

Supplemental Data

Transcription Factor Substitution during the Evolution of Fungal Ribosome Regulation

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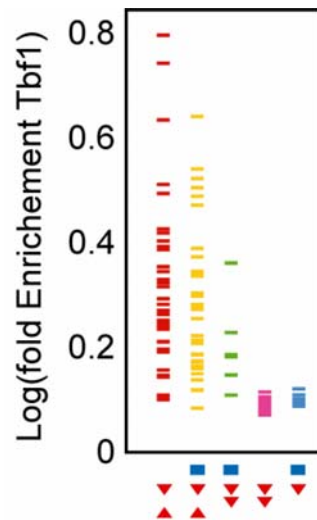


Figure S1. Tbf1 and Cbf1 elements organization predict Tbf1 binding in ChIP-CHIP experiments.

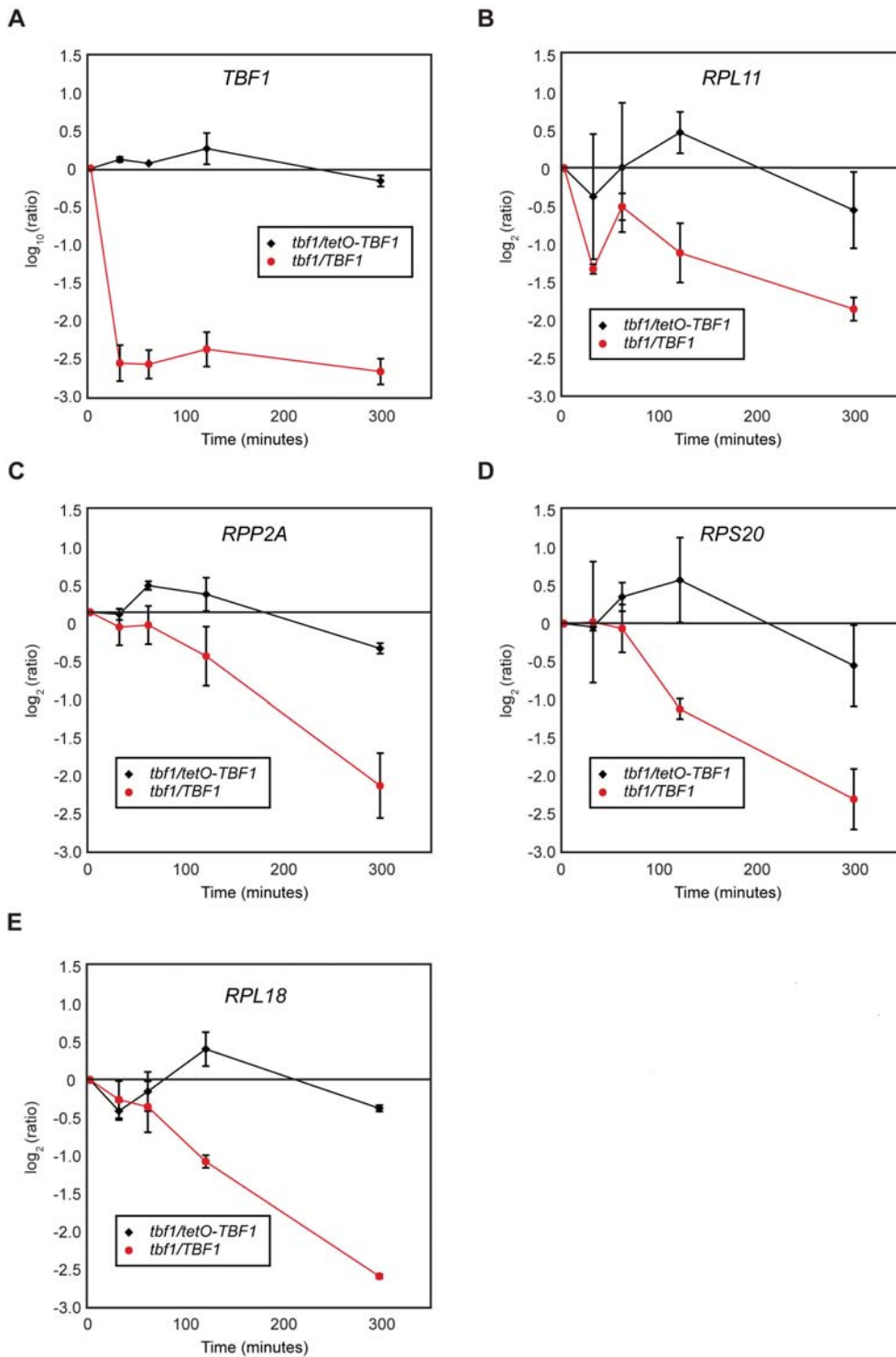


Figure S2. RT-qPCR validates the down-regulation of *TBF1* (A) and four target RP genes (B-E) in the *tbf1/tetO-TBF1* strain but not in the heterozygous *tbf1/TBF1* strain after tetracycline addition.

Species:

Necr_Neurospora crassa
 Boci_Botrytis cinerea
 Magr_Magnaporthe grisea
 Asni_Aspergillus nidulans
 Scpo_Schizosaccharomyces pombe
 Yali_Yarrowia lipolytica
 Caal_Candida albicans
 Catr_Candida tropicalis
 Deha_Debaryomyces hansenii
 Cagu_Candida guilliermondii
 Calu_Candida lusitanae
 Sace_Saccharomyces cerevisiae
 Cagl_Candida glabrata
 Klla_Kluyveromyces lactis

CLUSTAL W (1.83) multiple sequence alignment

