Figure S1

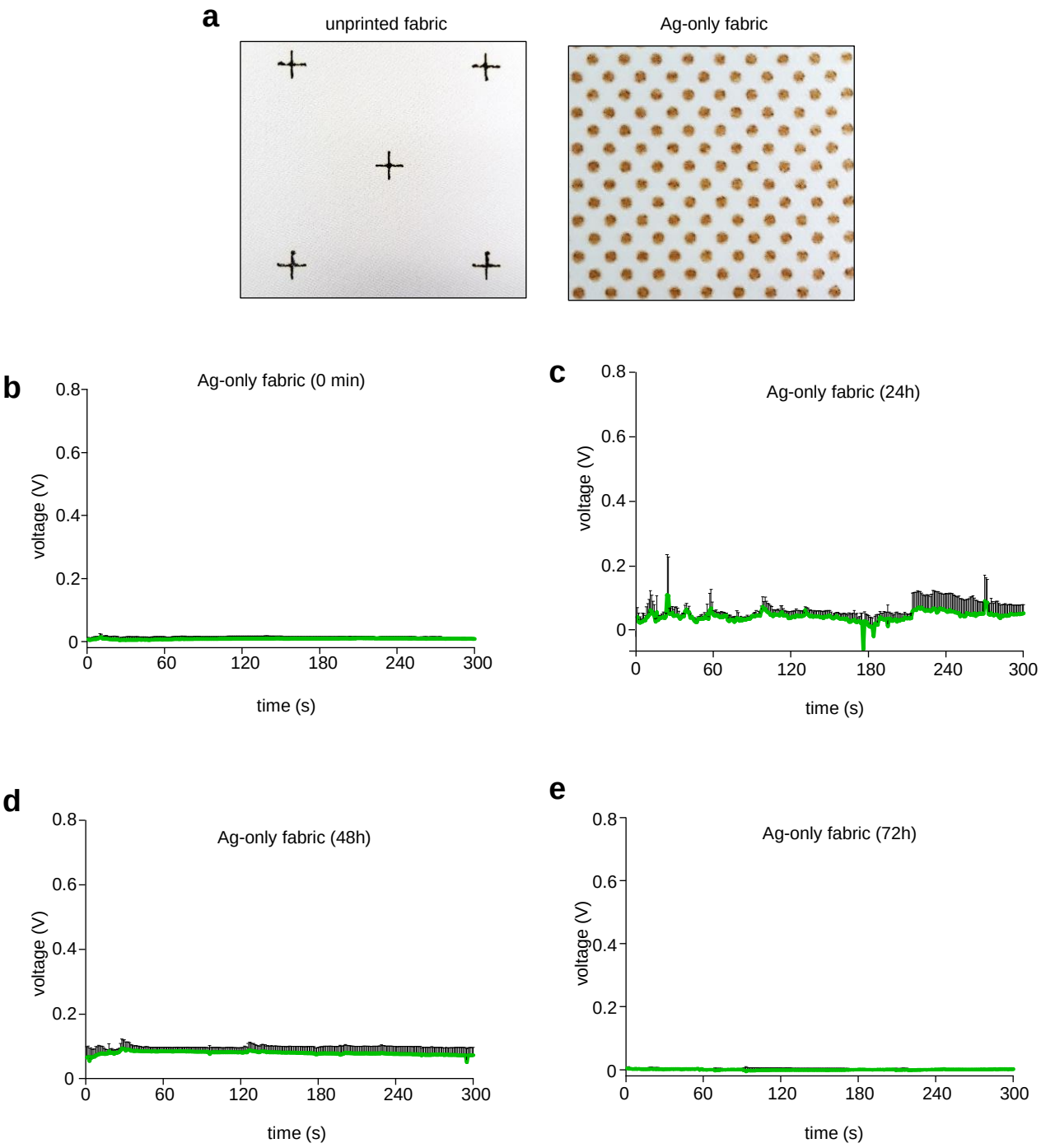

Figure S1: (**a**) Photomicrographs of unprinted fabric and silver only fabric (Ag-only fabric). (**b**–**e**) Voltage measurements for Ag-only fabric. Voltage generated by Ag-only fabric was measured using the Amprobe multimeter in presence of YPD broth. The multimeter probes were placed on adjacent Ag dots. At 0s, 200 microliters of YPD broth was added to the fabric and DC voltage was measured. Further, voltage measurements were recorded for this fabric after incubation in YPD broth for 24h, 48h and 72h. n = 4. Data are represented as the mean ± SD.

