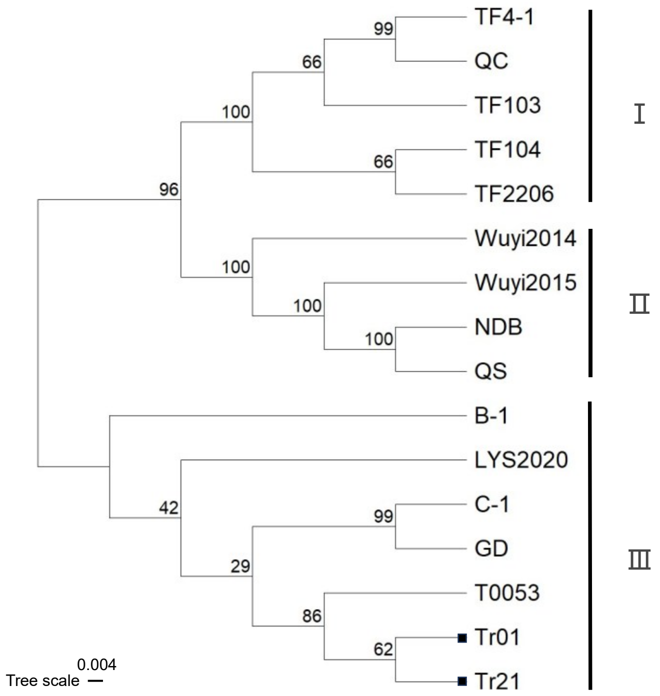
Supplementary Table 1. Source information of *T. fuciformis* strains.

Strain ID	Source Location	Type	Morphotype	Nuclear Status	Associated *A. stygium*
TF2206	Tongjiang County, Bazhong, Sichuan, China	Wild	M/Y	Heterokaryon	+
4-1	Tongjiang, Bazhong, Sichuan, China	Wild	M/Y	Heterokaryon	+
QC	Tongjiang, Bazhong, Sichuan, China	Wild	M/Y	Heterokaryon	+
TF103	Tongjiang, Bazhong, Sichuan, China	Wild	M/Y	Heterokaryon	+
TF104	Tongjiang, Bazhong, Sichuan, China	Wild	M/Y	Haploid	+
NDB	Mangdang Mountain, Nanping, Fujian, China	Wild	M/Y	Heterokaryon	+
QS	Qishan National Forest Park, Fuzhou, Fujian, China	Wild	M/Y	Heterokaryon	+
Wuyi2015	Wuyishan Biosphere Reserve, Nanping, Fujian, China	Wild	Y	Haploid	-
Wuyi2014	Wuyishan Biosphere Reserve, Nanping, Fujian, China	Wild	Y	Haploid	-
Tr01	Gutian County, Ningde, Fujian, China	Cultivated	M/Y	Heterokaryon	+
Tr21	Gutian County, Ningde, Fujian, China	Cultivated	M/Y	Heterokaryon	+
GD	Shaoguan, Guangdong, China	Wild	M/Y	Heterokaryon	+
B-1	Tengchong, Yunnan, China	Wild	M/Y	Heterokaryon	+
C-1	Tengchong, Yunnan, China	Wild	M/Y	Heterokaryon	+
LYS2020	Liangyeshan Mountain, Wuping County, Longyan, Fujian, China	Wild	Y	Haploid	-
T0053	Wuping Longyan, Fujian, China	Wild	Y	Haploid	-

Note: M/Y indicates that the strain exhibits both mycelial (M) and yeast-like/ (Y) morphological states; “+” indicates presence of an associated *A. stygium* strain; “–” indicates absence.

