipid Metabolic Process
RPL8B	YLL045C	No	Ribosomal 60S Subunit Protein L8B	Miscellaneous
KSP1	YHR082C	No	Serine/Threonine Protein Kinase	Signaling
KRE1	YNL322C	No	Cell Wall Glycoprotein Involved In Beta-Glucan Assembly	Miscellaneous
CNB1	YKL190W	No	Calcineurin B	Response To Chemical
SRL2	YLR082C	No	Protein Of Unknown Function	Miscellaneous
YCK1	YHR135C	No	Palmitoylated Plasma Membrane-Bound Casein Kinase I Isoform	Response To Chemical
MON2	YNL297C	No	Protein With A Role In Endocytosis And Vacuole Integrity	Protein Targeting
PAC10	YGR078C	No	Part Of The Heteromeric Co-Chaperone Gimc/Prefoldin Complex	Protein Complex Biogenesis
HRT3	YLR097C	No	Putative Scf-Ubiquitin Ligase F-Box Protein	Response To Chemical
STB5	YHR178W	No	Transcription Factor	Transcription From Rna Polymerase Ii Promoter
GIS2	YNL255C	No	Translational Activator For Mrnas With Internal Ribosome Entry Sites	Miscellaneous
CLB1	YGR108W	No	B-Type Cyclin Involved In Cell Cycle Progression	Mitotic Cell Cycle
NTE1	YML059C	No	Serine Esterase	Lipid Metabolic Process
RER1	YCL001W	No	Protein Involved In Retention Of Membrane Proteins	Golgi Vesicle Transport
ERP4	YOR016C	No	Member Of The P24 Family Involved In Er To Golgi Transport	Golgi Vesicle Transport
AZF1	YOR113W	No	Zinc-Finger Transcription Factor	Transcription From Rna Polymerase Ii Promoter
RAD52	YML032C	No	Protein That Stimulates Strand Exchange	Cellular Response To DNA Damage Stimulus
GFD2	YCL036W	No	Protein Of Unknown Function	Biological_Process
SHE4	YOR035C	No	Protein Containing A Ucs (Unc-45/Cro1/She4) Domain	Cytoskeleton Organization
ELG1	YOR144C	No	Subunit Of An Alternative Replication Factor C Complex	Mitotic Cell Cycle
ERV25	YML012W	No	Member Of The P24 Family Involved In Er To Golgi Transport	Golgi Vesicle Transport
RVS161	YCR009C	No	Amphiphysin-Like Lipid Raft Protein	Cytoskeleton Organization
CKA2	YOR061W	No	Alpha' Catalytic Subunit Of Casein Kinase 2 (Ck2)	Cellular Response To DNA Damage Stimulus
IES4	YOR189W	No	Component Of The Ino80 Chromatiin Remodeling Complex	Cellular Response To DNA Damage Stimulus
ERG5	YMR015C	No	C-22 Sterol Desaturase	Lipid Metabolic Process
DCN1	YLR128W	No	Scaffold-Type E3 Ligase	Protein Modification By Small Protein Conjugation Or Removal
GYP1	YOR070C	No	Cis-Golgi Gtpase-Activating Protein (Gap) For Yeast Rabs	Miscellaneous
RUD3	YOR216C	No	Golgi Matrix Protein	Golgi Vesicle Transport
FAR8	YMR029C	No	Protein Involved In Recovery From Arrest In Response To Pheromone	Response To Chemical
RNH203	YLR154C	No	Ribonuclease H2 Subunit	Miscellaneous
OST3	YOR085W	No	Gamma Subunit Of The Oligosaccharyltransferase Complex Of The Er Lumen	Protein Complex Biogenesis
DSE3	YOR264W	No	Daughter Cell-Specific Protein, May Help Establish Daughter Fate	Biological_Process
JJJ1	YNL227C	No	Co-Chaperone That Stimulates The Atpase Activity Of Ssa1P	Miscellaneous
KGD1	YIL125W	No	Subunit Of The Mitochondrial Alpha-Ketoglutarate Dehydrogenase Complex	Miscellaneous

YAP5	YIR018W	No	Basic Leucine Zipper (Bzip) Iron-Sensing Transcription Factor	Transcription From Rna Polymerase Ii Promoter
SYC1	YOR179C	No	Subunit Of The Apt Subcomplex Of Cleavage And Polyadenylation Factor	Transcription From Rna Polymerase Ii Promoter
IES2	YNL215W	No	Protein That Associates With The Ino80 Chromatin Remodeling Complex	Biological_Process
TPM2	YIL138C	No	Minor Isoform Of Tropomyosin	Cytoskeleton Organization
AIM29	YKR074W	No	Putative Protein Of Unknown Function	Biological_Process
PBS2	YJL128C	No	Map Kinase Kinase Of The Hog Signaling Pathway	Signaling
WHI3	YNL197C	No	Rna Binding Protein That Sequesters Cln3 Mrna In Cytoplasmic Foci	Miscellaneous
UBP7	YIL156W	No	Ubiquitin-Specific Protease That Cleaves Ubiquitin-Protein Fusions	Protein Modification By Small Protein Conjugation Or Removal
AVO2	YMR068W	No	Component Of A Complex Containing The Tor2P Kinase And Other Proteins	Signaling
SMA2	YML066C	No	Meiosis-Specific Prospore Membrane Protein	Meiotic Cell Cycle
PEX1	YKL197C	No	Aaa-Peroxin	Signaling
MSL1	YIR009W	No	U2B Component Of U2 Snrnp	Miscellaneous
AIP1	YMR092C	No	Actin Cortical Patch Component	Protein Complex Biogenesis
RPL43A	YPR043W	No	Ribosomal 60S Subunit Protein L43A	Miscellaneous
DOA1	YKL213C	No	Wd Repeat Protein Required For Ubiquitin-Mediated Protein Degradation	Cellular Response To DNA Damage Stimulus
RNH201	YNL072W	No	Ribonuclease H2 Catalytic Subunit	Miscellaneous
MSN1	YOL116W	No	Transcriptional Activator	Transcription From Rna Polymerase Ii Promoter
PHO88	YBR106W	No	Probable Membrane Protein	Miscellaneous
NAP1	YKR048C	No	Histone Chaperone	Transcription From Rna Polymerase Ii Promoter
INP52	YNL106C	No	Polyphosphatidylinositol Phosphatase	Lipid Metabolic Process
CAF130	YGR134W	No	Subunit Of The Ccr4-Not Transcriptional Regulatory Complex	Transcription From Rna Polymerase Ii Promoter
SLI15	YBR156C	No	Subunit Of The Conserved Chromosomal Passenger Complex (Cpc)	Regulation Of Cell Cycle
RMD5	YDR255C	No	Component Of Gid Complex That Confers Ubiquitin Ligase (U3) Activity	Protein Modification By Small Protein Conjugation Or Removal
PIL1	YGR086C	No	Primary Protein Component Of Eisosomes	Protein Phosphorylation
GIM5	YML094W	No	Subunit Of The Heterohexameric Cochaperone Prefoldin Complex	Transcription From Rna Polymerase Ii Promoter
NHP10	YDL002C	No	Protein Related To Mammalian High Mobility Group Proteins	Chromatin Organization
SSD1	YDR293C	No	Translational Repressor With A Role In Polar Growth And Wall Integrity	Miscellaneous
TOF2	YKR010C	No	Protein Required For RDNA Silencing And Mitotic RDNA Condensation	Mitotic Cell Cycle
	YML108W	No	Protein Of Unknown Function	Biological_Process
SLC1	YDL052C	No	1-Acyl-Sn-Glycerol-3-Phosphate Acyltransferase	Lipid Metabolic Process
IPK1	YDR315C	No	Inositol 1,3,4,5,6-Pentakisphosphate 2-Kinase	Miscellaneous
PTC4	YBR125C	No	Cytoplasmic Type 2C Protein Phosphatase (Pp2C)	Miscellaneous
MUB1	YMR100W	No	Mynd Domain-Containing Protein	Protein Modification By Small Protein Conjugation Or Removal
RPL13A	YDL082W	No	Ribosomal 60S Subunit Protein L13A	Miscellaneous
MSN5	YDR335W	No	Karyopherin	Miscellaneous
SAF1	YBR280C	No	F-Box Protein Involved In Proteasome-Dependent Degradation Of Aah1P	Proteolysis Involved In Cellular Protein Catabolic Process
PKR1	YMR123W	No	V-Atpase Assembly Factor	Protein Complex Biogenesis
LRS4	YDR439W	No	Nucleolar Protein That Forms A Complex With Csm1P	Mitotic Cell Cycle
CST6	YIL036W	No	Basic Leucine Zipper (Bzip) Transcription Factor, In Atf/Creb Family	Transcription From Rna Polymerase Ii Promoter
SED4	YCR067C	No	Integral Er Membrane Protein That Stimulates Sar1P Gtpase Activity	Protein Complex Biogenesis
RLF2	YPR018W	No	Largest Subunit (P90) Of The Chromatin Assembly Complex (Caf-1)	Chromatin Organization
PKH3	YDR466W	No	Protein Kinase With Similarity To Mammalian Pdk1 And Yeast Pkh1P/Phk2P	Signaling
DFG10	YIL049W	No	Probable Polyprenol Reductase	Lipid Metabolic Process
HCR1	YLR192C	No	Eif3J Component Of Translation Initiation Factor 3 (Eif3)	Miscellaneous
MAK3	YPR051W	No	Catalytic Subunit Of The Natc Type N-Terminal Acetyltransferase	Miscellaneous
PKH1	YDR490C	No	Serine/Threonine Protein Kinase	Signaling
PHO80	YOL001W	No	Cyclin	Transcription From Rna Polymerase Ii Promoter
CHS5	YLR330W	No	Component Of The Exomer Complex	Mitotic Cell Cycle
	YDR061W	No	Protein With Similarity To Abc Transporter Family Members	Biological_Process
LGE1	YPL055C	No	Protein Of Unknown Function	Chromatin Organization
MDM12	YOL009C	No	Mitochondrial Outer Membrane Protein	Protein Complex Biogenesis
BUD8	YLR353W	No	Protein Involved In Bud-Site Selection	Mitotic Cell Cycle
PPH3	YDR075W	No	Catalytic Subunit Of Protein Phosphatase Pp4 Complex	Cellular Response To DNA Damage Stimulus
SSN3	YPL042C	No	Cyclin-Dependent Protein Kinase	Transcription From Rna Polymerase Ii Promoter
TLG2	YOL018C	No	Syntaxin-Like T-Snare	Protein Targeting
ROM2	YLR371W	No	Gdp/Gtp Exchange Factor (Gef) For Rho1P And Rho2P	Signaling
GIS1	YDR096W	No	Histone Demethylase And Transcription Factor	Transcription From Rna Polymerase Ii Promoter
CHL1	YPL008W	No	Probable DNA Helicase	Mitotic Cell Cycle
PEX15	YOL044W	No	Tail-Anchored Type Ii Integral Peroxisomal Membrane Protein	Signaling
VAC14	YLR386W	No	Enzyme Regulator	Lipid Metabolic Process
DPB4	YDR121W	No	Subunit Of DNA Pol Epsilon And Of Isw2 Chromatin Accessibility Complex	Chromatin Organization
MSS18	YPR134W	No	Nuclear Encoded Protein Needed For Splicing Of Mitochondrial Intron	Miscellaneous
MET22	YOL064C	No	Bisphosphate-3'-Nucleotidase	Miscellaneous
RPN13	YLR421C	No	Subunit Of The 19S Regulatory Particle Of The 26S Proteasome Lid	Proteolysis Involved In Cellular Protein Catabolic Process
MKC7	YDR144C	No	Gpi-Anchored Aspartyl Protease	Miscellaneous
VPS4	YPR173C	No	Aaa-Atpase Involved In Multivesicular Body (Mvb) Protein Sorting	Protein Complex Biogenesis
HFI1	YPL254W	No	Adaptor Protein Required For Structural Integrity Of The Saga Complex	Transcription From Rna Polymerase Ii Promoter
RPS28B	YLR264W	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
RPP2B	YDR382W	No	Ribosomal Protein P2 Beta	Protein Phosphorylation
RMD8	YFR048W	No	Cytosolic Protein Required For Sporulation	Biological_Process
THI6	YPL214C	No	Thiamine-Phosphate Diphosphorylase And Hydroxyethylthiazole Kinase	Miscellaneous
RPS30A	YLR287C-A	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
SXM1	YDR395W	No	Nuclear Transport Factor (Karyopherin)	Miscellaneous
SCT1	YBL011W	No	Glycerol 3-Phosphate/Dihydroxyacetone Phosphate Sn-1 Acyltransferase	Lipid Metabolic Process
MRN1	YPL184C	No	Rna-Binding Protein That May Be Involved In Translational Regulation	Chromatin Organization
MMS22	YLR320W	No	Subunit Of E3 Ubiquitin Ligase Complex Involved In Replication Repair	Cellular Response To DNA Damage Stimulus
GIM4	YEL003W	No	Subunit Of The Heterohexameric Cochaperone Prefoldin Complex	Protein Complex Biogenesis
PSY4	YBL046W	No	Regulatory Subunit Of Protein Phosphatase Pp4	Cellular Response To DNA Damage Stimulus
SET6	YPL165C	No	Set Domain Protein Of Unknown Function	Biological_Process
CWC15	YDR163W	No	Non-Essential Protein Involved In Pre-Mrna Splicing	Miscellaneous
GDA1	YEL042W	No	Guanosine Diphosphatase Located In The Golgi	Carbohydrate Metabolic Process
RPS8A	YBL072C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
FRK1	YPL141C	No	Protein Kinase Of Unknown Cellular Role	Protein Phosphorylation
NUP42	YDR192C	No	Fg-Nucleoporin Component Of Central Core Of The Nuclear Pore Complex	Protein Targeting
CIN8	YEL061C	No	Kinesin Motor Protein	Mitotic Cell Cycle
	YBL086C	No	Protein Of Unknown Function	Biological_Process
VPS30	YPL120W	No	Subunit Of Phosphatidylinositol (Ptdins) 3-Kinase Complexes I And Ii	Protein Targeting
RTN1	YDR233C	No	Reticulon Protein	Protein Complex Biogenesis
ISC1	YER019W	No	Inositol Phosphosphingolipid Phospholipase C	Lipid Metabolic Process
PUF4	YGL014W	No	Member Of The Puf Protein Family	Chromatin Organization
SSE1	YPL106C	No	Atpase Component Of Heat Shock Protein Hsp90 Chaperone Complex	Miscellaneous
KEX1	YGL203C	No	Cell Death Protease Essential For Hypochlorite-Induced Apoptosis	Miscellaneous
JHD1	YER051W	No	Jmjc Domain Family Histone Demethylase Specific For H3-K36	Chromatin Organization
SCW11	YGL028C	No	Cell Wall Protein With Similarity To Glucanases	Miscellaneous
	YJL055W	No	Putative Protein Of Unknown Function	Response To Chemical
HUR1	YGL168W	No	Protein Of Unknown Function	Miscellaneous
RPS14A	YCR031C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
GYP8	YFL027C	No	Gtpase-Activating Protein For Yeast Rab Family Members	Miscellaneous
SNX4	YJL036W	No	Sorting Nexin	Protein Targeting
SWI4	YER111C	No	DNA Binding Component Of The Sbf Complex (Swi4P-Swi6P)	Transcription From Rna Polymerase Ii Promoter
	YCR061W	No	Protein Of Unknown Function	Miscellaneous
SDS3	YIL084C	No	Component Of The Rpd3L Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
HSE1	YHL002W	No	Subunit Of The Endosomal Vps27P-Hse1P Complex	Protein Targeting
SAK1	YER129W	No	Upstream Serine/Threonine Kinase For The Snf1 Complex	Protein Phosphorylation
SRB8	YCR081W	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter

TAF12	YDR145W	Yes	Subunit (61/68 Kda) Of Tfiid And Saga Complexes	Transcription From Rna Polymerase Ii Promoter
HTD2	YHR067W	No	Mitochondrial 3-Hydroxyacyl-Thioester Dehydratase	Lipid Metabolic Process
SPT2	YER161C	No	Protein Involved In Negative Regulation Of Transcription	Transcription From Rna Polymerase Ii Promoter
APS3	YJL024C	No	Small Subunit Of The Clathrin-Associated Adaptor Complex Ap-3	Protein Targeting
CDC27	YBL084C	Yes	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Protein Modification By Small Protein Conjugation Or Removal
EMC2	YJR088C	No	Member Of Conserved Er Transmembrane Complex	Miscellaneous
BMH1	YER177W	No	14-3-3 Protein, Major Isoform	Transcription From Rna Polymerase Ii Promoter
ISY1	YJR050W	No	Member Of The Nineteen Complex (Ntc)	Miscellaneous
RPB3	YIL021W	Yes	Rna Polymerase Ii Third Largest Subunit B44	Transcription From Rna Polymerase Ii Promoter
NFT1	YKR103W	No	Putative Transporter Of The Mrp Subfamily	Miscellaneous
DJP1	YIR004W	No	Cytosolic J-Domain-Containing Protein	Protein Targeting
UBP1	YDL122W	No	Ubiquitin-Specific Protease	Protein Modification By Small Protein Conjugation Or Removal
TFB3	YDR460W	Yes	Subunit Of Tfiih And Nucleotide Excision Repair Factor 3 Complexes	Transcription From Rna Polymerase Ii Promoter
SST2	YLR452C	No	Gtpase-Activating Protein For Gpa1P	Response To Chemical
DEG1	YFL001W	No	Trna:Pseudouridine Synthase	Miscellaneous
UGA3	YDL170W	No	Transcriptional Activator For Gaba-Dependent Induction Of Gaba Genes	Transcription From Rna Polymerase Ii Promoter
TAF4	YMR005W	Yes	Tfiid Subunit (48 Kda)	Transcription From Rna Polymerase Ii Promoter
MOG1	YJR074W	No	Conserved Nuclear Protein That Interacts With Gtp-Gsp1P	Protein Targeting
VRP1	YLR337C	No	Proline-Rich Actin-Associated Protein	Mitotic Cell Cycle
HDA1	YNL021W	No	Putative Catalytic Subunit Of A Class Ii Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
POL2	YNL262W	Yes	Catalytic Subunit Of DNA Polymerase (Ii) Epsilon	Mitotic Cell Cycle
MNS1	YJR131W	No	Alpha-1,2-Mannosidase	Proteolysis Involved In Cellular Protein Catabolic Process
GIM3	YNL153C	No	Subunit Of The Heterohexameric Cochaperone Prefoldin Complex	Transcription From Rna Polymerase Ii Promoter
YIP3	YNL044W	No	Protein Localized To Copii Vesicles	Golgi Vesicle Transport
CDC20	YGL116W	Yes	Activator Of Anaphase-Promoting Complex/Cyclosome (Apc/C)	Mitotic Cell Cycle
SPE4	YLR146C	No	Spermine Synthase	Miscellaneous
BUD31	YCR063W	No	Component Of The Sf3B Subcomplex Of The U2 Snrnp	Mitotic Cell Cycle
SSK2	YNR031C	No	Map Kinase Kinase Kinase Of Hog1 Mitogen-Activated Signaling Pathway	Regulation Of Organelle Organization
TAF7	YMR227C	Yes	Tfiid Subunit (67 Kda)	Transcription From Rna Polymerase Ii Promoter
ACK1	YDL203C	No	Protein That Functions In The Cell Wall Integrity Pathway	Signaling
VMA1	YDL185W	No	Subunit A Of The V1 Peripheral Membrane Domain Of V-Atpase	DNA Recombination
RTG3	YBL103C	No	Bhlh/Zip Transcription Factor For Retrograde (Rtg) And Tor Pathways	Transcription From Rna Polymerase Ii Promoter
RPB8	YOR224C	Yes	Rna Polymerase Subunit Abc14.5	Transcription From Rna Polymerase Ii Promoter
GCS1	YDL226C	No	Adp-Ribosylation Factor Gtpase Activating Protein (Arf Gap)	Cytoskeleton Organization
CGR1	YGL029W	No	Protein Involved In Nucleolar Integrity And Processing Of Pre-Rrna	Miscellaneous
OLA1	YBR025C	No	P-Loop Atpase With Similarity To Human Ola1 And Bacterial Ychf	Biological_Process
CDC34	YDR054C	Yes	Ubiquitin-Conjugating Enzyme (E2)	Mitotic Cell Cycle
SWC3	YAL011W	No	Protein Of Unknown Function	Chromatin Organization
OCA5	YHL029C	No	Cytoplasmic Protein Required For Replication Of Brome Mosaic Virus	Biological_Process
ZDS1	YMR273C	No	Protein With A Role In Regulating Swe1P-Dependent Polarized Growth	Mitotic Cell Cycle
SMY1	YKL079W	No	Protein That Interacts With Myo2P	Miscellaneous
SWD1	YAR003W	No	Subunit Of The Compass (Set1C) Complex	Chromatin Organization
YAP3	YHL009C	No	Basic Leucine Zipper (Bzip) Transcription Factor	Transcription From Rna Polymerase Ii Promoter
RIT1	YMR283C	No	2'-O-Ribosyl Phosphate Transferase	Miscellaneous
HAP4	YKL109W	No	Transcription Factor	Transcription From Rna Polymerase Ii Promoter
SPA2	YLL021W	No	Component Of The Polarisome	Mitotic Cell Cycle
MSC7	YHR039C	No	Protein Of Unknown Function	Organelle Fission
UBP15	YMR304W	No	Ubiquitin-Specific Protease Involved In Protein Deubiquitination	Protein Modification By Small Protein Conjugation Or Removal
DBR1	YKL149C	No	Rna Lariat Debranching Enzyme	Miscellaneous
BRE2	YLR015W	No	Subunit Of Compass (Set1C) Complex	Chromatin Organization
NAM8	YHR086W	No	Rna Binding Protein, Component Of The U1 Snrnp Protein	Miscellaneous
SKP2	YNL311C	No	F-Box Protein Of Unknown Function	Miscellaneous
ACB1	YGR037C	No	Acyl-Coa-Binding Protein	Miscellaneous
EMP70	YLR083C	No	Protein With A Role In Cellular Adhesion And Filamentous Growth	Miscellaneous
CHS7	YHR142W	No	Protein Of Unknown Function	Carbohydrate Metabolic Process
RIM21	YNL294C	No	Ph Sensor Molecule, Component Of The Rim101 Pathway	Meiotic Cell Cycle
SLX9	YGR081C	No	Protein Required For Pre-Rrna Processing	Miscellaneous
APC9	YLR102C	No	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Chromatin Organization
OYE2	YHR179W	No	Conserved Nadph Oxidoreductase Containing Flavin Mononucleotide (Fmn)	Miscellaneous
TEX1	YNL253W	No	Protein Involved In Mrna Export	Miscellaneous
CLB6	YGR109C	No	B-Type Cyclin Involved In DNA Replication During S Phase	Mitotic Cell Cycle
CMP2	YML057W	No	Calcineurin A	Response To Chemical
STP22	YCL008C	No	Component Of The Escrt-I Complex	Protein Modification By Small Protein Conjugation Or Removal
AHC1	YOR023C	No	Subunit Of The Ada Histone Acetyltransferase Complex	Chromatin Organization
TRS33	YOR115C	No	One Of 10 Subunits Of The Transport Protein Particle (Trapp) Complex	Protein Complex Biogenesis
USA1	YML029W	No	Scaffold Subunit Of The Hrd1P Ubiquitin Ligase	Protein Complex Biogenesis
SRO9	YCL037C	No	Cytoplasmic Rna-Binding Protein	Miscellaneous
HIR2	YOR038C	No	Subunit Of Hir Nucleosome Assembly Complex	Transcription From Rna Polymerase Ii Promoter
SLP1	YOR154W	No	Glycosylated Integral Er Membrane Protein Of Unknown Function	Miscellaneous
ERG6	YML008C	No	Delta(24)-Sterol C-Methyltransferase	Lipid Metabolic Process
POL4	YCR014C	No	DNA Polymerase Iv	Cellular Response To DNA Damage Stimulus
YNG1	YOR064C	No	Subunit Of The Nua3 Histone Acetyltransferase Complex	Chromatin Organization
ULS1	YOR191W	No	Protein Involved In Proteolytic Control Of Sumoylated Substrates	Chromatin Organization
SOK2	YMR016C	No	Nuclear Protein That Negatively Regulates Pseudohyphal Differentiation	Miscellaneous
ACE2	YLR131C	No	Transcription Factor Required For Septum Destruction After Cytokinesis	Transcription From Rna Polymerase Ii Promoter
SKI7	YOR076C	No	Coupling Protein For The Ski Complex And Cytoplasmic Exosome	Miscellaneous
MKK1	YOR231W	No	Mapkk Involved In The Protein Kinase C Signaling Pathway	Signaling
IMP2	YMR035W	No	Catalytic Subunit Of Mitochondrial Inner Membrane Peptidase Complex	Protein Targeting
	YLR177W	No	Putative Protein Of Unknown Function	Biological_Process
VPS21	YOR089C	No	Endosomal Rab Family Gtpase	Protein Targeting
HUA2	YOR284W	No	Cytoplasmic Protein Of Unknown Function	Biological_Process
RPS16A	YMR143W	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
RPL37A	YLR185W	No	Ribosomal 60S Subunit Protein L37A	Miscellaneous
ISW2	YOR304W	No	Atp-Dependent DNA Translocase Involved In Chromatin Remodeling	Transcription From Rna Polymerase Ii Promoter
PEX17	YNL214W	No	Peroxisomal Membrane Peroxin And Subunit Of Docking Complex	Protein Complex Biogenesis
REV7	YIL139C	No	Accessory Subunit Of DNA Polymerase Zeta	Cellular Response To DNA Damage Stimulus
MSA2	YKR077W	No	Putative Transcriptional Activator	Transcription From Rna Polymerase Ii Promoter
MLP1	YKR095W	No	Myosin-Like Protein Associated With The Nuclear Envelope	Transcription From Rna Polymerase Ii Promoter
CHS1	YNL192W	No	Chitin Synthase I	Miscellaneous
BNR1	YIL159W	No	Formin	Protein Complex Biogenesis
MOT3	YMR070W	No	Transcriptional Repressor And Activator With Two C2-H2 Zinc Fingers	Transcription From Rna Polymerase Ii Promoter
POP2	YNR052C	No	Rnase Of The Dedd Superfamily	Transcription From Rna Polymerase Ii Promoter
LOS1	YKL205W	No	Nuclear Pore Protein	Miscellaneous
SNF3	YDL194W	No	Plasma Membrane Low Glucose Sensor, Regulates Glucose Transport	Response To Chemical
HXT17	YNR072W	No	Hexose Transporter	Miscellaneous
SPT7	YBR081C	No	Subunit Of The Saga Transcriptional Regulatory Complex	Chromatin Organization
VPS1	YKR001C	No	Dynamin-Like Gtpase Required For Vacuolar Sorting	Organelle Fission
MKS1	YNL076W	No	Pleiotropic Negative Transcriptional Regulator	Transcription From Rna Polymerase Ii Promoter
DYN2	YDR424C	No	Cytoplasmic Light Chain Dynein, Microtubule Motor Protein	Mitotic Cell Cycle
IML3	YBR107C	No	Outer Kinetochore Protein And Component Of The Ctf19 Complex	Mitotic Cell Cycle
DYN1	YKR054C	No	Cytoplasmic Heavy Chain Dynein	Mitotic Cell Cycle
YAF9	YNL107W	No	Subunit Of Nua4 Histone H4 Acetyltransferase And Swr1 Complexes	Chromatin Organization
SNF6	YHL025W	No	Subunit Of The Swi/Snf Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
IFA38	YBR159W	No	Microsomal Beta-Keto-Reductase	Lipid Metabolic Process
RKM4	YDR257C	No	Ribosomal Lysine Methyltransferase	Miscellaneous