Figure S2

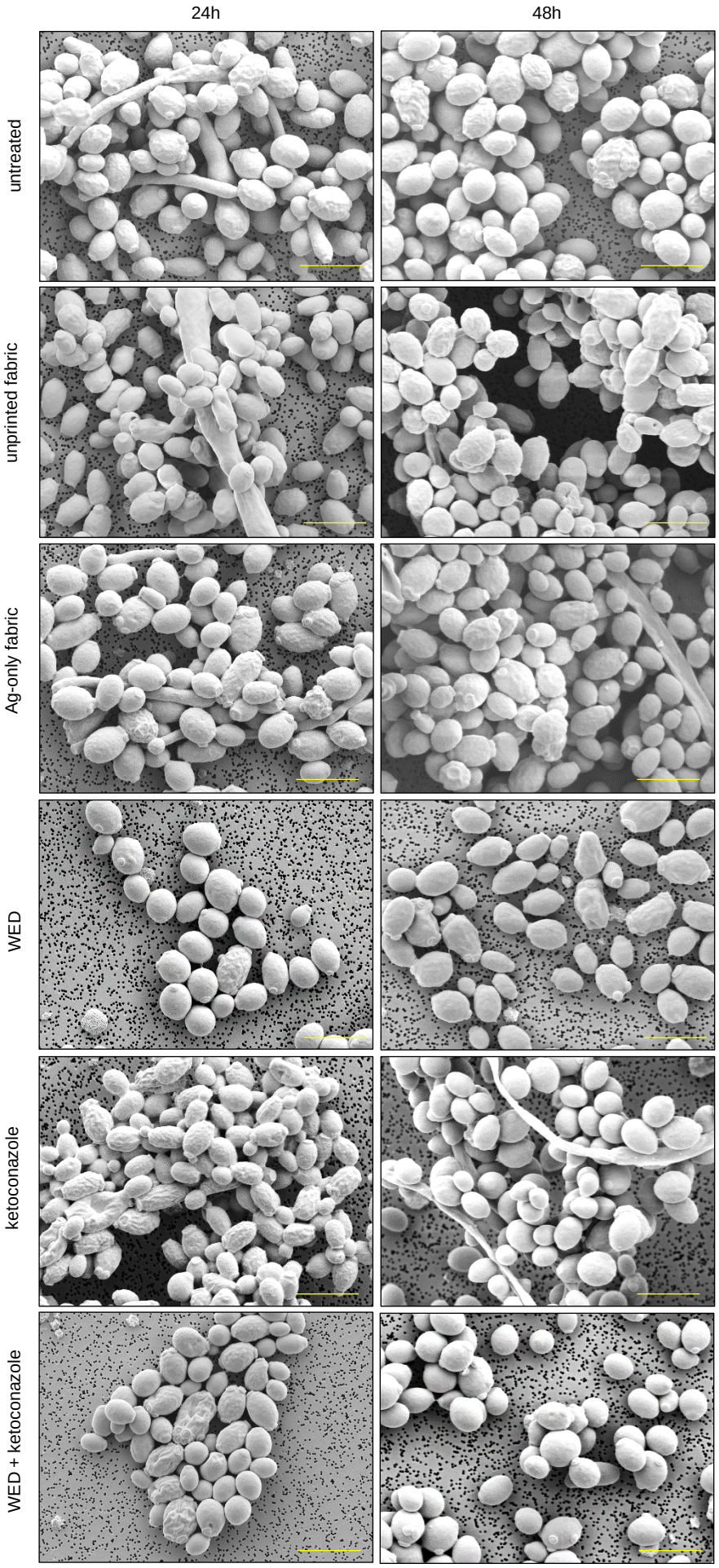

Figure S2: Enlarged representative SEM images for *C albicans in vitro* biofilm. *In vitro* biofilms (24h and 48h old) formed on polycarbonate membrane discs were processed for SEM and images were captured at 4000X magnification. These images are enlarged version of images shown in main figure 2B. Scale bar represents 5 µm.

Figure S3

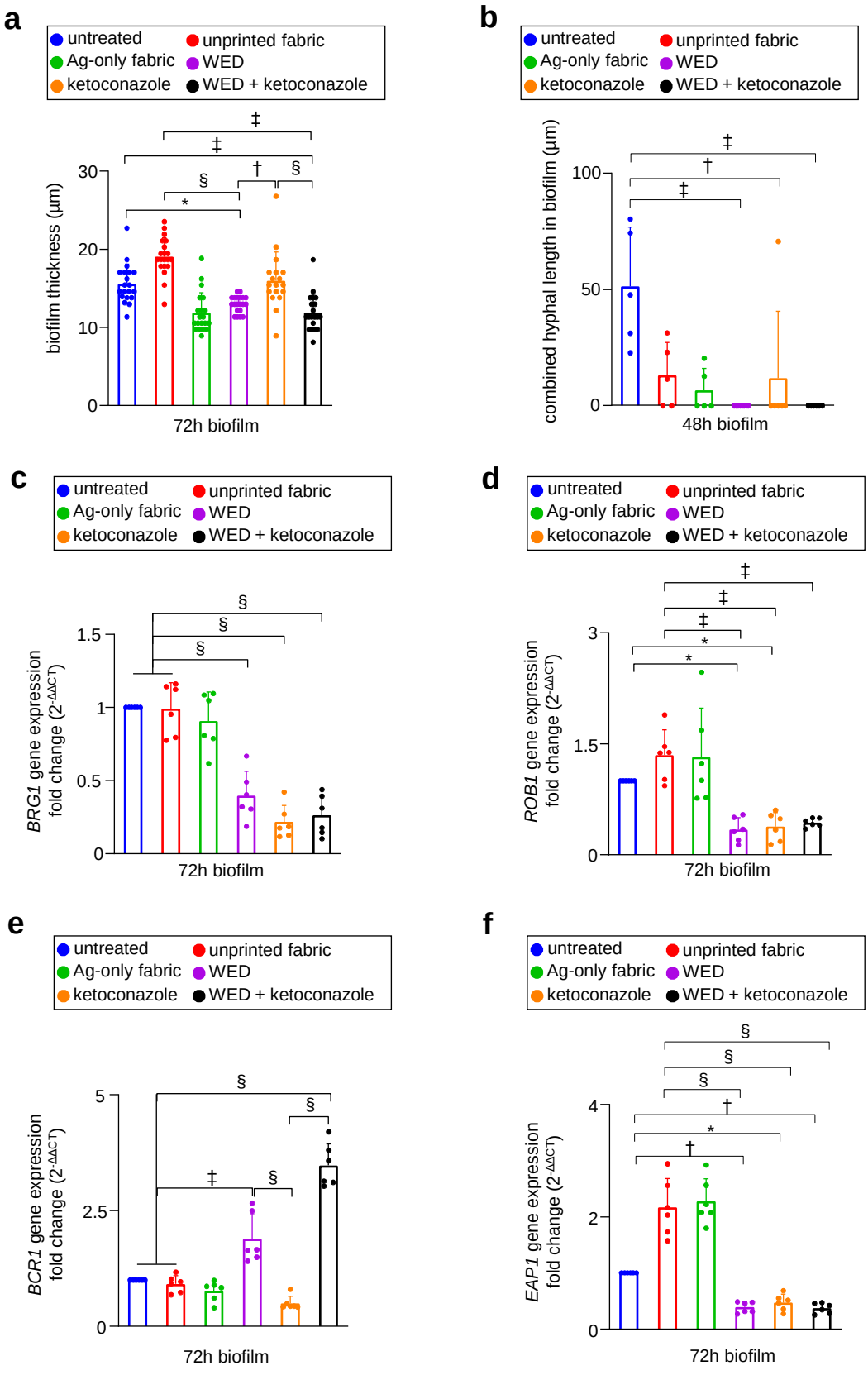
a
untreated
unprinted fabric
Ag-only fabric
WED
ketoconazole
WED + ketoconazole
biofilm thickness (µm)
72h biofilm
b
combined hyphal length in biofilm (µm)
48h biofilm
c
BRG1 gene expression fold change (2-ΔΔCT)
72h biofilm
d
ROB1 gene expression fold change (2-ΔΔCT)
72h biofilm
e
BCR1 gene expression fold change (2-ΔΔCT)
72h biofilm
f
EAP1 gene expression fold change (2-ΔΔCT)
72h biofilm

