

Table S1. Primers used for qPCR experiments in this study.

Primer	Sequence (5' – 3')	Reference
B-actin_F	GCTGACAGGATGCAGAAGGA	[66]
B-actin_R	TAGAAGCATTTGCGGTGGAC	
IL1-B_F	TTGTGGGAGACAGACAGTGC	
IL1-B_R	GATTGGGGTTTGATGTGCTT	
TNF-a_F	ACAAGGCAATTTCACTTCCA	
TNF-a_R	AGCTGATGTGCAAAGACACC	
IL-10_F	TCACGTCATGAACGAGATCC	
IL-10_R	CACCATATCCCGCTTGAGTT	
iNOS_F	GAGCAGGCCCAATGCATTT	
iNOS_R	TGCGCTGCTGCCAGAAAC	
IFN-γ_F	CTATGGGCGATCAAGGAAAA	[67]
IFN-γ_R	CTTAGCCTGCCGTCTCTTG	
MyD88_F	TAAACGGCTAATCCCTGTCTG	
MyD88_R	TCGAGTCCAGAACCAGACCT	
IL-6_F	GGACGTGAAGACACTCAGAGACG	[28]
IL-6_R	AAGGTTTGAGGAGAGGAGTGCTG	
IL-17a_F	CAATCTGAGGACGGAAGGG	
IL-17a_R	ACTGGGCTTCAAAGATGACC	
NF-κB P65F1	GGCAGGTGGCGATAGTGTT	[68]
NF-κB P65R1	CATTCTTCAGTTCTCTTGCG	
jak2F1	TCGCTGCTTCTTCTGTCAGG	
jak2R1	ACAGCCGTCCATTTTGGCTT	
stat3F1	CATTCCCAAAGAGGAGGCGT	
stat3R1	ATTTGGCTCGGAGAGAAAGCA	
foxp3a_F	ACCTCACCAAAACCAATGGC	
foxp3a_R	TCTGATTGCGAGATGAGCCG	[63]
foxp3b_F	GCGTGGACGAGACTTTTCT	
foxp3b_R	GCAGCTGAAGAACTGCATTC	
mpx_F	TTCCAGAAAATCCGAGATGG	
mpx_R	CCATTGACACAGAAGCCAGA	[22]
IL-8_F	TTTCCTGGCATTCTGACC	
IL-8_R	CGTCGGCTTTCTGTTTCAAT	
mmp9_F	CCCTGGCTCTGGACCAGCC	[69]
mmp9_R	CTGTGCGGCCCTCAGTGGTG	
mmp13_F	CCGCCTGCTGGAGGAGACCA	
mmp13_R	GACGGGCTCGGGTTCTGTGC	

Table S2. Average of gene expression levels of zebrafish infected with *C. auris* and *C. haemulonii* at different timepoints, compared with the expression level of β -actin in each group.

Genes	<i>C. auris</i>			<i>C. haemulonii</i>		
	8 hpi	96 hpi	<i>P</i> value#	8 hpi	96 hpi	<i>P</i> value#
Proinflammatory and inflammatory cytokines						
<i>tnfa</i>	1.57**	1.13 ^{NS}	0.0077	1.04 ^{NS}	1.09 ^{NS}	0.9579
<i>ifng</i>	0.78*	0.40****	0.0007	0.81 ^{NS}	0.76 ^{NS}	0.8620
<i>il1b</i>	1.55**	0.70*	0.0003	0.78 ^{NS}	1.24 ^{NS}	0.0443
<i>il6</i>	0.88 ^{NS}	1.47*	0.0130	1.14 ^{NS}	2.46****	<0.0001
<i>il8</i>	2.98****	0.84 ^{NS}	<0.0001	1.49**	1.03 ^{NS}	0.0093
<i>il10</i>	1.48*	1.01 ^{NS}	0.0242	0.81 ^{NS}	1.52**	0.0394
<i>il17a</i>	1.11 ^{NS}	1.97**	0.0019	2.17***	1.24 ^{NS}	0.0040
Leukocyte activities						
<i>inos</i>	0.78 ^{NS}	1.87***	<0.0001	0.68 ^{NS}	1.66**	0.0003
<i>mpx</i>	1.09 ^{NS}	1.22 ^{NS}	0.4064	0.92 ^{NS}	3.06****	<0.0001
Matrix metalloproteinases						
<i>mmp9</i>	0.39****	1.13 ^{NS}	<0.0001	1.95****	1.30****	<0.0001
<i>mmp13</i>	1.28 ^{NS}	1.22 ^{NS}	0.8342	1.36 ^{NS}	1.32 ^{NS}	0.9638
Inflammatory regulators						
<i>myd88</i>	1.61*	0.95 ^{NS}	0.0107	1.11 ^{NS}	1.10 ^{NS}	0.9960
<i>nfkb</i>	0.85 ^{NS}	1.03 ^{NS}	0.0353	1.29*	1.86***	0.0014
<i>jak2</i>	2.16****	0.37***	<0.0001	0.33***	0.21****	0.0342
<i>stat3</i>	1.56*	1.19 ^{NS}	0.0003	2.11***	1.49*	<0.0001
Regulatory T-cells						
<i>foxp3a</i>	2.02***	0.87 ^{NS}	0.0002	0.72 ^{NS}	2.44***	<0.0001
<i>foxp3b</i>	1.25*	0.82 ^{NS}	0.0016	0.80 ^{NS}	1.41*	0.0001