NNF2	YGR089W	No	Protein That Exhibits Physical And Genetic Interactions With Rpb8P	Biological_Process
RAD10	YML095C	No	Single-Stranded DNA Endonuclease (With Rad1P)	Cellular Response To DNA Damage Stimulus
PTC1	YDL006W	No	Type 2C Protein Phosphatase (Pp2C)	Response To Chemical
DPL1	YDR294C	No	Dihydrosphingosine Phosphate Lyase	Signaling
IRS4	YKR019C	No	Eh Domain-Containing Protein	Signaling
NAB6	YML117W	No	Putative Rna-Binding Protein	Biological_Process
MBP1	YDL056W	No	Transcription Factor	Transcription From Rna Polymerase Ii Promoter
MCM21	YDR318W	No	Component Of The Kinetochore Sub-Complex Coma	Mitotic Cell Cycle
CCZ1	YBR131W	No	Protein Involved In Vacuolar Assembly	Protein Targeting
	YMR102C	No	Protein Of Unknown Function	Biological_Process
RPS16B	YDL083C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
INP51	YIL002C	No	Phosphatidylinositol 4,5-Bisphosphate 5-Phosphatase	Lipid Metabolic Process
APM3	YBR288C	No	Mu3-Like Subunit Of The Clathrin Associated Protein Complex (Ap-3)	Protein Targeting
SAS2	YMR127C	No	Histone Acetyltransferase (Hat) Catalytic Subunit Of The Sas Complex	Chromatin Organization
DOT1	YDR440W	No	Nucleosomal Histone H3-Lys79 Methylase	Mitotic Cell Cycle
PRM2	YIL037C	No	Pheromone-Regulated Protein	Miscellaneous
TUP1	YCR084C	No	General Repressor Of Transcription	Transcription From Rna Polymerase Ii Promoter
CSR2	YPR030W	No	Nuclear Ubiquitin Protein Ligase Binding Protein	Transcription From Rna Polymerase Ii Promoter
SDC1	YDR469W	No	Subunit Of The Compass (Set1C) Complex	Chromatin Organization
SEC28	YIL076W	No	Epsilon-Cop Subunit Of The Coatomer	Golgi Vesicle Transport
DCR2	YLR361C	No	Phosphoesterase	Mitotic Cell Cycle
NHP6A	YPR052C	No	High-Mobility Group (Hmg) Protein, Binds To And Remodels Nucleosomes	Transcription From Rna Polymerase Ii Promoter
PUF6	YDR496C	No	Pumilio-Homology Domain Protein	Miscellaneous
PRK1	YIL095W	No	Protein Serine/Threonine Kinase	Cytoskeleton Organization
YMD8	YML038C	No	Putative Nucleotide Sugar Transporter	Miscellaneous
ROX1	YPR065W	No	Heme-Dependent Repressor Of Hypoxic Genes	Transcription From Rna Polymerase Ii Promoter
GNP1	YDR508C	No	High-Affinity Glutamine Permease	Miscellaneous
PLB3	YOL011W	No	Phospholipase B (Lysophospholipase) Involved In Lipid Metabolism	Lipid Metabolic Process
RSC2	YLR357W	No	Component Of The Rsc Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
RAD55	YDR076W	No	Protein That Stimulates Strand Exchange	Cellular Response To DNA Damage Stimulus
	YPL041C	No	Protein Of Unknown Function Involved In Maintenance Of Telomere Length	Biological_Process
TAT2	YOL020W	No	High Affinity Tryptophan And Tyrosine Permease	Miscellaneous
SUR4	YLR372W	No	Elongase	Lipid Metabolic Process
MSH6	YDR097C	No	Protein Required For Mismatch Repair In Mitosis And Meiosis	Cellular Response To DNA Damage Stimulus
HAT1	YPL001W	No	Catalytic Subunit Of The Hat1P-Hat2P Histone Acetyltransferase Complex	Chromatin Organization
PSK2	YOL045W	No	Pas-Domain Containing Serine/Threonine Protein Kinase	Protein Phosphorylation
RPS29A	YLR388W	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
KIN1	YDR122W	No	Serine/Threonine Protein Kinase Involved In Regulation Of Exocytosis	Protein Phosphorylation
CTF4	YPR135W	No	Chromatin-Associated Protein	Mitotic Cell Cycle
INP54	YOL065C	No	Phosphatidylinositol 4,5-Bisphosphate 5-Phosphatase	Lipid Metabolic Process
ECM22	YLR228C	No	Sterol Regulatory Element Binding Protein	Transcription From Rna Polymerase Ii Promoter
SWI5	YDR146C	No	Transcription Factor That Recruits Mediator And Swi/Snf Complexes	Transcription From Rna Polymerase Ii Promoter
	YPR174C	No	Protein Of Unknown Function	Biological_Process
VIK1	YPL253C	No	Protein That Forms A Kinesin-14 Heterodimeric Motor With Kar3P	Mitotic Cell Cycle
NEJ1	YLR265C	No	Protein Involved In Regulation Of Nonhomologous End Joining	Cellular Response To DNA Damage Stimulus
NKP1	YDR383C	No	Central Kinetochore Protein And Subunit Of The Ctf19 Complex	Biological_Process
HXK1	YFR053C	No	Hexokinase Isoenzyme 1	Carbohydrate Metabolic Process
LEA1	YPL213W	No	Component Of U2 Snrnp Complex	Miscellaneous
GUF1	YLR289W	No	Mitochondrial Matrix Gtpase	Miscellaneous
SIZ1	YDR409W	No	Sumo/Smt3 Ligase	Protein Modification By Small Protein Conjugation Or Removal
FUS3	YBL016W	No	Mitogen-Activated Serine/Threonine Protein Kinase Involved In Mating	Response To Chemical
CTI6	YPL181W	No	Component Of The Rpd3L Histone Deacetylase Complex	Miscellaneous
NUM1	YDR150W	No	Protein Required For Nuclear Migration	Organelle Fission
MIT1	YEL007W	No	Transcriptional Regulator Of Pseudohyphal Growth	Biological_Process
EDE1	YBL047C	No	Endocytic Protein	Response To Chemical
BEM4	YPL161C	No	Protein Involved In Establishment Of Cell Polarity And Bud Emergence	Signaling
HSP42	YDR171W	No	Small Heat Shock Protein (Shsp) With Chaperone Activity	Cytoskeleton Organization
	YEL043W	No	Predicted Cytoskeleton Protein Involved In Intracellular Signaling	Biological_Process
SSA3	YBL075C	No	Atpase Involved In Protein Folding And The Response To Stress	Protein Targeting
MKK2	YPL140C	No	Mapkk Involved In The Protein Kinase C Signaling Pathway	Signaling
UME6	YDR207C	No	Component Of The Rpd3L Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
NPR2	YEL062W	No	Subunit Of Sea (Seh1-Associated), Npr2/3, And Iml1P Complexes	Response To Chemical
RPL23A	YBL087C	No	Ribosomal 60S Subunit Protein L23A	Miscellaneous
DBP1	YPL119C	No	Putative Atp-Dependent Rna Helicase Of The Dead-Box Protein Family	Miscellaneous
HOS2	YGL194C	No	Histone Deacetylase And Subunit Of Set3 And Rpd3L Complexes	Chromatin Organization
GPA2	YER020W	No	Nucleotide Binding Alpha Subunit Of The Heterotrimeric G Protein	Response To Chemical
KAP122	YGL016W	No	Karyopherin Beta	Protein Targeting
ELP4	YPL101W	No	Subunit Of Hexameric Reca-Like Atpase Elp456 Elongator Subcomplex	Transcription From Rna Polymerase Ii Promoter
VAM7	YGL212W	No	Vacuolar Snare Protein	Miscellaneous
HOM3	YER052C	No	Aspartate Kinase (L-Aspartate 4-P-Transferase)	Miscellaneous
RPL24A	YGL031C	No	Ribosomal 60S Subunit Protein L24A	Miscellaneous
PCH2	YBR186W	No	Hexameric Ring Atpase That Remodels Chromosome Axis Protein Hop1P	Organelle Fission
VID30	YGL227W	No	Central Component Of Gid Complex, Involved In Fbpase Degradation	Proteolysis Involved In Cellular Protein Catabolic Process
PTP3	YER075C	No	Phosphotyrosine-Specific Protein Phosphatase	Response To Chemical
TIF4632	YGL049C	No	Translation Initiation Factor Eif4G	Miscellaneous
MAD2	YJL030W	No	Component Of The Spindle-Assembly Checkpoint Complex	Mitotic Cell Cycle
BOI2	YER114C	No	Protein Implicated In Polar Growth, Functionally Redundant With Boi1P	Signaling
HCM1	YCR065W	No	Forkhead Transcription Factor	Transcription From Rna Polymerase Ii Promoter
GEF1	YJR040W	No	Voltage-Gated Chloride Channel	Miscellaneous
NEM1	YHR004C	No	Probable Catalytic Subunit Of Nem1P-Spo7P Phosphatase Holoenzyme	Lipid Metabolic Process
RTR1	YER139C	No	Ctd Phosphatase	Transcription From Rna Polymerase Ii Promoter
AHC2	YCR082W	No	Component Of The Ada Histone Acetyltransferase Complex	Chromatin Organization
APC4	YDR118W	Yes	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Protein Modification By Small Protein Conjugation Or Removal
PFS1	YHR185C	No	Sporulation Protein Required For Prospore Membrane Formation	Meiotic Cell Cycle
RAD4	YER162C	No	Protein That Recognizes And Binds Damaged DNA (With Rad23P) During Ner	Cellular Response To DNA Damage Stimulus
SPC1	YJR010C-A	No	Subunit Of The Signal Peptidase Complex (Spc)	Protein Targeting
TFG1	YGR186W	Yes	Tfiif (Transcription Factor Ii) Largest Subunit	Transcription From Rna Polymerase Ii Promoter
MCM22	YJR135C	No	Outer Kinetochore Protein And Component Of The Ctf3 Subcomplex	Mitotic Cell Cycle
PDA1	YER178W	No	E1 Alpha Subunit Of The Pyruvate Dehydrogenase (Pdh) Complex	Miscellaneous
RAD7	YJR052W	No	Protein That Binds Damaged DNA During Ner	Cellular Response To DNA Damage Stimulus
STH1	YIL126W	Yes	Atpase Component Of The Rsc Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
ATG17	YLR423C	No	Scaffold Protein Responsible For Phagophore Assembly Site Organization	Protein Phosphorylation
BRE1	YDL074C	No	E3 Ubiquitin Ligase	Transcription From Rna Polymerase Ii Promoter
HNT1	YDL125C	No	Adenosine 5'-Monophosphoramidase	Miscellaneous
RSC58	YLR033W	Yes	Component Of The Rsc Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
FMP27	YLR454W	No	Putative Protein Of Unknown Function	Biological_Process
MSH4	YFL003C	No	Protein Involved In Meiotic Recombination	Organelle Fission
AIR2	YDL175C	No	Rna-Binding Subunit Of The Tramp Nuclear Rna Surveillance Complex	Miscellaneous
CDC39	YCR093W	Yes	Component Of The Kinetochore-Associated Ndc80 Complex	Transcription From Rna Polymerase Ii Promoter
	YJR084W	No	Protein That Forms A Complex With Thp3P	Response To Chemical
BDF1	YLR399C	No	Protein Involved In Transcription Initiation	Chromatin Organization
SSN8	YNL025C	No	Cyclin-Like Component Of The Rna Polymerase Ii Holoenzyme	Transcription From Rna Polymerase Ii Promoter
NUT2	YPR168W	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
SGM1	YJR134C	No	Protein Of Unknown Function	Biological_Process
MNN10	YDR245W	No	Subunit Of A Golgi Mannosyltransferase Complex	Carbohydrate Metabolic Process

