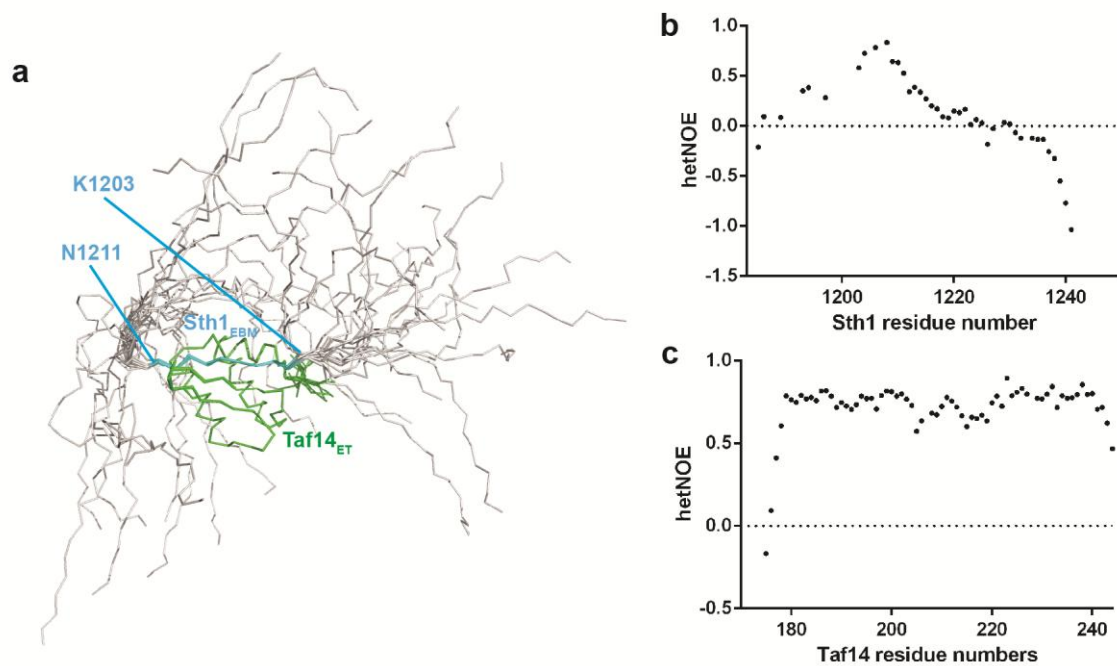


Supplementary Information

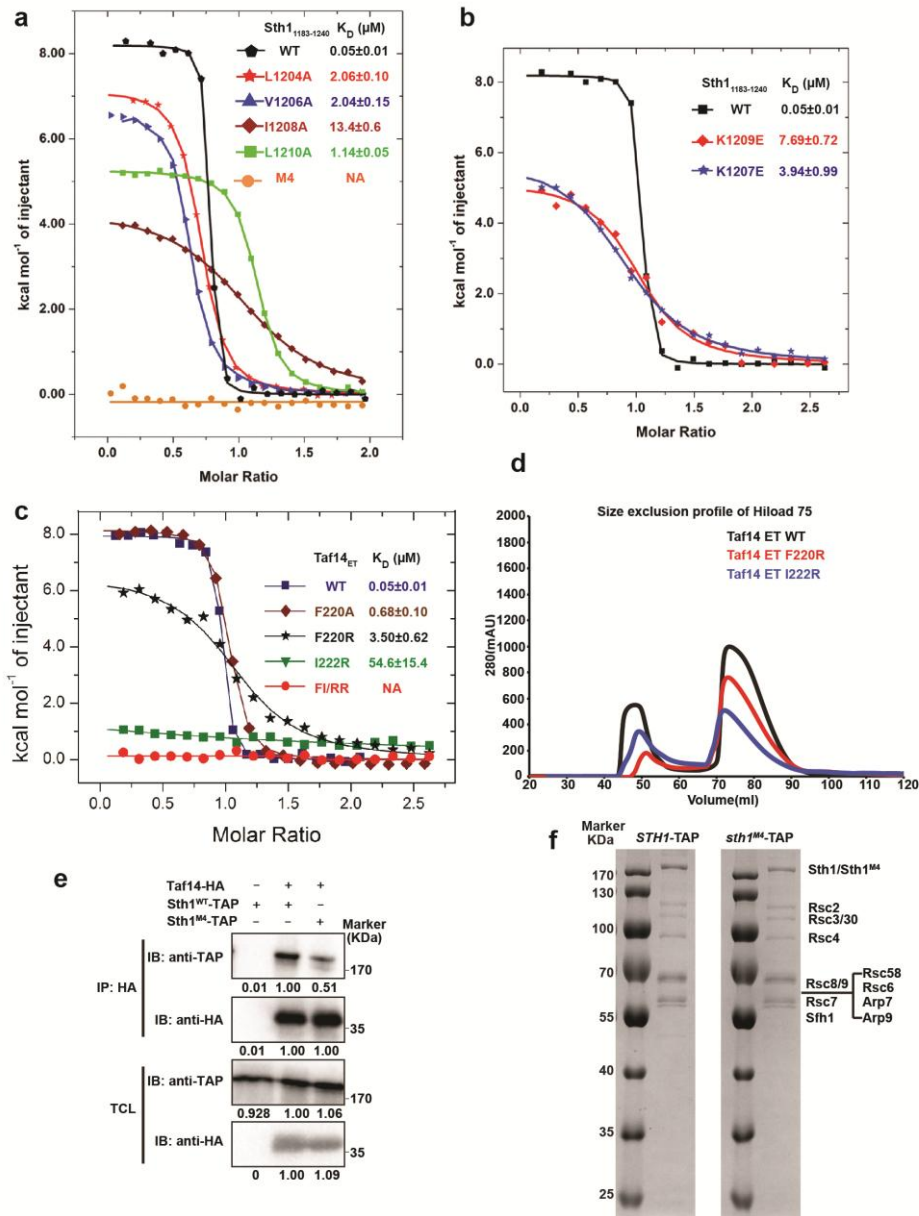
**Taf14 recognizes a common motif in transcriptional machineries and facilitates their  
clustering by phase separation**

Guochao Chen, Duo Wang, Bin Wu et al.



