

Supplemental Table 1 *S. cerevisiae* strains used in this study (K. Ohtsuki *et al.*)

Strain	Genotype	Source
Y13.2	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1</i> pYN1/ <i>TAF1</i>	Kokubo <i>et al</i> (1998)
Y22.1	<i>MATα ura3-52 trp1-63 leu2-3,112 Δtaf1</i> pYN1/ <i>TAF1</i>	Kokubo <i>et al</i> (1998)
YTK2741	<i>MATα ura3-52 trp1-63 leu2-3,112 Δtaf1</i> pM1169/ <i>TAF1</i>	Takahata <i>et al</i> (2004)
YTK3780	<i>MATα ura3-52 trp1-63 leu2-3,112 Δtaf1</i> pM1747/ <i>taf1-T657K</i>	this study
YTK6760	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF2::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6761	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF3::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6762	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF4::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6763	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF5::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6764	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF6::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6765	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF7::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6766	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF8::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6767	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF9::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6768	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF10::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6769	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF11::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6770	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF12::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6771	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF13::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6772	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF14::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6773	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 GCN5::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6779	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 SUA7::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6780	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TFA2::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6781	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TFG1::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6782	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TFB3::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6783	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 SPT15::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6784	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 BUR6::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6785	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 NCB2::3xPK-kanMX6</i> pYN1/ <i>TAF1</i>	this study
YTK6818	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF2::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6819	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF3::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6820	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF4::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6821	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF5::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6822	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF6::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6823	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF7::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6824	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF8::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6825	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF9::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study
YTK6826	<i>MATα ura3-52 trp1-63 leu2-3,112 his3-609 Δtaf1 TAF10::3xPK-kanMX6</i> pM1169/ <i>TAF1</i>	this study

YTK6827	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF11::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6828	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF12::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6829	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF13::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6830	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF14::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6831	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 GCN5::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6837	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 SUA7::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6838	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TFA2::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6839	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TFG1::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6840	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TFB3::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6841	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 SPT15::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6842	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 BUR6::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6843	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 NCB2::3xPK-kanMX6 pM1169/TAF1</i>	this study
YTK6845	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF2::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6846	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF3::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6847	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF4::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6848	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF5::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6849	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF6::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6850	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF7::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6851	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF8::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6852	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF9::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6853	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF10::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6854	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF11::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6855	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF12::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6856	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF13::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6857	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TAF14::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6858	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 GCN5::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6864	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 SUA7::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6865	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TFA2::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6866	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TFG1::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6867	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 TFB3::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6868	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 SPT15::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6869	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 BUR6::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study
YTK6870	<i>MATα ura3-52 trp1-63 leu2-3, 112 his3-609 Δtaf1 NCB2::3xPK-kanMX6 pM1747/taf1-T657K</i>	this study

Supplemental Table 2 Oligonucleotides used in this study (K. Ohtsuki *et al.*)

