

**TABLE S1** Primers used for PCR and sequencing of the target genes.

Oligo Name	Sequence	Target gene/Purpose	PCR product sizes	PCR program	Reference
Cp-ERG11-Fexternal	AACAAAGATCATACGACTG	<i>CpERG11</i> /PCR and sequencing	1805bps	5min 95°C, 35 cycles of [30sec, 95°C; 30sec, 52°C; and 2min, 72°C], 8min, 72°C	This study
Cp-ERG11-R1	TAGTCAAATGTTGATAGG	<i>CpERG11</i> /sequencing	---		This study
Cp-ERG11-F1	AAGGGTCATGAATTTGTG	<i>CpERG11</i> /sequencing	---		This study
Cp-ERG11-R2	GAGGTAATGGCAAGTGTG	<i>CpERG11</i> /sequencing	---		This study
Cp-ERG11-F2	AGGAGAAGCAATGAGGAA	<i>CpERG11</i> /sequencing	---		This study
Cp-ERG11-R3	TTGTATGAGCATAACCTG	<i>CpERG11</i> /sequencing	---		This study
Cp-ERG11-F3	CCATTACATTCCATATTCA	<i>CpERG11</i> /sequencing	---		This study
Cp-ERG11-Rexternal	CATTCTGCATTAAACCCC	<i>CpERG11</i> /PCR and sequencing	1805bps		This study
Cp-TAC1-Fexternal	GTCCAACCTTAGCTTCTT	<i>CpTAC1</i> /PCR and sequencing	3096ps	5min 95°C, 35 cycles of [30sec, 95°C; 30sec, 52°C; and 3min, 72°C], 8min, 72°C	This study
Cp-TAC1--R1	TCCTTCTTCTCGTGAC	<i>CpTAC1</i> /sequencing	---		This study
Cp-TAC1-F1	CATGGATATAGATTCGC	<i>CpTAC1</i> /sequencing	---		This study
Cp-TAC1-R2	TAGAGTCACAATAGGAAA	<i>CpTAC1</i> /sequencing	---		This study
Cp-TAC1-F2	GCAAAGTTAAATCACTTG	<i>CpTAC1</i> /sequencing	---		
Cp-TAC1-R3	CTTCAGGTCAATAAAAATG	<i>CpTAC1</i> /sequencing	---		
Cp-TAC1-F4	CATATCAGTTGTACAGAA	<i>CpTAC1</i> /sequencing	---		
Cp-TAC1-F3	CTACGTGACTTTGATGC	<i>CpTAC1</i> /sequencing	---		This study
Cp-TAC1-R4	TTCTTGGTACAATTCGG	<i>CpTAC1</i> /sequencing	---		
Cp-TAC1-Rexternal	TCTCTAAAATACAGCTCTC	<i>CpTAC1</i> /PCR and sequencing	3096bps		This study
Cp-MRR1-Fexternal	CTGTATGGAGAGTGAGAT	<i>CpMRR1</i> /PCR and sequencing	3850bps	5min 95°C, 35 cycles of [30sec, 95°C; 30sec, 52°C; and 4min, 72°C], 8min, 72°C	This study
Cp-MRR1-F1	AAACTGTGTAAAGGCTA	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-F2	AATTTATCAAACACGAGA	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-F3	AGAAGAGTTTATCGAGTG	<i>CpMRR1</i> /sequencing	---		This study