### Supplementary Figure 1. NMR analyses of Taf14<sub>ET</sub>-Sth1<sub>EBM</sub> complex

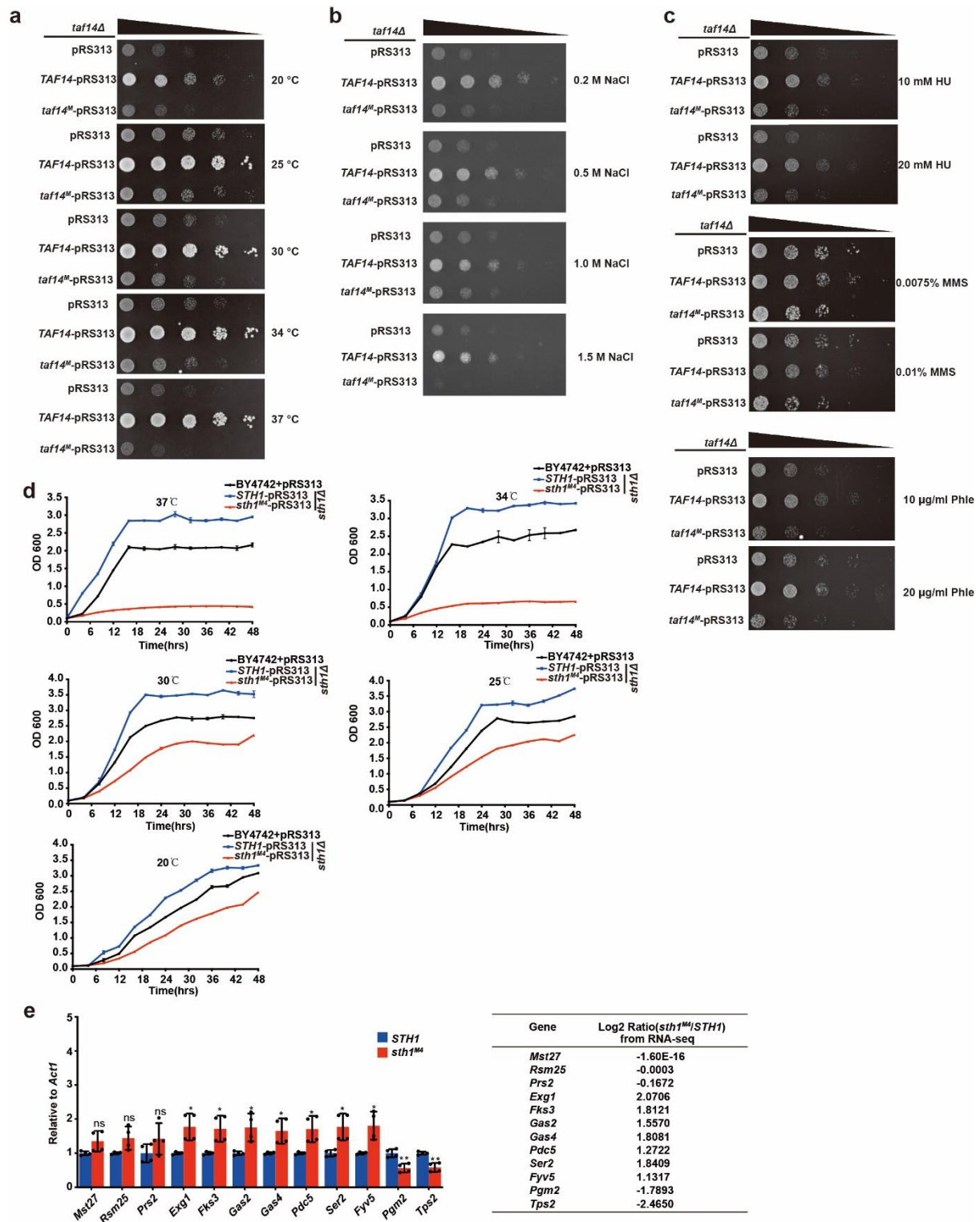
- The ensemble of the 20 lowest energy conformers of the Taf14<sub>ET</sub>-Sth1<sub>EBM</sub> complex. Taf14<sub>ET</sub> is shown in green. The core regions of Sth1<sub>EBM</sub> converge from K1203 to N1211. Other parts of Sth1<sub>EBM</sub> are flexible.
- Heteronuclear NOE values measured at 25 °C for <sup>15</sup>N-labeled Sth1<sub>EBM</sub> in complex with unlabeled Taf14<sub>ET</sub>.
- Heteronuclear NOE values measured at 25 °C for <sup>15</sup>N-labeled Taf14<sub>ET</sub> in complex with unlabeled Sth1<sub>EBM</sub>.