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Necr_gi|85082158|ref|XP_956863      -----STRRPWTPDEEKALMMGLDM 732
Boci_BC1G_06358.1                  -----MAGLDS 6
Magr_gi|39943776|ref|XP_361425     -----STRRPWSPEEERALMTGLDL 803
Asni_gi|67515743|ref|XP_657757     -----SQRPPWTEEEENALMAGLDR 677
Scpo_gi|19112771|ref|NP_595979     -----RRSWTKEEEEALDGLDL 422
Yali_gi|50547139|ref|XP_501039     -----PVRPWSKAEAAALMNGLRT 458
Caal_gi|68469830|ref|XP_720925     -----RRAWSREEEKALRHAELEL 669
Catr_CTRG_01572.3                  -----RRPWTRREEEKALRHAELEL 817
Deha_gi|50419739|ref|XP_458398     -----KSLQRRPWTRREEEKALRHAELEL 721
Cagu_PGUG_03851.1                  -----RNPQRRPWTRDEEKALRQALEL 625
Calu_CLUG_01092.1                  -----KVTNRRPWTRREEEKALRHAELEL 732
Sace_gi|6325129|ref|NP_015197.     -----HNNSSNSNN-----NGSIGLRKPKAKRTWSKEEEEALVEGLKE 426
Cagl_gi|50294111|ref|XP_449467     GGENVHSQLVDSNNSILSDVISKSPSVKVVAKARTWSKEEEKTLITGLID 447
Klla_gi|50306773|ref|XP_453362     -----PKQKMMWTQEEEDCLKSGLQK 396

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Pfam00249 (myb domain)