SFB2	YNL049C	No	Component Of The Sec23P-Sfb2P Heterodimer Of The Copii Vesicle Coat	Protein Complex Biogenesis
CDC48	YDL126C	Yes	Aaa Atpase	Mitotic Cell Cycle
ERV41	YML067C	No	Protein Localized To Copii-Coated Vesicles	Golgi Vesicle Transport
SYS1	YJL004C	No	Integral Membrane Protein Of The Golgi	Protein Targeting
PPG1	YNR032W	No	Putative Serine/Threonine Protein Phosphatase	Carbohydrate Metabolic Process
FCP1	YMR277W	Yes	Carboxy-Terminal Domain (Ctd) Phosphatase	Transcription From Rna Polymerase Ii Promoter
RTN2	YDL204W	No	Reticulon Protein	Miscellaneous
ECM33	YBR078W	No	Gpi-Anchored Protein Of Unknown Function	Miscellaneous
HHT1	YBR010W	No	Histone H3	Mitotic Cell Cycle
ESA1	YOR244W	Yes	Catalytic Subunit Of The Histone Acetyltransferase Complex (Nua4)	Transcription From Rna Polymerase Ii Promoter
PTP1	YDL230W	No	Phosphotyrosine-Specific Protein Phosphatase	Miscellaneous
ROX3	YBL093C	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
RPL4A	YBR031W	No	Ribosomal 60S Subunit Protein L4A	Miscellaneous
TAF3	YPL011C	Yes	Tfiid Subunit (47 Kda)	Transcription From Rna Polymerase Ii Promoter
MAF1	YDR005C	No	Highly Conserved Negative Regulator Of Rna Polymerase Iii	Transcription From Rna Polymerase Ii Promoter
PUS4	YNL292W	No	Pseudouridine Synthase	Miscellaneous
MUM2	YBR057C	No	Protein Essential For Meiotic DNA Replication And Sporulation	Organelle Fission
CDC23	YHR166C	Yes	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Protein Modification By Small Protein Conjugation Or Removal
BUD14	YAR014C	No	Protein Involved In Bud-Site Selection	Protein Complex Biogenesis
QCR10	YHR001W-A	No	Subunit Of The Ubiqunol-Cytochrome C Oxidoreductase Complex	Miscellaneous
YKU70	YMR284W	No	Subunit Of The Telomeric Ku Complex (Yku70P-Yku80P)	Chromatin Organization
KTI12	YKL110C	No	Protein That Plays A Role In Modification Of Trna Wobble Nucleosides	Transcription From Rna Polymerase Ii Promoter
SSA2	YLL024C	No	Atp-Binding Protein	Protein Targeting
SSF1	YHR066W	No	Constituent Of 66S Pre-Ribosomal Particles	Miscellaneous
GAS1	YMR307W	No	Beta-1,3-Glucanosyltransferase	Miscellaneous
ELF1	YKL160W	No	Transcription Elongation Factor With A Conserved Zinc Finger Domain	Transcription From Rna Polymerase Ii Promoter
POM34	YLR018C	No	Subunit Of The Transmembrane Ring Of The Nuclear Pore Complex (Npc)	Protein Complex Biogenesis
GGA2	YHR108W	No	Protein That Regulates Arf1P, Arf2P To Facilitate Golgi Trafficking	Protein Targeting
STB1	YNL309W	No	Protein With Role In Regulation Of Mbf-Specific Transcription At Start	Transcription From Rna Polymerase Ii Promoter
	YGR054W	No	Eukaryotic Initiation Factor (Eif) 2A	Miscellaneous
ARP6	YLR085C	No	Actin-Related Protein That Binds Nucleosomes	Chromatin Organization
MTC6	YHR151C	No	Protein Of Unknown Function	Biological_Process
MID1	YNL291C	No	N-Glycosylated Integral Membrane Protein Of The Er And Plasma Membrane	Miscellaneous
RPL11B	YGR085C	No	Ribosomal 60S Subunit Protein L11B	Miscellaneous
HOG1	YLR113W	No	Mitogen-Activated Protein Kinase Involved In Osmoregulation	Transcription From Rna Polymerase Ii Promoter
PTH1	YHR189W	No	One Of Two Mitochondrially-Localized Peptidyl-Trna Hydrolases	Miscellaneous
VPS75	YNL246W	No	Nap Family Histone Chaperone	Chromatin Organization
RPS23A	YGR118W	No	Ribosomal Protein 28 (Rp28) Of The Small (40S) Ribosomal Subunit	Miscellaneous
SPC2	YML055W	No	Subunit Of Signal Peptidase Complex	Protein Targeting
SGF29	YCL010C	No	Component Of The Hat/Core Module Of The Saga, Slik, And Ada Complexes	Transcription From Rna Polymerase Ii Promoter
HST3	YOR025W	No	Member Of The Sir2 Family Of Nad(+)-Dependent Protein Deacetylases	Chromatin Organization
LEO1	YOR123C	No	Component Of The Paf1 Complex	Transcription From Rna Polymerase Ii Promoter
TSA1	YML028W	No	Thioredoxin Peroxidase	Cellular Response To DNA Damage Stimulus
EMC1	YCL045C	No	Member Of Conserved Endoplasmic Reticulum Membrane Complex	Miscellaneous
CKB2	YOR039W	No	Beta' Regulatory Subunit Of Casein Kinase 2 (Ck2)	Cellular Response To DNA Damage Stimulus
NFI1	YOR156C	No	Sumo E3 Ligase	Protein Modification By Small Protein Conjugation Or Removal
YAP1	YML007W	No	Basic Leucine Zipper (Bzip) Transcription Factor	Transcription From Rna Polymerase Ii Promoter
CWH43	YCR017C	No	Putative Sensor/Transporter Protein Involved In Cell Wall Biogenesis	Lipid Metabolic Process
CYT1	YOR065W	No	Cytochrome C1	Miscellaneous
SLK19	YOR195W	No	Kinetochore-Associated Protein Required For Chromosome Segregation	Mitotic Cell Cycle
PEP8	YJL053W	No	Vacuolar Protein Component Of The Retromer	Miscellaneous
CKI1	YLR133W	No	Choline Kinase	Lipid Metabolic Process
BUD21	YOR078W	No	Component Of Small Ribosomal Subunit (Ssu) Processosome	Miscellaneous
KIN4	YOR233W	No	Serine/Threonine Protein Kinase	Mitotic Cell Cycle
MIH1	YMR036C	No	Protein Tyrosine Phosphatase Involved In Cell Cycle Control	Mitotic Cell Cycle
SAM1	YLR180W	No	S-Adenosylmethionine Synthetase	Miscellaneous
SNF2	YOR290C	No	Catalytic Subunit Of The Swi/Snf Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
MPD1	YOR288C	No	Member Of The Protein Disulfide Isomerase (Pdi) Family	Miscellaneous
NUP53	YMR153W	No	Fg-Nucleoporin Component Of Central Core Of Nuclear Pore Complex (Npc)	Mitotic Cell Cycle
MMR1	YLR190W	No	Phosphorylated Protein Of The Mitochondrial Outer Membrane	Miscellaneous
SLY41	YOR307C	No	Protein Involved In Er-To-Golgi Transport	Golgi Vesicle Transport
RCY1	YJL204C	No	F-Box Protein Involved In Recycling Endocytosed Proteins	Golgi Vesicle Transport
SPT21	YMR179W	No	Protein With A Role In Transcriptional Silencing	Transcription From Rna Polymerase Ii Promoter
ENT2	YLR206W	No	Epsin-Like Protein Required For Endocytosis And Actin Patch Assembly	Cytoskeleton Organization
RPL20B	YOR312C	No	Ribosomal 60S Subunit Protein L20B	Miscellaneous
RPS22A	YJL190C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
NPR1	YNL183C	No	Protein Kinase	Lipid Metabolic Process
SGN1	YIR001C	No	Cytoplasmic Rna-Binding Protein	Miscellaneous
IRC21	YMR073C	No	Putative Protein Of Unknown Function	Response To Chemical
	YPR022C	No	Putative Transcription Factor, As Suggested By Computational Analysis	Biological_Process
ADD66	YKL206C	No	Protein Involved In 20S Proteasome Assembly	Protein Complex Biogenesis
IOC3	YFR013W	No	Subunit Of The Isw1A Complex	Chromatin Organization
MSH2	YOL090W	No	Protein That Binds To DNA Mismatches	Cellular Response To DNA Damage Stimulus
UBC4	YBR082C	No	Ubiquitin-Conjugating Enzyme (E2)	Protein Modification By Small Protein Conjugation Or Removal
MEH1	YKR007W	No	Component Of The Ego And Gse Complexes	Miscellaneous
TPM1	YNL079C	No	Major Isoform Of Tropomyosin	Cytoskeleton Organization
VHR2	YER064C	No	Non-Essential Nuclear Protein	Miscellaneous
AIM3	YBR108W	No	Protein Interacting With Rvs167P	Protein Complex Biogenesis
RHO4	YKR055W	No	Non-Essential Small Gtpase	Regulation Of Organelle Organization
NCS2	YNL119W	No	Protein Required For Uridine Thiolation Of Lys(Uuu) And Glu(Uuc) Trnas	Protein Modification By Small Protein Conjugation Or Removal
SVP26	YHR181W	No	Integral Membrane Protein Of The Early Golgi Apparatus And Er	Carbohydrate Metabolic Process
TOS1	YBR162C	No	Covalently-Bound Cell Wall Protein Of Unknown Function	Biological_Process
SWM1	YDR260C	No	Subunit Of The Anaphase-Promoting Complex (Apc)	Mitotic Cell Cycle
DBF2	YGR092W	No	Ser/Thr Kinase Involved In Transcription And Stress Response	Organelle Fission
VPS9	YML097C	No	Guanine Nucleotide Exchange Factor (Gef)	Protein Targeting
SLX5	YDL013W	No	Subunit Of The Slx5-Slx8 Sumo-Targeted Ubiquitin Ligase Complex	Cellular Response To DNA Damage Stimulus
SUR2	YDR297W	No	Sphinganine C4-Hydroxylase	Lipid Metabolic Process
SAP190	YKR028W	No	Protein That Forms A Complex With The Sit4P Protein Phosphatase	Mitotic Cell Cycle
	YML119W	No	Putative Protein Of Unknown Function	Biological_Process
RAD59	YDL059C	No	Protein Involved DNA Double-Strand Break Repair	Cellular Response To DNA Damage Stimulus
SWA2	YDR320C	No	Auxilin-Like Protein Involved In Vesicular Transport	Miscellaneous
TBS1	YBR150C	No	Putative Protein Of Unknown Function	Biological_Process
YKU80	YMR106C	No	Subunit Of The Telomeric Ku Complex (Yku70P-Yku80P)	Chromatin Organization
ASM4	YDL088C	No	Fg-Nucleoporin Component Of Central Core Of Nuclear Pore Complex (Npc)	Mitotic Cell Cycle
TIR3	YIL011W	No	Cell Wall Mannoprotein	Biological_Process
SNF5	YBR289W	No	Subunit Of The Swi/Snf Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
POM152	YMR129W	No	Glycoprotein Subunit Of Transmembrane Ring Of Nuclear Pore Complex	Protein Complex Biogenesis
SSN2	YDR443C	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
TED1	YIL039W	No	Conserved Phosphoesterase Domain-Containing Protein	Golgi Vesicle Transport
ABP1	YCR088W	No	Actin-Binding Protein Of The Cortical Actin Cytoskeleton	Protein Complex Biogenesis
SRO7	YPR032W	No	Effector Of Rab Gtpase Sec4P	Signaling
PEX29	YDR479C	No	Peroxisomal Integral Membrane Peroxin	Miscellaneous
AIR1	YIL079C	No	Zinc Knuckle Protein	Miscellaneous
ARC18	YLR370C	No	Subunit Of The Arp2/3 Complex	Cytoskeleton Organization
SMK1	YPR054W	No	Middle Sporulation-Specific Mitogen-Activated Protein Kinase (Mapk)	Meiotic Cell Cycle

ITR1	YDR497C	No	Myo-Inositol Transporter	Miscellaneous
URM1	YIL008W	No	Ubiquitin-Like Protein Involved In Thiolation Of Cytoplasmic Trnas	Response To Chemical
VPS71	YML041C	No	Nucleosome-Binding Component Of The Swr1 Complex	Chromatin Organization
HOS1	YPR068C	No	Class I Histone Deacetylase (Hdac) Family Member	Transcription From Rna Polymerase Ii Promoter
EMI1	YDR512C	No	Non-Essential Protein Of Unknown Function	Transcription From Rna Polymerase Ii Promoter
RPL34B	YIL052C	No	Ribosomal 60S Subunit Protein L34B	Miscellaneous
CSM3	YMR048W	No	Replication Fork Associated Factor	Mitotic Cell Cycle
OPY2	YPR075C	No	Integral Membrane Protein That Acts As A Membrane Anchor For Ste50P	Response To Chemical
CUE3	YGL110C	No	Protein Of Unknown Function	Biological_Process
MDM38	YOL027C	No	Mitochondrial Protein	Protein Complex Biogenesis
VID22	YLR373C	No	Glycosylated Integral Membrane Protein Localized To Plasma Membrane	Miscellaneous
BMH2	YDR099W	No	14-3-3 Protein, Minor Isoform	Mitotic Cell Cycle
ISR1	YPR106W	No	Predicted Protein Kinase	Biological_Process
GSH2	YOL049W	No	Glutathione Synthetase	Miscellaneous
ATP10	YLR393W	No	Assembly Factor For The F0 Sector Of Mitochondrial F1F0 Atp Synthase	Protein Complex Biogenesis
ECM18	YDR125C	No	Protein Of Unknown Function	Biological_Process
TAZ1	YPR140W	No	Lyso-Phosphatidylcholine Acyltransferase	Protein Complex Biogenesis
RTG1	YOL067C	No	Transcription Factor (Bhlh) Involved In Interorganelle Communication	Transcription From Rna Polymerase Ii Promoter
EST1	YLR233C	No	Tlc1 Rna-Associated Factor Involved In Telomere Length Regulation	Miscellaneous
GGA1	YDR358W	No	Golgi-Localized Protein With Homology To Gamma-Adaptin	Protein Targeting
SKI3	YPR189W	No	Ski Complex Component And Tpr Protein	Miscellaneous
GAL4	YPL248C	No	DNA-Binding Transcription Factor Required For Activating Gal Genes	Transcription From Rna Polymerase Ii Promoter
PDR8	YLR266C	No	Transcription Factor	Transcription From Rna Polymerase Ii Promoter
EFT2	YDR385W	No	Elongation Factor 2 (Ef-2), Also Encoded By Eft1	Miscellaneous
HSV2	YGR223C	No	Phosphatidylinositol 3,5-Bisphosphate-Binding Protein	Miscellaneous
PUS1	YPL212C	No	Trna:Pseudouridine Synthase	Miscellaneous
SEC72	YLR292C	No	Non-Essential Subunit Of Sec63 Complex	Protein Targeting
ERD1	YDR414C	No	Predicted Membrane Protein Required For Lumenal Er Protein Retention	Carbohydrate Metabolic Process
PEP1	YBL017C	No	Type I Transmembrane Sorting Receptor For Multiple Vacuolar Hydrolases	Protein Targeting
TCO89	YPL180W	No	Subunit Of Torc1 (Tor1P Or Tor2P-Kog1P-Lst8P-Tco89P)	Signaling
ENT5	YDR153C	No	Protein Containing An N-Terminal Epsin-Like Domain	Golgi Vesicle Transport
VAC8	YEL013W	No	Phosphorylated And Palmitoylated Vacuolar Membrane Protein	Protein Targeting
PIN4	YBL051C	No	Protein Involved In G2/M Phase Progression And Response To DNA Damage	Mitotic Cell Cycle
TGS1	YPL157W	No	Trimethyl Guanosine Synthase, Conserved Nucleolar Methyl Transferase	Organelle Fission
ARG82	YDR173C	No	Inositol Polyphosphate Multikinase (Ipmk)	Transcription From Rna Polymerase Ii Promoter
FRD1	YEL047C	No	Soluble Fumarate Reductase	Response To Chemical
ATG8	YBL078C	No	Component Of Autophagosomes And Cvt Vesicles	Protein Targeting
UME1	YPL139C	No	Component Of Both The Rpd3S And Rpd3L Histone Deacetylase Complexes	Transcription From Rna Polymerase Ii Promoter
RAD9	YDR217C	No	DNA Damage-Dependent Checkpoint Protein	Transcription From Rna Polymerase Ii Promoter
AVT2	YEL064C	No	Putative Transporter	Miscellaneous
TEL1	YBL088C	No	Protein Kinase Primarily Involved In Telomere Length Regulation	Chromatin Organization
HOS3	YPL116W	No	Trichostatin A-Insensitive Homodimeric Histone Deacetylase (Hdac)	Transcription From Rna Polymerase Ii Promoter
GCN1	YGL195W	No	Positive Regulator Of The Gcn2P Kinase Activity	Miscellaneous
CHZ1	YER030W	No	Histone Chaperone For Htz1P/H2A-H2B Dimer	Chromatin Organization
CKB1	YGL019W	No	Beta Regulatory Subunit Of Casein Kinase 2 (Ck2)	Cellular Response To DNA Damage Stimulus
ATG21	YPL100W	No	Phosphoinositide Binding Protein	Protein Targeting
SKI8	YGL213C	No	Ski Complex Component And Wd-Repeat Protein	Organelle Fission
CEM1	YER061C	No	Mitochondrial Beta-Keto-Acyl Synthase	Lipid Metabolic Process
MIG1	YGL035C	No	Transcription Factor Involved In Glucose Repression	Transcription From Rna Polymerase Ii Promoter
AIM4	YBR194W	No	Protein Proposed To Be Associated With The Nuclear Pore Complex	Biological_Process
SHE10	YGL228W	No	Protein Involved In Outer Spore Wall Assembly	Meiotic Cell Cycle
GET2	YER083C	No	Subunit Of The Get Complex	Golgi Vesicle Transport
ERV14	YGL054C	No	Copii-Coated Vesicle Protein	Mitotic Cell Cycle
NGR1	YBR212W	No	Rna Binding Protein That Negatively Regulates Growth Rate	Miscellaneous
RTF1	YGL244W	No	Subunit Of Rnapii-Associated Chromatin Remodeling Paf1 Complex	Transcription From Rna Polymerase Ii Promoter
PEX4	YGR133W	No	Peroxisomal Ubiquitin Conjugating Enzyme	Protein Modification By Small Protein Conjugation Or Removal
SGF73	YGL066W	No	Saga Complex Subunit	Transcription From Rna Polymerase Ii Promoter
STP2	YHR006W	No	Transcription Factor	Transcription From Rna Polymerase Ii Promoter
PEA2	YER149C	No	Coiled-Coil Polarisome Protein	Mitotic Cell Cycle
CSM1	YCR086W	No	Nucleolar Protein That Mediates Homolog Segregation During Meiosis I	Mitotic Cell Cycle
TAF10	YDR167W	Yes	Subunit (145 Kda) Of Tfiid And Saga Complexes	Transcription From Rna Polymerase Ii Promoter
MDM31	YHR194W	No	Mitochondrial Protein That May Have A Role In Phospholipid Metabolism	Lipid Metabolic Process
CHD1	YER164W	No	Chromatin Remodeler That Regulates Various Aspects Of Transcription	Transcription From Rna Polymerase Ii Promoter
	YJR011C	No	Putative Protein Of Unknown Function	Biological_Process
TFA1	YKL028W	Yes	Tfiie Large Subunit	Transcription From Rna Polymerase Ii Promoter
SRP40	YKR092C	No	Nucleolar Serine-Rich Protein	Miscellaneous
FAR3	YMR052W	No	Protein Of Unknown Function	Response To Chemical
BFA1	YJR053W	No	Component Of The Gtpase-Activating Bfa1P-Bub2P Complex	Mitotic Cell Cycle
CKS1	YBR135W	Yes	Cyclin-Dependent Protein Kinase Regulatory Subunit And Adaptor	Mitotic Cell Cycle
TUS1	YLR425W	No	Guanine Nucleotide Exchange Factor (Gef) That Modulate Rho1P Activity	Signaling
SNF1	YDR477W	No	Amp-Activated Serine/Threonine Protein Kinase	Protein Phosphorylation
RPP1B	YDL130W	No	Ribosomal Protein P1 Beta	Protein Phosphorylation
RGR1	YLR071C	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
SAM37	YMR060C	No	Component Of The Sorting And Assembly Machinery (Sam) Complex	Protein Complex Biogenesis
BLM10	YFL007W	No	Proteasome Activator	Protein Complex Biogenesis
	YDL176W	No	Protein Of Unknown Function	Biological_Process
APC11	YDL008W	Yes	Catalytic Core Subunit, Anaphase-Promoting Complex/Cyclosome (Apc/C)	Protein Modification By Small Protein Conjugation Or Removal
IME1	YJR094C	No	Master Regulator Of Meiosis That Is Active Only During Meiotic Events	Transcription From Rna Polymerase Ii Promoter
DOC1	YGL240W	No	Processivity Factor	Mitotic Cell Cycle
CRZ1	YNL027W	No	Transcription Factor, Activates Transcription Of Stress Response Genes	Transcription From Rna Polymerase Ii Promoter
MET30	YIL046W	Yes	F-Box Protein Containing Five Copies Of The Wd40 Motif	Transcription From Rna Polymerase Ii Promoter
HOM6	YJR139C	No	Homoserine Dehydrogenase (L-Homoserine:Nadp Oxidoreductase)	Miscellaneous
LPD1	YFL018C	No	Dihydrolipoamide Dehydrogenase	Miscellaneous
SWM2	YNR004W	No	Protein With A Role In Snrna And Snorna Cap Trimethylation	Miscellaneous
RPB11	YOL005C	Yes	Rna Polymerase Ii Subunit B12.5	Transcription From Rna Polymerase Ii Promoter
TCB3	YML072C	No	Cortical Er Protein Involved In Er-Plasma Membrane Tethering	Lipid Metabolic Process
MAD3	YJL013C	No	Subunit Of Spindle-Assembly Checkpoint Complex	Mitotic Cell Cycle
COQ2	YNR041C	No	Para Hydroxybenzoate Polyprenyl Transferase	Miscellaneous
MED4	YOR174W	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
NOP6	YDL213C	No	Rrna-Binding Protein Required For 40S Ribosomal Subunit Biogenesis	Miscellaneous
NAT1	YDL040C	No	Subunit Of Protein N-Terminal Acetyltransferase Nata	Miscellaneous
MNN2	YBR015C	No	Alpha-1,2-Mannosyltransferase	Carbohydrate Metabolic Process
HRT1	YOL133W	Yes	Ring-H2 Domain Core Subunit Of Multiple Ubiquitin Ligase Complexes	Mitotic Cell Cycle
OST4	YDL232W	No	Subunit Of The Oligosaccharyltransferase Complex Of The Er Lumen	Carbohydrate Metabolic Process
CYC8	YBR112C	No	General Transcriptional Co-Repressor	Transcription From Rna Polymerase Ii Promoter
HMT1	YBR034C	No	Nuclear Sam-Dependent Mono- And Asymmetric Methyltransferase	Transcription From Rna Polymerase Ii Promoter
APC5	YOR249C	Yes	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Chromatin Organization
GAL3	YDR009W	No	Transcriptional Regulator	Transcription From Rna Polymerase Ii Promoter
SAP30	YMR263W	No	Component Of Rpd3L Histone Deacetylase Complex	Transcription From Rna Polymerase Ii Promoter
UBP14	YBR058C	No	Ubiquitin-Specific Protease	Proteolysis Involved In Cellular Protein Catabolic Process
MED7	YOL135C	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
FMP21	YBR269C	No	Putative Protein Of Unknown Function	Biological_Process
MRPL36	YBR122C	No	Mitochondrial Ribosomal Protein Of The Large Subunit	Miscellaneous
TAT1	YBR069C	No	Amino Acid Transporter For Valine, Leucine, Isoleucine, And Tyrosine	Miscellaneous
BST1	YFL025C	No	Gpi Inositol Deacylase Of The Endoplasmic Reticulum (Er)	Proteolysis Involved In Cellular Protein Catabolic Process

