

FIG S1 The effect of RF on *C. parapsilosis* hyphal and biofilm formation. (A) Hyphae formation was evaluated in a 1640 RPMI + 10 % (v/v) FBS liquid medium and the uniformly enlarged image is presented in the black boxes on the left hand. Scale bar: 20  $\mu$ m. (B) Hyphae formation was evaluated on YPD+10 % (v/v) FBS agar plates. (C) The biomass of *C. albicans* biofilm was observed by a crystal violet (CV) assay. (D) Metabolic activity of *C. albicans* biofilm was determined by 2,3-bis-(2-methoxy-4-nitro-5-sulphophenyl)-2H-tetrazolium-5-carboxanilide (XTT) assay and the results are presented as relative percentages. Data were analyzed by t test (ns  $P > 0.05$ , \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ , \*\*\*\*  $P < 0.0001$ ).

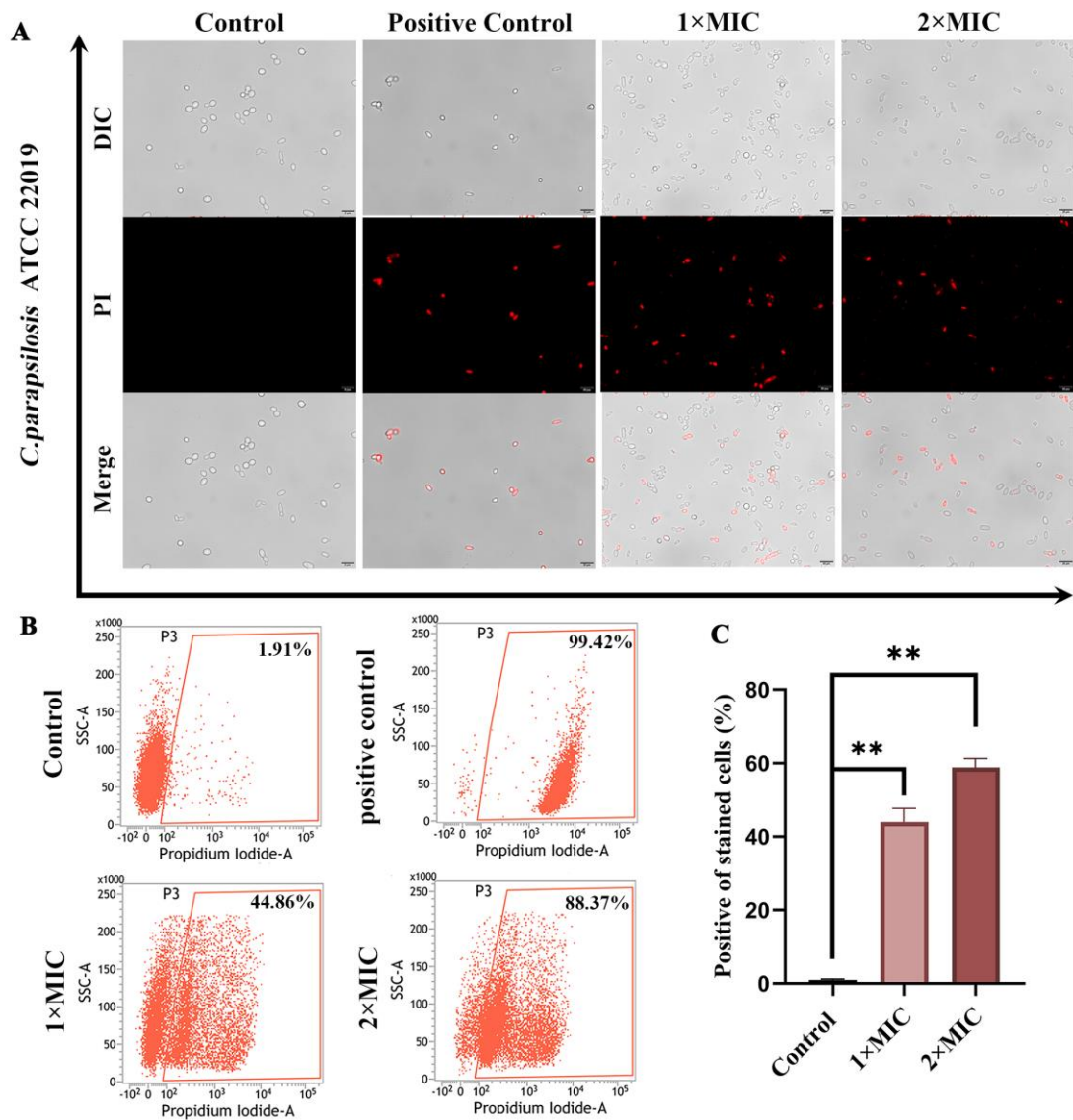


FIG S2 The effect of RF on *C. parapsilosis* cell membrane. *C. parapsilosis* cells with or without RF treatment were stained with propidium iodide (PI) and analyzed by (A) fluorescence microscopy and (B) flow cytometry. Scale bar: 20  $\mu\text{m}$ . (C) Histogram analysis shows the percentage of PI-positive cells. Data were analyzed by ANOVA (ns  $P > 0.05$ , \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ , \*\*\*\*  $P < 0.0001$ ).