**Supplementary Figure 2. Mutation analyses of Taf14-Sth1 complex.**

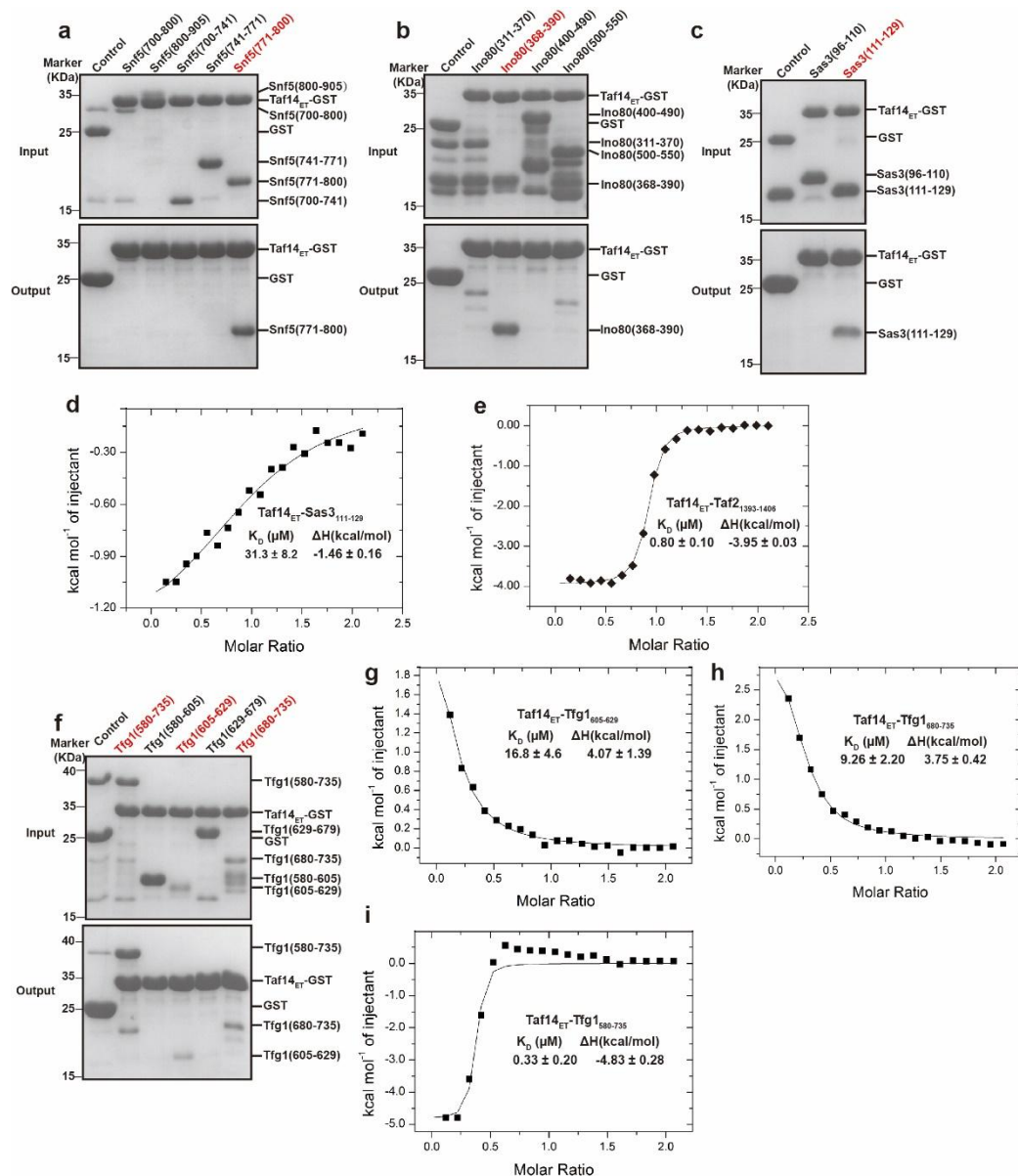
- ITC assays show that mutations of hydrophobic residues of Sth1 decrease the interaction between Taf14<sub>ET</sub> and Sth1<sub>EBM</sub>.
- ITC assays show that mutations of positively charged residues of Sth1 decrease the interaction between Taf14<sub>ET</sub> and Sth1<sub>EBM</sub>.
- ITC assays show that mutations of hydrophobic residues of Taf14 decrease the interaction between Taf14<sub>ET</sub> and Sth1<sub>EBM</sub>.

- d. Gel-filtration profiles of Taf14<sub>ET</sub> mutations showed that these mutations did not affect the overall structural integrity of Taf14<sub>ET</sub>.
- e. Another batch of co-immunoprecipitation experiment using an HA antibody showed that Sth1<sup>M4</sup> mutation weakened the interaction with Taf14. Taf14 was tagged with HA; Sth1 was tagged with TAP. TCL, total cell lysate; IP, immunoprecipitation; IB, immune-blot.
- f. TAP purification shows that *sth1*<sup>M4</sup> mutation does not affect the integrity of the RSC complex.



Supplementary Figure 3. Functional analyses of Taf14 and Sth1 mutations in yeast cells.

- a. Spotting assays with *taf14* $\Delta$  and *taf14*<sup>M</sup> strains compared with WT strains at various temperatures. The *taf14*<sup>M</sup> is Taf14 F220R/I222R mutation that disrupts Sth1<sub>EBM</sub> binding. The *taf14* $\Delta$  and *taf14*<sup>M</sup> strains showed growth defects at all the temperatures.
- b. Spotting assays with *taf14* $\Delta$  and *taf14*<sup>M</sup> strains compared with WT strains on plates containing different NaCl concentrations at 30 °C. The *taf14* $\Delta$  and *taf14*<sup>M</sup> strains showed growth defects at all the NaCl concentrations.
- c. Spotting assays with *taf14* $\Delta$  and *taf14*<sup>M</sup> strains compared with WT strains on plates containing indicated DNA-damage agents at 30 °C.
- d. Growth curves at *STH1* and *sth1*<sup>M4</sup> at different temperatures. The *sth1*<sup>M4</sup> mutant showed much delayed growth when the temperature was above 30 °C, but had similar (albeit slightly slow) growth rate compared to the WT strains. Data are presented as mean  $\pm$ SD, n = 3.
- e. The qPCR validation of the RNA-seq results. The change levels from RNA-seq were shown. Error bars represent standard deviations of four replicates. The relative expression level of wild-type *STH1* strain genes was set to 1. \**P* < 0.05; \*\**P* < 0.01; \*\*\**P* < 0.001; \*\*\*\**P* < 0.0001. Two-tailed Student's *t*-test. Data are presented as mean  $\pm$ SD, n = 4.