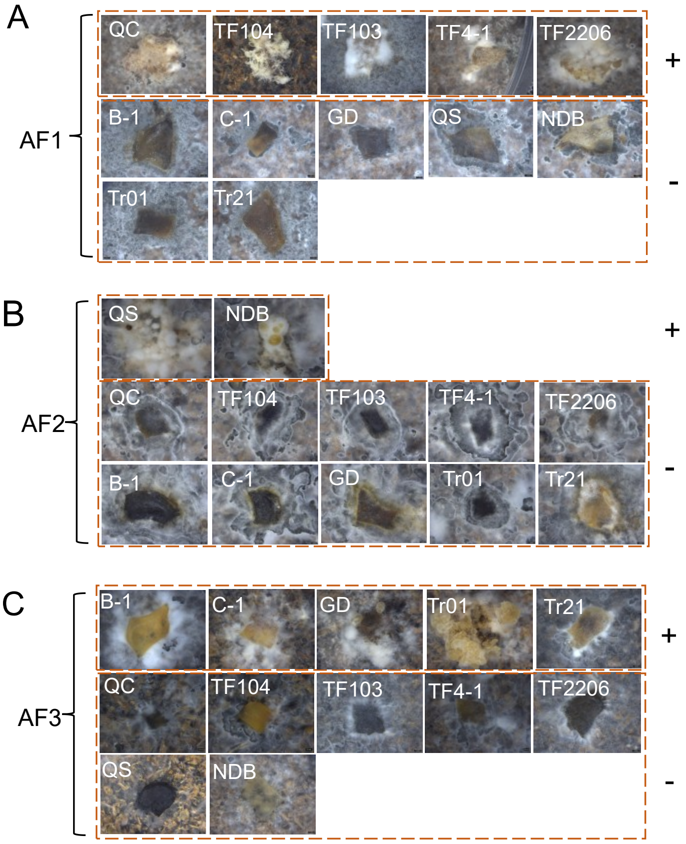
Supplementary Table 2. *T. fuciformis* genome assembly statistics using Hi-C.

Strain ID	HiFi reads number	Total data (Gb)	Contig N50 (Kb)	Coverage (×)
TF2206	540,905	10.58	19.71	441
4-1	361,242	6.76	18.78	273
QC	247,810	5.42	22.15	222
TF103	332,323	6.34	19.58	259
TF104	321,258	6.89	21.97	282
NDB	329,762	7.27	22.06	232
QS	393,337	8.87	22.49	265
Wuyi2015	180,615	3.37	18.44	103
Wuyi2014	406,556	4.07	12.25	131
Tr01	211,688	3.34	21.17	120
Tr21	575,272	9.52	16.96	142
GD	389,229	9.21	23.57	321
B-1	365,840	7.87	21.6	286
C-1	280,680	5.97	21.31	221
LYS2020	286,678	4.47	15.67	159
T0053	224,771	3.96	17.27	139

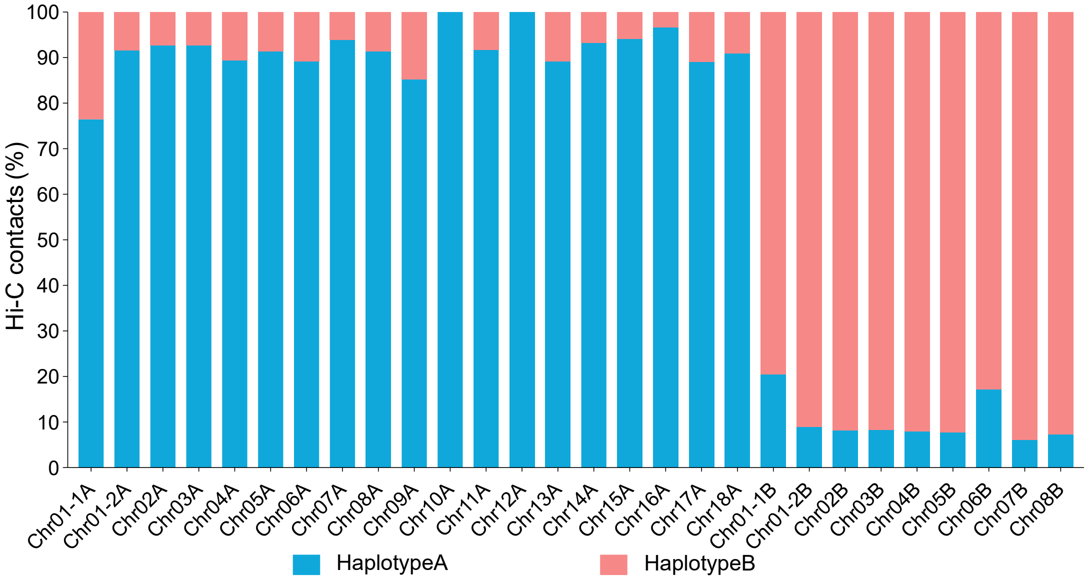


Supplementary Figure 1. Neighbor-Joining phylogenetic tree of 16 *T. fuciformis* strains based on ITS sequences (bootstrap = 1000 replicates). Strains are color-coded by origin: ■ cultivateds (n=2), other branches represent wild isolates (n=14).

Supplementary Figure 2. Field-collected fruiting bodies of representative strains from three Clusters of *T. fuciformis*. The images display wild fruiting bodies of typical strains from Cluster I (TF2206), Cluster II (QS), and Cluster III (Tr21), which were selected from the 16 analyzed strains in this study. All specimens were collected from natural habitats in China and photographed under native growth conditions.