Figure S3: (**a**) Graphical representation of *C albicans* biofilm thickness. The z-axis measurements from CLSM images were plotted to depict the changes in biofilm thickness. n = 18-20 biofilms. $^{\S}P < 0.0001$, $^{\ddagger}P < 0.0005$, $^{\dagger}P \leq 0.001$ and $^{*}P < 0.05$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD. (**b**) Hyphal length measurement in *C albicans* biofilms (48h). Hyphal lengths were measured from SEM images using ImageJ software. Graph represents combined hyphal lengths for respective experimental groups. n = 5-7. $^{\ddagger}P < 0.0005$ and $^{\dagger}P \leq 0.001$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD. (**c**-**f**) Quantitative real-time PCR analysis of yeast biofilm related genes – *BCR1, BRG1, ROB1* and *EAP1*, respectively*. C albicans* cells were allowed to form biofilms on six well polystyrene plates (all six experimental groups) for 72h at 27°C. RNA was extracted from these cells and cDNA was prepared. Real time PCR analysis was performed for transcripts: *BCR1, BRG1, ROB1* and *EAP1* with aforementioned cDNA. *C albicans* actin gene (*ACT1*) was used as a housekeeping control. Expression levels were quantified employing the $2^{(-\Delta\Delta ct)}$ relative quantification method. n = 6. $^{\S}P < 0.0001$, $^{\ddagger}P < 0.0005$, $^{\dagger}P \leq 0.001$ and $^{*}P < 0.05$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Figure S4

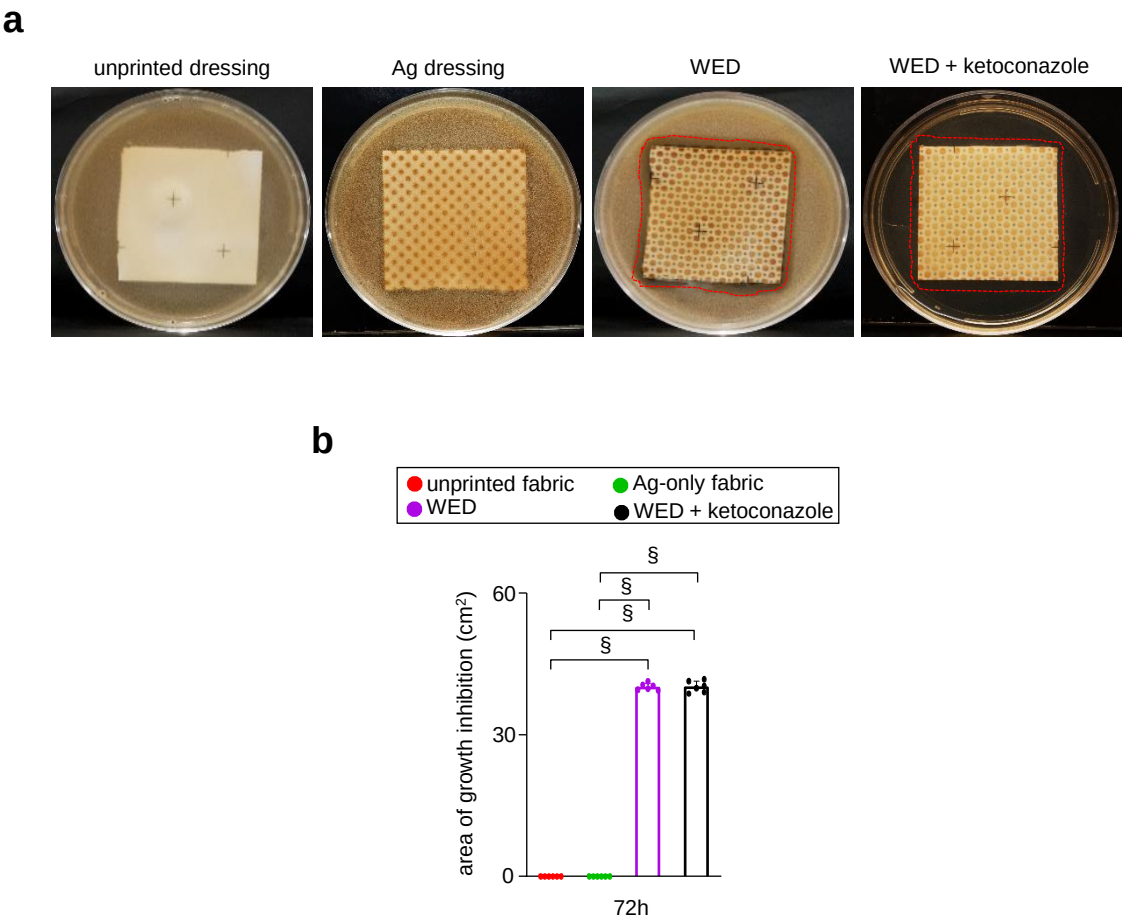

Figure S4: (**a**) Representative images for agar lawn assay. Log phase *C albicans* cells were mixed with molten YPD agar and poured in petri plates containing moist fabrics (5 cm x 5 cm). After 48h incubation at 27°C, plates were observed for area of growth inhibition around dressings. (**b**) Graphical representation of area of growth inhibition. Images were captured for aforementioned agar lawn assay plates and area of growth inhibition around farics was calculated using ImageJ software. n = 6. §$P < 0.0001$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Figure S5