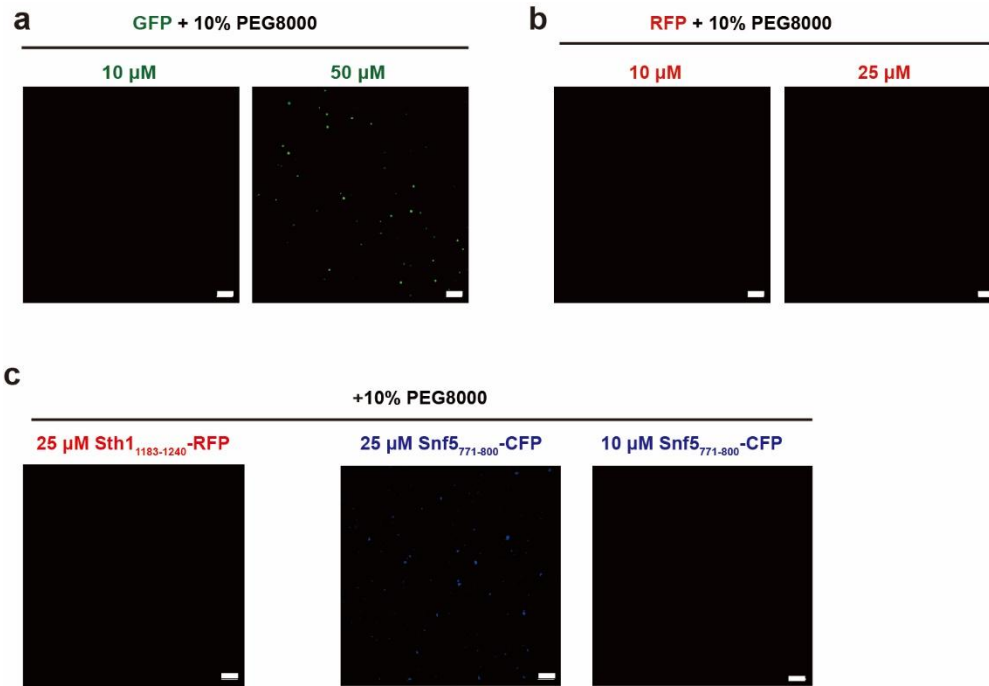


**Supplementary Figure 4. GST pull-down assays to map the Taf14<sub>ET</sub>-binding fragments.**

- Mapping the Taf14<sub>ET</sub>-interaction regions of Snf5. Snf5<sub>771-800</sub> is pulled down by GST-Taf14<sub>ET</sub>. All the Snf5 proteins are Sumo-fusion proteins to increase the visibility of the short peptides on SDS-PAGE. The Snf5 fragment binding Taf14<sub>ET</sub> was labeled red. The input controls were shown as 10% of the total proteins used to pull-down assays.
- Mapping the Taf14<sub>ET</sub>-interaction regions of Ino80. Ino80<sub>368-390</sub> has the strongest interaction with GST-Taf14<sub>ET</sub>. All the Ino80 proteins are Sumo-fusion proteins to

increase the visibility of the short peptides on SDS-PAGE. The Ino80 fragment binding Taf14<sub>ET</sub> was labeled red.

- c. Mapping the Taf14<sub>ET</sub>-interaction regions of Sas3. Sas3<sub>111-129</sub> is pulled down by GST-Taf14<sub>ET</sub>. All the Sas3 proteins are Sumo-fusion proteins to increase the visibility of the short peptides on SDS-PAGE. The Sas3 fragment binding Taf14<sub>ET</sub> was labeled red.
- d. The ITC plot for Sas3<sub>111-129</sub> (1 mM) titrated into Taf14<sub>ET</sub> (0.1 mM). The dissociation constant ( $K_D$ ), enthalpy change ( $\Delta H$ ), and their fitting errors from this ITC plot were shown.
- e. The ITC plot for Taf2<sub>1393-1406</sub> (1 mM) titrated into Taf14<sub>ET</sub> (0.1 mM).
- f. Mapping the Taf14<sub>ET</sub>-interaction regions of Tfg1. Tfg1<sub>605-629</sub> and Tfg1<sub>680-735</sub> have weak interactions with GST-Taf14<sub>ET</sub>, while Tfg1<sub>580-735</sub> has a much stronger interaction with GST-Taf14<sub>ET</sub>. All the Tfg1 proteins are Sumo-fusion proteins to increase the visibility of the short peptides on SDS-PAGE. The Tfg1 fragments binding Taf14<sub>ET</sub> were labeled red.
- g. The ITC plot for Tfg1<sub>605-629</sub> (1 mM) titrated into Taf14<sub>ET</sub> (0.1 mM).
- h. The ITC plot for Tfg1<sub>680-735</sub> (1 mM) titrated into Taf14<sub>ET</sub> (0.1 mM).
- i. The ITC plot for Tfg1<sub>580-735</sub> (1 mM) titrated into Taf14<sub>ET</sub> (0.1 mM).



**Supplementary Figure 5. Phase separation of some control proteins.**

- a. Representative images of GFP at two different concentrations in the droplet formation buffer (25 mM Tris-HCl, pH 8.0, 150 mM NaCl, 10% PEG8000). GFP alone formed small droplets at 50  $\mu$ M concentration, but not at 25 (Fig.5a) or 10  $\mu$ M, so we kept the protein concentration below 25  $\mu$ M in the droplet formation assays.
- b. Representative images of RFP at two different concentrations in the droplet formation buffer (25 mM Tris-HCl, pH 8.0, 150 mM NaCl, 10% PEG8000). At these concentrations, RFP did not form any droplet.
- c. Representative images of Sth1<sub>1183-1240</sub>-RFP and Snf5<sub>771-800</sub>-CFP in the same droplet formation buffer. Sth1<sub>1183-1240</sub>-RFP did not form any droplet at 25  $\mu$ M concentration. It should be noted that Snf5<sub>771-800</sub>-CFP did not form any droplet at 10  $\mu$ M concentration but formed small non-spherical aggregates at 25  $\mu$ M concentration. So in the droplet formation assays with Snf5<sub>771-800</sub>-CFP, the protein concentration was kept below 10  $\mu$ M.

