SUPPLEMENTARY INFORMATION

Supplemental Materials and methods

Yeast strains and media
All yeast strains are derivative of the SK1 background and are listed in Supplemental Table S5. For synchronous meiosis, cells were grown in SPS presporulation medium and transferred to 1% potassium acetate with vigorous shaking at 30˚C as described (Murakami and Nicolas 2009). For all strains, spore viability was measured after sporulation on solid sporulation medium for two days at 30˚C.

Yeast strains construction
Yeast strains were obtained by direct transformation or crossing to obtain the desired genotype. Site directed mutagenesis and C-terminal deletions were introduced by PCR. All transformants were confirmed using PCR discriminating between correct and incorrect integrations and sequencing for epitope tag insertion or mutagenesis. The functionality of the tagged proteins was measured by spore viability assays (Supplemental Table S6). All tagged proteins were functional.

Two-hybrid analyses
ZIP2, ZIP3, ZIP4, SPO16, RED1 and MSH5 ORFs were PCR-amplified from SK1 genomic DNA. ZIP4 cDNA sequence was amplified from SK1 genomic DNA by fusion of 2 PCR products eliminating ZIP4’s intron. PCR products were cloned in pDNOR207 Gateway plasmid and subcloned in Gateway plasmids derived from the two hybrid vectors pGADT7 (GAL4-activating domain) and pGBKKT7 (GAL4-binding domain) creating N terminal fusions (gift from M. Grelon). For C terminal fusions, ZIP2, ZIP4, SPO16, RED1 and MSH5 ORFs were PCR-amplified without stop codon SK1 genomic DNA and cloned in pDONR207 plasmid and subcloned in Gateway plasmids derived from the two hybrid vectors pGADCr and pGBKCr (Stellberger et al. 2010).
Yeast strains and two-hybrid experiments were performed as in (Kumar et al. 2010). Interaction is defined compared to the growth seen in the negative control consisting of the combination between the Gal4BD-bait protein in the presence of Gal4AD-only
or Gal4AD-bait protein in the presence of Gal4BD-only. Any combination that grows better than this control on the selective media is considered as an interaction.

**Tandem affinity purification**

2.10¹⁰ cells (1 liter) were processed for proteomic analysis. We chose the 4.25 hr time-point instead of 4 hr in the other smaller scale assays, because meiotic progression is slightly slower when we use a large 1 liter volume culture. 2. 10¹⁰ cells were harvested and 2 ml of PMSF (0.5M in DMSO) is immediately added. Cells were washed two times with ice-cold TNG buffer (50 mM Tris/HCl pH 8; 150 mM NaCl, 10% Glycerol; 1 mM PMSF; 1X Complete Mini EDTA-Free (Roche); 1X PhosSTOP (Roche) and flash-frozen in liquid nitrogen. Frozen cells were mechanically ground in liquid nitrogen with the 6775 Freezer/Mill cryogenic grinder (SPEX SamplePrep). The resulting powder was resuspended in 50 mL of lysis buffer (50 mM Tris/HCl pH 7.5; 1 mM EDTA; 0.5% NP-40; 10% glycerol; 300 mM NaCl; 1 mM PMSF; 10 mM NEM; 1X Complete Mini EDTA-Free (Roche); 1X PhosSTOP (Roche)). The lysate was cleared by centrifugation at 4000 rpm for 10 min and then incubated with 1 ml of IgG Sepharose beads (GE Healthcare) for 1 hr at 4 °C. The beads were collected in 2 ml tubes, washed two times with lysis buffer and once with TEV-C buffer (20 mM Tris/HCl pH 8; 0.5 mM EDTA; 150 mM NaCl; 0.1% NP-40; 5% glycerol; 1 mM MgCl₂; 1 mM DTT). The beads were resuspended in 1 ml of TEV-C buffer and transferred into 1.2 ml Bio-Spin Chromatography Column (BioRad). The beads were incubated with 60 µl TEV protease (1mg/ml) and 125 units of Benzonase Nuclease (Sigma) at 4°C overnight. The eluate was transferred into Poly-Prep Chromatography Column (BioRad) containing 6ml of CAM-B buffer (20 mM Tris/HCl pH 8; 150 mM NaCl; 1mM Imidazole; 5% glycerol; 1 mM MgCl₂; 2 mM CaCl₂). The beads were washed three times with TEV-C 300 mM NaCl buffer (20 mM Tris/HCl pH 8; 0.5 mM EDTA; 300 mM NaCl; 0.1% NP-40; 5% glycerol; 1 mM MgCl₂; 1 mM DTT). The eluate was then incubated with 400 µl of Calmodulin Sepharose Beads (GE Healthcare) for 3 hr at 4°C. The beads were washed three times with CAM-B/NP-40 buffer (20 mM Tris/HCl pH 8; 150 mM NaCl; 1mM Imidazole; 5% glycerol; 1 mM MgCl₂; 2 mM CaCl₂; 0.05% NP-40; 10 mM β-Mercaptoethanol). For Zip2-TAP purification, the column was eluted with 350 µl and 700 µl of CAM-E 4/150 (10 mM Tris/HCl pH 8; 150 mM NaCl; 4 mM EGTA; 1 mM Imidazole; 5% glycerol; 1 mM MgCl₂; 0.02% NP-40; 10 mM β-Mercaptoethanol), and with 700 µl and 300 µl of
CAM-E 20/500 (10 mM Tris/HCl pH 8; 500 mM NaCl; 20mM EGTA; 1 mM Imidazole; 5% glycerol; 1 mM MgCl2; 0,02% NP-40; 10 mM β-Mercaptoethanol). For Zip4-TAP and Spo16-TAP purifications, the column was eluted once with 350 µl of CAM-E 20/500 and twice with 700 µl of CAM-E 20/500, and once with CAM-E 50/1000 (10 mM Tris/HCl pH 8; 1 M NaCl; 50 mM EGTA; 1 mM Imidazole; 5% glycerol; 1 mM MgCl2; 0,02% NP-40; 10 mM β-Mercaptoethanol). Eluate fractions was concentrated by TCA purification and resuspended in one tube with 45 µl of loading buffer.