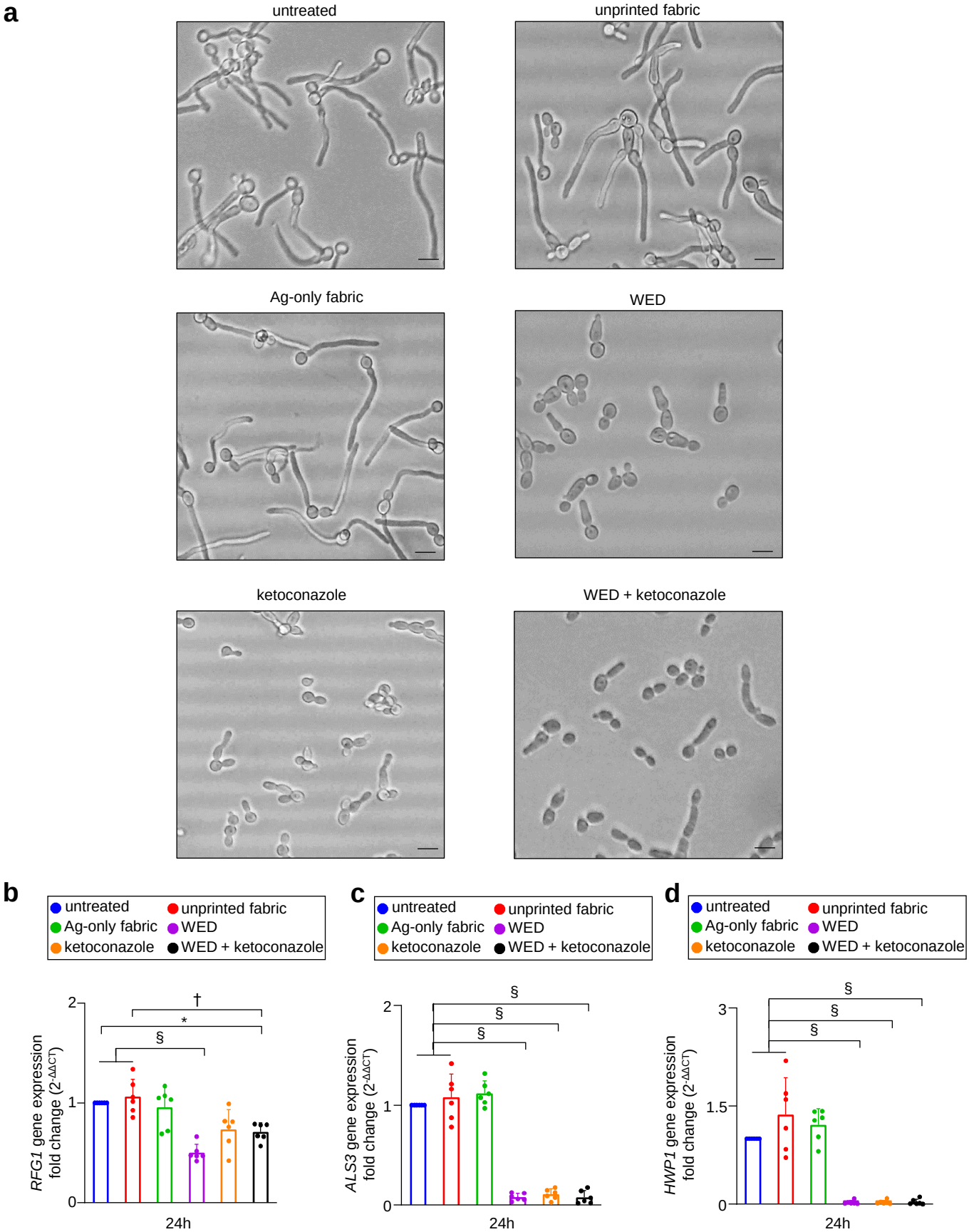
a
untreated
unprinted fabric
Ag-only fabric
WED
ketoconazole
WED + ketoconazole
b
untreated
unprinted fabric
Ag-only fabric
WED
ketoconazole
WED + ketoconazole
RFG1 gene expression fold change (2-ΔΔCT)
24h
c
ALS3 gene expression fold change (2-ΔΔCT)
24h
d
HWP1 gene expression fold change (2-ΔΔCT)
24h

Figure S5: (**a**) Representative images for hyphal transition. *C albicans* cells were allowed to form hyphae in hyphae inducing conditions. After 2h, microscopic images were captured at 20X magnification to confirm the induction of filamentation. These images were used to calculate hyphal lengths as in main figure 3A. Scale bar represents 5 µm. (**b**–**d**) Quantitative real-time PCR analysis of yeast filamentation related genes – *RFG1, ALS3* and *HWP1. C albicans* cells were induced to form hyphae in hyphae induction medium for 24h. RNA was extracted from these cells and cDNA was prepared. Real time PCR analysis was performed for transcripts: *RFG1, ALS3* and *HWP1*with aforementioned cDNA. *C albicans* actin gene (*ACT1*) was used as a housekeeping control. Expression levels were quantified employing the $2^{(-\Delta\Delta ct)}$ relative quantification method. n = 6. $^{\S}P < 0.0001$, $^{\dagger}P \leq 0.001$ and $^{*}P < 0.05$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Figure S6

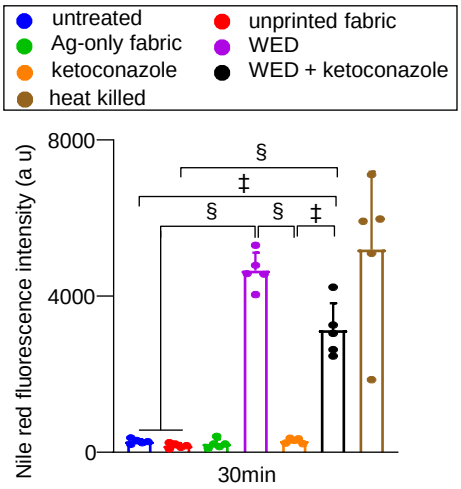

Figure S6: Graphical representation of Nile red fluorescence intensities. *C albicans* cells were assayed for accumulation of Nile red as a measure of efflux pump activity. Microscopy images were captured at 63X magnification (main figure 4C). Display settings for all images were kept same. Nile red fluorescence intensities were measured from these images using Zen Blue software and represented graphically. n = 5. $^{\S}P < 0.0001$, and $^{\ddagger}P < 0.0005$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Figure S7

