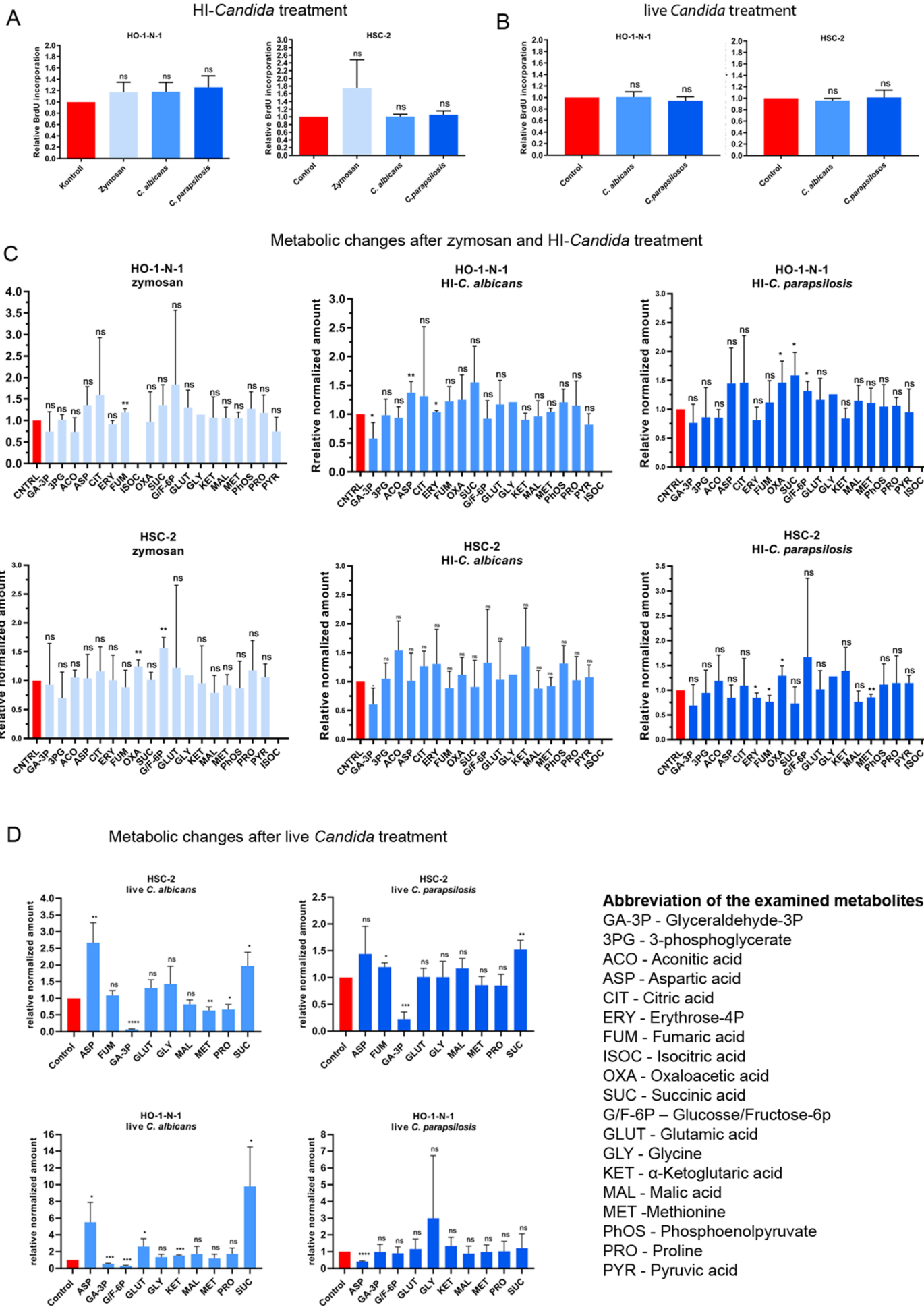


Abbreviation of the examined metabolites

GA-3P - Glyceraldehyde-3P
3PG - 3-phosphoglycerate
ACO - Aconitic acid
ASP - Aspartic acid
CIT - Citric acid
ERY - Erythrose-4P
FUM - Fumaric acid
ISOC - Isocitric acid
OXA - Oxaloacetic acid
SUC - Succinic acid
G/F-6P – Glucosse/Fructose-6p
GLUT - Glutamic acid
GLY - Glycine
KET - α-Ketoglutaric acid
MAL - Malic acid
MET -Methionine
PhOS - Phosphoenolpyruvate
PRO - Proline
PYR - Pyruvic acid