**Interactomic and stoichiometry analyses**

5 µl of the TAP-purified complexes were analyzed by SDS-PAGE by using Novex 4–12% gradient gels (Invitrogen) and visualized by staining with SilverQuest Silver Staining Kit (Thermo, LC6070). Protein preparation and mass spectrometry-based proteomic analyses were carried out as described in (Alfieri et al. 2017). Briefly, eluted proteins were stacked as a single band in a SDS-PAGE gel (NuPAGE 4–12%, Invitrogen) and submitted to in-gel digested using trypsin (Promega, sequencing grade). Resulting peptides were analyzed by online nanoLC-MS/MS (UltiMate 3000 and Q-Exactive Plus or LTQ-Orbitrap Velos Pro, Thermo Scientific) using a 120-min gradient. Peptides and proteins were identified and quantified using MaxQuant (version 1.5.3.30, (Cox and Mann 2008)) and the SwissProt database (August 2016 version, Saccharomyces cerevisiae S288c taxonomy). Proteins were quantified based on the iBAQ value (Schwanhäusser et al. 2011) calculated by MaxQuant. Statistical analysis were performed using ProStaR (Wieczorek et al. 2017). Proteins identified in the reverse and contaminant databases, proteins only identified by site and proteins exhibiting less than 3 intensity values in one condition were discarded from the list. After log2 transformation, intensity values were normalized by median centering before missing value imputation (replacing missing values by the 2.5 percentile value of each column); statistical testing was conducted using limma t-test. Differentially expressed proteins were sorted out using a log2 (fold change) cut-off of 3 and a FDR threshold on remaining p-values of 1% using the Benjamini-Hochberg method. The stoichiometries of Zip2-TAP, Spo16-TAP, Zip4-TAP and Zip2ΔXPF-TAP partners were determined using the mass spectrometry-based iBAQ metrics, as described (Smits et al. 2013).
The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE (Vizcaíno et al. 2016) partner repository with the dataset identifier PXD007735.