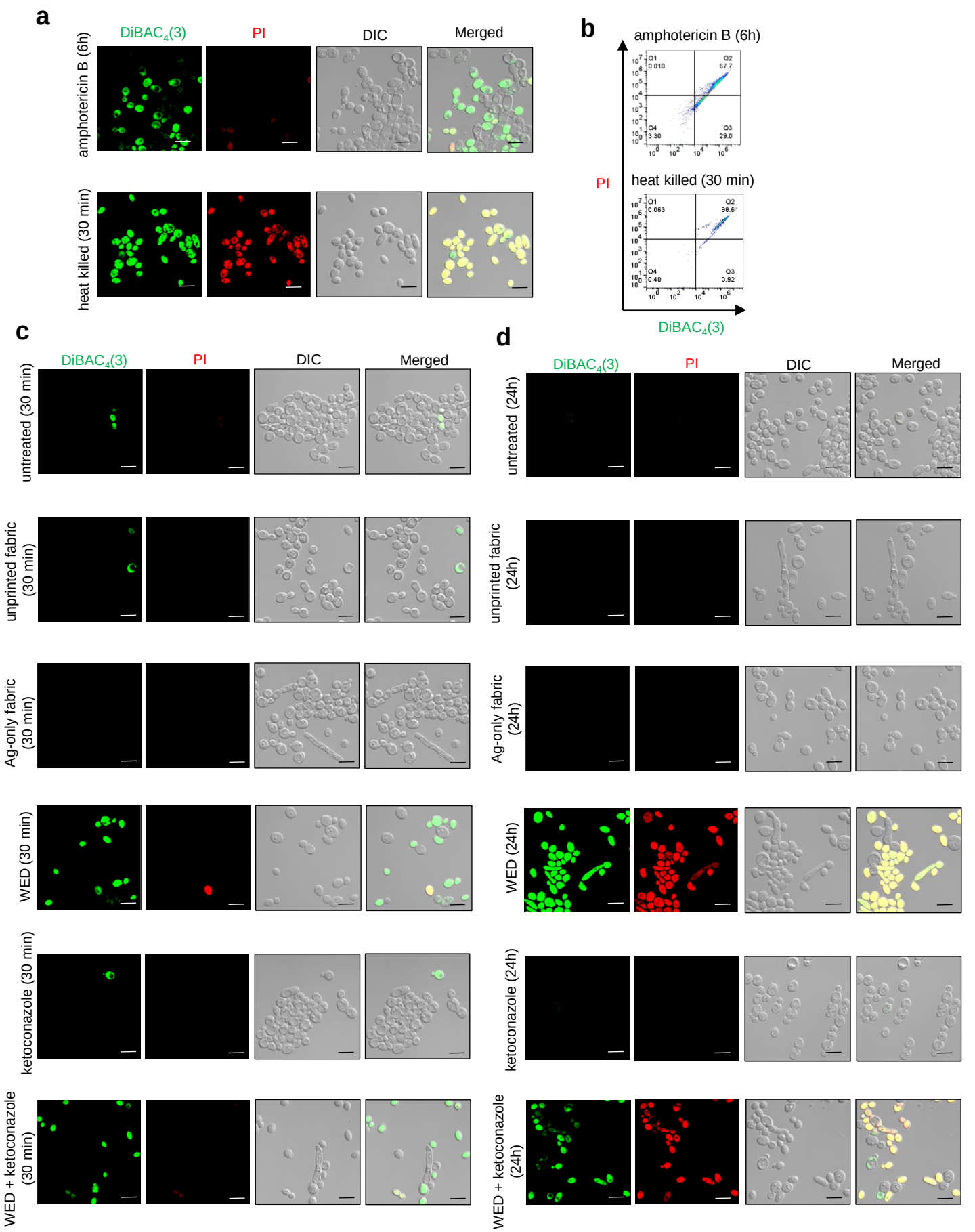
a
DiBAC4(3)
PI
DIC
Merged
amphotericin B (6h)
heat killed (30 min)
b
amphotericin B (6h)
heat killed (30 min)
PI
DiBAC4(3)
Q1 0.010
Q2 67.7
Q4 3.30
Q3 29.0
Q1 0.063
Q2 98.6
Q4 0.40
Q3 0.92
c
d
untreated (30 min)
unprinted fabric (30 min)
Ag-only fabric (30 min)
WED (30 min)
ketoconazole (30 min)
WED + ketoconazole (30 min)
untreated (24h)
unprinted fabric (24h)
Ag-only fabric (24h)
WED (24h)
ketoconazole (24h)
WED + ketoconazole (24h)

Figure S7: (**a**) Representative split channel images for $DiBAC_4(3)^+$ and PI^+ population in amphotericin B treated cells (6h) and heat killed cells (100°C for 30 mins). Display settings for all images were kept same. Scale bar represents 5 µm. (**b**) Representative scatter plots for flow cytometry analysis of $DiBAC_4(3)^+$ and PI^+ population in amphotericin B treated and heat killed cells. (**c-d**) Split channel images for *C albicans* cells, untreated or respective treatment groups, after $DiBAC_4(3)$ and PI staining. Merged images are in main figure 6C. Display settings for all images were kept same. Scale bar represents 5 µm.