Number	Sequence
TK178	5'-TTAACCATCTTTTAAAGGTTGGACAAACTTT-3'
TK4234	5'-AAGGGGGTGGTTTAGTTTAGTAGAA-3'
TK4235	5'-TGTTTTATTTTGTGTA AAAAGTA-3'
TK6352	5'-AGATCGTTTATGGTTAAGATAAGAACAAGAATGATGCTAAGAATATCTCCGGTTCTG CTGCTAGT-3'
TK6353	5'-ATGTATTTGTATAAAATATGATATTACTCAGACTCAAGCAAACAACGTCGACCTCGAG GCCAGAAG-3'
TK6354	5'-AGCACATTTCAACGTCGAACCTCACTAGATTATGGGGTACTTTATCTCCGGTTCTG CTGCTAGT-3'
TK6355	5'-AAATATGGATGAGATAATGACGAAAGAAAATGCAGAAATGTCGTTCTCGACCTCGAG GCCAGAAG-3'
TK6356	5'-AGCGTTCAGACTATTATTTCAAAGGGTTATGCCAAGATCAGAGATATCTCCGGTTCTG CTGCTAGT-3'
TK6357	5'-AACACTATACCTTTAAATATTATAGACAGTATAAGAGATGAGCAACGTCGACCTCGAG GCCAGAAG-3'
TK6358	5'-TTCAGCAGAAGCAATTTAGCCCTTGCCAGGAGGTGCTTTCAGGCCAATCTCCGGTTCTG CTGCTAGT-3'
TK6359	5'-ACTTATTACATATCACTTCCATGCTGTTATTTTTTTCAGTGTGAACGTCGACCTCGAGG CCAGAAG-3'
TK6360	5'-AGAGACGACGCAAAGAATTAATTAGTGCGATATTTTTTGCGAAATCTCCGGTTCTG CTGCTAGT-3'
TK6361	5'-GTTATATAACATTACCGTTGTACTATTAGTATAAACCGATTCTCACGTCGACCTCGAGG CCAGAAG-3'
TK6362	5'-AACGATCTCGATATGATGATGCTATTTGGTGCAGAGGGTGATGAGATCTCCGGTTCTG CTGCTAGT-3'
TK6363	5'-GAGTCGTATAGTGATAAGAGTAATATATAGATGATAAAGAGAACCGTCGACCTCGAG GCCAGAAG-3'
TK6364	5'-ACATCTCCTCCTGCAGATATAGCCACAGATCACGATATAACTATGATCTCCGGTTCTG CTGCTAGT-3'
TK6365	5'-TATTATTATATTAGGGACAAACACTGGTTCACTGAAAGCAGTTGTCGTCGACCTCGAG GCCAGAAG-3'
TK6366	5'-TGTCTCACAGCGAAGGAGTGGGACCTTGAGGACCCAAAGTCTATGATCTCCGGTTCT GCTGCTAGT-3'
TK6367	5'-CGGAAGAACTTGATTTAGTGACTTATGATATATAAGCGGTGCATCGTCGACCTCGAG GCCAGAAG-3'
TK6368	5'-GTTGCTGAATACGGGCTCAATATAGGTCGCCAGACTTTTATCGTATCTCCGGTTCTG CTGCTAGT-3'
TK6369	5'-CATACTGCTACACTATATACATATTTTCAATTCATTTGTTAGCCACGTCGACCTCGAGG CCAGAAG-3'
TK6370	5'-GCTTACTGGAGAACTCAAGGAGAAGGGCAGGGATCCATGTTCCAGAATCTCCGGTTCT GCTGCTAGT-3'
TK6371	5'-TATATAGATTGATATATGTTGGAGCCGTTGGACAATTATGGGCAGCGTCGACCTCGAG GCCAGAAG-3'
TK6372	5'-GCAAAAAACAATGGAAACAATGTTGCAAGCTTGAATACAAAAAAATCTCCGGTTCTG CTGCTAGT-3'
TK6373	5'-TTAGGAATTTTTTCTGTGGAAGAGTGGAGAATGTGGGTAACATAACGTCGACCTCGAG GCCAGAAG-3'
TK6374	5'-AAGATTAGGAAGCAGGGGCCTAAAAACCTCAAGAAAAACAAAAAAATCTCCGGTTCTG CTGCTAGT-3'
TK6375	5'-ATATCTGAATCAAGCCTACGTAAACGGGCCTGCCAAGTAGCTATACGTCGACCTCGAG GCCAGAAG-3'
TK6376	5'-GGATTATTGAAAAGTCTATGGGACTACGTTAAGAAAAATACCGAGATCTCCGGTTCTGC TGCTAGT-3'
TK6377	5'-TTATACAAACATAAAAAGCGCGCATTAAACGCCCTTTTACCTTTTACGTCGACCTCGAGG CCAGAAG-3'
TK6378	5'-AATAATAAAGTAAAAGAAATACCTGAATATTCTCACCTTATTGATATCTCCGGTTCTGCT GCTAGT-3'
TK6379	5'-TTTCTTCTTCGAAAGGAATAGTAGCGGAAAAGCTTCTTCTACGCACGTCGACCTCGAG GCCAGAAG-3'
TK6382	5'-ATCTCCGGTTCTGCTGCT-3'
TK6383	5'-CGTCGACCTCGAGGCCAG-3'