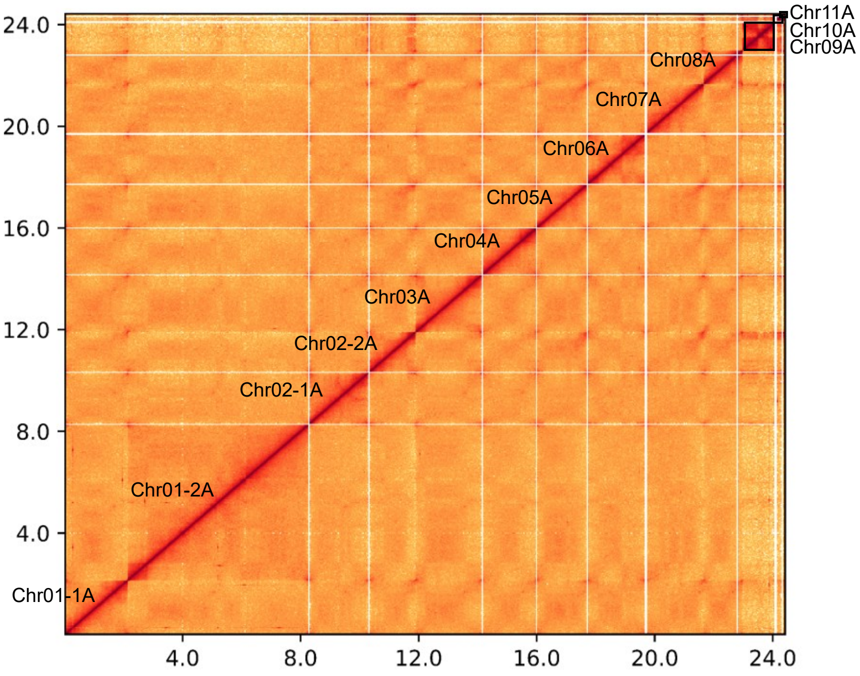


Supplementary Figure 3. Pairing compatibility between *T. fuciformis* strains and their associated fungus (AF) across phylogenetic clusters. (A-C) Representative *T. fuciformis* strains from Cluster I (A), Cluster II (B), and Cluster III (C), showing successful pairing (indicated by "+") with their native AF isolates (e.g., AF1, AF2, AF3), but incompatibility with strains from other clusters.

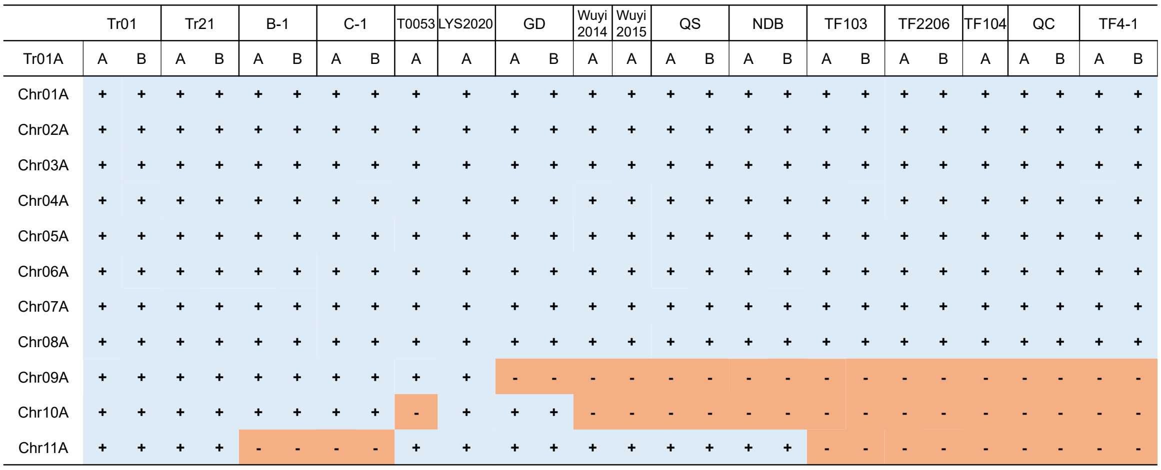


Supplementary Figure 4. NDB Haplotype-resolved Hi-C contact profiles.

Heatmap depicts the distribution of Hi-C contact frequencies (%) between haplotypeA and haplotypeB across 18 chromosomes (Chr01-Chr18). The x-axis indicates chromosome numbers (suffix A/B denotes haplotype assignment), while the y-axis represents normalized Hi-C contact frequency (%). Color gradient reflects haplotype-specific interaction intensity, with haplotypeA (blue) and haplotypeB (red) showing distinct interaction partitioning.