**Co-immunoprecipitation**

6.10^8 cells were harvested, washed one time with PBS, and lyzed in 1.5 ml lysis buffer (20 mM HEPES/KOH pH7.5; 150 mM NaCl; 0.5% Triton X-100; 10% Glycerol; 1 mM MgCl2; 2 mM EDTA; 1 mM PMSF; 1X Complete Mini EDTA-Free (Roche); 1X PhosSTOP (Roche); 125 U/mL benzonase nuclease (Sigma)) and glass beads three times for 30 s in a Fastprep instrument (MP Biomedicals, Santa Ana, CA). The lysate was cleared by centrifugation at 13,000 g for 5 min. 25 µl of Protein G magnetic beads (New England Biolabs, Ipswich, MA) (equilibrated 1:1 with lysis buffer) was directly added for TAP pull-down assay or 25 µl of Protein G magnetic beads and 5 mg of mouse monoclonal anti-FLAG primary antibody M2 (Sigma) were added for anti-FLAG immunoprecipitation. The tubes were incubated overnight at 4°C. The magnetic beads were washed four times with 1 mL of wash buffer (20 mM HEPES/KOH pH7.5; 150 mM NaCl; 0.5% Triton X-100; 5% Glycerol; 1 mM MgCl2; 2 mM EDTA; 1 mM PMSF; 1X Complete Mini EDTA-Free (Roche); 1X Phos-STOP (Roche)) and resuspended in 30 µl of 2xSDS protein sample buffer. The beads were heated at 95°C for 3 min and loaded in duplicate or triplicate onto a 4–12% SDS-polyacrylamide gel. The proteins were then blotted to PVDF and probed for TAP, Flag, V5 or Myc-tagged protein with corresponding antibodies. Signal was detected using the SuperSignal West Pico Chemiluminescent Substrate (ThermoFisher), excepted Red1 detection for which a combination of SuperSignal West Femto and Pico Chemiluminescent Substrate (ThermoFisher) was used.

**Size exclusion chromatography**

8.10^9 cells of VBD1735 were harvested and prepared as described above, except that frozen cells were ground in liquid nitrogen with the 6775 Freefer/Mill cryogenic grinder (SPEX SamplePrep). Spo16-TAP complexes were eluted by TEV cleavage in 100 µl of TEV-C buffer. Eluate was injected onto a Superdex 200 Increase 3.2/300 column and elution was performed at 4°C with buffer containing 50 mM Tris-HCl (pH 7.9), 300 mM KCl and 2mM EDTA Chromatography was performed on an
ATKA purifier UPCV (GE Healthcare) at 0.075 mL/min and fifty-one fractions 0.1 mL were collected. The column was calibrated with molecular weight standards. Individual fractions, eluted from 0.8 ml and 1.8 ml after injection, were analyzed by Western blot and probed as described above.

**TCA extraction and Western blot analysis**
Protein extracts were prepared by trichloroacetic acid (TCA) precipitation method. 1.5 ml of sporulating cell culture was harvested and pellet was immediately frozen in liquid nitrogen. Cells were resuspended in 100 µl of ice-cold NaOH solution (1.85N NaOH, 7.5% β-mercaptoethanol) and incubated for 10 min on ice. Samples were then mixed with 30 µl of ice-cold TCA 50% and incubated for 10 min on ice. Cell suspension was then harvested for 5 min at 15000g at 4°C and the pellet was resuspended in 100 µl of loading buffer (55 mM Tris pH 6.8, 6.6 M Urea, 4.2% SDS, 0.083 mM EDTA, 0.001% bromophenol blue, 1.5% β-mercaptoethanol). Protein samples were dipped in liquid nitrogen and then incubated at 65°C for 3 min. Samples were centrifuged 5 min at 20000 g and the supernatant was kept at -80°C. Samples were loaded on precast acrylamide gel (4-12% Bis-Tris gel (Invitrogen)) and transferred on PVDF membrane in MOPS SDS Running Buffer (Life Technologies). Proteins were detected using, c-Myc (clone 9E10) mouse monoclonal antibody (Santa Cruz, 1:500), Flag M2 mouse monoclonal antibody (Sigma, 1:1000). For normalization, Pgk1 mouse monoclonal antibody was used (Invitrogen, 1:3000). Signal was quantified after image acquisition with Chemidoc system (Biorad). To quantify protein levels, the band intensity in each lane was measured by the Fiji software and divided by the corresponding Pgk1 band intensity in the same lane.