**Supplementary Table 1. *Saccharomyces cerevisiae* strains used in this study.**

Names of strains	Genotype
Fig.2e and Supplementary Fig. 2e, 2f	
BY4742	<i>MAT<math>\alpha</math> his3<math>\Delta</math>1 leu2<math>\Delta</math>0 lys2<math>\Delta</math>0 ura3<math>\Delta</math>0</i>
BY4742-1 ( <i>TAF14-HA</i> )	BY4742 <i>TAF14-3HA::KanMX6</i>
BY4742-2( <i>STH1-TAP/TAF14-HA</i> )	BY4742 <i>STH1-TAP::URA3,TAF14-3HA ::KanMX6</i>
BY4742-2-Cas9 ( <i>STH1-TAP/TAF14-HA</i> )	BY4742 <i>STH1-TAP::URA3,TAF14-3HA::KanMX6, pCas9</i>
BY4742-3 ( <i>sth1<sup>M4</sup>-TAP/TAF14-HA</i> )	BY4742 <i>sth1<sup>M4</sup>-TAP::URA3,TAF14-3HA::KanMX6</i>
Fig. 3a-c, Supplementary Fig. 3d	
BY4742-4 (pRS313)	BY4742, pRS313
BY4742-5 ( <i>STH1</i> -pRS313)	BY haploid <i>sth1<math>\Delta</math> :: KanMX4, pRS313-STH1</i>
BY4742-6 ( <i>sth1<sup>M4</sup></i> -pRS313)	BY haploid <i>sth1<math>\Delta</math> :: KanMX4, pRS313-sth1<sup>M4</sup></i>
Supplementary Figure 3a-c	
BY4742-7 (pRS313)	BY4742 <i>taf14<math>\Delta</math> :: KanMX4, pRS313</i>
BY4742-8 ( <i>TAF14</i> -pRS313)	BY4742 <i>taf14<math>\Delta</math> :: KanMX4, pRS313-TAF14</i>
BY4742-9 ( <i>taf14<sup>M</sup></i> -pRS313)	BY4742 <i>taf14<math>\Delta</math> :: KanMX4, pRS313-taf14<sup>M</sup></i>

**Supplementary Table 2. Plasmids used in this study.**

Names of plasmids	Purpose
Fig. 1	
pet28b-Sth1 <sub>(1183-1359)</sub>	Purification of Sth1 fragments 1183-1259
pet28b-Sth1 <sub>(1183-1240)</sub>	Purification of Sth1 fragments 1183-1240
pet28b-Sth1 <sub>(1248-1359)</sub>	Purification of Sth1 fragments 1248-1359
pet28b-Sth1 <sub>(1199-1225)</sub>	Purification of Sth1 fragments 1199-1225
pGEX6P-1-Taf14 <sub>174-244</sub>	Purification of Taf14 ET domain
Fig. 2 and Supplementary Fig. 2	
pet28b-Sth1 <sub>(1183-1240)</sub> L1204A	Purification of Sth1 <sub>EBM</sub> mutant L1204A
pet28b-Sth1 <sub>(1183-1240)</sub> V1206A	Purification of Sth1 <sub>EBM</sub> mutant V1206A
pet28b-Sth1 <sub>(1183-1240)</sub> I1208A	Purification of Sth1 <sub>EBM</sub> mutant I1208A
pet28b-Sth1 <sub>(1183-1240)</sub> L1210A	Purification of Sth1 <sub>EBM</sub> mutant L1210A
pet28b-Sth1 <sub>(1183-1240)</sub> <sup>M4</sup>	Purification of Sth1 <sub>EBM</sub> <sup>L1204A/V1206A/I1208A/L1210A</sup>
pet28b-Sth1 <sub>(1183-1240)</sub> K1207E	Purification of Sth1 <sub>EBM</sub> mutant K1207E
pet28b-Sth1 <sub>(1183-1240)</sub> K1209E	Purification of Sth1 <sub>EBM</sub> mutant K1209E
pGEX6P-1-Taf14 <sub>174-244</sub> F220A	Purification of Taf14 <sub>ET</sub> mutant F220A
pGEX6P-1-Taf14 <sub>174-244</sub> F220R	Purification of Taf14 <sub>ET</sub> mutant F220R
pGEX6P-1-Taf14 <sub>174-244</sub> I222R	Purification of Taf14 <sub>ET</sub> mutant I222R
pGEX6P-1-Taf14 <sub>174-244</sub> F220R/I222R	Purification of Taf14 <sub>ET</sub> mutant F220R/I222R
Fig. 4 and Supplementary Fig. 4	
pet28b-Sth1 <sub>(700-800)</sub>	Purification of Snf5 fragments with Sumo tag
pet28b-Snf5 <sub>(800-905)</sub>	Purification of Snf5 fragments with Sumo tag
pet28b-Snf5 <sub>(700-741)</sub>	Purification of Snf5 fragments with Sumo tag
pet28b-Snf5 <sub>(771-800)</sub>	Purification of Snf5 fragments with Sumo tag
pet28b-Ino80 <sub>(311-370)</sub>	Purification of Ino80 fragments with Sumo tag
pet28b-Ino80 <sub>(368-390)</sub>	Purification of Ino80 fragments with Sumo tag
pet28b-Ino80 <sub>(400-490)</sub>	Purification of Ino80 fragments with Sumo tag
pet28b-Ino80 <sub>(500-550)</sub>	Purification of Ino80 fragments with Sumo tag
pet28b-Sas3 <sub>(96-110)</sub>	Purification of Sas3 fragments with Sumo tag
pet28b-Sas3 <sub>(111-129)</sub>	Purification of Sas3 fragments with Sumo tag
pet28b-Tfg1 <sub>(580-735)</sub>	Purification of Tfg1 fragments with Sumo tag
pet28b-Tfg1 <sub>(580-605)</sub>	Purification of Tfg1 fragments with Sumo tag
pet28b-Tfg1 <sub>(629-679)</sub>	Purification of Tfg1 fragments with Sumo tag
pet28b-Tfg1 <sub>(680-735)</sub>	Purification of Tfg1 fragments with Sumo tag
Fig. 5 and Supplementary Fig. 5	
pet28b-GFP	Purification of GFP
pet28b-RFP	Purification of RFP
pet28b-CFP	Purification of CFP
pet28b-Taf14 <sub>174-244</sub> -GFP	Purification of Taf14 <sub>ET</sub> with C-terminal GFP
pet28b-Sth1 <sub>(1183-1240)</sub> -RFP	Purification of Sth1 <sub>EBM</sub> with C-terminal RFP
pet28b-Snf5 <sub>(771-800)</sub> -CFP	Purification of Snf5 <sub>EBM</sub> with C-terminal CFP
Fig. 6	
pGEX6P-1-Bdf1 <sub>525-595</sub>	Purification of Bdf1 ET domain with GST tag
pGEX6P-1-Bdf2 <sub>514-585</sub>	Purification of Bdf2 ET domain with GST tag
pGEX6P-1-AF9 <sub>490-568</sub>	Purification of AF9 ET domain with GST tag
pet28b-AF9 <sub>490-568</sub> -GFP	Purification of AF9 <sub>ET</sub> with C-terminal GFP
pet28b-BRD <sub>601-683</sub> -GFP	Purification of BRD4 <sub>ET</sub> with C-terminal GFP