Note: The normalized expression levels were analyzed with the Livak method ($2^{-\Delta\Delta CT}$): < 1, downregulation; 1, basal; > 1, upregulation.

Abbreviations and symbols: hpi, hour post infection; Compared gene expression level with β -actin in each group: ^{NS}, not significant; *, $P < 0.5$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; #, Comparison of expression level at different timepoint in each group.

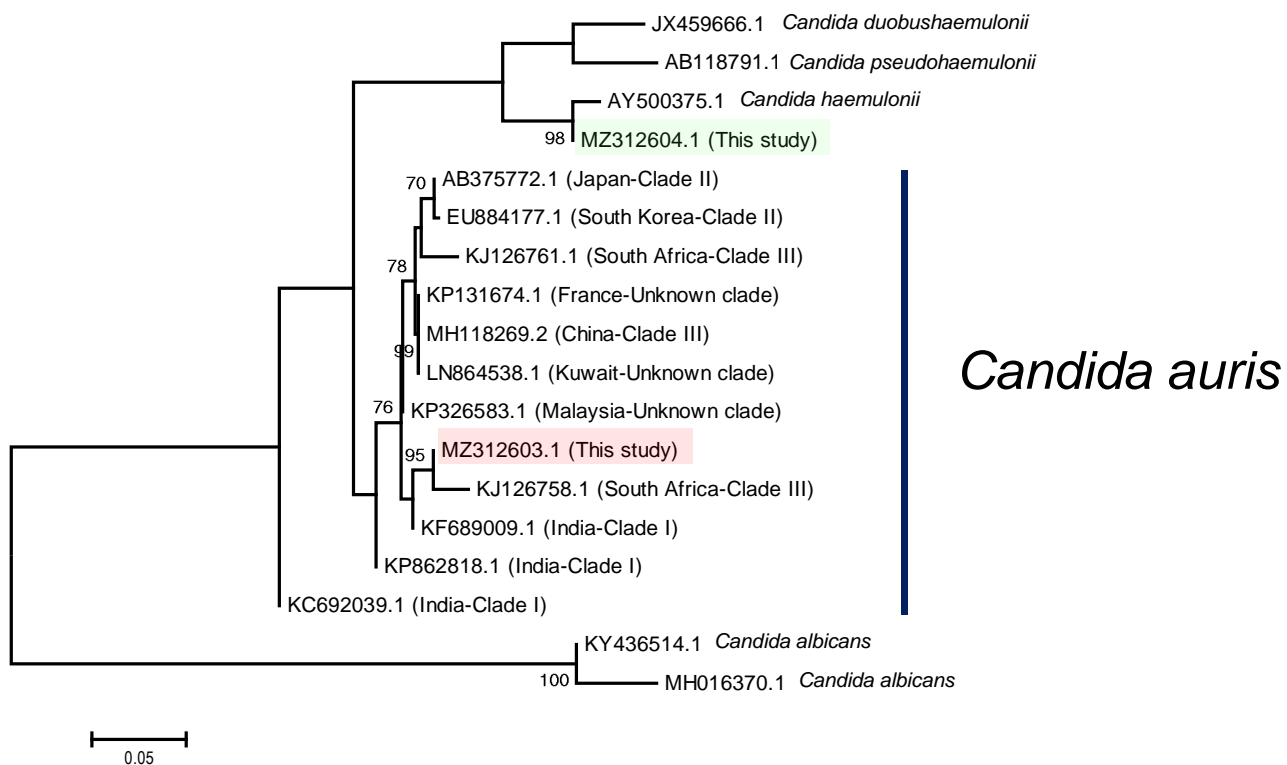


Figure S1. Phylogenetic tree using ITS sequences of emerging strains in this study (aligned by ClustalW and drawn by p-distance model and Neighbor-Joining with bootstrap analysis by MEGA program version 6). The information of ITS sequences in this analysis was adapted from [70].