Figure S8

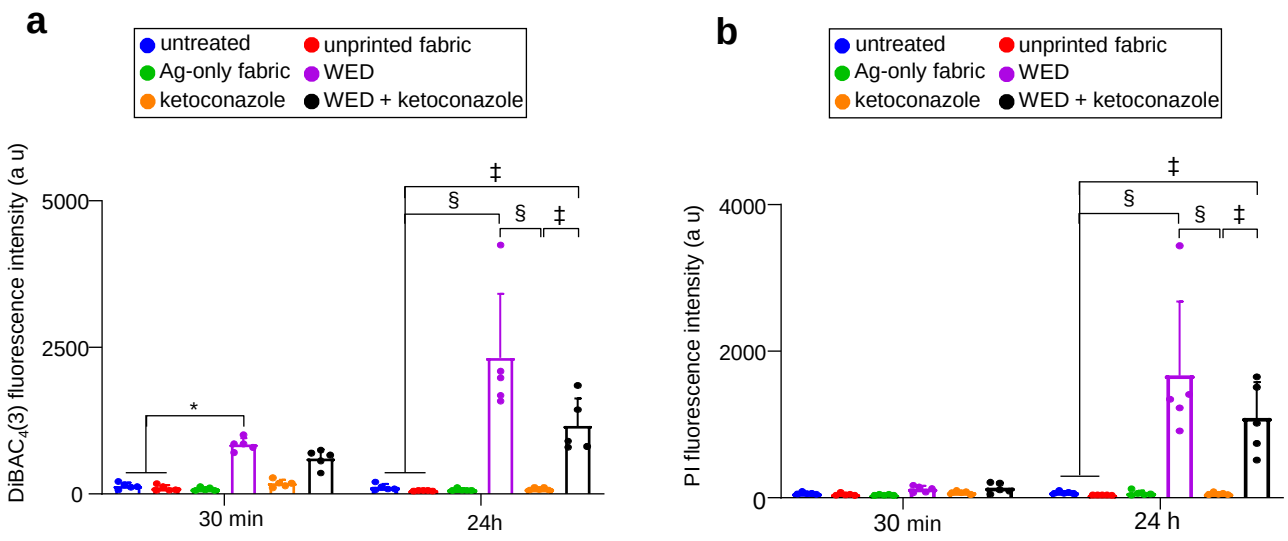

Figure S8: Graphical representation of (**a**) $DiBAC_4(3)$ and (**b**) PI fluorescence intensities measurements. Images were captured at 63X magnification (refer main figure 6C), after 30 min and 24h treatment. Display settings for all images were kept same. $DiBAC_4(3)$ and PI fluorescence intensities were measured from these images using Zen Blue software and represented graphically. n = 5. $^{\S}P < 0.0001$, $^{\ddagger}P < 0.0005$ and $^{*}P < 0.05$ (Two-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Figure S9

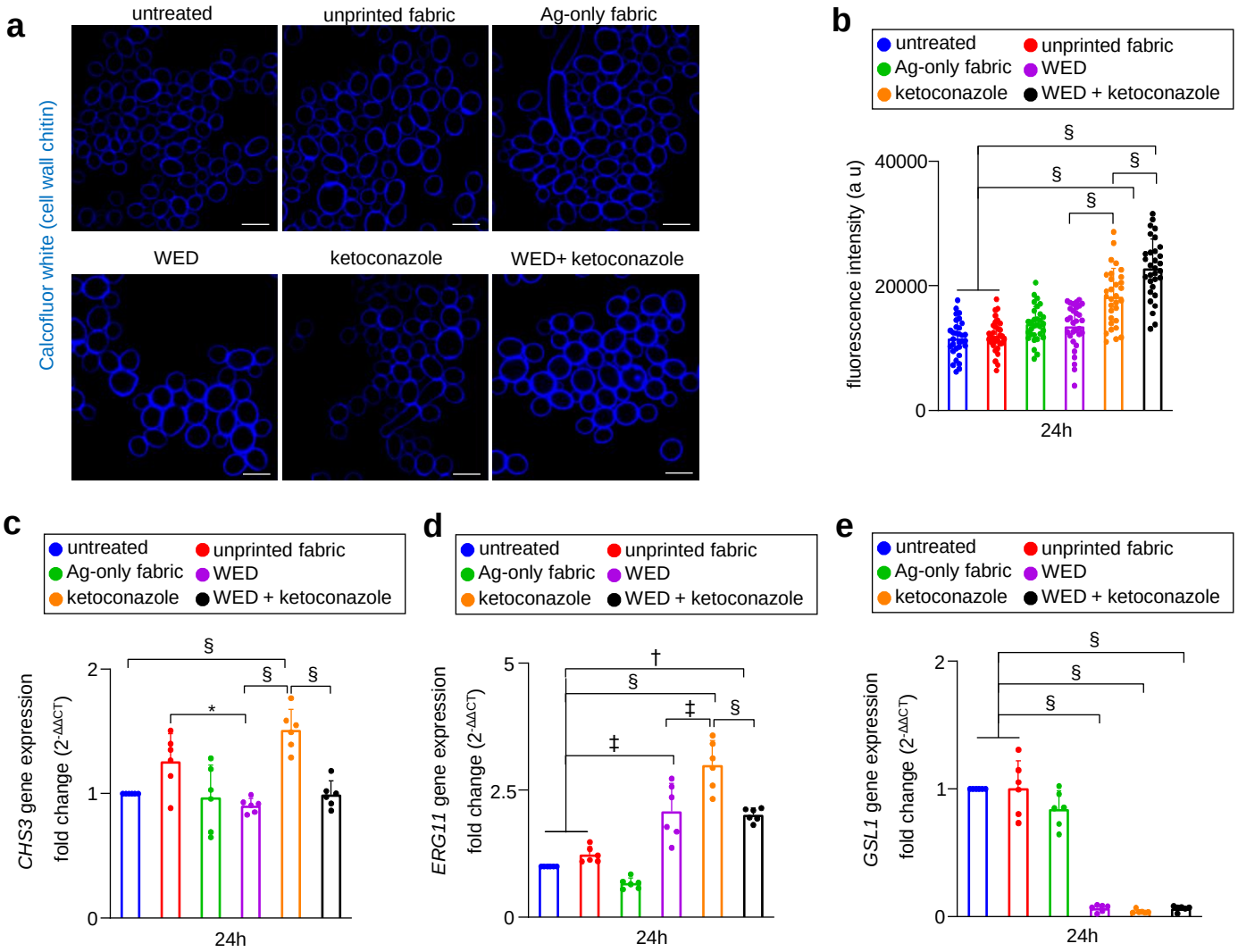
a
untreated
unprinted fabric
Ag-only fabric
WED
ketoconazole
WED+ ketoconazole
Calcofluor white (cell wall chitin)
b
untreated
unprinted fabric
Ag-only fabric
WED
ketoconazole
WED + ketoconazole
fluorescence intensity (a u)
40000
20000
0
24h
§
c
CHS3 gene expression
fold change (2-ΔΔCT)
2
1
0
*
24h
d
ERG11 gene expression
fold change (2-ΔΔCT)
5
2.5
0
†
‡
24h
e
GSL1 gene expression
fold change (2-ΔΔCT)
2
1
0
24h