**Supplementary Table 3. Primers used in this study.**

Names of constructs	primer sequence 5'-3'
Fig. 1	
Sth1 <sub>(1183-1359)</sub>	F:GCGCGGATCCGAAGTGAAAAGCTCTAGTGTTG R: GCGCCTCGAGTTATGAGGAGTGTCTTTAAACCATTC
Sth1 <sub>(1183-1240)</sub>	F: GCGCGGATCCGAAGTGAAAAGCTCTAGTGTTG R:GCGCCTCGAGTTACTTCGCAGCGGTTTTCTTCGCC
Sth1 <sub>(1248-1359)</sub>	F: GCGCAGATCTTCGCTTGGGATTTTTCCCACG R:GCGCCTCGAGTTACGAAGAGTGTTCCTTGAACCATTCATCAG TAAACTCATTTAACTTGTGAGCATCAACGTAAACCCAGGAGCC TC
Sth1 <sub>(1199-1225)</sub>	F: GCGCGGATCCAAGAAAAACCGAAACTGACCG R:GCCGCTCGAGTTAATATTCAGCGCGTTTACCATCATTGTTTT CAG
Taf14 <sub>(174-244)</sub>	F: GCGCGGATCCAAGGGAGCGTGGACCTAG R: GCCGCTCGAGTTACTCGGTATTTTTCTTAACGTAGTC
Fig. 2 and Supplementary Fig. 2	
Sth1 <sub>(1183-1240)</sub> L1204A	F:CAAAAAGAAAAACCGAAAGCAACCGTTAAAATCAA ACTGACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Sth1 <sub>(1183-1240)</sub> V1206A	F:CAAAAAGAAAAACCGAAACTGACCGCAAAAATCAA ACTGACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Sth1 <sub>(1183-1240)</sub> I1208A	F:CAAAAAGAAAAACCGAAACTGACCGTTAAAGCAA AACTGACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Sth1 <sub>(1183-1240)</sub> L1210A	F:CAAAAAGAAAAACCGAAACTGACCGTTAAAATCAA AGCAAACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Sth1 <sub>(1183-1240)</sub> <sup>M4</sup>	F:CAAAAAGAAAAACCGAAAGCAACCGCAAAAAGCAA AAGCAAACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Sth1 <sub>(1183-1240)</sub> K1207E	F:CAAAAAGAAAAACCGAAACTGACCGTTGAAATCAA ACTGACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Sth1 <sub>(1183-1240)</sub> K1209E	F:CAAAAAGAAAAACCGAAACTGACCGTTAAAATCGA AACTGACAAAACCACGGTCCTGG R: CTTTCAGAGCCGTTGATAATTTCAAC
Taf14 <sub>(174-244)</sub> F220A	F:GAATAATGTTGAAGAGGGTGAAGCAATAATTGACT TGTATAGTTTACCTGAG R: GTCACGTTCAATTTCTGGTGTGTTTTATTGTC
Taf14 <sub>(174-244)</sub> F220R	F:GAATAATGTTGAAGAGGGTGAACGTATAATTGACT TGTATAGTTTACCTGAG R: GTCACGTTCAATTTCTGGTGTGTTTTATTGTC
Taf14 <sub>(174-244)</sub> I222R	F:GAATAATGTTGAAGAGGGTGAATTTATACGTGACT TGTATAGTTTACCTGAG R: GTCACGTTCAATTTCTGGTGTGTTTTATTGTC
Taf14 <sub>(174-244)</sub> F220R/I222R	F:GAATAATGTTGAAGAGGGTGAACGTATAACGTGACT TGTATAGTTTACCTGAG R: GTCACGTTCAATTTCTGGTGTGTTTTATTGTC
Sth1 <sup>M4</sup> -gRNA	F1:CGGAATCCTCTTTGAAAAGATAATGTATGATTATG CTTTC R1:GCTCTAAAACAACTGACCGTCAAGATCAAGATCAT TTTATC TTTCACTGCGGAGAAG