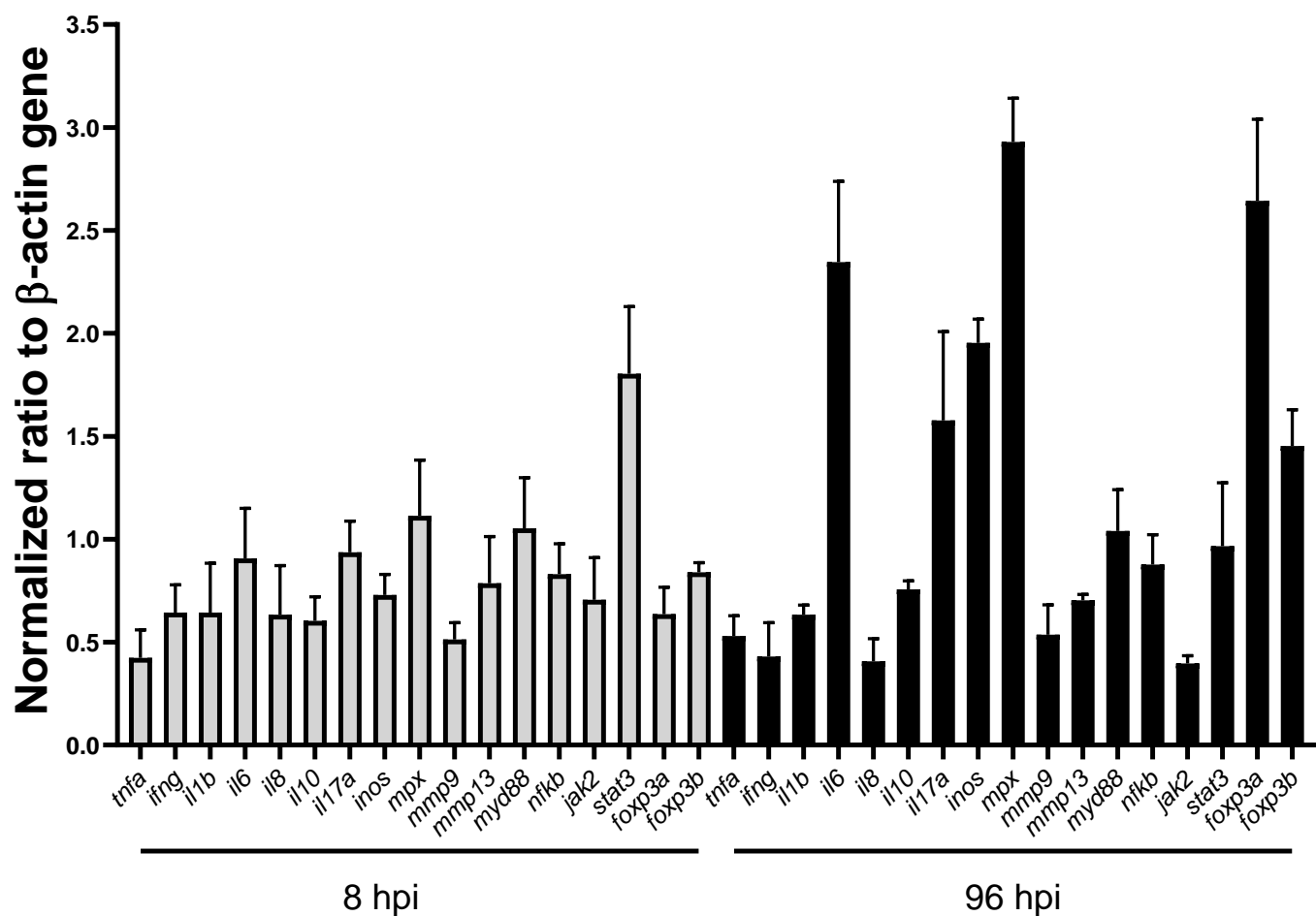


Figure S2. qPCR analysis of the gene expression levels in zebrafish infected with *Candida albicans* ATCC24433 as a control strain in this study. Each experimental group of 20 zebrafish was injected with 10^7 CFU yeast suspension. The normalized ratios of expression were calculated by comparison with the level of expression of the β -actin gene at 8 hpi. Each experiment was performed in triplicate. **Abbreviations:** hpi, hour-post-infection