Figure S9: (**a**) Representative images for qualitative assessment of cell wall chitin content. *C albicans* cells, after 24h of planktonic growth (untreated or with respective treatments) were stained with Calcofluor white and observed at 63X magnification. Display settings for all images within a group were same. Scale bar represents 5 µm. (**b**) Semi-quantitative assessment of cell wall chitin content. Microscopic images captured for aforementioned samples were analyzed for fluorescence intensities using Zen Blue software. These values are graphically represented in terms of arbitrary units (a u). n = 31 images. $^{\S}P \leq 0.0001$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD. (**c**–**e**) Quantitative real-time PCR analysis of *C albicans* cell wall related genes – *CHS3, ERG11* and *GSL1. C albicans* cells were cultured in presence of dressings for 24h at 27^{o}C. RNA was extracted from these cells and cDNA was prepared. Real time PCR analysis was performed for transcripts: *CHS3, ERG11* and *GSL1* with aforementioned cDNA. *C albicans* actin gene (*ACT1*) was used as a housekeeping control. Expression levels were quantified employing the $2^{(-\Delta\Delta ct)}$ relative quantification method. n = 6. $^{\S}P < 0.0001$, $^{\ddagger}P < 0.0005$, $^{\dagger}P \leq 0.001$ and $^{*}P < 0.05$ (One-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Figure S10

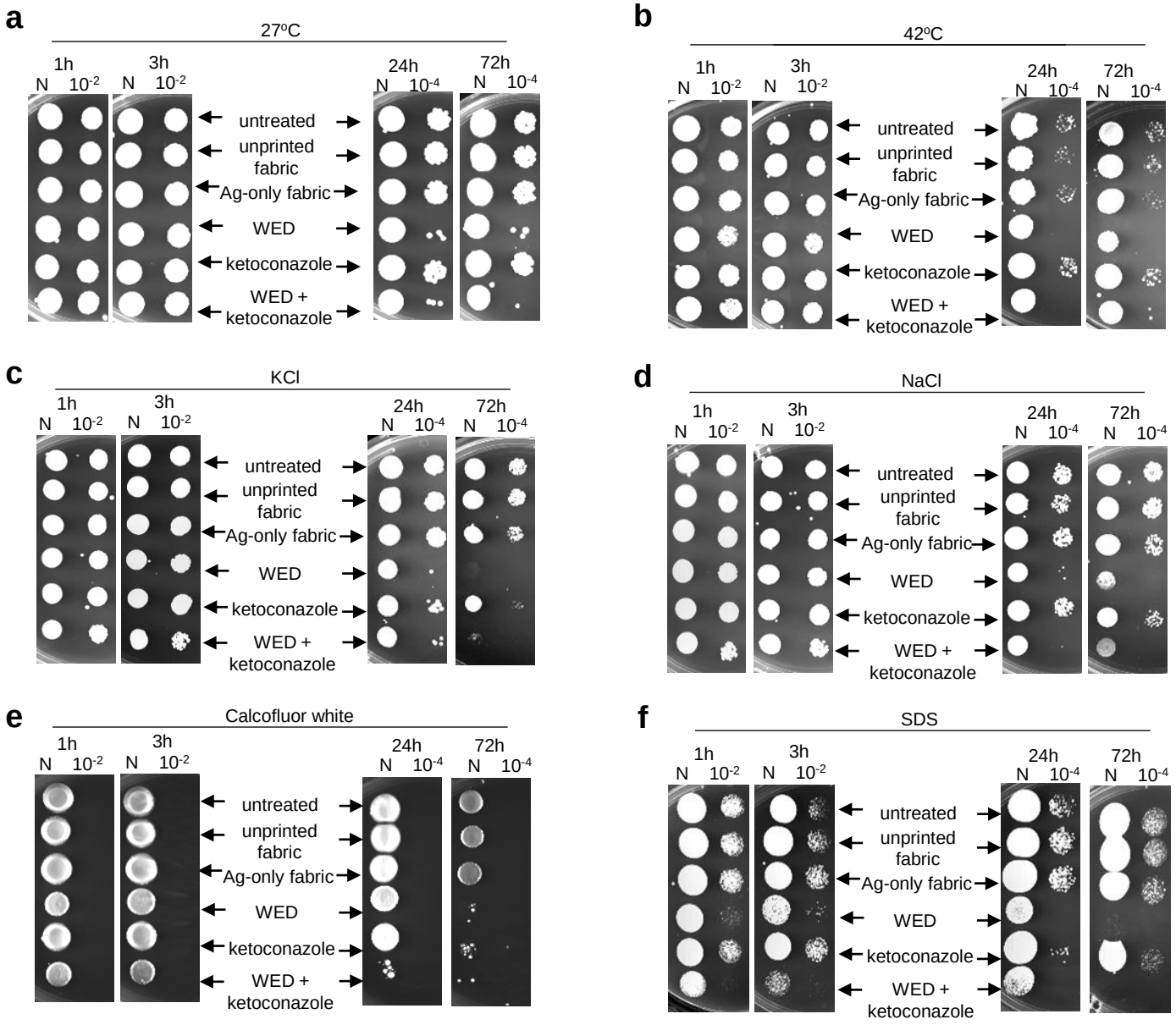

Figure S10: (**a**-**f**) Representative plate images for spot viability assay with secondary cell wall stressors. *Candida albicans* cells were first cultured in YPD broth with fabrics or ketoconazole or a combination of both. After respective time intervals (1h, 3h, 24h and 72h), these stressed cells were washed and spotted on to YPD agar plates with a secondary cell wall stress agent such as 1M KCl, 1M NaCl, 50 µg /ml Calcofluor white or 0.01% SDS. One set of cells were also incubated at 42°C (heat stress). All plates except heat stress plates were incubated at 27°C. After 48-72h incubation, plates were observed for growth.