**Preparation of expression plasmids**
The XPF domain of ZIP2 gene was amplified from SK1 using forward primer Zip2-P3_NcoI_New (catgCCATGGagaataaatgcatagccgtaaatg) and reverse primer Zip2-P2 linker10hisPvuII (CATGcagctgTTAATGGTGATGGTGATGGTGATGGGTGGGAACCGGAACCGGAACCccattctaaggttaataacttc). The reverse primer carried 10x histidine gene sequence. The amplified product was cloned into the acceptor plasmid pKL (Fitzgerald et al. 2006) to make pKL-XPF(Zip2)-10xHis. The SPO16 gene was amplified from SK1 using forward primer Spo16-P1_BamHI
(cgGGATCCatgtctgaattcttttgggatgtac) and reverse primer Spo16-P2_SalI (gcGTCGACttattcattaaaagcaaccaccaag). The amplified product was cloned into the donor plasmid pUCDM (Fitzgerald et al. 2006) to make pUCDM-SPO16. The cloned genes were verified by sequencing. pKL-XPF(Zip2)-10xHis and pUCDM-SPO16 were fused at loxP sites by in vitro Cre-Fusion as described before (Fitzgerald et al. 2006).

DNA extraction and Southern blot analysis
DNA samples were prepared using a CTAB extraction procedure (Allers and Lichten 2000) and were analyzed by Southern blot of one-dimensional agarose gels as described (Oh et al. 2007).

Chromatin immunoprecipitation
For each meiotic time point, 2.10⁸ cells were processed as described (Borde et al. 2009), with the following modifications: lysis was performed in Lysis buffer plus 1 mM PMSF, 50 µg/mL Aprotinin and 1X Complete Mini EDTA-Free (Roche), using 0.5 mm zirconium/silica beads (Biospec Products, Bartlesville, OK). We used 2 µg of the mouse monoclonal anti-FLAG antibody M2 (Sigma) and 30 µL Protein G magnetic beads (New England Biolabs) or 1.6 µg of c-Myc monoclonal antibody (9E10, Santa Cruz) and 50 µL PanMouse IgG magnetic beads (Thermo Scientific). Quantitative PCR was performed from the immunoprecipitated DNA or the whole-cell extract using a 7900HT Fast Real-Time PCR System (Applied Biosystems, Thermo Scientific) and SYBR Green PCR master mix (Applied Biosystems) as described (Borde et al. 2009). Results were expressed as % of DNA in the total input present in the immunoprecipitated sample and normalized to the negative control site in the middle of NFT1, a 3.5 kb long gene. Primers for GAT1, BUD23, HIS4LEU2, ERG1, Axis and NFT1 have been described (Brachet et al. 2015; Sommermeyer et al. 2013; Duroc et al. 2017).

For ChIP-seq experiments, 1.10⁹ cells were processed as described before, excepted that chromatin was further sonicated as described in Murakami and Keeney (2014). DNA fragments were purified by the IPure kit V2 (Diagenode).

Detection of (remote) homology relationships for Spo16
Direct detection of reliable homologs and construction of the Spo16 profile

The *S. cerevisiae* Spo16 sequence (Uniprot [PMID: 27899622] identifier P17122) was queried against the clustered Uniprot20 database (version 2016_06) with 3 iterations of HHblits [PMID: 22198341] using an e-value cutoff of 0.1. As a result, 16 homologous sequences were retrieved, all in closely related species including *Candida glabrata* (XP_447335.1, 18% sequence identity), *Zygosaccharomyces rouxii* (XP_002495594.1, 20% sequence identity) and *Kluyveromyces lactis* (XP_454656.1, 11% sequence identity).

Secondary structure predictions were made with PSIPRED [PMID: 10493868] as implemented in the HH-suite addss.pl script.

Querying the Spo16 profile against profile databases for several Ascomycete species

In order to detect remote homology relationships with proteins in Ascomycete species, databases of profiles for all proteins in several fully sequenced Ascomycete species (as reported in the OMA database [PMID: 25399418]) were built using the procedure described in the HH-suite user guide. This involved running 2 iterations of HHblits against the clustered Uniprot20 database (version 2016_06) and adding predicted secondary structure to the profiles as above. Seven Ascomycete species relatively divergent from *S. cerevisiae* were chosen: *Ashbya gossypii*; *Aspergillus oryzae*; *Candida albicans*; *Cryptococcus neoformans*; *Debaryomyces hansenii*; *Neurospora crassa*; *Schizosaccharomyces pombe*.

The Spo16 profile was queried against each of those databases and the 10 matches with highest probability were analyzed in each case to detect the presence of interesting functional domains. For this purpose, each of the 10 matches was queried with HHblits against the clustered Uniprot20 database (version 2016_06) in order to identify reliable homologs giving indications regarding the function of this match.

The results of this procedure are reported in Table S4.