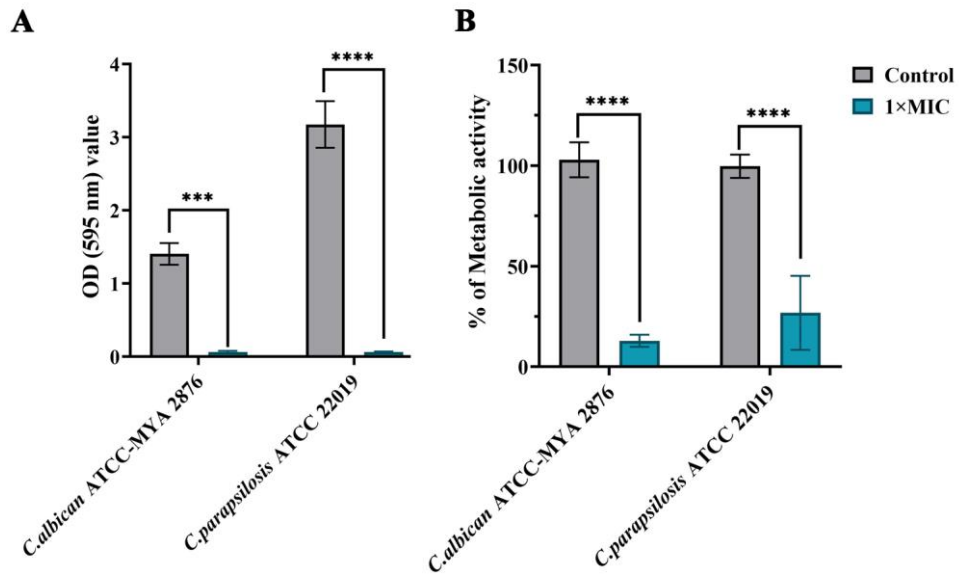


FIG S3 The effect of RF on adhesion. The adhesion of *C. albicans* and *C. parapsilosis* were examined by (A) CV assay and (B) XTT assay. Data were analyzed by t test (ns  $P > 0.05$ , \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ , \*\*\*\*  $P < 0.0001$ ).

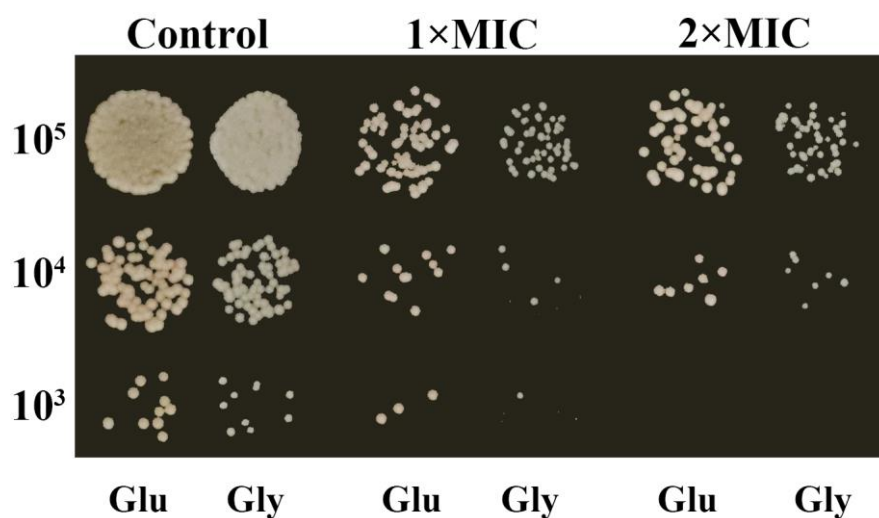


FIG S4 Effects of RF on glucose (Glu) and glycerol (Gly) utilization in *C. albicans*. Strains with defective respiratory function are unable to utilize non-fermentative carbon sources (glycerol).