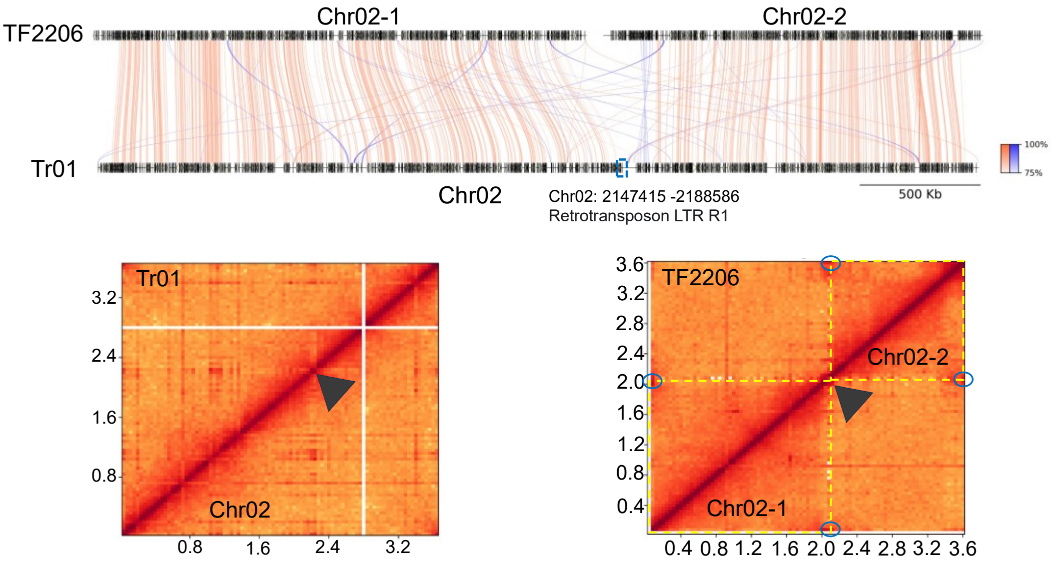


Supplementary Figure 5. Hi-C interaction heatmaps produced by Hi-C Pro validated the assembled genomic architecture of TF2206.

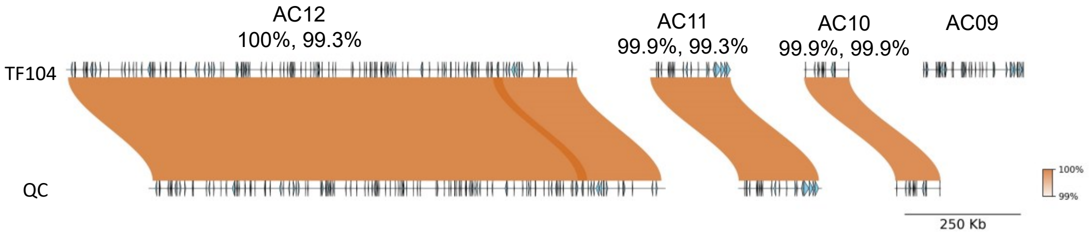


	Tr01		Tr21		B-1		C-1		T0053	LYS2020	GD		Wuyi 2014	Wuyi 2015	QS		NDB		TF103		TF2206		TF104	QC		TF4-1	
Tr01A	A	B	A	B	A	B	A	B	A	A	A	B	A	A	A	B	A	B	A	B	A	B	A	A	B	A	B
Chr01A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr02A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr03A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr04A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr05A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr06A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr07A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr08A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chr09A	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Chr10A	+	+	+	+	+	+	+	+	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Chr11A	+	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-

Supplementary Figure 6. Synteny analysis of chromosomes between the Tr01 hapA genome and 26 haploid genomes. the "+" symbol on a blue background indicates synteny between the Tr01 hapA chromosome and chromosomes in other haploid genomes, while the "-" symbol on a yellow background indicates the absence of synteny between the Tr01 hapA chromosome and chromosomes in other haploid genomes.



Supplementary Figure 7. Syntenic conservation analysis of Chr02 between Tr01 and TF2206 strains Blue box delineates syntenic region boundaries. Hi-C contact heatmaps of Chr01 (40-Kb resolution) are shown for Tr01 (left) and TF2206 (right). Black triangles indicate syntenic boundaries, while solid black circles mark telomere interaction hotspots.



Supplementary Figure 8. Synteny analysis of accessory chromosomes in the QCA and TF104A genomes. The homologous chromosomes AC10 to AC12 show near-identical synteny between the QCA and TF104A genomes, with sequence similarity >99.9% and coverage ≥99.3%.