Supplemental Fig. S1. The occupancies of Rad6, Bre1 and Lge1 in UAS region of the *PMA1* gene. ChIP analyses were carried out in cells TAP-tagged with Rad6, Bre1, or Lge1 at the indicated region of *PMA1* gene. The quantitated results are graphed at the bottom

Supplemental Table 1. *Saccharomyces cerevisiae* strains used in this study. Individual TAP-tagged and deletion strains were obtained from Open Biosystems or Euroscarf. For gene disruptions, the indicated gene was deleted by high efficiency transformation of a PCR product amplified from genomic DNA containing the target gene of interest, which had been replaced by the *KanMX4* gene (Euroscarf). All deletion strains and genomically tagged strains were confirmed by PCR and/or Western blot analysis.

Strain	Genotype	Reference of source
BY4741	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0*	-
YKH045	*MATa ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	(31)
YKH046	*MAT*a, *ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, pRS314 [Flag-*htb1*-K123R-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	(31)
YKH047	*MAT*a, *ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, *ubp8*::*KanMX4*, pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	(31)
YKL142	*MAT*a, *ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, *sgf11*::*LEU2*, pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	(31)
YKL143	*MAT*a, *ura3-1 leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, *gcn5*::*LEU2* pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	(31)
SY082	*MAT*a, *ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, *rad6*::*KanMX4*, pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	This study
SY083	*MAT*a, *ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, *bre1*::*KanMX4*, pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4*-URA3 Integrative]	This study
SY084	*MAT*a, *ura3-1, leu2-3,112, trp1-1, his3-11,15, ade2-1, htb1-1, htb2-1*, *lge1*::*KanMX4*, pRS314 [Flag-*HTB1*-CEN-*TRP1*], pRG145 [GAPDHprom-3HA-*UBI4-URA3* Integrative]	This study
FY067	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, RAD6*-TAP tag::*HIS3MX6*	Open Biosystems
FY068	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, BRE1*-TAP tag::*HIS3MX6*	Open Biosystems

FY089	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, UBP8*-TAP tag::*HIS3MX6*	Open Biosystems
FY168	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, LGE1*-TAP tag::*HIS3MX6*	Open Biosystems
FY090	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, SGF11*-TAP tag::*HIS3MX6*	Open Biosystems
SY197	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, RAD6*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study
SY198	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, BRE1*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study
SY199	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, UBP8*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study
FY280	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, GCN5*-TAP tag::*HIS3MX6*	Open Biosystems
FY281	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, TAF6*-TAP tag::*HIS3MX6*	Open Biosystems
FY282	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, SPT8*-TAP tag::*HIS3MX6*	Open Biosystems
SY275	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, SGF11*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study
SY276	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, GCN5*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study
SY277	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, TAF6*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study
SY278	*MAT*a, *ura3Δ0, leu2Δ0, his3Δ1, met15Δ0, SPT8*-TAP tag::*HIS3MX6*, *lge1Δ*::*KanMX4*	This study

Supplemental Table 2. Oligonucleotides used in this study.

Name (Location, ATG: +1)	Primer position in Fig. 1A	Sequence	Reference or source
PMA1-UAS-for (-927 ~ -906)	UAS	GAAACGGAGAAACATAAACAGG	(14, 15)
PMA1-UAS-rev (-697 ~ -678)	UAS	GTCTCGAGGCCTGGAAGTGC	(14, 15)
PMA1-PRO-for (-371 ~ -348)	1	GGTACCGCTTATGCTCCCCTCCAT	(14, 15)
PMA1-PRO-rev (-115 ~ -90)	1	CTTTTGAATGTGTGTATAAAAGAGAG	(14, 15)
PMA1-CDS1-for (168 ~ 190)	2	CGACGACGAAGACAGTGATAACG	(14, 15)
PMA1-CDS1-rev (349 ~ 376)	2	ATTGAATTGGACCGACGAAAAACATAAC	(14, 15)
PMA1-CDS2-for (584 ~ 608)	3	AAGTCGTCCCAGGTGATATTTTGCA	(14, 15)
PMA1-CDS2-rev (784 ~ 807)	3	AACGAAAGTGTTGTCACCGGTAGC	(14, 15)
PMA1-CDS4-for (2018 ~ 2045)	5	CTATTATTGATGCTTTGAAGACCTCCAG	(14, 15)
PMA1-CDS4-rev (2263 ~ 2290)	5	TGCCCAAAATAATAGACATACCCCATAA	(14, 15)
PMA1-3UTR2-for (3287 ~ 3313)	7	GAAAATATTTGGTATCTTTGCAAGATG	(14, 15)
PMA1-3UTR2-rev (3474 ~ 3500)	7	GTAAATTTGTATACGTTCATGTAAGTG	(14, 15)
ADH1-PRO-for (-236 ~ -213)	1	TTCCTTCCTTCATTCACGCACACT	(14, 15)
ADH1-PRO-rev (-39 ~ -14)	1	GTTGATTGTATGCTTGGTATAGCTTG	(14, 15)
ADH1-CDS-for (844 ~ 871)	2	TTCAACCAAGTCGTCAAGTCCATCTCTA	(14, 15)
ADH1-CDS-rev (987 ~ 1013)	2	ATTTGACCCTTTTCCATCTTTTCGTAA	(14, 15)
ADH1-3UTR-for (1231 ~ 1254)	3	ACCGGCATGCCGAGCAAATGCCTG	(14, 15)
ADH1-3UTR-rev (1378 ~ 1400)	3	CCCAACTGAAGGCTAGGCTGTGG	(14, 15)
GAL10-PRO1-for (-393 ~ -374)	1	TTACTGCCAATTTTTCCTCT	This study
GAL10-PRO1-rev (-151 ~ -133)	1	GAGCCCCATTATCTTAGCC	This study
GAL10-PRO2-for (-58 ~ -37)	2	TTAAACTTCTTTGCGTCCATCC	This study
GAL10-PRO2-rev (161-182)	2	TGCTTGGTCAAGACCTCTAACC	This study
GAL10-CDS1-for (401-424)	3	CTTCTGCTACTGTCTATGGTGATG	This study
GAL10-CDS1-rev (667-687)	3	CTTCTCGCGCCTACCAACAGC	This study

GAL10-CDS2-for (823-844)	4	TGTCGTGAGTGGAACTTGGGTT	This study
GAL10-CDS2-rev (1084-1108)	4	GCATATCTTCAGCGGAAAATCTGGC	This study
GAL10-CDS3-for (1869-1892)	5	TGTCAAGGCTTTTCATCCCGATTC	This study
GAL10-CDS3-rev (2057-2078)	5	TTGGACCCGTAAGTTTCACCGT	This study
*ChrV NO-ORF-for	-	GGCTGTCAGAATATGGGGCCGTAGTA	(14, 15)
*ChrV NO-ORF-rev	-	CACCCCGAAGCTGCTTTCACAATAC	(14, 15)

*These primers were used for the amplification of a non-transcribed region of chromosome V.