ENT4	YLL038C	No	Protein Of Unknown Function	Cytoskeleton Organization
NMD2	YHR077C	No	Protein Involved In The Nonsense-Mediated Mrna Decay (Nmd) Pathway	Miscellaneous
RPD3	YNL330C	No	Histone Deacetylase, Component Of Both The Rpd3S And Rpd3L Complexes	Transcription From Rna Polymerase Ii Promoter
TPK3	YKL166C	No	Camp-Dependent Protein Kinase Catalytic Subunit	Signaling
IRC25	YLR021W	No	Component Of A Heterodimeric Poc4P-Irc25P Chaperone	Protein Complex Biogenesis
UBA4	YHR111W	No	Protein That Activates Urm1P Before Urmylation	Response To Chemical
MSG5	YNL053W	No	Dual-Specificity Protein Phosphatase	Response To Chemical
RSC1	YGR056W	No	Component Of The Rsc Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
CSF1	YLR087C	No	Protein Required For Fermentation At Low Temperature	Miscellaneous
RTT107	YHR154W	No	Protein Implicated In Mms22-Dependent DNA Repair During S Phase	Cellular Response To DNA Damage Stimulus
CAF40	YNL288W	No	Component Of The Ccr4-Not Transcriptional Complex	Transcription From Rna Polymerase Ii Promoter
ASK10	YGR097W	No	Component Of Rna Polymerase Ii Holoenzyme	Transcription From Rna Polymerase Ii Promoter
AVL9	YLR114C	No	Conserved Protein Involved In Exocytic Transport From The Golgi	Golgi Vesicle Transport
RPN10	YHR200W	No	Non-Atpase Base Subunit Of The 19S Rp Of The 26S Proteasome	Proteolysis Involved In Cellular Protein Catabolic Process
RRP6	YOR001W	No	Nuclear Exosome Exonuclease Component	Miscellaneous
	YGR122W	No	Protein That May Be Involved In Ph Regulation	Transcription From Rna Polymerase Ii Promoter
GAL80	YML051W	No	Transcriptional Regulator Involved In The Repression Of Gal Genes	Transcription From Rna Polymerase Ii Promoter
GBP2	YCL011C	No	Poly(A+) Rna-Binding Protein	Miscellaneous
BUB3	YOR026W	No	Kinetochore Checkpoint Wd40 Repeat Protein	Mitotic Cell Cycle
UBP2	YOR124C	No	Ubiquitin-Specific Protease	Protein Modification By Small Protein Conjugation Or Removal
OST6	YML019W	No	Subunit Of The Oligosaccharyltransferase Complex Of The Er Lumen	Protein Complex Biogenesis
APA1	YCL050C	No	Ap4A Phosphorylase	Miscellaneous
CUE5	YOR042W	No	Ubiquitin-Binding Protein	Biological_Process
SEY1	YOR165W	No	Dynamin-Like Gtpase That Mediates Homotypic Er Fusion	Miscellaneous
YPT7	YML001W	No	Rab Family Gtpase	Regulation Of Organelle Organization
MAK32	YCR019W	No	Protein Necessary For Stability Of L-A Dsrna-Containing Particles	Miscellaneous
ALG8	YOR067C	No	Glucosyl Transferase	Lipid Metabolic Process
PTP2	YOR208W	No	Phosphotyrosine-Specific Protein Phosphatase	Signaling
UBC7	YMR022W	No	Ubiquitin Conjugating Enzyme	Chromatin Organization
SLX4	YLR135W	No	Endonuclease Involved In Processing DNA	Cellular Response To DNA Damage Stimulus
DIA2	YOR080W	No	Origin-Binding F-Box Protein	Protein Modification By Small Protein Conjugation Or Removal
RPL33B	YOR234C	No	Ribosomal 60S Subunit Protein L33B	Miscellaneous
SUB1	YMR039C	No	Transcriptional Coactivator	Transcription From Rna Polymerase Ii Promoter
VTA1	YLR181C	No	Multivesicular Body (Mvb) Protein	Protein Complex Biogenesis
TIM18	YOR297C	No	Component Of The Mitochondrial Tim22 Complex	Response To Chemical
HXT8	YJL214W	No	Protein Of Unknown Function With Similarity To Hexose Transporters	Miscellaneous
HLJ1	YMR161W	No	Co-Chaperone For Hsp40P	Proteolysis Involved In Cellular Protein Catabolic Process
PEX13	YLR191W	No	Integral Peroxisomal Membrane Protein	Protein Complex Biogenesis
SNU66	YOR308C	No	Component Of The U4/U6.U5 Snrnp Complex	Miscellaneous
PHO90	YJL198W	No	Low-Affinity Phosphate Transporter	Miscellaneous
HSC82	YMR186W	No	Cytoplasmic Chaperone Of The Hsp90 Family	Protein Complex Biogenesis
HRD3	YLR207W	No	Er Membrane Protein That Plays A Central Role In Erad	Proteolysis Involved In Cellular Protein Catabolic Process
PMT3	YOR321W	No	Protein O-Mannosyltransferase	Carbohydrate Metabolic Process
SWE1	YJL187C	No	Protein Kinase That Regulates The G2/M Transition	Mitotic Cell Cycle
CIK1	YMR198W	No	Kinesin-Associated Protein	Mitotic Cell Cycle
CPR6	YLR216C	No	Peptidyl-Prolyl Cis-Trans Isomerase (Cyclophilin)	Miscellaneous
SNC2	YOR327C	No	Vesicle Membrane Receptor Protein (V-Snare)	Golgi Vesicle Transport
SWI3	YJL176C	No	Subunit Of The Swi/Snf Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
EMC3	YKL207W	No	Member Of Conserved Er Transmembrane Complex	Miscellaneous
COG5	YNL051W	No	Component Of The Conserved Oligomeric Golgi Complex	Protein Targeting
TRM10	YOL093W	No	Trna Methyltransferase	Miscellaneous
PHO5	YBR093C	No	Repressible Acid Phosphatase	Miscellaneous
VPS51	YKR020W	No	Component Of The Garp (Golgi-Associated Retrograde Protein) Complex	Protein Targeting
EOS1	YNL080C	No	Protein Involved In N-Glycosylation	Response To Chemical
	YER077C	No	Putative Protein Of Unknown Function	Biological_Process
RAD16	YBR114W	No	Protein That Binds Damaged DNA During Ner	Cellular Response To DNA Damage Stimulus
TIF1	YKR059W	No	Translation Initiation Factor Eif4A	Miscellaneous
RPL41B	YDL133C-A	No	Ribosomal 60S Subunit Protein L41B	Miscellaneous
RAD5	YLR032W	No	DNA Helicase/Ubiquitin Ligase	Cellular Response To DNA Damage Stimulus
YSY6	YBR162W-A	No	Protein Of Unknown Function	Miscellaneous
PEX10	YDR265W	No	Peroxisomal Membrane E3 Ubiquitin Ligase	Protein Modification By Small Protein Conjugation Or Removal
RPS21B	YJL136C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
TSL1	YML100W	No	Large Subunit Of Trehalose 6-Phosphate Synthase/Phosphatase Complex	Carbohydrate Metabolic Process
RPN4	YDL020C	No	Transcription Factor That Stimulates Expression Of Proteasome Genes	Transcription From Rna Polymerase Ii Promoter
CPR5	YDR304C	No	Peptidyl-Prolyl Cis-Trans Isomerase (Cyclophilin) Of The Er	Biological_Process
SET3	YKR029C	No	Defining Member Of The Set3 Histone Deacetylase Complex	Chromatin Organization
GTR1	YML121W	No	Cytoplasmic Gtpase	Signaling
RPS29B	YDL061C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
PEX3	YDR329C	No	Peroxisomal Membrane Protein (Pmp)	Protein Targeting
PEX32	YBR168W	No	Peroxisomal Integral Membrane Protein	Miscellaneous
MYO5	YMR109W	No	One Of Two Type I Myosins	Mitotic Cell Cycle
NUR1	YDL089W	No	Protein Of Unknown Function	Miscellaneous
EMC5	YIL027C	No	Member Of Conserved Er Transmembrane Complex	Miscellaneous
RIM1	YCR028C-A	No	SsDNA-Binding Protein Essential For Mitochondrial Genome Maintenance	Miscellaneous
REC114	YMR133W	No	Protein Involved In Early Stages Of Meiotic Recombination	Organelle Fission
ADA2	YDR448W	No	Transcription Coactivator	Transcription From Rna Polymerase Ii Promoter
APQ12	YIL040W	No	Protein Required For Nuclear Envelope Morphology	Lipid Metabolic Process
FIG2	YCR089W	No	Cell Wall Adhesin, Expressed Specifically During Mating	Response To Chemical
THP3	YPR045C	No	Protein That May Have A Role In Transcription Elongation	Miscellaneous
CWC21	YDR482C	No	Protein Involved In Rna Splicing By The Spliceosome	Miscellaneous
CST9	YLR394W	No	Sumo E3 Ligase	Organelle Fission
BRR1	YPR057W	No	Snrnp Protein Component Of Spliceosomal Snrnps	Miscellaneous
RPL37B	YDR500C	No	Ribosomal 60S Subunit Protein L37B	Miscellaneous
NOT3	YIL038C	No	Subunit Of Ccr4-Not Global Transcriptional Regulator	Transcription From Rna Polymerase Ii Promoter
PRM6	YML047C	No	Potassium Transporter That Mediates K+ Influx	Miscellaneous
SPE3	YPR069C	No	Spermidine Synthase	Miscellaneous
KRE28	YDR532C	No	Subunit Of A Kinetochore-Microtubule Binding Complex	Biological_Process
HXT10	YFL011W	No	Putative Hexose Transporter	Miscellaneous
CIN4	YMR138W	No	Gtp-Binding Protein Involved In Beta-Tubulin (Tub2P) Folding	Protein Complex Biogenesis
	YPR084W	No	Putative Protein Of Unknown Function	Biological_Process
SNF4	YGL115W	No	Activating Gamma Subunit Of The Amp-Activated Snf1P Kinase Complex	Transcription From Rna Polymerase Ii Promoter
RTT10	YPL183C	No	Wd40 Domain-Containing Protein Involved In Endosomal Recycling	Miscellaneous
LSM1	YJL124C	No	Lsm (Like Sm) Protein	Miscellaneous
SCS3	YGL126W	No	Protein Required For Inositol Prototrophy	Lipid Metabolic Process
GAL11	YOL051W	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
SKI2	YLR398C	No	Ski Complex Component And Putative Rna Helicase	Miscellaneous
SWF1	YDR126W	No	Palmitoyltransferase That Acts On Transmembrane Proteins	Meiotic Cell Cycle
KAR3	YPR141C	No	Minus-End-Directed Microtubule Motor	Mitotic Cell Cycle
HST1	YOL068C	No	Nad(+)-Dependent Histone Deacetylase	Chromatin Organization
TOP3	YLR234W	No	DNA Topoisomerase Iii	Mitotic Cell Cycle
EAF1	YDR359C	No	Component Of The Nua4 Histone Acetyltransferase Complex	Chromatin Organization
SEM1	YDR363W-A	No	Component Of Lid Subcomplex Of 26S Proteasome Regulatory Subunit	Protein Complex Biogenesis
BOP2	YLR267W	No	Protein Of Unknown Function	Biological_Process
MUS81	YDR386W	No	Subunit Of Structure-Specific Mms4P-Mus81P Endonuclease	Cellular Response To DNA Damage Stimulus
DIE2	YGR227W	No	Dolichyl-Phosphoglucose-Dependent Alpha-1,2 Glucosyltransferase	Carbohydrate Metabolic Process