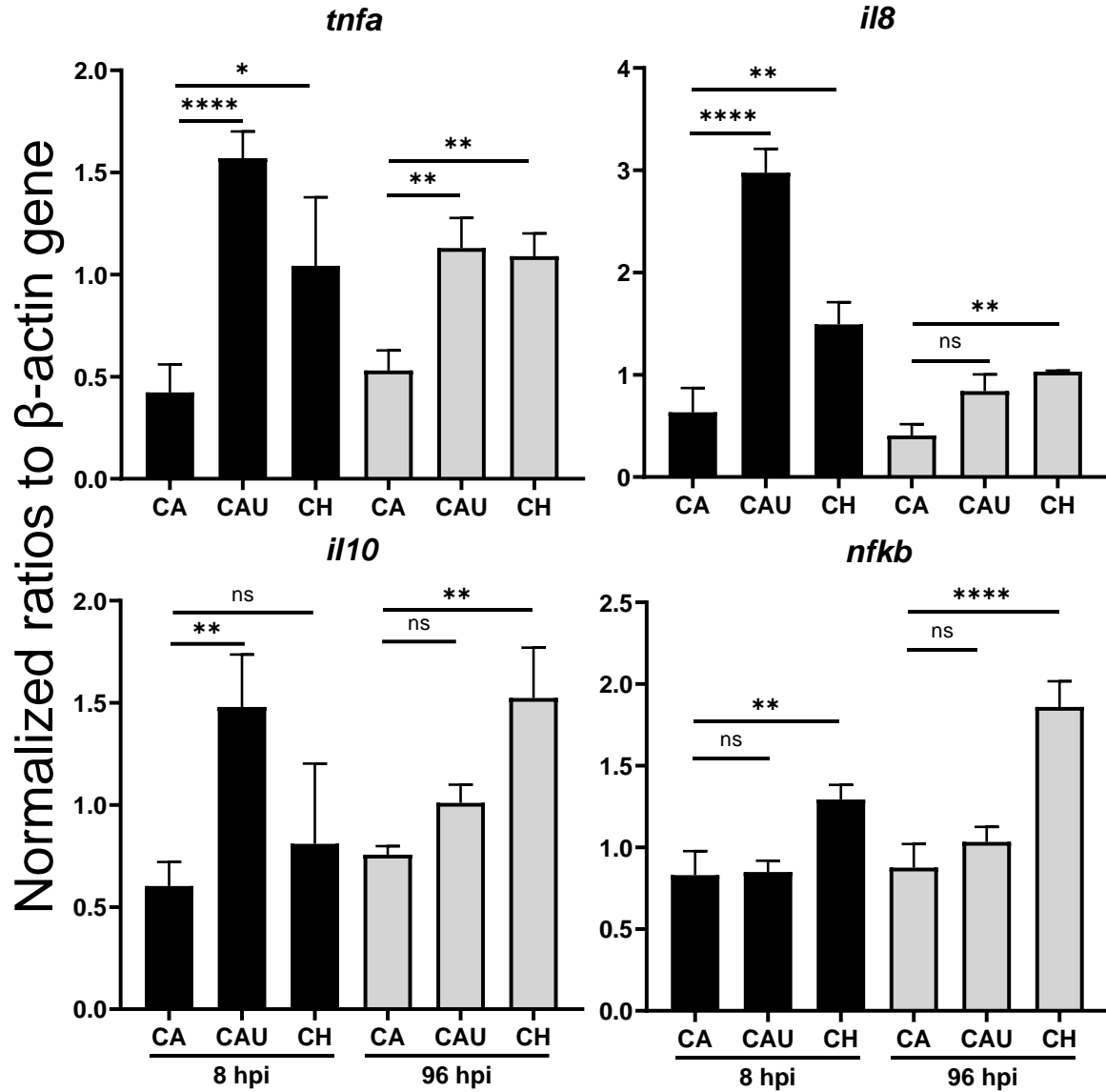


Figure S3. qPCR analysis indicating the high alterations of the expression levels of *tnfa*, *il8*, *il10*, and *nfkb* in zebrafish infected with emerging *Candida* strains. Each experimental group of 20 zebrafish was injected with 10^7 CFU cells of one of *C. albicans* ATCC24433 (CA), *C. auris* strain SI-18-CAU-HEM (CAU), or *C. haemulonii* strain SI-21-CH-PLF (CH). The normalized ratios of expression were calculated by comparison with the level of expression of the β -actin gene in each group at 8 hpi. Each experiment was performed in triplicate. **Abbreviations and symbols:** hpi, hour-post-infection; ns, not significant; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.