	F2:ATGATCTTGATCTTGACGGTCAGTTTGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAG R2:AAGGAAAAAAGCGGCCGCAGACATAAAAAACAAAAAAGC ACCACCG
Sth1-TAP	F:TTAAATGAGTTTACTGATGAATGGTTCAAGGAACACTCTTCG TCCATGGAAAAGAGAAG R:GGATATAGTCGTAAAAAATAACATGTGGTGATGAAAAC GTACGACTCACTATAGGG
Taf14-HA	F:ATTGAAAAGTCTATGGGACTACGTTAAGAAAAATACCGAGCG GATCCCCGGGTTAATTAA R:ATACAAACATAAAAGCGCGCATTAAACGCCCTTTTACCTTGA ATTCGAGCTCGTTAAAC
Fig. 3 and Supplementary Fig. 3	
Sth1-pRS313	F: GGACTAGTCACTAGAGTCTTCCTCGTCGC R: CTCGAGGATGCTGAACGAGAATCGCTTC
Taf14-pRS313	F1: CCCCCGGGGGATTCTTCTCTAGAATGGCA R1:CGGATGGTTCTTTTTACTGTAGCTACCATGATTAGTTATCT F2:GATAACTAATCATGGTAGCTACAGTAAAAAGAACCATCCG R2: CCCTCGAGGG TCAAACATCAAGAGGATTC
Act1	F: TCGTTCCAATTTACGCTGGTT R: CGGCCAAATCGATTCTCAA
Mgm1	F: AAAGTCCGTTGGTGCACCTTACA R: TGGCATGTGCTGATCTGTGA
Tir4	F: TGCCGACTACATCACCTATCC R: GGCATTTGGTCCAAGGAAAA
Yml045w	F: GAAATCCGAGTGATGAGAAGAATGA R: CCGAGCTATAACTTTGGGTTTG
Hlr1	F: GGAGAACCCCTCCACGTATACA R: TCGTCGGCAAATGACACTTT
Hsp30	F: ACCATGCTACGGACGATGTG R: GCTCTCTGGAACAGCTTCTTTTG
Tps1	F: TTGCACGCCATGGAAGTG R: AACAACTTGCCCCTCCATT
Gpx1	F: TGCAACGGGCAAAGCA R: CAGACTTCCCGCTTACTGAATTC
Mst27	F: CAAGGCAGCGGAGATCGA R: GCCGCCTTCGCCAGTAA
Rsm25	F: TGGGCGTGAAAAGGCTGTA R: GCGATCTGAGCCTATCCTCAA
Prs2	F: CCACACCGGAGATCCTTTTG R: TCTTGGAACCCGCATTGC
Exg1	F: CCATCGGTTGGGCTAGAAAC R: CGGCACCATGCAAATCAA
Fks3	F: ACTTGGGTGCGTTGAACCA R: CAACGGGTGTCTCAAGATTTGTAA
Gas2	F: GCGCCTGTTTGGATGAGATT R: TCCAGATTCAGCACCAAAAGG
Gas4	F: GGCTCTCCGACGTTAGTGAA R: GAGCGCATGCATCTGGATT
Pdc5	F: TTGGGACCACTTGGCCTTATT R: GGTAGCAACTCTGTGGGTTTCG
Ser2	F: TTTGTTATCACCTGCATAGCTCATG R: TCGCAATCTGGTCGATGGT

Fyv5	F: TCTGTCCGAATTTGCTCTCGTA R: RGCCGAGGAGCTGATCAAG
Pgm2	F: GGTTACGGCCCATCTTTCGT R: GCTGCATATTCGGCAATAATTG
Tps2	F: CACTGTGGGATCTGCATCCA R: GGACTTGCTGAGGATCGGTAA
Fig. 4 and Supplementary Fig. 4	
INO80 <sub>(368-390)</sub>	F: GCGCGGATCCGATTCCAAGTTGAACATCAAAATAAC R: GCGCTCGAGTTAGTTAATCAGTTTTTCAACCTTTTGAC
Ino80 <sub>(311-370)</sub>	F: CGGGATCCATGAACTCGCTGTCTTTAATAACG R: CGCTCGAGTACTTGGAAATCGATTGGATTGTA
Ino80 <sub>(400-490)</sub>	F: CGGGATCCGAGGCCTTGAAGAACAACGTTGG R: CGCTCGAGTTATCTTGACATTTTCGTAGAATCC
Ino80 <sub>(500-550)</sub>	F: CGGGATCCTCTACAAATTTTAGGAAAACCTC R: CGCTCGAGTTATTCTTCACGCTCATTCTTCTTCC
Ino80 <sub>EBM</sub> L371A	F: GCAAACATCAAAATAACTTTGAAACAG R: CTTGGAATCGATTGGATTG
Ino80 <sub>EBM</sub> I373A	F: GCAAAAATAACTTTGAAACAGTACCAC R: GTTCAACTTGGAAATCGATTGGATT
Ino80 <sub>EBM</sub> I375A	F: GCAACTTTGAAACAGTACCACGTC R: TTTGATGTTCAACTTGGAAATC
Ino80 <sub>EBM</sub> L377A	F: GCAAAACAGTACCACGTCAAAAGGTT R: AGTTATTTTGATGTTCAACTTGGAA
Ino80 <sub>EBM</sub> <sup>M4</sup>	F: GCAAACGCAAAAGCAACTGCAAAACAGTACCACGTCAAAAG GTT R: CTTGGAATCGATTGGATTG
Sas3 <sub>(111-129)</sub>	F: GCGCGGATCCAGCGAGGAGTTGAAGGTTAGAATTAAG R: GCGCTCGAGTTATTCAAATTTGAAAATTTGATAGAATC
Sas3 <sub>(96-110)</sub>	F: CGGGATCCATGGGAGCAGTAAGTTCCCATATTGAACCTA ATATTGAAGTC R: CGCTCGAGTTAGACTTCAATATTAGGTTCAATAATGGGGAAA CTTACTGCTCCCAT
Snf5 <sub>(771-800)</sub>	F: CGGGATCCGCCAGATAGACCTAAGCCAGTT R: CGCTCGAGTACTCTTCTTTTGTATTAACCTTCC
Snf5 <sub>(700-800)</sub>	F: CGGGATCCACACAGTAGCAGCAGGAAATGC R: CGCTCGAGTACTCTTCTTTTGTATTAACCTTCCC
Snf5 <sub>(800-905)</sub>	F: CGGGATCCGAGTTCGCAGCAGCGCCCAATG R: CGCTCGAGTACTATGTATTCTGTGTGTTATTGTTACTGC
Snf5 <sub>(700-741)</sub>	F: CGGGATCCACACAGTAGCAGCAGGAAATGC R: CGCTCGAGTTAACCAGGCATTAAGTGCTAGG
Snf5 <sub>(741-771)</sub>	F: CGGGATCCGGTGGTGTTGACGTAGGCCCTTC R: CGCTCGAGTTATGAAACTGGCTTAGGTCTATCTGGCCT
Snf5 <sub>EBM</sub> L785A	F: GCACTACTTTCTATTAACCTGCCTG R: CGAATGACCCGGAATATGG
Snf5 <sub>EBM</sub> L787A	F: GCATCTATTAACCTGCCTGGGAAAG R: TAGTAGCGAATGACCCGGAATATG
Snf5 <sub>EBM</sub> I789A	F: GCAAAACTGCCTGGGAAAGTTAATAC R: AGAAAGTAGTAGCGAATGACCCGG
Snf5 <sub>EBM</sub> L791A	F: GCACCTGGGAAAGTTAATACAAAAGA R: TTTAATAGAAAGTAGTAGCGAATGAC
Snf5 <sub>EBM</sub> <sup>M4</sup>	F: GCACTAGCATCTGCAAAAGCACCTGGGAAAGTTAA R: CGAATGACCCGGAATATGGTC
Taf2 <sub>(1393-1406)</sub>	F: CGGGATCCTCAAGATCGTTTATGGTTAAGATAAGAACAAAGA