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Necr_gi|85082158|ref|XP_956863     VKGPHWSQILSLFGAHGSVSDILKDRDQVQLKDKARNLKLFFLKTNSEMP 782
Boci_BC1G_06358.1                   VKGPHWSQILALYGDGKGSVSTILDRNQVQLKDKARNLKLFFLKSNIIEVP 56
Magr_gi|39943776|ref|XP_361425     VKGPHWSQILSLFPGNGTLDVVKDRSQVQLKDKARNLKLFFLKTNSEMP 853
Asni_gi|67515743|ref|XP_657757     VKGPHWSQILAMFPGGGTISEALKDRNQVQLKDKARNLKLFFLKSGLIEVP 727
Scpo_gi|19112771|ref|NP_595979     VKGPRWSQILELYGPGGKSEVLKYRNQVQLKDKARNMKLFFLKSQGVVP 472
Yali_gi|50547139|ref|XP_501039     VNGPYWSQILEIYGGGTVSEVLKDRNQVQLKDKARNLKLFFLKSGLIEVP 508
Caal_gi|68469830|ref|XP_720925     K-GPHWATILELFGQGGKI SEALKNRTQVQLKDKARNWKKFFLRSGLIEIP 718
Catr_CTRG_01572.3                   K-GPHWATILELFGQGGKI SEALKGRTQVQLKDKARNWKKFFLRSGLIEVP 866
Deha_gi|50419739|ref|XP_458398     K-GPLWSNILELFGAGGKI SEALKNRSQVQLKDKARNWKMFFLKSGLPVP 770
Cagu_PGUG_03851.1                   K-GPQWSTILELFGAGGKI SEALKNRRNQMLKDKARNWKMFFLKTGMPPVP 674
Calu_CLUG_01092.1                   K-GPSWSTILELFGQGGKINESLKNRTQVQLKDKARNWKMFFLKSGLPVP 781
Sace_gi|6325129|ref|NP_015197.     V-GPSWSKILDLYGPGGKITENLKNRTQVQLKDKARNWKLQYLKSGKPLP 475
Cagl_gi|50294111|ref|XP_449467     L-GPAWAKILDLYGPGGKINENLKNRTQVQLKDKARNWKLHLYLKTGKPLP 496
Klla_gi|50306773|ref|XP_453362     C-GPAWAKILSLYGGGTVSESLKNRSQVQLKDKARNWKMHYLKNMKPVP 445

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Pfam00249 (myb domain)

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Necr_gi|85082158|ref|XP_956863     YYLQSVTGELKTRAPGQAAR--KEAEKARLNAEDEQARLAGIMTLGGLH 830
Boci_BC1G_06358.1                   YYLQCVTGELKTRAPTQAAR--KEAEERARLAGNEESARFHGVLALAAGM 104
Magr_gi|39943776|ref|XP_361425     YYLQSVTGELKTRAPNLSARKAREMEQAGVNAATEEQARAQGMAGLAHDS 903
Asni_gi|67515743|ref|XP_657757     YYLKQVVTGELKTRAPAQAAR--REARERQKKQGEEDKAHVEGIKGMMLA 775
Scpo_gi|19112771|ref|NP_595979     AALQCVTGDLRRD----- 485
Yali_gi|50547139|ref|XP_501039     DCLQFVTGGIKKGRRRGGAVEQRQRVQPQQVMQQVQQQQQQQQQQG 558
Caal_gi|68469830|ref|XP_720925     SYLRGVTGGVD-DGKRK---KDNVTKTAAAPVPMNSEQLQQQQQ----- 759
Catr_CTRG_01572.3                   SYLQGVVTGGVD-DNKNK---KSRRTKTSAAPVPMNQKQKAKSKENEADK 912
Deha_gi|50419739|ref|XP_458398     AYLQKVTGDLERDRLRQNKRLNRRKTAAPVPTPIQNQKSPGQ----- 815
Cagu_PGUG_03851.1                   TYLQKVTGDLEREDRSREAKRS-RSRKTAAPVPS-IK----- 710
Calu_CLUG_01092.1                   AYLKSVTGDLERDDKSR--AKNARNKTAAPVPTVAKKDGEGETAFNG 829
Sace_gi|6325129|ref|NP_015197.     DYLIKVTGNLEKIYKAKKFKSPSPNSSTIMEQNLSQLHSSAASATEDTQT 525
Cagl_gi|50294111|ref|XP_449467     EYLNKVTGNLDKIAKTKRR----- 515
Klla_gi|50306773|ref|XP_453362     EYLEKVTGDLERGLKSKKK----- 464

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Figure S3. Multiple sequence alignment of Tbf1 orthologs in ascomycetes species showing conservation of the myb DNA-binding domain (pfam00249).