TK6745 5'-GGTGAGATAATCGAATTG-3'
TK6746 5'-TCTGAACATGGATCCCTG-3'
TK6747 5'-CTGCCATAATTGTCCAA-3'
TK6748 5'-CGAGGAGGAATTCCAATG-3'
TK6749 5'-CACCGGTAGCTTATAGAT-3'
TK6750 5'-TTTTTTTGTATTCAAGCT-3'
TK6751 5'-TTATGTTACCCACATTCT-3'
TK6752 5'-GAATGATTTGCAGCGGTG-3'
TK6905 5'-AGAGAAGACTTGTGGCGA-3'
TK6906 5'-ATTCTTAGCATCATTCTT-3'
TK6907 5'-TTGTTTGCTTGAGTCTGA-3'
TK6908 5'-CTCAGTTTCGACAGTTCA-3'
TK6909 5'-ACAACGTATAAACATGAT-3'
TK6910 5'-AAAGTAACCCCAATC-3'
TK6911 5'-AACGACATTTCTGCATTT-3'
TK6912 5'-CTAAACCCTCTACTAATG-3'
TK6913 5'-AGTGCCTGCGAAAATAT-3'
TK6914 5'-ATCTCTGATCTTGGCATA-3'
TK6915 5'-TTGCTCATCTCTTATACT-3'
TK6916 5'-CTCAAATTCTTCATCCTC-3'
TK6917 5'-TCACATATATCCATTAAG-3'
TK6918 5'-TGGCCTGAAAGCACCTCC-3'
TK6919 5'-TTCACACTGAAAAAATA-3'
TK6920 5'-GGTTTAGTGCTGGAGGCG-3'
TK6921 5'-GCATCTTTGTTGGACTAT-3'
TK6922 5'-TTCGCCAAAAATATCGC-3'
TK6923 5'-TGAGAATCGGTTTATACT-3'
TK6924 5'-TACGCCTACATGAACGTG-3'
TK6925 5'-CTGCTGGTGGGGAAAGTG-3'
TK6926 5'-CTCATCACCCCTCTGCACC-3'
TK6927 5'-GTTCTCTTTATCATCTAT-3'
TK6928 5'-TTGAACCTTTGTGGCAAG-3'
TK6929 5'-TACCTAAGGTCCAGAAGT-3'
TK6930 5'-CATAGTTATATCGTGATC-3'
TK6931 5'-ACAACCTGCTTTTCAAGTAA-3'
TK6932 5'-AAATGATATAAAGAGATA-3'
TK6933 5'-AGAAAAGACTAGAGGACT-3'
TK6934 5'-CATAGACTTTGGGTCCCTC-3'
TK6935 5'-ATGCACCGCTTATATATC-3'
TK6936 5'-TGAAGTTGCTCCGTTATC-3'
TK6937 5'-GCAGAAAACATGAAGAAG-3'
TK6938 5'-ACGATAAAAGTCTGGGCG-3'
TK6939 5'-TGGCTAACAAATGGAAAT-3'
TK6940 5'-AATCAGTAAGAGAAGTTT-3'
TK6941 5'-ATGTCTAGGAAGCTGAAA-3'
TK6942 5'-TTTTTTTGTCTTTCTTGAG-3'
TK6943 5'-TATAGCTACTTGGCAGGC-3'
TK6944 5'-TCCTGCGGTAAGTTATTT-3'
TK6945 5'-AAGGTTGGGGTGGATTTT-3'
TK6946 5'-CTCGGTATTTTTCTTAAC-3'
TK6947 5'-TAAAAGGTAAAAGGGCGT-3'
TK6948 5'-GATTCACATGGGCAAAAT-3'
TK6949 5'-TGCGAAGAAAAATAAGAA-3'
TK6950 5'-ATCAATAAGGTGAGAATA-3'
TK6951 5'-TGCGTAGAAGAAGCTTTT-3'
TK6952 5'-TGGTTATCAACTTTTCCA-3'
TK7112 5'-GATTGGTTGCAGACGTGC-3'
TK7114 5'-CTGGCCTCGAGGTCGACGAGTGATAAACAGTAAAT-3'
TK7115 5'-CAAACATGCCTGGTATGC-3'
TK7117 5'-AGCAGCAGAACCGGAGATTACTCTATGGGAATAATC-3'
TK7118 5'-CTGGCCTCGAGGTCGACGGGTTGTTTTGATTAAATC-3'
TK7119 5'-TTGATAGCACAGTGGAAA-3'
TK7120 5'-AGAGAATGAATCGCCCGT-3'
TK7121 5'-AGCAGCAGAACCGGAGATCTCTTTCTTTAATTCCAT-3'
TK7122 5'-CTGGCCTCGAGGTCGACGGTTAGTTTATAATGTTAT-3'