Cp-MRR1-F4	TTTATCAGCGTTGGTTG	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-F5	TTGACGTATTTTACTTG	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-F6	GGTCAATTTGTGTGAAG	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-Rexternal	GTTACAGGTGTATAGTGG	<i>CpMRR1</i> /PCR and sequencing	3850bps		This study
Cp-MRR1-R1	GAATTTCTGTCTCTGATT	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-R2	ATTTGTCCTTGAATCAG	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-R3	CAAGTCTAGTCTTTTCTC	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-R4	TCTTTCTCTTATCTGTT	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-R5	GATAAACATATCACAAATCA	<i>CpMRR1</i> /sequencing	---		This study
Cp-MRR1-R6	TATCCTTTGATGTCGATG	<i>CpMRR1</i> /sequencing	---		This study
Cp-UPC2-Fexternal	AGAGTGAGAGACAGTATC	<i>CpUPC2</i> /PCR and sequencing	2750bps	5min 95°C,35 cycles of [	This study
Cp-UPC2-R1	TACCGAACTGTCCAAAC	<i>CpUPC2</i> /sequencing	---	30sec, 95°C; 30sec, 52°C; and 3min, 72°C], 8min, 72°C	This study
Cp-UPC2-F1	GATCTTTGGATGGGTTG	<i>CpUPC2</i> /sequencing	---		This study
Cp-UPC2-R2	TGTTGCTGTTGTTGTTGA	<i>CpUPC2</i> /sequencing	---		This study
Cp-UPC2-F2	CGAGACCAATTGAATATG	<i>CpUPC2</i> /sequencing	---		This study
Cp-UPC2-R3	TGTTGCTGCACCTTTTAC	<i>CpUPC2</i> /sequencing	---		This study
Cp-UPC2-F3	GATTATGGACTCATTGGC	<i>CpUPC2</i> /sequencing	---		This study
Cp-UPC2-R4	AAATCCATCATCATATGC	<i>CpUPC2</i> /sequencing	---		This study
Cp-UPC2-Rexternal	TTCAGTTGAAATCTCCTTC	<i>CpUPC2</i> /PCR and sequencing	2750bps		This study

**TABLE S2** Results of the comparative biofilm production assay for selected isolates.

The data are expressed as the mean  $\pm$  standard deviation for crystal violet and resazurin-based viability staining ( $n = 12$  wells).

Starin #	Erg11p	AVG CTB	AVG CV	SD CTB	SD CV
**17P	Y132F	62129,75	0,84975	7392,21	0,152901
**19P	Y132F	47658,5	0,563167	16486,37	0,106059
**2P	Y132F	72496	0,911167	11591,54	0,11853
**3P	Y132F	68093,83	0,904583	9833,773	0,124455
**30P	Y132F	220660,8	6,682	10473,24	0,114979
**45P	Y132F	46916,25	0,569333	7045,647	0,065245
**56FS	Y132F	74271,33	2,4625	10517,19	0,197098
**67FS	Y132F	220025,2	2,562667	12514	0,020861
**68FS	Y132F+K143R	157217,6	1,916	15421,05	0,021894
**96P	Y132F+K143R	186353,4	3,370667	22637,79	0,079691
**97FS	Y132F	179695,8	3,082667	9885,604	0,0251
10P	G458S, T519A	233358,6	4,6325	18999,61	0,321584
26R	Q250K, R398I, G458S	207154,2	8,824667	11208,06	0,065908
31P	G458S	242899,1	5,804	20401,04	0,050735
34R	R398I	154564,8	2,317917	13999,69	0,210447
36P	G458S	248692,6	5,861333	11939,6	0,116
37R	R398I	57344,92	0,396917	13438,28	0,122315
54R	None	178940,9	2,401333	28932,24	0,025882
65P	G458S	215346,3	3,93	9241,754	0,042824
91P	G458S	217026,8	5,161333	20360,58	0,100241