Figure S11

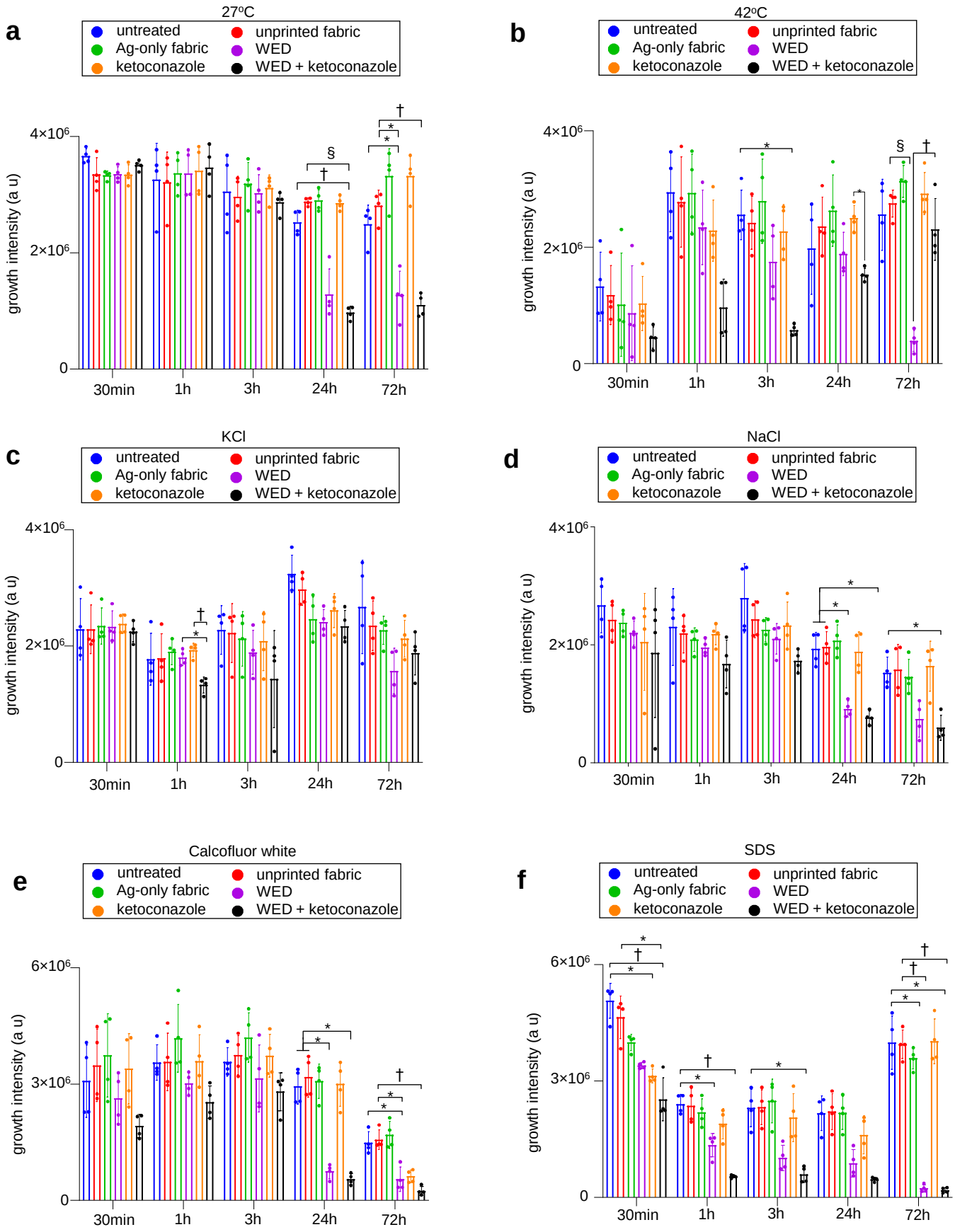
a
27ºC
untreated
Ag-only fabric
ketoconazole
unprinted fabric
WED
WED + ketoconazole
growth intensity (a u)
4×10⁶
2×10⁶
0
30min
1h
3h
24h
72h
b
42ºC
c
KCl
d
NaCl
e
Calcofluor white
6×10⁶
3×10⁶
f
SDS

Figure S11: (**a-f**) Growth intensity measurement plots for secondary cell wall stress assay plates. An area of interest was selected around the growth spots on secondary cell wall stress assay plate images and the intensity of growth was calculated using ImageJ software. This data was graphically represented for 27°C, 42°C, KCl, NaCl, Calcofluor white and SDS, respectively. n = 4 plates. $^{\S}P < 0.0001$, $^{\ddagger}P < 0.0005$ and $^{*}P < 0.05$ (Two-way ANOVA followed by *post-hoc* Sidak multiple comparison test). Data are represented as the mean ± SD.

Table 1: Primers used in this study

Gene	Forward primer (5' – 3')	Reverse primer (5' – 3')	Reference
ACT1	TGATTTGGCTGGTAGAGACT	ATGGCAGAAGATTGAGAAGA	This study
ALS3	CCAAGTGTTCCAACAACTGAA	GAACCGGTTGTTGCTATGGT	[1]
BCR1	TTATGCCGTGCCTCCTTTAC	AACTTGATGCCGACGATTCA	[2]
BRG1	GGGAAGAACGGTCGAAGAATAA	GATATTGGCCGTGCATCAAAG	[2]
CDR1	TTTAGCCAGAACTTTCACTCATGATT	TATTTATTTCTTCATGTTCATATGGATTGA	[3]
CHS3	TATGTTGCTGTTGCCCAAGG	GTTGCTTTTCTGGTGGCACA	This study
EAP1	TGCCCCAGGTACTGAAACCACTC	AGTGCCTGGGATAACGGGTTGAG	[4]
EFG1	AACAACTACCATGTGGGAAG	TGATTTCAAAATCCCATCTC	This study
ERG11	AACTACTTTTGTTTATAATTTAAGATGGACTATTGA	AATGATTTCTGCTGGTTCAGTAGGT	[3]
GSL1	AACTTCAGCCGCATTTGGAT	GCGGTGACTTATTGGGGGTA	[5]
HWP1	TCTACTGCTCCAGCCACTGA	CCAGCAGGAATTGTTTCCAT	This study
MDR1	TTACCTGAAACTTTTGGCAAAACA	ACTTGTGATTCTGTCGTTACCG	[3]
NRG1	CCCAAGTACCTCCACCAGCA	CGACAAAGCAAGGGAGTTGG	This study
RFG1	AACCCTGAAGTTTCCCGAGAA	CAGCAAGATTATTCCAATGTTCCTT	This study
ROB1	GAACCACAACCACAAGAAGAAC	ACATGTCCTCAGCTGGATTG	[2]
TUP1	CTCTTGGCGACAGGTGCAG	GTGGTGACGCCGTCTTCGA	[6]

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