Structural modeling of the Zip2/Spo16 complex

Using a single iteration of HHblits on the HHpred web server [PMID: 15980461], FANCM (PDB identifier 4bxo, chain A) was straightforwardly identified as a suitable structural template for *S. cerevisiae* Zip2 with high confidence (HHpred probability 97%).
Since remote homology relationships pointed at the possible presence of a divergent form of an XPF/ERCC1 domain in *S. cerevisiae* Spo16, an alignment was built between Spo16 and FAAP24 (PDB identifier 4bxo, chain B, in complex with FANCM) using a global profile-profile alignment with weak probability and matching predicted secondary structure of Spo16 with the secondary structure of FAAP24 as assigned by DSSP [PMID: 6667333]. This alignment is displayed in Supplemental Fig. S5A.

The Zip2/Spo16 complex was then modeled using RosettaCM [PMID: 24035711] with default parameters, using the 4bxo PDB structure as a template. The region where the predicted Spo16 secondary structure best matches the FAAP24 secondary structure is also the interface region with Zip2 in this model.

Evolutionary conservation was assessed for Spo16 using the Rate4Site software [PMID: 15201400] which runs behind the widely-used ConSurf web server [PMID: 27166375] and mapped on the surface of the model as displayed in Supplemental Fig. S5B.

**Supplemental Tables**

**Supplemental Table S1. List of partners identified by mass spectrometry of Zip2-TAP, Zip4-TAP, Spo16-TAP and Zip2ΔXPF-TAP purifications.**

Stoichiometries of Zip2-TAP, Zip4-TAP, Spo16-TAP and Zip2ΔXPF-TAP are also shown.

**Supplemental Table S2. Yeast two hybrid assays results.**

AD constructs were transformed into the AH109 strain while BD constructs were transformed into Y187 cells. After mating, diploids cells were selected on SD medium lacking leucine, and tryptophan (SD-LW). Interactions were scored in parallel on SD medium lacking leucine, tryptophan, histidine and adenine (SD-LWHA). White boxes indicate a lack of interaction, green indicates growth on SD-LWAH. All interactions were tested with Gal4 AD and BD fused to the N-terminal or the N-terminal extremities of pray and bait proteins were also tested.

**Supplemental Table S3. Search for Spo16 orthologs in several Ascomycete species.**
The search for Spo16 orthologs involved running HHsearch with the Spo16 profile against the database of profiles for all protein sequences in several fully sequenced Ascomycete species and looking for short proteins of unknown function that might be Spo16 orthologs. This was done only in species for which a Zip2 ortholog was found.

Supplemental Table S4. Spo16 profile matches in several Ascomycete species.
While running HHsearch with the Spo16 profile against the databases of profiles in several fully sequenced Ascomycete species, several well-ranked hits homologous to proteins of the XPF-ERCC1 superfamily (and at least one in each analyzed species) were spotted.

Supplemental Table S5. List of strains used in this study.

Supplemental Table S6. Spore viability profile of tagged proteins used in this study.

Supplemental Figures

Supplemental Figure S1. Correlation heatmap using Spearman method focused on the signal extracted from the union of the strongest 1000 per-sample peaks.
For each experiment, peaks were determined and ranked, and the correlation between the strongest 1000 peaks of each experiment measured using the deepTools modules (multiBigwigSummary and plotCorrelation, v2.2.4, (Ramírez et al. 2016). Peaks for Red1 and Spo11 oligos are from (Sun et al. 2015) and (Zhu and Keeney 2015), respectively.

Supplemental Figure S2. Zip2, Zip3, Zip4 and Spo16 bind to centromeric regions during meiosis.
DNA binding profiles for Zip3-Flag, Zip2-Flag, Zip4-Flag, Spo16-Myc and Red1 at all the centromeres of budding yeast. The map of Spo11-oligos is also presented. Chromosome number, location and coordinates of centromeric regions are shown.

Supplemental Figure S3. Zip2, Zip4 and Spo16 recruitment in absence of recombination.
Analysis of Zip2, Zip4 and Spo16 association with different chromosomal regions in \(spo11\Delta\) and \(dmc1\Delta\) mutant backgrounds. Cells from a synchronous time-course were processed for ChIP of Zip2-Flag, Zip4-Flag and Spo16-Myc and the association is quantified by qPCR using primers that cover the indicated regions.