TK7123 5'-CTGGAAGAGAATACTTAA-3'
TK7124 5'-AGATAGAAAGTTTCGAAC-3'
TK7125 5'-AGCAGCAGAACCGGAGATAAGCTCCTCGGATATAAC-3'
TK7126 5'-CTGGCCTCGAGGTCGACGAACATCAGGATAGTGTGC-3'
TK7478 5'-TTTCCACCTACGATGTCC-3'
TK7479 5'-GGTAGATGGTTGCATTTTC-3'
TK7772 5'-ACAAAACATTGTGGCAAC-3'
TK7773 5'-AGCAGCAGAACCGGAGATCATTTTTCTAAATTC-3'
TK7774 5'-CTGGCCTCGAGGTCGACGTGGGGAAGGAGTAGACGA-3'
TK7775 5'-AAAGCCAACAACAAGCTG-3'
TK7884 5'-ATGGCAGATCAAGTACCA-3'
TK7885 5'-AGCAGCAGAACCGGAGATGGCACTCTTCTCCTCCGG-3'
TK7886 5'-CTGGCCTCGAGGTCGACGGCAGAACGGGGCGATGTA-3'
TK7887 5'-TCCTTTGGCACTTGAAAG-3'
TK7888 5'-ATGGCTGGAGACTCCGAT-3'
TK7889 5'-AGCAGCAGAACCGGAGATAGAAGAATCCTCCGACTT-3'
TK7890 5'-CTGGCCTCGAGGTCGACGATAGAAGCTTCTAAACAA-3'
TK7891 5'-GAAACCGTGATGCTGTTA-3'
TK8413 5'-CGACTTAGTTCGGAAAATATTTCC-3'
TK8414 5'-GGCCGTCATAATTCTTATATATGC-3'
TK9359 5'-AGCAGCAGAACCGGAGATTTTTCTTTTCAACGCCCGG-3'
TK9483 5'-ATATGCTACGAATTTCCACCATG-3'
TK9484 5'-GTCCGTTTCATGTATATTCATCTC-3'
TK9487 5'-CTTTTCTTTCTGGCATTTCGTTTC-3'
TK9488 5'-AAGTTAATGGTGTATTCACGAGTG-3'
TK9493 5'-TAAGTTTACGCGGACCCAAAATTC-3'
TK9494 5'-ACGGTTAATTCAGTGGACATCTTG-3'
TK9497 5'-CGCATTGATTGATATCGTTTTCTC-3'
TK9498 5'-CTCGTGGTACGTACCATTTTTATC-3'
TK9501 5'-CTAGCGTTTTGTTTTGGTACTAC-3'
TK9502 5'-CTGCTTTCAAAAATTTAGCCATGG-3'
TK9614 5'-TCACATAATAGGTAGCTTAAATTG-3'
TK9615 5'-AGTCTTTATTATTTTGTTCATCTC-3'
TK10334 5'-TGTGTATGGTTTTCTTTTTTTGG-3'
TK10335 5'-TACGAGGTATTTACTAAACATTGG-3'
TK10475 5'-CAAATACTACCTTGGTTGGTTATC-3'
TK10476 5'-TAGCAGACATTGTATGTGTGTATG-3'

Supplemental Figure 1. Expression of non-tagged Rpb1 (pol II), HA-Taf1 (TFIID), PK-Taf2-14 (TFIID and/or SAGA), PK-TBP (TFIID), PK-Sua7 (TFIIB), PK-Tfa2 (TFIIE), PK-Tfg1 (TFIIF), PK-Tfb3 (TFIIH), PK-Gcn5 (SAGA), PK-Ncb2 (NC2) and PK-Bur6 (NC2) in yeast strains that were used in this study.

Specifically, yeast strains expressing HA-Taf1 (YTK2741), PK-Taf2 (YTK6760), PK-Taf3 (YTK6761), PK-Taf4 (YTK6762), PK-Taf5 (YTK6763), PK-Taf6 (YTK6764), PK-Taf7 (YTK6765), PK-Taf8 (YTK6766), PK-Taf9 (YTK6767), PK-Taf10 (YTK6768), PK-Taf11 (YTK6769), PK-Taf12 (YTK6770), PK-Taf13 (YTK6771), PK-Taf14 (YTK6772), PK-TBP (YTK6783), PK-Sua7 (YTK6779), PK-Tfa2 (YTK6780), PK-Tfg1 (YTK6781), PK-Tfb3 (YTK6782), PK-Gcn5 (YTK6773), PK-Ncb2 (YTK6785) and PK-Bur6 (YTK6784) were grown in YPD medium to mid-log phase at 25°C. Whole cell extracts were prepared with a cracking buffer (1) and then analyzed by immunoblotting using the primary antibodies indicated at the bottom. The percentage of polyacrylamide in the gel used for isocratic or gradient SDS-polyacrylamide gel electrophoresis (SDS-PAGE) is also shown at the bottom. Size markers (kDa) are indicated to the left of each panel. Note that the expression of Rpb1 and HA-Taf1 was examined for the same extract derived from YTK2741.