OXR1	YPL196W	No	Protein Of Unknown Function Required For Oxidative Damage Resistance	Response To Chemical
UBC12	YLR306W	No	Enzyme That Mediates The Conjugation Of Rub1P	Protein Modification By Small Protein Conjugation Or Removal
HKR1	YDR420W	No	Mucin Family Member That Functions As An Osmosensor In The Hog Pathway	Mitotic Cell Cycle
HAP3	YBL021C	No	Subunit Of The Hap2P/3P/4P/5P Ccaat-Binding Complex	Transcription From Rna Polymerase Ii Promoter
CBC2	YPL178W	No	Small Subunit Of The Heterodimeric Cap Binding Complex With Sto1P	Miscellaneous
CPR1	YDR155C	No	Cytoplasmic Peptidyl-Prolyl Cis-Trans Isomerase (Cyclophilin)	Chromatin Organization
EDC3	YEL015W	No	Non-Essential Conserved Protein With A Role In Mrna Decapping	Miscellaneous
SAS3	YBL052C	No	Histone Acetyltransferase Catalytic Subunit Of Nua3 Complex	Chromatin Organization
KIP2	YPL155C	No	Kinesin-Related Motor Protein Involved In Mitotic Spindle Positioning	Regulation Of Organelle Organization
NGG1	YDR176W	No	Subunit Of Chromatin Modifying Histone Acetyltransferase Complexes	Chromatin Organization
TCA17	YEL048C	No	Subunit Of Trappii	Protein Complex Biogenesis
NUP170	YBL079W	No	Subunit Of The Inner Ring Of The Nuclear Pore Complex (Npc)	Mitotic Cell Cycle
MFB1	YDR219C	No	Mitochondria-Associated F-Box Protein	Proteolysis Involved In Cellular Protein Catabolic Process
NOP16	YER002W	No	Constituent Of 66S Pre-Ribosomal Particles	Miscellaneous
AIM44	YPL158C	No	Protein That Regulates Cdc42P And Rho1P	Miscellaneous
BEM3	YPL115C	No	Rho Gtpase Activating Protein (Rhogap)	Signaling
DSD1	YGL196W	No	D-Serine Dehydratase (Aka D-Serine Ammonia-Lyase)	Miscellaneous
FIR1	YER032W	No	Protein Involved In 3' Mrna Processing	Miscellaneous
PGD1	YGL025C	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
SWD3	YBR175W	No	Essential Subunit Of The Compass (Set1C) Complex	Chromatin Organization
KIP3	YGL216W	No	Kinesin-Related Motor Protein Involved In Mitotic Spindle Positioning	Mitotic Cell Cycle
MOT2	YER068W	No	Ubiquitin-Protein Ligase Subunit Of The Ccr4-Not Complex	Transcription From Rna Polymerase Ii Promoter
DST1	YGL043W	No	General Transcription Elongation Factor Tfiis	Transcription From Rna Polymerase Ii Promoter
MSI1	YBR195C	No	Subunit Of Chromatin Assembly Factor I (Caf-1)	Chromatin Organization
TAN1	YGL232W	No	Putative Trna Acetyltransferase	Miscellaneous
PPT1	YGR123C	No	Protein Serine/Threonine Phosphatase	Miscellaneous
RAD6	YGL058W	No	Ubiquitin-Conjugating Enzyme (E2)	Transcription From Rna Polymerase Ii Promoter
HPC2	YBR215W	No	Subunit Of The Hir Complex	Transcription From Rna Polymerase Ii Promoter
RMR1	YGL250W	No	Protein Required For Meiotic Recombination And Gene Conversion	Organelle Fission
PRE9	YGR135W	No	Alpha 3 Subunit Of The 20S Proteasome	Protein Complex Biogenesis
NPY1	YGL067W	No	Nadh Diphosphatase (Pyrophosphatase)	Miscellaneous
TDP1	YBR223C	No	Tyrosyl-DNA Phosphodiesterase I	Cellular Response To DNA Damage Stimulus
HXK2	YGL253W	No	Hexokinase Isoenzyme 2	Response To Chemical
GTR2	YGR163W	No	Putative Gtp Binding Protein	Transcription From Rna Polymerase Ii Promoter
DBP3	YGL078C	No	Rna-Dependent Atpase, Member Of Dexd/H-Box Family	Miscellaneous
RIM13	YMR154C	No	Calpain-Like Cysteine Protease	Miscellaneous
DNF1	YER166W	No	Aminophospholipid Translocase (Flippase)	Miscellaneous
RAV1	YJR033C	No	Subunit Of Rave Complex (Rav1P, Rav2P, Skp1P)	Protein Complex Biogenesis
TAF9	YMR236W	Yes	Subunit (17 Kda) Of Tfiid And Saga Complexes	Transcription From Rna Polymerase Ii Promoter
PTR2	YKR093W	No	Integral Membrane Peptide Transporter	Miscellaneous
STV1	YMR054W	No	Subunit A Of The Vacuolar-Atpase V0 Domain	Miscellaneous
KCH1	YJR054W	No	Potassium Transporter That Mediates K+ Influx	Miscellaneous
SRB7	YDR308C	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
TDA5	YLR426W	No	Putative Protein Of Unknown Function	Response To Chemical
SSK1	YLR006C	No	Cytoplasmic Response Regulator	Regulation Of Organelle Organization
PPH21	YDL134C	No	Catalytic Subunit Of Protein Phosphatase 2A (Pp2A)	Mitotic Cell Cycle
APC1	YNL172W	Yes	Largest Subunit Of The Anaphase-Promoting Complex/Cyclosome	Mitotic Cell Cycle
BRE5	YNR051C	No	Ubiquitin Protease Cofactor	Protein Modification By Small Protein Conjugation Or Removal
IES1	YFL013C	No	Subunit Of The Ino80 Chromatin Remodeling Complex	Chromatin Organization
PPH22	YDL188C	No	Catalytic Subunit Of Protein Phosphatase 2A (Pp2A)	Mitotic Cell Cycle
TFB4	YPR056W	Yes	Subunit Of Tfiih Complex	Transcription From Rna Polymerase Ii Promoter
STE24	YJR117W	No	Highly Conserved Zinc Metalloprotease	Miscellaneous
RMI1	YPL024W	No	Subunit Of The Recq (Sgs1P) - Topo Iii (Top3P) Complex	Mitotic Cell Cycle
HHF2	YNL030W	No	Histone H4	Chromatin Organization
DPB2	YPR175W	Yes	Second Largest Subunit Of DNA Polymerase Ii (DNA Polymerase Epsilon)	Chromatin Organization
HIR3	YJR140C	No	Subunit Of The Hir Complex	Transcription From Rna Polymerase Ii Promoter
BUL2	YML111W	No	Component Of The Rsp5P E3-Ubiquitin Ligase Complex	Protein Modification By Small Protein Conjugation Or Removal
VPS27	YNR006W	No	Endosomal Protein That Forms A Complex With Hse1P	Protein Targeting
SGT1	YOR057W	Yes	Cochaperone Protein	Protein Complex Biogenesis
HOT1	YMR172W	No	Transcription Factor For Glycerol Biosynthetic Genes	Transcription From Rna Polymerase Ii Promoter
CPR7	YJR032W	No	Peptidyl-Prolyl Cis-Trans Isomerase (Cyclophilin)	Miscellaneous
FPK1	YNR047W	No	Ser/Thr Protein Kinase	Response To Chemical
DPB11	YJL090C	Yes	DNA Replication Initiation Protein	Mitotic Cell Cycle
HBT1	YDL223C	No	Shmoo Tip Protein, Substrate Of Hub1P Ubiquitin-Like Protein	Response To Chemical
NOT5	YPR072W	No	Subunit Of Ccr4-Not Global Transcriptional Regulator	Transcription From Rna Polymerase Ii Promoter
POA1	YBR022W	No	Phosphatase That Is Highly Specific For Adp-Ribose 1''-Phosphate	Miscellaneous
TFB2	YPL122C	Yes	Subunit Of Tfiih And Nucleotide Excision Repair Factor 3 Complexes	Transcription From Rna Polymerase Ii Promoter
AAD4	YDL243C	No	Putative Aryl-Alcohol Dehydrogenase	Miscellaneous
GCN5	YGR252W	No	Catalytic Subunit Of Ada And Saga Histone Acetyltransferase Complexes	Transcription From Rna Polymerase Ii Promoter
CSG2	YBR036C	No	Endoplasmic Reticulum Membrane Protein	Lipid Metabolic Process
SUA7	YPR086W	Yes	Transcription Factor Tfiib	Transcription From Rna Polymerase Ii Promoter
RAD61	YDR014W	No	Subunit Of A Complex That Inhibits Sister Chromatid Cohesion	Mitotic Cell Cycle
MCK1	YNL307C	No	Dual-Specificity Ser/Thr And Tyrosine Protein Kinase	Mitotic Cell Cycle
TRM7	YBR061C	No	2'-O-Ribose Methyltransferase	Miscellaneous
ORC1	YML065W	Yes	Largest Subunit Of The Origin Recognition Complex	Miscellaneous
UBX7	YBR273C	No	Ubx (Ubiquitin Regulatory X) Domain-Containing Protein	Proteolysis Involved In Cellular Protein Catabolic Process
DER1	YBR201W	No	Endoplasmic Reticulum Membrane Protein	Proteolysis Involved In Cellular Protein Catabolic Process
RDH54	YBR073W	No	DNA-Dependent Atpase	Cellular Response To DNA Damage Stimulus
LDB18	YLL049W	No	Component Of The Dynactin Complex	Mitotic Cell Cycle
DPB3	YBR278W	No	Third-Largest Subunit Of DNA Polymerase Ii (DNA Polymerase Epsilon)	Chromatin Organization
CBF1	YJR060W	No	Basic Helix-Loop-Helix (Bhlh) Protein	Transcription From Rna Polymerase Ii Promoter
EAF7	YNL136W	No	Subunit Of The Nua4 Histone Acetyltransferase Complex	Transcription From Rna Polymerase Ii Promoter
UBA3	YPR066W	No	Protein That Activates Rub1P (Nedd8) Before Neddylation	Protein Modification By Small Protein Conjugation Or Removal
PDC1	YLR044C	No	Major Of Three Pyruvate Decarboxylase Isozymes	Carbohydrate Metabolic Process
BZZ1	YHR114W	No	Sh3 Domain Protein Implicated In Regulating Actin Polymerization	Protein Complex Biogenesis
RPS19B	YNL302C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
PEF1	YGR058W	No	Penta-Ef-Hand Protein	Mitotic Cell Cycle
ALT1	YLR089C	No	Alanine Transaminase (Glutamic Pyruvic Transaminase)	Miscellaneous
LIN1	YHR156C	No	Non-Essential Component Of U5 Snrnp	Biological_Process
CAF120	YNL278W	No	Part Of The Ccr4-Not Transcriptional Regulatory Complex	Transcription From Rna Polymerase Ii Promoter
PCP1	YGR101W	No	Mitochondrial Serine Protease	Regulation Of Organelle Organization
SRN2	YLR119W	No	Component Of The Escrt-I Complex	Protein Targeting
RPS4B	YHR203C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
ALG6	YOR002W	No	Alpha 1,3 Glucosyltransferase	Lipid Metabolic Process
RAS1	YOR101W	No	Gtpase Involved In G-Protein Signaling In Adenylate Cyclase Activation	Signaling
AIM32	YML050W	No	Putative Protein Of Unknown Function	Biological_Process
DCC1	YCL016C	No	Subunit Of A Complex With Ctf8P And Ctf18P	Mitotic Cell Cycle
STI1	YOR027W	No	Hsp90 Cochaperone	Miscellaneous
RGA1	YOR127W	No	Gtpase-Activating Protein For Polarity-Establishment Protein Cdc42P	Response To Chemical
PSP2	YML017W	No	Asn Rich Cytoplasmic Protein That Contains Rgg Motifs	Biological_Process
PEX34	YCL056C	No	Protein That Regulates Peroxisome Populations	Miscellaneous
WHI2	YOR043W	No	Protein Required For Full Activation Of The General Stress Response	Cytoskeleton Organization
LCB4	YOR171C	No	Sphingoid Long-Chain Base Kinase	Signaling
AIM34	YMR003W	No	Protein Of Unknown Function	Biological_Process
PET18	YCR020C	No	Protein Of Unknown Function	Miscellaneous