**Supplemental Figure S4. Zip2, Zip4 and Spo16 are mutually dependent for chromosome binding.**
Analysis of Zip2, Zip4 and Spo16 association with different chromosomal regions in several mutant backgrounds. Cells from a synchronous time-course were processed for ChIP of Zip2-Flag, Zip4-Flag and Spo16-Myc and the association is quantified by qPCR using primers that cover the indicated regions. Error bars indicate SEM from two independent experiments.

**Supplemental Figure S5. Analysis of zip2\DeltaXPF protein expression and Zip2\DeltaXPF-TAP partners.**
(A) Comparison of protein expression between Zip2\DeltaXPF-Flag and Zip2-Flag. Pgk1 is used as a loading control.
(B) Mass spectrometry analysis of Zip2\DeltaXPF-TAP partners during meiosis (t= 4.25 hr). The volcano plot indicates in red the proteins significantly co-purified with Zip2 (Log2(Fold Change)>3 and log10(p-value)<2). Selected top candidates are indicated. The entire list can be found as Supplemental Table S1. Zip3 protein is also shown despite being just below the fixed cut-off. The experiment was done in triplicate.
(C) Comparison of stoichiometry between zip2\DeltaXPF-Flag (green) and Zip2-Flag (orange) partners. Values are the average of three independent experiments ± SD.
(D) Zip4 interacts with Msh5 in in yeast two-hybrid assays. +His/Ade (SD-Leu-Trp+His+Ade) was used to test the cotransformation efficiency. -His/Ade (SD-Leu-Trp-His-Ade) was used as the selective medium to verify the interactions. AD, GAL4 activation domain; BD, Gal4 binding domain.

**Supplemental Figure S6. Spo16 model and amino acids conservation.**
(A) Spo16/FAAP24 alignment used to build the structural model of Zip2-Spo16 based on FANCM-FAAP24 (PDB 4b xo). The grey box corresponds to the grey region in the model (Fig. 5C), i.e. the region where the structural alignment is rather unreliable (secondary structure not well-matched) therefore the Spo16 model might be
unreliable. This region does not belong to the interface with Zip2 in the Zip2-Spo16 interface model.

(B) Spo16 mapping conservation in complex with Zip2 XPF domain (green) and DNA. Surface of the Spo16 protein showing amino acid conservation, from low (white) to high (red).

Supplemental Figure S7. Complementary information about the XPF(Zip2)-Spo16 complex.

(A) Gel filtration profile of the XPF(Zip2)-Spo16 complex (49 kDa), Ovalbumin (44 kDa) and Albumin (66 kDa). XPF(Zip2)-Spo16 elutes as a mono-disperse entity between the ovalbumine (44kDa) and the albumin (66kDa) which is compatible with a 1:1 stoichiometry.

(B) Comparison of migration profiles between XPF(Zip2)-Spo16 and Ku70-80 complexes bound to Holliday junctions. The binding of the XPF(Zip2)-Spo16 complex was compared to that of the yeast Ku70-80 heterodimer with a strong DNA end binding capacity. The experiment indicated that the dispersed signal obtained with the XPF(Zip2)-Spo16 complex reflects unstable and dynamic DNA binding, in contrast to Ku under the same experimental conditions. The Ku heterodimer is expected to bind the ends of the four DNA arms.

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A

Zip2-Flag

Control (Pgk1)

zip2△XPF-Flag

Control (Pgk1)

B

Zip2△XPF-TAP MS analysis

D

+His/Ade  -His/Ade

Msh5-AD/Zip4-BD
Msh5-AD/BD
AD/Zip4-BD

C

Relative abundance

Zip2/TAP experiments
Zip2△XPF-TAP experiments

Dilution

Msh5-AD/Zip4-BD
Msh5-AD/BD
AD/Zip4-BD
Spo16 predicted secondary structure
Spo16 confidence of predicted ss
Spo16 consensus sequence based on profile
Spo16 sequence (P17122)
FAAP24 (4bbox_B) secondary structure
FAAP24 predicted secondary structure
FAAP24 confidence of predicted ss
FAAP24 consensus sequence based on profile
FAAP24 sequence (4bbox_B)

Spo16 predicted secondary structure
Spo16 confidence of predicted ss
Spo16 consensus sequence based on profile
Spo16 sequence (P17122)
FAAP24 (4bbox_B) secondary structure
FAAP24 predicted secondary structure
FAAP24 confidence of predicted ss
FAAP24 consensus sequence based on profile
FAAP24 sequence (4bbox_B)

B

180°

Conservation

A

De Muyt_Supplemental Fig. S6
A

B