Supplemental Figure 2. Growth comparison of epitope-tagged strains at 25 and 37 °C. Strains expressing HA-tagged *TAF1* (YTK2741) alone or in combination with PK-tagged *TAF2* (YTK6760), PK-tagged *TAF3* (YTK6761), PK-tagged *TAF4* (YTK6762), PK-tagged *TAF5* (YTK6763), PK-tagged *TAF6* (YTK6764), PK-tagged *TAF7* (YTK6765), PK-tagged *TAF8* (YTK6766), PK-tagged *TAF9* (YTK6767), PK-tagged *TAF10* (YTK6768), PK-tagged *TAF11* (YTK6769), PK-tagged *TAF12* (YTK6770), PK-tagged *TAF13* (YTK6771), PK-tagged *TAF14* (YTK6772), PK-tagged *SUA7* (YTK6779), PK-tagged *TFA2* (YTK6780), PK-tagged *TFG1* (YTK6781), PK-tagged *TFB3* (YTK6782), PK-tagged *GCN5* (YTK6773), PK-tagged *SPT15(TBP)*

(YTK6783), PK-tagged *BUR6* (YTK6784) or PK-tagged *NCB2* (YTK6785), were grown on YPD plates for 2 days at the indicated temperatures.

Supplemental Figure 3. A control experiment for sequential chromatin immuno-precipitation analysis conducted for Figure 3.

A. Strains expressing either HA-tagged *TAF1* (YTK2741) or PK-tagged *GCN5* (YTK6773), or both (YTK6831), were used for this experiment. Chromatin immuno-precipitation was performed successively with anti-HA and anti-PK monoclonal antibodies as described in Figure 3. **B.** The results obtained for the promoters of two ribosomal protein genes (i.e., *RPL10* and *RPL35A*) and *POL1*-ORF (negative control) are summarized here. Significant occupancy of both Taf1 and Gcn5 at these promoters was observed for YTK6831 (#3), but not for YTK2741 (#1) or YTK6773 (#2), indicating that the signals detected in Figure 3 are specific.

Supplemental Figure 4. Cluster analysis of factor localization on chromosomes III, IV and V in wild-type strains.

Each column represents a single ChIP-chip experiment conducted for a factor shown above the column. Each row represents “fold change value” (signal log₂ ratio as scaled in a color from “red” to “blue” as shown at the top) for a given probe set. Primary data were obtained using Affymetrix microarray Suite software version 5.0 as described in “Experimental Procedures” and are summarized in Supplemental Figures 5, 6 and 7. Hierarchical clustering analysis was performed with Genesis software (2) using average linkage algorithm and euclidean distance as a measure of similarity.

Supplemental Figure 5. Localization of a complete set of Tafs (Taf1-Taf14), other GTFs (TBP, Sua7, Tfa2, Tfg1 and Tfb3), SAGA (Gcn5), NC2 (Bur6 and Ncb2) and pol II (Rpb1) on chromosome III.

Localization of each factor (indicated at left, orange signal) was compared with that of Rpb1 (blue signal) by generating merged images for the entire region of chromosome III as described in Figure 1. ChIP analysis was also conducted as described in Figure 1. Note that it is difficult to compare directly the localization of TBP (top panel) to those of other factors (the rest panels) because TBP occupancy signals at class II promoters were less significantly detected in our system due to the much stronger signals at class III promoters. Because of this technical limitation, TBP occupancy signals were not analyzed further and not compared with those of other factors in this study.

Supplemental Figure 6. Localization of a complete set of Tafs (Taf1-Taf14), other GTFs (TBP, Sua7, Tfa2, Tfg1 and Tfb3), SAGA (Gcn5), NC2 (Bur6 and Ncb2) and pol II (Rpb1) on chromosome IV.

Localization of each factor (indicated at left, orange signal) was compared with that of Rpb1 (blue signal) on chromosome IV as described in Supplemental Figure 5.