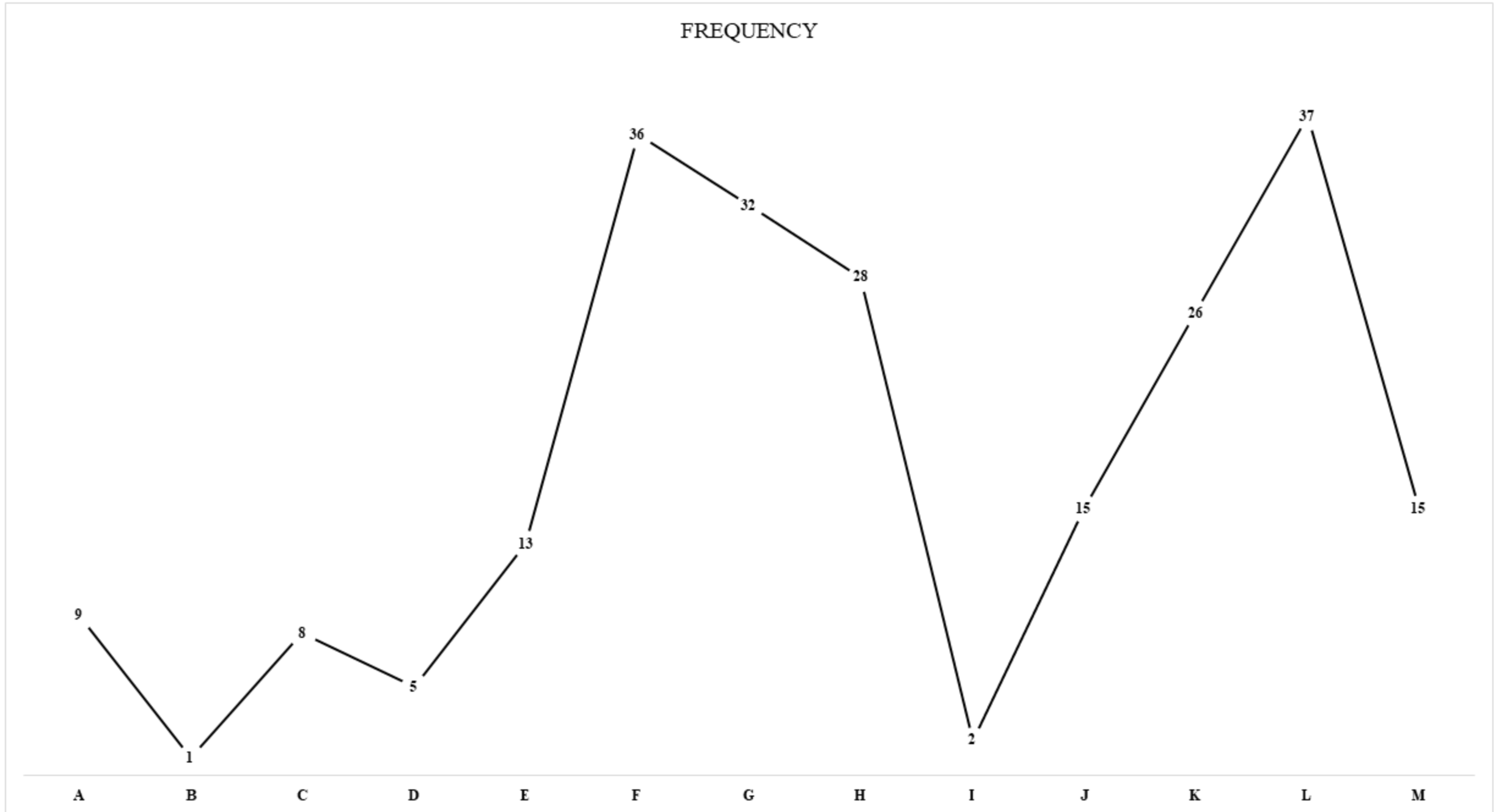
**TABLE S3** Results of the azole antifungal susceptibility assay and amino acid substitutions found in proteins implicated in azole resistance.