VAM10	YOR068C	No	Protein Involved In Vacuole Morphogenesis	Miscellaneous
NPT1	YOR209C	No	Nicotinate Phosphoribosyltransferase	Miscellaneous
PEX12	YMR026C	No	C3Hc4-Type Ring-Finger Peroxin And E3 Ubiquitin Ligase	Protein Targeting
STM1	YLR150W	No	Protein Required For Optimal Translation Under Nutrient Stress	Signaling
WHI5	YOR083W	No	Repressor Of G1 Transcription	Transcription From Rna Polymerase Ii Promoter
PUS7	YOR243C	No	Pseudouridine Synthase	Miscellaneous
ARG80	YMR042W	No	Transcription Factor Involved In Regulating Arginine-Responsive Genes	Transcription From Rna Polymerase Ii Promoter
SWI6	YLR182W	No	Transcription Cofactor	Transcription From Rna Polymerase Ii Promoter
CPA1	YOR303W	No	Small Subunit Of Carbamoyl Phosphate Synthetase	Miscellaneous
ECM5	YMR176W	No	Subunit Of The Snt2C Complex	Response To Chemical
YKE2	YLR200W	No	Subunit Of The Heterohexameric Gim/Prefoldin Protein Complex	Transcription From Rna Polymerase Ii Promoter
DGK1	YOR311C	No	Diacylglycerol Kinase	Lipid Metabolic Process
UBP12	YJL197W	No	Ubiquitin-Specific Protease	Biological_Process
SGS1	YMR190C	No	Nucleolar DNA Helicase Of The Recq Family	Mitotic Cell Cycle
CLB4	YLR210W	No	B-Type Cyclin Involved In Cell Cycle Progression	Mitotic Cell Cycle
LDB19	YOR322C	No	Protein Involved In Ubiquitin-Dependent Endocytosis	Miscellaneous
MNN11	YJL183W	No	Subunit Of A Golgi Mannosyltransferase Complex	Carbohydrate Metabolic Process
CLN1	YMR199W	No	G1 Cyclin Involved In Regulation Of The Cell Cycle	Regulation Of Cell Cycle
MSC3	YLR219W	No	Protein Of Unknown Function	Organelle Fission
MIP1	YOR330C	No	Mitochondrial DNA Polymerase	Miscellaneous
SET2	YJL168C	No	Histone Methyltransferase With A Role In Transcriptional Elongation	Chromatin Organization
RAD14	YMR201C	No	Protein That Recognizes And Binds Damaged DNA During Ner	Cellular Response To DNA Damage Stimulus
RSA3	YLR221C	No	Protein With A Likely Role In Ribosomal Maturation	Miscellaneous
UBC11	YOR339C	No	Ubiquitin-Conjugating Enzyme	Protein Modification By Small Protein Conjugation Or Removal
HAL5	YJL165C	No	Putative Protein Kinase	Protein Phosphorylation
DBP7	YKR024C	No	Putative Atp-Dependent Rna Helicase Of The Dead-Box Family	Miscellaneous
PMS1	YNL082W	No	Atp-Binding Protein Required For Mismatch Repair	Cellular Response To DNA Damage Stimulus
DOT6	YER088C	No	Protein Involved In Rrna And Ribosome Biogenesis	Transcription From Rna Polymerase Ii Promoter
MUD1	YBR119W	No	U1 Snrnp A Protein	Miscellaneous
KTR2	YKR061W	No	Mannosyltransferase Involved In N-Linked Protein Glycosylation	Carbohydrate Metabolic Process
HMO1	YDR174W	No	Chromatin Associated High Mobility Group (Hmg) Family Member	Transcription From Rna Polymerase Ii Promoter
RIC1	YLR039C	No	Protein Involved In Retrograde Transport To The Cis-Golgi Network	Miscellaneous
ARL1	YBR164C	No	Soluble Gtpase With A Role In Regulation Of Membrane Traffic	Protein Targeting
HEL2	YDR266C	No	Ring Finger Ubiquitin Ligase (E3)	Chromatin Organization
RPL17B	YJL177W	No	Ribosomal 60S Subunit Protein L17B	Miscellaneous
CUE4	YML101C	No	Protein Of Unknown Function	Biological_Process
RTK1	YDL025C	No	Putative Protein Kinase, Potentially Phosphorylated By Cdc28P	Biological_Process
	YDR306C	No	F-Box Protein Of Unknown Function	Proteolysis Involved In Cellular Protein Catabolic Process
ERP1	YAR002C-A	No	Member Of The P24 Family Involved In Er To Golgi Transport	Golgi Vesicle Transport
PHO84	YML123C	No	High-Affinity Inorganic Phosphate (Pi) Transporter	Miscellaneous
PEX19	YDL065C	No	Chaperone And Import Receptor For Newly-Synthesized Class I Pmps	Protein Targeting
UBX5	YDR330W	No	Ubx Domain-Containing Protein That Interacts With Cdc48P	Proteolysis Involved In Cellular Protein Catabolic Process
TEC1	YBR083W	No	Transcription Factor Targeting Filamentation Genes And Ty1 Expression	Transcription From Rna Polymerase Ii Promoter
	YMR111C	No	Protein Of Unknown Function	Biological_Process
UBX3	YDL091C	No	Subunit Of The Dsc Ubiquitin Ligase Complex	Biological_Process
CAP2	YIL034C	No	Beta Subunit Of The Capping Protein Heterodimer (Cap1P And Cap2P)	Protein Complex Biogenesis
SNT1	YCR033W	No	Subunit Of The Set3C Deacetylase Complex	Chromatin Organization
SUT2	YPR009W	No	Putative Transcription Factor Of The Zn2Cys6 Family	Transcription From Rna Polymerase Ii Promoter
YHP1	YDR451C	No	Homeobox Transcriptional Repressor	Transcription From Rna Polymerase Ii Promoter
AGE2	YIL044C	No	Adp-Ribosylation Factor (Arf) Gtpase Activating Protein (Gap) Effector	Golgi Vesicle Transport
TPS2	YDR074W	No	Phosphatase Subunit Of The Trehalose-6-P Synthase/Phosphatase Complex	Carbohydrate Metabolic Process
MCM16	YPR046W	No	Component Of The Ctf19 Complex And The Coma Subcomplex	Mitotic Cell Cycle
PAC11	YDR488C	No	Dynein Intermediate Chain, Microtubule Motor Protein	Mitotic Cell Cycle
ICE2	YIL090W	No	Integral Er Membrane Protein With Type-Iii Transmembrane Domains	Protein Complex Biogenesis
APT1	YML022W	No	Adenine Phosphoribosyltransferase	Miscellaneous
	YPR063C	No	Er-Localized Protein Of Unknown Function	Biological_Process
PSP1	YDR505C	No	Asn And Gln Rich Protein Of Unknown Function	Biological_Process
SYG1	YIL047C	No	Plasma Membrane Protein Of Unknown Function	Signaling
HMG1	YML075C	No	Hmg-Coa Reductase	Lipid Metabolic Process
MED1	YPR070W	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
ARC1	YGL105W	No	Protein That Binds Trna And Methionyl- And Glutamyl-Trna Synthetases	Miscellaneous
BUD27	YFL023W	No	Unconventional Prefoldin Protein Involved In Translation Initiation	Protein Complex Biogenesis
MBF1	YOR298C-A	No	Transcriptional Coactivator	Transcription From Rna Polymerase Ii Promoter
ASR1	YPR093C	No	Ubiquitin Ligase That Modifies And Regulates Rna Pol Ii	Response To Chemical
MON1	YGL124C	No	Protein Required For Cvt-Vesicle/Autophagosome Fusion With The Vacuole	Protein Targeting
AGX1	YFL030W	No	Alanine:Glyoxylate Aminotransferase (Agt)	Miscellaneous
COS6	YGR295C	No	Protein Of Unknown Function	Biological_Process
MTC1	YJL123C	No	Protein Of Unknown Function That May Interact With Ribosomes	Biological_Process
SOH1	YGL127C	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
HAC1	YFL031W	No	Basic Leucine Zipper (Bzip) Transcription Factor (Atf/Creb1 Homolog)	Transcription From Rna Polymerase Ii Promoter
SSM4	YIL030C	No	Ubiquitin-Protein Ligase Involved In Er-Associated Protein Degradation	Proteolysis Involved In Cellular Protein Catabolic Process
ALB1	YJL122W	No	Shuttling Pre-60S Factor	Miscellaneous
SNT2	YGL131C	No	Subunit Of Snt2C Complex, Ring Finger Ubiquitin Ligase (E3)	Transcription From Rna Polymerase Ii Promoter
REX4	YOL080C	No	Putative Rna Exonuclease	Miscellaneous
FAR10	YLR238W	No	Protein Involved In Recovery From Arrest In Response To Pheromone	Response To Chemical
ESC2	YDR363W	No	Sumo-Like Domain Protein	Mitotic Cell Cycle
UBP5	YER144C	No	Putative Ubiquitin-Specific Protease	Protein Modification By Small Protein Conjugation Or Removal
CIN2	YPL241C	No	Gtpase-Activating Protein (Gap) For Cin4P	Protein Complex Biogenesis
SEC22	YLR268W	No	R-Snare Protein	Golgi Vesicle Transport
RVS167	YDR388W	No	Actin-Associated Protein With Roles In Endocytosis And Exocytosis	Miscellaneous
PHB2	YGR231C	No	Subunit Of The Prohibitin Complex (Phb1P-Phb2P)	Miscellaneous
APL5	YPL195W	No	Delta Adaptin-Like Subunit Of The Clathrin Associated Protein Complex	Protein Targeting
	YLR312C	No	Putative Protein Of Unknown Function	Biological_Process
ARO80	YDR421W	No	Zinc Finger Transcriptional Activator Of The Zn2Cys6 Family	Transcription From Rna Polymerase Ii Promoter
NCL1	YBL024W	No	S-Adenosyl-L-Methionine-Dependent Trna: M5C-Methyltransferase	Response To Chemical
CUP9	YPL177C	No	Homeodomain-Containing Transcriptional Repressor	Transcription From Rna Polymerase Ii Promoter
RPA14	YDR156W	No	Rna Polymerase I Subunit A14	Miscellaneous
SPF1	YEL031W	No	P-Type Atpase, Ion Transporter Of The Er Membrane	Miscellaneous
SHP1	YBL058W	No	Ubx (Ubiquitin Regulatory X) Domain-Containing Protein	Mitotic Cell Cycle
RRD2	YPL152W	No	Peptidyl-Prolyl Cis/Trans-Isomerase	Mitotic Cell Cycle
SAS4	YDR181C	No	Subunit Of The Sas Complex (Sas2P, Sas4P, Sas5P)	Miscellaneous
MAK10	YEL053C	No	Non-Catalytic Subunit Of N-Terminal Acetyltransferase Of The Natc Type	Miscellaneous
	YBL081W	No	Non-Essential Protein Of Unknown Function	Biological_Process
HHO1	YPL127C	No	Histone H1, Linker Histone With Roles In Meiosis And Sporulation	DNA Recombination
GTB1	YDR221W	No	Glucosidase Ii Beta Subunit, Forms A Complex With Alpha Subunit Rot2P	Carbohydrate Metabolic Process
YND1	YER005W	No	Apyrase With Wide Substrate Specificity	Carbohydrate Metabolic Process
CDH1	YGL003C	No	Activator Of Anaphase-Promoting Complex/Cyclosome (Apc/C)	Mitotic Cell Cycle
	YPL113C	No	Glyoxylate Reductase	Miscellaneous
MDS3	YGL197W	No	Putative Component Of The Tor Regulatory Pathway	Signaling
CAJ1	YER048C	No	Nuclear Type Ii J Heat Shock Protein Of The E. Coli DNAj Family	Miscellaneous
CWH41	YGL027C	No	Processing Alpha Glucosidase I	Carbohydrate Metabolic Process
RPS6B	YBR181C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
OST5	YGL226C-A	No	Zeta Subunit Of The Oligosaccharyltransferase Complex Of The Er Lumen	Carbohydrate Metabolic Process
VTC1	YER072W	No	Subunit Of The Vacuolar Transporter Chaperone (Vtc) Complex	Miscellaneous
BEM1	YBR200W	No	Protein Containing Sh3-Domains	Response To Chemical

	YGL242C	No	Putative Protein Of Unknown Function	Biological_Process
SYF2	YGR129W	No	Member Of The Nineteen Complex (Ntc)	Miscellaneous
YBP2	YGL060W	No	Central Kinetochore Associated Protein	Mitotic Cell Cycle
PDB1	YBR221C	No	E1 Beta Subunit Of The Pyruvate Dehydrogenase (Pdh) Complex	Miscellaneous
RTG2	YGL252C	No	Sensor Of Mitochondrial Dysfunction	Transcription From Rna Polymerase Ii Promoter
CHO2	YGR157W	No	Phosphatidylethanolamine Methyltransferase (Pemt)	Lipid Metabolic Process
AFT1	YGL071W	No	Transcription Factor Involved In Iron Utilization And Homeostasis	Transcription From Rna Polymerase Ii Promoter
SLX1	YBR228W	No	Endonuclease Involved In DNA Recombination And Repair	Miscellaneous
ZRT1	YGL255W	No	High-Affinity Zinc Transporter Of The Plasma Membrane	Miscellaneous
TRS65	YGR166W	No	Subunit Of Trappii	Protein Complex Biogenesis
	YGL081W	No	Putative Protein Of Unknown Function	Biological_Process
ROT2	YBR229C	No	Glucosidase Ii Catalytic Subunit	Miscellaneous
CUL3	YGR003W	No	Ubiquitin-Protein Ligase	Protein Modification By Small Protein Conjugation Or Removal
PSD2	YGR170W	No	Phosphatidylserine Decarboxylase Of The Golgi And Vacuolar Membranes	Lipid Metabolic Process
GUP1	YGL084C	No	Plasma Membrane Protein Involved In Remodeling Gpi Anchors	Lipid Metabolic Process
UBP11	YKR098C	No	Ubiquitin-Specific Protease	Biological_Process
BUB2	YMR055C	No	Mitotic Exit Network Regulator	Mitotic Cell Cycle
PTK2	YJR059W	No	Putative Serine/Threonine Protein Kinase	Mitotic Cell Cycle
MED6	YHR058C	Yes	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
CRN1	YLR429W	No	Coronin	Protein Complex Biogenesis
CCS1	YMR038C	No	Copper Chaperone For Superoxide Dismutase Sod1P	Miscellaneous
RDI1	YDL135C	No	Rho Gdp Dissociation Inhibitor	Regulation Of Organelle Organization
TFB1	YDR311W	Yes	Subunit Of Tfiih And Nucleotide Excision Repair Factor 3 Complexes	Transcription From Rna Polymerase Ii Promoter
FRE4	YNR060W	No	Ferric Reductase	Miscellaneous
RIM15	YFL033C	No	Protein Kinase Involved In Cell Proliferation In Response To Nutrients	Response To Chemical
UFD2	YDL190C	No	Ubiquitin Chain Assembly Factor (E4)	Response To Chemical
RSC3	YDR303C	Yes	Component Of The Rsc Chromatin Remodeling Complex	Transcription From Rna Polymerase Ii Promoter
ILM1	YJR118C	No	Protein Of Unknown Function	Miscellaneous
SMI1	YGR229C	No	Protein Involved In The Regulation Of Cell Wall Synthesis	Mitotic Cell Cycle
HHT2	YNL031C	No	Histone H3	Mitotic Cell Cycle
MPE1	YKL059C	Yes	Essential Conserved Subunit Of Cpf Cleavage And Polyadenylation Factor	Miscellaneous
CTK3	YML112W	No	Gamma Subunit Of C-Terminal Domain Kinase I	Protein Phosphorylation
CSE2	YNR010W	No	Subunit Of The Rna Polymerase Ii Mediator Complex	Transcription From Rna Polymerase Ii Promoter
RPB2	YOR151C	Yes	Rna Polymerase Ii Second Largest Subunit B150	Transcription From Rna Polymerase Ii Promoter
RPL35A	YDL191W	No	Ribosomal 60S Subunit Protein L35A	Miscellaneous
ECM21	YBL101C	No	Protein Involved In Regulating Endocytosis Of Plasma Membrane Proteins	Miscellaneous
CDC4	YFL009W	Yes	F-Box Protein Required For Both The G1/S And G2/M Phase Transitions	Mitotic Cell Cycle
WHI4	YDL224C	No	Putative Rna Binding Protein	Miscellaneous
RPS27B	YHR021C	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
CHS3	YBR023C	No	Chitin Synthase Iii	Meiotic Cell Cycle
ARP7	YPR034W	Yes	Component Of Both The Swi/Snf And Rsc Chromatin Remodeling Complexes	Transcription From Rna Polymerase Ii Promoter
RAD57	YDR004W	No	Protein That Stimulates Strand Exchange	Cellular Response To DNA Damage Stimulus
MRPL10	YNL284C	No	Mitochondrial Ribosomal Protein Of The Large Subunit	Miscellaneous
FAT1	YBR041W	No	Very Long Chain Fatty Acyl-Coa Synthetase And Fatty Acid Transporter	Lipid Metabolic Process
CDC16	YKL022C	Yes	Subunit Of The Anaphase-Promoting Complex/Cyclosome (Apc/C)	Protein Modification By Small Protein Conjugation Or Removal
RPS11A	YDR025W	No	Protein Component Of The Small (40S) Ribosomal Subunit	Miscellaneous
MMS4	YBR098W	No	Subunit Of Structure-Specific Mms4P-Mus81P Endonuclease	Cellular Response To DNA Damage Stimulus
ECM2	YBR065C	No	Pre-Mrna Splicing Factor	Miscellaneous
CHK1	YBR274W	No	Serine/Threonine Kinase And DNA Damage Checkpoint Effector	Cellular Response To DNA Damage Stimulus
BUD3	YCL014W	No	Protein Involved In Bud-Site Selection	Mitotic Cell Cycle
ECM8	YBR076W	No	Non-Essential Protein Of Unknown Function	Biological_Process
UBR2	YLR024C	No	Cytoplasmic Ubiquitin-Protein Ligase (E3)	Protein Modification By Small Protein Conjugation Or Removal
DUG2	YBR281C	No	Component Of Glutamine Amidotransferase (Gatase Ii)	Miscellaneous
TMA23	YMR269W	No	Nucleolar Protein Implicated In Ribosome Biogenesis	Miscellaneous
FPR1	YNL135C	No	Peptidyl-Prolyl Cis-Trans Isomerase (Ppiase)	Chromatin Organization
VPS53	YJL029C	No	Component Of The Garp (Golgi-Associated Retrograde Protein) Complex	Golgi Vesicle Transport
SSH1	YBR283C	No	Subunit Of The Ssh1 Translocon Complex	Protein Targeting
LSM7	YNL147W	No	Lsm (Like Sm) Protein	Miscellaneous
TEP1	YNL128W	No	Pten Homolog With No Demonstrated Inositol Lipid Phosphatase Activity	Meiotic Cell Cycle
RIM8	YGL046W	No	Merged Open Reading Frame	Miscellaneous
RIM8	YGL045W	No	Protein Involved In Proteolytic Activation Of Rim101P	Miscellaneous
LAG1	YHL003C	No	Ceramide Synthase Component	Lipid Metabolic Process

Query strains

NOTE: Gene description taken from the SGD Database (March 17th, 2007). Essentiality status taken from Saccharomyces Genome Deletion Project.
NOTE: The Primary Functional category was defined by the the top ranked GO term in the list of the 25 most frequently found GO slim terms (taken from SGD) for all array and query genes.