Supplemental Figure 7. Localization of a complete set of Tafs (Taf1-Taf14), other GTFs (TBP, Sua7, Tfa2, Tfg1 and Tfb3), SAGA (Gcn5), NC2 (Bur6 and Ncb2) and pol II (Rpb1) on chromosome V.

Localization of each factor (indicated at left, orange signal) was compared with that of Rpb1 (blue signal) on chromosome V as described in Supplemental Figure 5.

Supplemental Figure 8. Effects of *taf1-T657K* mutation on the localization of a complete set of Tafs (Taf1-Taf14), other GTFs (TBP, Sua7, Tfa2, Tfg1 and Tfb3), SAGA (Gcn5), NC2 (Bur6 and Ncb2) and pol II (Rpb1) on chromosome III.

Localization of each factor (indicated at left) was compared in wild-type (orange bars) and *taf1-T657K* (blue bars) strains by generating merged images for the entire region of chromosome III as described in Figure 4. ChIP analysis was conducted as described in

Figure 4. The numbers at the top and bottom connected by a vertical line indicate a locus where the occupancy signal(s) can be significantly detected for at least one factor (except TBP) and correspond to the numbers in Supplemental Table 3 (on the far left side) where the effects of *taf1-T657K* mutation on the occupancy of all factors were scored at five levels and summarized. The regions of ARS (autonomously replicating sequence) and/or CEN (centromere) are marked with pink rectangles.

Supplemental Figure 9. Effects of *taf1-T657K* mutation on the localization of a complete set of Tafs (Taf1-Taf14), other GTFs (TBP, Sua7, Tfa2, Tfg1 and Tfb3), SAGA (Gcn5), NC2 (Bur6 and Ncb2) and pol II (Rpb1) on chromosome IV.

Localization of each factor (indicated at left) was compared in wild-type (orange bars) and *taf1-T657K* (blue bars) strains on chromosome IV as described in Supplemental Figure 8.

Supplemental Figure 10. Effects of *taf1-T657K* mutation on the localization of a complete set of Tafs (Taf1-Taf14), other GTFs (TBP, Sua7, Tfa2, Tfg1 and Tfb3), SAGA (Gcn5), NC2 (Bur6 and Ncb2) and pol II (Rpb1) on chromosome V.

Localization of each factor (indicated at left) was compared in wild-type (orange bars) and *taf1-T657K* (blue bars) strains on chromosome V as described in Supplemental Figure 8.

Supplemental Figure 11. Effects of the *taf1-T657K* mutation on the localization of TBP at a subset of class II gene promoters.

Strains expressing HA-tagged *TAF1* (YTK2741) or *taf1-T657K* (YTK3780) alone or in combination with PK-tagged *SPT15* (YTK6841/YTK6868; this depicts *TAF1/taf1-T657K* strains, respectively) were cultured and cross-linked as described in Figure 1. The cross-linked chromatin was prepared and precipitated with anti-PK

monoclonal antibodies as described in Figure 2. After cross-link reversal, quantitative PCR was carried out in triplicate to determine the recovery ratio of DNA corresponding to the promoters of several genes or *POL1* ORF (negative control), as indicated at the bottom of each panel. The average values from three independent experiments with the standard deviations of the ratios of precipitated DNA to the inputs are shown as blue (*TAF1*) or red (*taf1-T657K*) bars in each panel. YTK6841/YTK6868 and YTK2741/YTK3780 strains were used to assess TBP occupancy levels (left panel) and background levels (right panel; untagged strain), respectively.

Supplemental Figure 12. Immunoprecipitation of TFIID via PK-tagged Taf3, PK-tagged Taf4, PK-tagged Taf8 and PK-tagged Taf11.

Yeast strains expressing PK-Taf3 (YTK6819/YTK6846; this depicts *TAF1/taf1-T657K* strains, respectively), PK-Taf4 (YTK6820/YTK6847), PK-Taf8 (YTK6824/YTK6851) and PK-Taf11 (YTK6827/YTK6854) were grown in YPD medium to mid-log phase at 25°C and then shifted to 37°C for further incubation for 2 hrs. Whole cell extracts were prepared as described in Materials and Methods, except that crosslinking and chromatin shearing steps were omitted and the extracts were centrifuged at 15,000 rpm for 30 min (instead of 5 min) at the final step. Immunoprecipitation was conducted as described previously (3) using anti-PK monoclonal antibody. Precipitates were analyzed by immunoblotting using the primary antibodies indicated above each blot (IB).

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