Strain #	Erg11p	Mrr1p	Tac1p	Upc2p	Fluconazole (mg/L)	Voriconazole (mg/L)
1R	Y132F, K143R			L38I	>32	2
21R			F186I		2	<0,03
22R				G342S	16	<0,03
23R					4	<0,03
25R	R398I			A793S	2	<0,03
26R	Q250K, R398I, G458S	P295L, Q1074*	L390I		16	0,25
27R	R398I				4	0,25
28R			L578M	L38I, A793S	1	0,06
30R	Y132F, K143R				>32	1
31R	R398I				2	0,06
33R					0,5	0,0156
34R	R398I		G490R		32	0,25
37R	R398I				>32	0,5
38R	R398I		G490R, S760R, A761G		32	0,5
39R	R398I		L578M	A793S	4	0,125
41R	Y132F, K143R			L38I	32	0,06
42R	R398I				2	<0,03
43R	K143R			L38I	16	0,5
44R		K606E	E312D		2	0,06
46R				A793S	0,5	0,0156
47R	R398I			Q348P	0,5	<0,03
48R	R398I		N7I		0,5	<0,03
49R	R398I				0,25	0,0156
50R	Y132F, K143R			L38I	>32	1
51R	R398I		L390I		2	0,03
52R	R398I				2	0,03
54R					32	0,125
70R				A793S	0,125	<0,03
72R			N7I	L38I, A793S	0,5	<0,03
105R				L38I	0,5	0,0156
127R	R398I			P201S	2	<0,03
5FS	Y132F (A395W)			L38I, A793S	>32	0,25
6FS	Y132F, K143R			L38I, A793S	>32	1
15FS	Y132F, K143R			A793S	>32	1
56FS	Y132F				>32	2
59FS	Y132F, K143R				>32	1
62R	R398I				0,5	<0,03
63R			L574F		0,25	<0,03
64R			N7Y, A352V	A793S	0,25	<0,03
67FS	Y132F (A395W)				32	0,5

68FS	Y132F, K143R				32	0,5
69FS	Y132F, K143R			L38I, A793S	>32	1
76R				S577*	0,06	0,0156
94FS	Y132F			L38I, A793S	>32	0,125
97FS	Y132F (A395W)				32	0,5
101FS	Y132F, K143R			L38I, A793S	>32	1
106FS	Y132F, K143R			A793S	>32	1
107FS	Y132F, K143R		A21V		>32	1
108FS	Y132F		A21V		8	0,06
112FS	K143R		A21V	A793S	>32	0,5
1P			L578M, N602Y	A793S	0,5	<0,03
2P	Y132F		L578M	A793S	8	0,25
3P	Y132F		N7Y, L578M	A793S	8	0,25
4P		NA	NA	NA	0,5	<0,03
5P					0,125	<0,03
6P	R398I				0,5	<0,03
7P	Y132F, K143R	L926*			>32	0,5
9P	Y132F			A793S	>32	2
10P	G458S, T519A			A793S	16	0,5
15P	Y132F			A793S	8	0,125
16P	R398I				2	0,06
17P	Y132F				8	0,25
18P	Y132F, K143R				>32	4
19P	Y132F				8	0,125
25P	Y132F	G427V	P150H		8	0,25
30P	Y132F				16	0,25
31P	G458S				>32	1
35P	Y132F, G307A				>32	2
36P	G458S				16	0,5
37P	Y132F				>32	0,5
38P	R398I		G490R		0,06	0,03
40P	Y132F			L38I	16	0,25
41P	Y132F			A793S	8	0,125
42P	Y132F			E7*	8	0,25
43P	Y132F, K143R				>32	1
45P	Y132F				8	0,25
47P	Y132F			P45H	8	0,25
49P	Y132F, G307A				>32	2
50P	Y132F			P45H, A793S	8	0,125
54P	Y132F, K143R		Q965K, M966V		>32	1
55P		L419F			8	0,25
59P	Y132F			Q372H	8	0,25
60P	Y132F	Q1027R	D603V, P803L		8	0,125
65P	G458S			Q371H	16	0,5
75P	Y132F	Q1027R			8	0,25
77P	Y132F, G307A			L38I, Q371H	16	0,5

81P	Y132F, K143R	G472V			>32	0,5
87P	Y132F, K143R			P45H	>32	1
91P	G458S				16	0,5
96P	Y132F, K143R				>32	1
97P					0,5	<0,03

FIG S1. Frequency of isolation of the *C. parapsilosis* species complex per year. (A) 2007, (B) 2008, (C) 2009, (D) 2010, (E) 2011, (F) 2012, (G) 2013, (H) 2014, (I) 2015, (J) 2016, (K) 2017, (L) 2018, and (M) 2019.