Gene	ORF	Essential?	Description	Primary Functional Category
ASF1	YJL115W	No	Nucleosome Assembly Factor	Histone Modification
RTT101	YJL047C	No	Cullin Subunit Of A Roc1P-Dependent E3 Ubiquitin Ligase Complex	Proteolysis Involved In Cellular Protein Catabolic Process
NUP133	YKR082W	No	Subunit Of Nup84P Subcomplex Of Nuclear Pore Complex (Npc)	Protein Targeting
RTT109	YLL002W	No	Histone Acetyltransferase	Histone Modification
RAD5	YLR032W	No	DNA Helicase/Ubiquitin Ligase	Protein Modification By Small Protein Conjugation Or Removal
RAD52	YML032C	No	Protein That Stimulates Strand Exchange	DNA Recombination
SGS1	YMR190C	No	Nucleolar DNA Helicase Of The Recq Family	DNA Recombination
MRE11	YMR224C	No	Nuclease Subunit Of The Mrx Complex With Rad50P And Xrs2P	DNA Recombination
YKU70	YMR284W	No	Subunit Of The Telomeric Ku Complex (Yku70P-Yku80P)	DNA Recombination
RPD3	YNL330C	No	Histone Deacetylase, Component Of Both The Rpd3S And Rpd3L Complexes	DNA Recombination
TOF1	YNL273W	No	Subunit Of A Replication-Pausing Checkpoint Complex	DNA Repair
PSY2	YNL201C	No	Subunit Of Protein Phosphatase Pp4 Complex	Signaling
HTZ1	YOL012C	No	Histone Variant H2Az	Chromatin Organization
HST3	YOR025W	No	Member Of The Sir2 Family Of Nad(+)-Dependent Protein Deacetylases	Histone Modification
EXO1	YOR033C	No	5'-3' Exonuclease And Flap-Endonuclease	DNA Recombination
ARP8	YOR141C	No	Nuclear Actin-Related Protein Involved In Chromatin Remodeling	DNA Recombination
RAD17	YOR368W	No	Checkpoint Protein	DNA Recombination
MRC1	YCL061C	No	S-Phase Checkpoint Protein Required For DNA Replication	Regulation Of Cell Cycle
DCC1	YCL016C	No	Subunit Of A Complex With Ctf8P And Ctf18P	Organelle Fission
RAD18	YCR066W	No	E3 Ubiquitin Ligase	Protein Modification By Small Protein Conjugation Or Removal
BRE1	YDL074C	No	E3 Ubiquitin Ligase	DNA Recombination
SLX5	YDL013W	No	Subunit Of The Slx5-Slx8 Sumo-Targeted Ubiquitin Ligase Complex	Protein Modification By Small Protein Conjugation Or Removal
PPH3	YDR075W	No	Catalytic Subunit Of Protein Phosphatase Pp4 Complex	DNA Recombination
UBC13	YDR092W	No	E2 Ubiquitin-Conjugating Enzyme	Protein Modification By Small Protein Conjugation Or Removal
RAD9	YDR217C	No	DNA Damage-Dependent Checkpoint Protein	Regulation Of Cell Cycle
SWR1	YDR334W	No	Swi2/Snf2-Related Atpase	Chromatin Organization
DOT1	YDR440W	No	Nucleosomal Histone H3-Lys79 Methylase	DNA Recombination
SLX8	YER116C	No	Subunit Of Slx5-Slx8 Sumo-Targeted Ubiquitin Ligase (Stubl) Complex	Protein Modification By Small Protein Conjugation Or Removal
RAD24	YER173W	No	Checkpoint Protein	DNA Recombination
SAE2	YGL175C	No	Endonuclease Involved In Processesing Hairpin DNA Structures	DNA Recombination
RSC1	YGR056W	No	Component Of The Rsc Chromatin Remodeling Complex	DNA Repair
DDC1	YPL194W	No	DNA Damage Checkpoint Protein	DNA Recombination
mec1-100	YBR136W	yes	Genome integrity checkpoint protein and PI kinase superfamily member	cellular response to DNA damage stimulus
rfa1-t11	YAR007C	yes	Subunit of heterotrimeric Replication Protein A (RPA)	cellular response to DNA damage stimulus
sgs1-r1	YMR190C	no	RecQ family nucleolar DNA helicase	mitotic cell cycle

CURRICULUM VITAE

Davidsbodenstrasse 34
CH-4056 Basel
Switzerland
T: +41 61 5344190

Friedrich Miescher Institute for Biomedical Research
Maulbeerstrasse 66
CH-4058 Basel
Switzerland
T: +41 61 697 5583

nicole.hustedt@fmi.ch

EDUCATION

GRADUATE STUDIES

since 6/2010 — PhD thesis
Thesis advisor: Susan M. Gasser
Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland
Title: Regulation of Mec1 (ATR) signalling in budding yeast

UNDERGRADUATE STUDIES

4/2009 - 12/2009 — Diploma thesis
Thesis advisor: Silke Hauf
Friedrich Miescher Laboratory of the Max Planck Society, Tuebingen, Germany
Title: Aurora B function in the spindle assembly checkpoint

10/2004 - 12/2009 — Degree in biochemistry (core areas: immunology, pharmaceutical chemistry, cell biology, structural biology, protein biochemistry)
Eberhard Karls University, Tübingen, Germany
Grade: 1.0 on a scale of 1 (best) to 6 (worst)

SCHOOL

06/2004 — A level (Abitur) in biology, chemistry, politics and latin
Hermann-Billung-Gymnasium, Celle, Germany
Grade: 1.0 on a scale of 1 (best) to 6 (worst), best of class

SCIENTIFIC EXPERIENCE

since 6/2010 — **PhD student**, group of Susan Gasser
Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland
Topic: Regulation of Mec1 (ATR) signalling in budding yeast
Techniques used: budding yeast genetics, molecular biology (PCR, cloning, mutagenesis), biochemistry (radioactivity and non-radioactivity based *in vitro* kinase assays), cell biological techniques (immunoblotting, immunoprecipitation, yeast-two-hybrid assay, chromatin immunoprecipitation) tissue culture (culturing of cancer cell lines, transfection, gene knockdown with siRNA oligos, FACS), high-throughput techniques (yeast genetic interaction screen, suppressor screen, non-labelled phosphoproteomics), programming in *R* (basic knowledge)

4/2009 - 05/2010 — **Diploma student/research assistant**, group of Silke Hauf
Friedrich Miescher Laboratory of the Max Planck Society, Tuebingen, Germany
Topic: Aurora B function in the spindle assembly checkpoint
Techniques used: fission yeast genetics, cell biological techniques (immunoblotting, immunoprecipitation, immunostaining, protein sample preparation for mass spectrometry), microscopy (wide field fluorescence imaging of living and fixed cells)

08/2008 - 09/2008 **internship**, group of Stefan Stevanović
Department of Immunology, Eberhard Karls University, Tuebingen, Germany
Topic: Methods in immunology

04/2008 - 03/2009 **research assistant**, group of Silke Hauf
Friedrich Miescher Laboratory of the Max Planck Society, Tuebingen, Germany
Topic: Creating analog-sensitive kinase alleles

02/2008 - 03/2008 **lab rotation**, group of Klaus Wanner
Department of Pharmaceutical Chemistry, Ludwigs Maximilian University, Munich
Topic: Establishment of a LC-MS/MS method for quantification of substances in biological matrices

11/2007 - 01/2008 **lab rotation**, group of Stefan Jentsch
Department of Molecular Cell Biology MPI for Biochemistry, Martinsried, Germany
Topic: Genetic and biochemical analysis of Mgs1 in DNA damage bypass

10/2007 - 11/2007 **lab rotation**, group of Reinhard Fässler
Department of Molecular Medicine, MPI for Biochemistry, Martinsried, Germany
Topic: Generation of αv integrin fluorescent reporter protein constructs

04/2007 - 09/2007 **research assistant**, group of Andrei Lupas
Department of Protein Evolution, MPI for Developmental Biology, Tübingen, Germany
Topic: Isolation of chaperone proteins

11/2006 - 12/2006 **research assistant**, group of Volker Lipka
Center for Plant Molecular Biology, Eberhard Karls University Tübingen, Germany
Topic: Molecular biological work in *A. thaliana* and *E. coli*

PUBLICATIONS

Hustedt N, Seeber A, , Sack R, Tsai M, Bhupinder B, van Leeuwen F, Guenole A, van Attikum H, Srivas R, Ideker T, Shimada K, Gasser SM
Yeast PP4 interacts with ATR homologue Ddc2-Mec1 and regulates checkpoint signaling.
in revision at Molecular Cell

Seeber A*, Hegnauer A*, **Hustedt N**, van Leeuwen F, van Attikum H, Srivas R, Ideker T, Pasero P, Vogel M, Amsler P, Thomae N, Shimada K, Gasser SM
RFA1 recruits MRX to forks and double strand breaks in budding yeast. *in preparation*
*These authors contributed equally to this work

Hustedt, N., and Shimada, K. (2014). Analyzing DNA replication checkpoint in budding yeast. ***Methods Mol Biol*** 1170, 321-341.

Heinrich S, Sewart K, Windecker H, Langegger M, Schmidt N, **Hustedt N**, Hauf S (2014) Mad1 contribution to spindle assembly checkpoint signalling goes beyond presenting Mad2 at kinetochores. ***EMBO Rep*** 15: 291-298

Hustedt N, Gasser SM, Shimada K (2013) Replication Checkpoint: Tuning and Coordination of Replication Forks in S Phase. ***Genes*** 4: 388-434

Hegnauer AM*, **Hustedt N***, Shimada K, Pike BL, Vogel M, Amsler P, Rubin SM, van Leeuwen F, Guenole A, van Attikum H, Thoma NH, Gasser SM (2012) An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. ***EMBO J*** 31: 3768-3783
*These authors contributed equally to this work.

Heinrich S, Windecker H, **Hustedt N**, Hauf S (2012) Mph1 kinetochore localization is crucial and upstream in the hierarchy of spindle assembly checkpoint protein recruitment to kinetochores. ***J Cell Sci*** 125: 4720-4727

CONFERENCE PRESENTATIONS

Abcam conference on Maintenance of Genome Stability 2014, St Kitts
Title: Protein Phosphatase 4: A new player in ATR/Mec1 regulation. (talk)

Cold Spring Harbor Eukaryotic DNA Replication & Genome Maintenance meeting 2013,
Cold Spring Harbor, USA
Title: Genetic and physical interaction between the ATR kinase and PP4 phosphatase in yeast. (poster)

Keystone symposium on Genomic Instability and DNA Repair 2013, Banff, Canada
Title: Mec1 checkpoint kinase regulation by the PP4 phosphatase. (poster)

Yeast Systems Biology Workshop 2012
Fribourg, Switzerland

Swiss meeting on Genome Stability and Chromatin Dynamics 2012, Weggis, Switzerland
Title: Exploring the S-phase function of the Mec1 checkpoint kinase: Genetic and biochemical analysis of a S-phase defective Mec1 mutant. (poster)

Cold Spring Harbor Eukaryotic DNA Replication & Genome Maintenance meeting 2011
Cold Spring Harbor, USA
Title: Mec1 dependent phosphorylation of Sgs1 facilitates replication checkpoint activation by direct interaction with Rad53 at stalled forks. (poster)

TEACHING EXPERIENCE

02/2014 - 03/2014	Supervising and teaching undergraduate student in yeast genetics and molecular biology techniques
06/2012 - 08/2012	Supervising and teaching undergraduate student in yeast genetics and molecular biology techniques
04/2006 - 07/2006	Teaching a practical course in chemistry for students of human medicine

GRANTS

2013	**travel grant from Swiss Society for Molecular and Cellular Biosciences** to to attend a scientific conference

PROFESSIONAL MEMBERSHIPS

since 03/2012	Swiss Society for Molecular and Cellular Biosciences
06/2010 - 10/2012	Image DNA damage response (EU training network)

OTHER SKILLS / INTERESTS

SOFT SKILLS

02/2014	Project Management Workshopt Friedrich Miescher Institute, Basel, Switzerland
08/2012	Team Work, Carreer planning and Leadership Competencies Workshop Friedrich Miescher Institute, Basel, Switzerland
06/2012	Effective Scientific Communication Workshop University of Basel, Basel, Switzerland

ORGANIZATION SKILLS

since 11/2011	Initiation and organization of literature seminar (Journal Club)
since 06/2010	Organization of lab events (lab hikes, ski days)

LANGUANGE SKILLS:

German:	native speaker
English:	fluent
Spanish:	basic knowledge
Latin:	advanced certificate (Großes Latinum)

NON-SCIENTIFIC INTERESTS:

Outdoor Sports (hiking, climbing, alpine skiing)
Running (e.g. Dreilaenderlauf 2011- 13, Lucerne Marathon 2011)

Dr. Susan Gasser

Friedrich Miescher Institute for Biomedical Research
Maulbeerstrasse 66
P.O. Box 3775
4002 Basel
Switzerland
T: +41 61 69 75025

susan.gasser@fmi.ch

Dr. John Diffley

London Research Institute
44 Lincoln's Inn Fields
London
WC2A 3LY
United Kingdom
T: +44 1707 625869

john.diffley@cancer.org.uk

Dr. Silke Hauf

Virginia Bioinformatics Institute
1015 Life Science Circle (MC 0477)
Blacksburg, VA 24061
United States
T: +1 540 231 7318

silke.hauf@vt.edu

Dr. Fred van Leeuwen

The Netherlands Cancer Institute
Postbus 90203
1006 BE Amsterdam
The Netherlands
31 20 512 1973

fred.v.leeuwen@nki.nl

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