TABLE S1 Primers sequence of target genes

Gene	Sequence (5'-3')
<i>ACT1-F</i>	CCAGGTATTGCTGAACGTATGC
<i>ACT1-R</i>	ACTCTGTCTGGATTGGTGGTTC
<i>HWP1-F</i>	TCTCTACGACTGAAGGTGCTATTC
<i>HWP1-R</i>	GACTTTCGGTGCTGCTATTATTGG
<i>ALS3-F</i>	CCTATACCACTGCTACTACCGTT
<i>ALS3-R</i>	CGTCCTCATTACACCAACCATAAC
<i>BCR1-F</i>	TACACCTAAAAGAAGACCCGAACC
<i>BCR1-R</i>	ACCAACACCAATATGAACACGG
<i>NDT80-F</i>	AATCTACCCTGCAGTTCCTTCAG
<i>NDT80-R</i>	AGGGGAAACTACTACCAAGAGTAC
<i>ERG11-F</i>	TGGAGACGTGATGCTGCTCA
<i>ERG11-R</i>	ACGTGGTGATATTGATCCAAATCGT
<i>ECE1-F</i>	CCAGAAATTGTTGCTCGTGTTG
<i>ECE1-R</i>	CTTGTTGAACAGTTTCCAGGACG
<i>CDA2-F</i>	GTGGCGGCAGTGGATTAC
<i>CDA2-R</i>	AGGTGGATCTAAATCTGGCCATT
<i>ERG2-F</i>	GCCACGGCCATTATGATTGA
<i>ERG2-R</i>	AGTCCCAATTGCTGTACCGA
<i>ERG11-F</i>	TGGAGACGTGATGCTGCTCA
<i>ERG11-R</i>	ACGATTTGGATCAATATCACCACGT
<i>RIB4-F</i>	TGGTATTCTTCATGCCAGATGGA
<i>RIB4-R</i>	AGGTAAACCATTAGACGCCA
<i>RIB5-F</i>	ACTCTCCGCAGAACCAATCT
<i>RIB5-R</i>	TGGCCACCCAATCTAACTTCA

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<i>THI4-F</i>	GCCACTGCCGTTGAAGATTT
<i>THI4-R</i>	CTTCTGGTCACGATGGACCT
<i>THI13-F</i>	GAGCCCTCCAATCCATCTGA
<i>THI13-R</i>	TGGGAGTCCTCTAGCTTTGG
<i>PGM2-F</i>	ACCAGGAGATTCCGTTGCTA
<i>PGM2-R</i>	TCCAACCAGTAGGAACTTCA
<i>TPH1-F</i>	ACCAAGTTTGCCTTGGACAC
<i>TPH1-R</i>	GGGTAGCGGCTAAACCAGTA
<i>RHR2-F</i>	GGATACCATGACGCCCACTA
<i>RHR2-R</i>	GCACCTTTACCTGCGGTTAT
<i>MLS1-F</i>	AGAAACAGAGCTGCTTTGGC
<i>MLS1-R</i>	TGGTTCCTTTGGTGGCAATG
<i>PCK1-F</i>	CTTGGTGTGACCCCAATGA
<i>PCK1-R</i>	AGAACCAACCAACCAGTGT
<i>FDH1-F</i>	AGAGGTATCGCTGCCATTGA
<i>FDH1-R</i>	AACAGCAGCAACATCCCAAG
<i>ADH2-F</i>	TTAGAAGCCGGTCAATGGGT
<i>ADH2-R</i>	CATGGCCTTGGCGTATTGAA
<i>RPL3-F</i>	ACGTCACGGTTCCTTAGGTT
<i>RPL3-R</i>	AAGGCAGTCAAAGCAACTGG
<i>RPL4B-F</i>	AAGGCAGTCAAAGCAACTGG
<i>RPL4B-R</i>	GCTTGTTCAACCTTGGCAGA
<i>RPL10-F</i>	AGGTATGAGAGGTGCTTGGG
<i>RPL10-R</i>	TTGTTGACCTGGGAACTTGT
<i>RPL17B-F</i>	CCTGCTAACCCAGCCAAATC
<i>RPL17B-R</i>	TGGCTTGAGCAGTTTCTCTG
<i>RPP1A-F</i>	TCAACTTCTCTGCTGCTCCA
<i>RPP1A-R</i>	TTCTTCAGCAGCTTCTTCGG
<i>YST1-F</i>	CCCAAGAACCGATGCTCAAG
<i>YST1-R</i>	TCTCTAGCAAGCAACCACCA
<i>RPS14B-F</i>	TTGCCAGAGTTACTGGTGGT
<i>RPS14B-R</i>	AGCTCTTAAAGCGGATTGACC
<i>ASC1-F</i>	CGCTGACTTCATTGGTCACA
<i>ASC1-R</i>	AAGCATGAACTTCGGCCTTG

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