# FREQUENCY

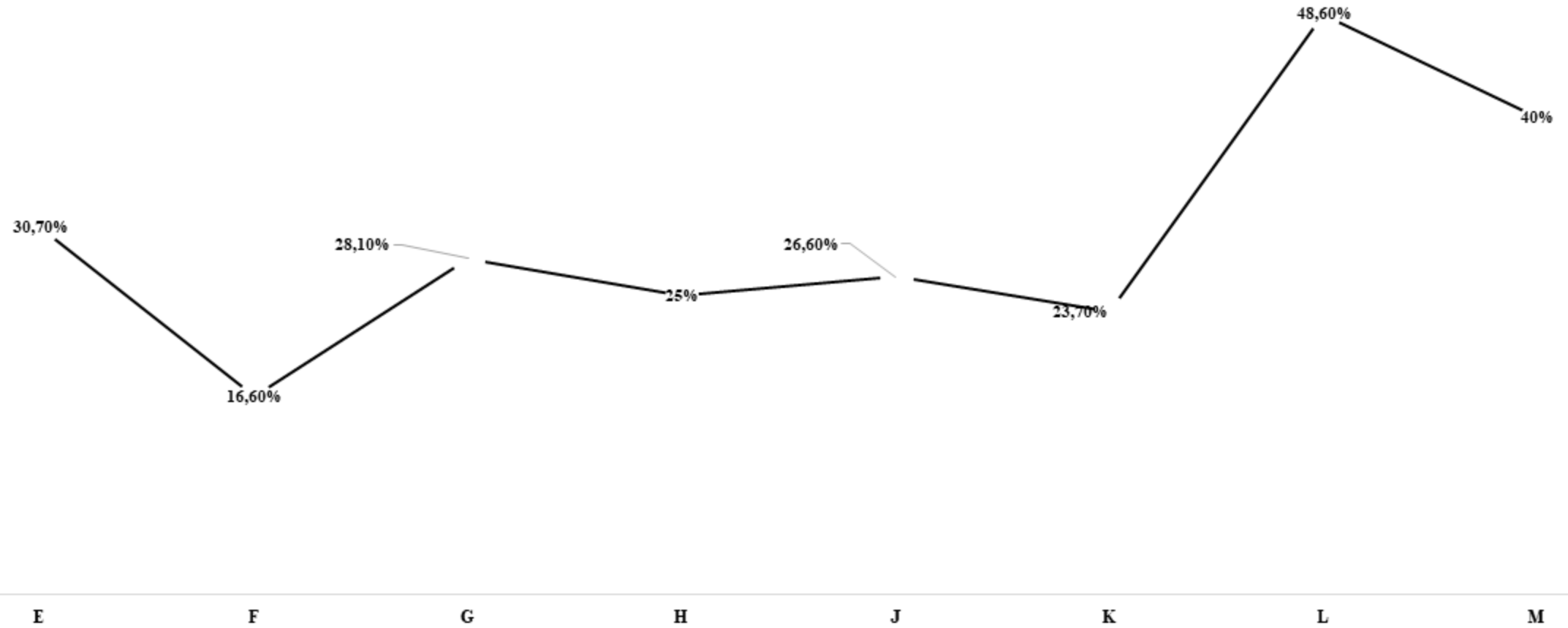


FIG S2 Dynamic frequency (percentage) of FLZR isolates in each year.