	ATGATGCTAAG R:CGCTCGAGTAACTTAGCATCATTCTTTGTTCTTATCTTAACCA TAAACGATCTTGA
Tfg1 <sub>(580-605)</sub>	F:CGGGATCCGACACTCTATCCAAATCCAAGAGATCTTCTCAA AGAAACAGCAAAGAAAGCTACAAATGCGCATGTGCATAAAG AG R:CGCTCGAGTTACTCTTTATGCACATGCGCATTGTAGCTTTCT TTTGCTGTTTCTTTGGAGAAGATCTCTTGGATTGGATAGAGTG TC
Tfg1 <sub>(605-629)</sub>	F:CGGGATCCGAGCCAACCTTTGAGGGTGAAAAGTATTA AAAACT GTGTCATTATCTTGAAGGGGGATAAGAAAATACTGAAAAGC R:CGCTCGAGTTAGCTTTTCAGTATTTTCTTATCCCCCTTCAAGA TAATGACACAGTTTTTAATACTTTTCACCCTCAAAGTTGGCTC
Tfg1 <sub>(629-679)</sub>	F:CGGGATCCAGCTTCCAGAGGGAGAA R: CGCTCGAGTTATGTTATTGTAGGCGCTGGAGTTTC
Tfg1 <sub>(580-735)</sub>	F: GCGCGGATCCGACACTCTATCCAAATCCAAGAGATC R: GCGCCTCGAGTTACTCTTTCTTTAATTCCATGTGGTC
Tfg1 <sub>(680-735)</sub>	F: GCGC GGATCC GAAAAGATATCATCGAGGCTATTG R: GCGCCTCGAGTTACTCTTTCTTTAATTCCATGTGGTC
Fig. 5 and Supplementary Fig. 5	
Sth1 <sub>(1183-1240)</sub> -RFP	F1:CGGGATCCGAAGTAAAAAGTAGCTCCGTTG R1:CCTCGGAGGAGGCTTTGGCGTCAGTCTTCTTCGCG F2:GACTGCAGCCAAAGCCTCCTCCGAGGACGTCATC R2:CCGCTCGAGTTAGGCGCCGGTGGAGTGGC
Snf5 <sub>(771-800)</sub> -CFP	F1:ATGTCGGA CT CAGAAGTCAATC R1:AAAAGTTCTTCTCCTTTGCTCTCTTCTTTGTATTA ACTTTCC CAGGC F2:AAGTTAATA CAAAAGAAGAGAGCAAAGGAGAAGAACTTTTC AC R2:CCGCTCGAGTTATTTGTAGAGCTCATCCATGCCA
Taf14 <sub>(174-244)</sub> -GFP	F:CGGGATCCAAAGGGACGGTGGACCTAGAA R:CCGCTCGAGCTCGGTATTTTTCTTAACGTAGTCC
Fig. 6	
Bdf1 <sub>(525-595)</sub>	F: GCGCGGATCCAAAACAGTAGTGACATATGATATG R: GCCGCTCGAGTTAGGATGAGCTTTCATATTGTCTAAAG
Bdf2 <sub>(514-585)</sub>	F: GCGC GGATCC AAGCATTCAGTTGACGATTTAAAG R:GCCGCTCGAGTTAGTTATTTTTTTTCTCAAATATCTCTC
AF9 <sub>(490-568)</sub>	F: CGGGATCCTCAGATAAGCAAATAAAGAATGGTG R: CCGCTCGAGTCAGGATGTTCCAGATGTTTCC
AF9 <sub>(490-568)</sub> -GFP	F: CGGGATCCTCAGATAAGCAAATAAAGAATGGTG R: CCGCTCGAGTCAGGATGTTCCAGATGTTTCC
BRD <sub>(601-683)</sub> -GFP	F: CGGGATCCTCGGAGGAAGAGGACAAGTGC R: CCGCTCGAGAGCTTGAGGTTTCCTTTTCTTCCG