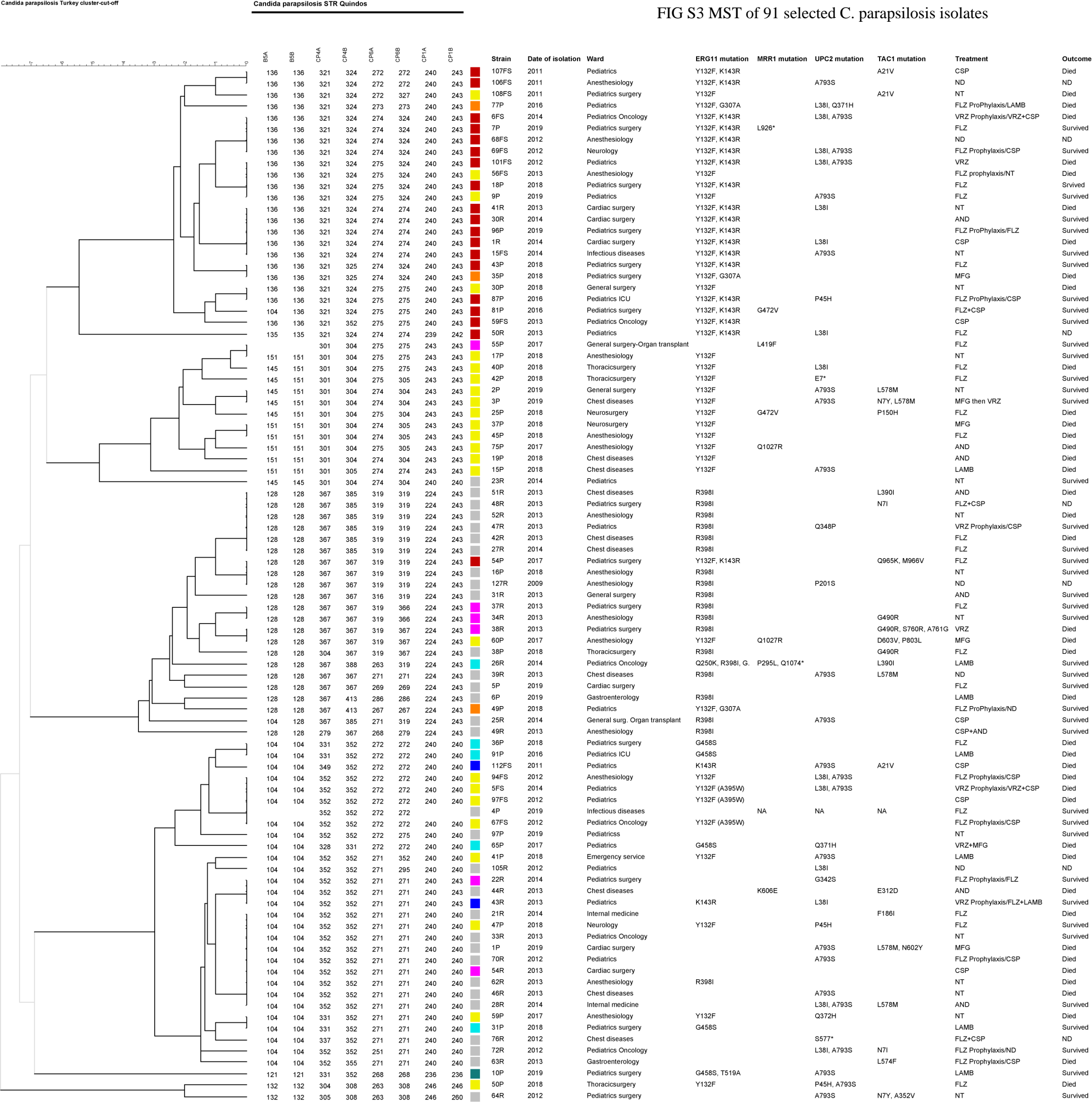






FIG S6 AFLP typing of 91 selected *C. parapsilosis* isolates

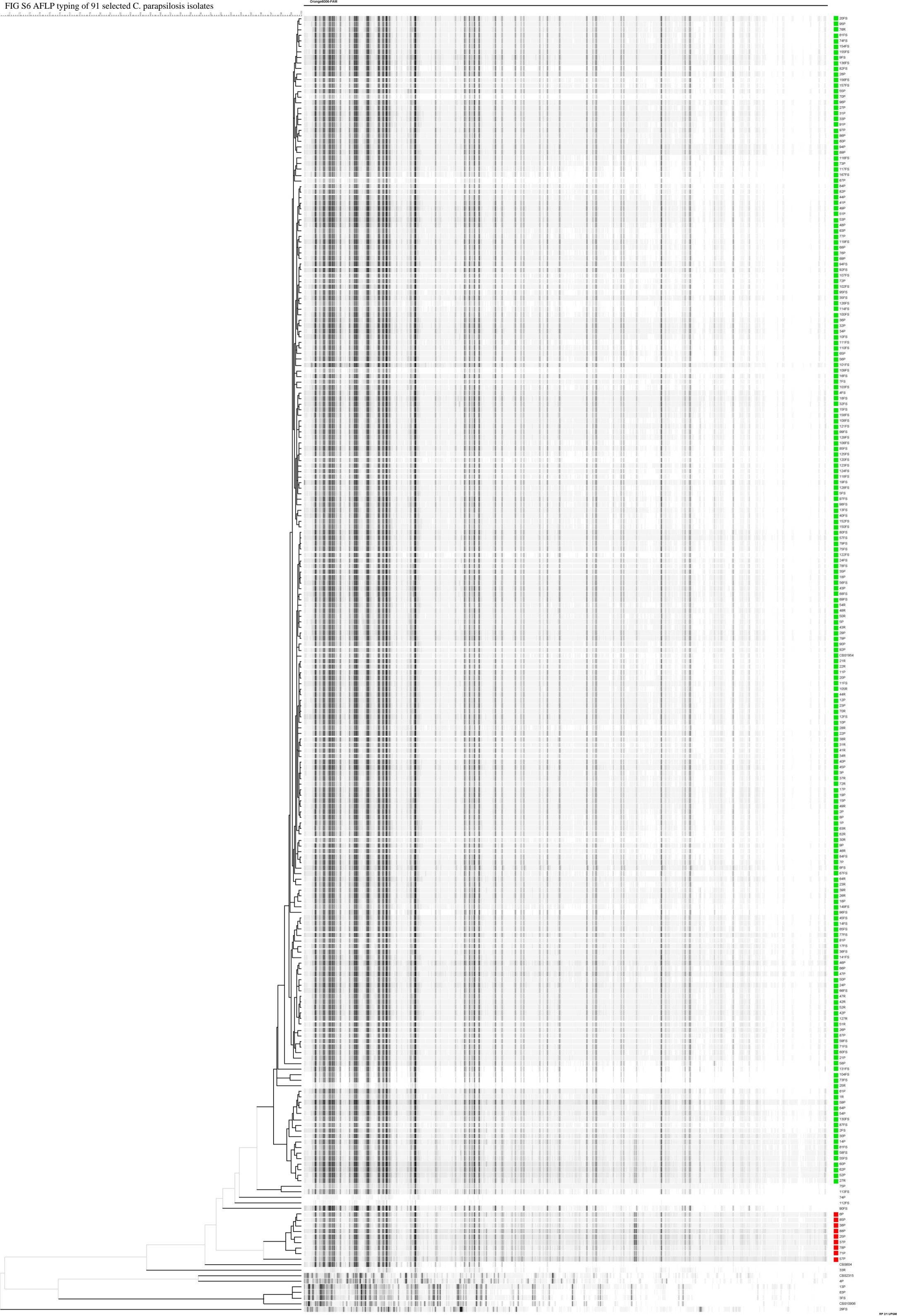


FIG S7 Biofilm formation by isolates with the Y132F mutation and other FLZR isolates. The data are expressed as the mean  $\pm$  standard deviation for crystal violet and resazurin-based viability staining (n = 12 wells).