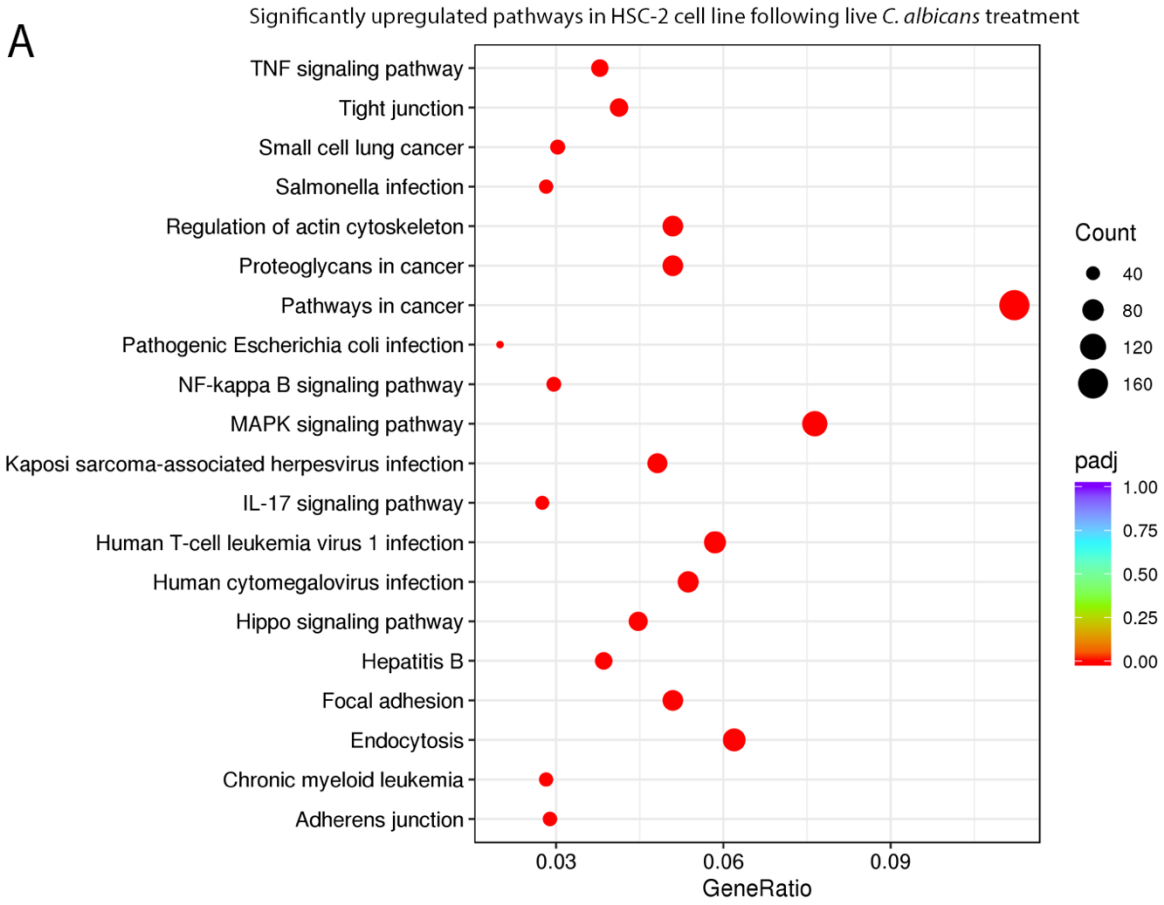
Supp Fig1

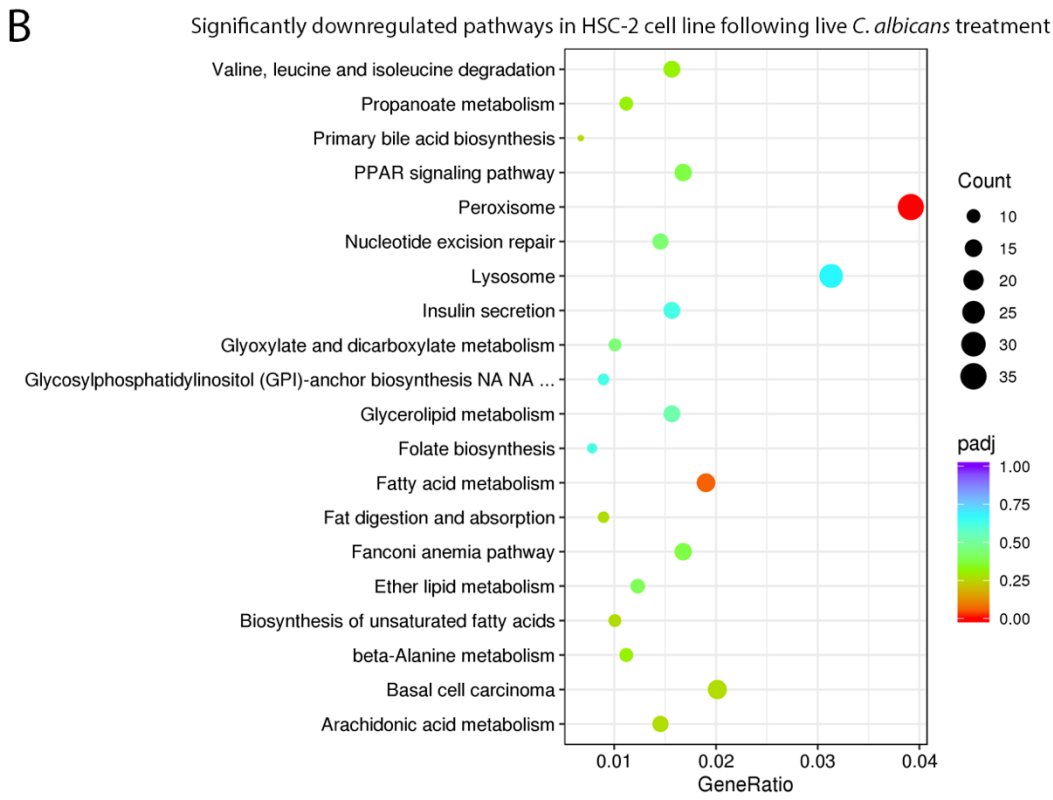
(A) Normalized proliferation activity of OSCC cells in the presence of heat- killed *C. albicans*, C. *parapsilosis* and zymosan measured by BrdU incorporation assay.

(B) Normalized proliferation activity of OSCC cells in the presence of live *C. albicans* and *C. parapsilosis* measured by BrdU incorporation assay.

(C) Normalized amount of metabolites of OSCC cells in the presence of heat- killed *C. albicans*, *C. parapsilosis* and zymosan measured by HPLC-HRMS.

(D) Normalized amount of metabolites of OSCC cells in the presence of live *C. albicans* and *C. parapsilosis* measured by HPLC-HRMS.

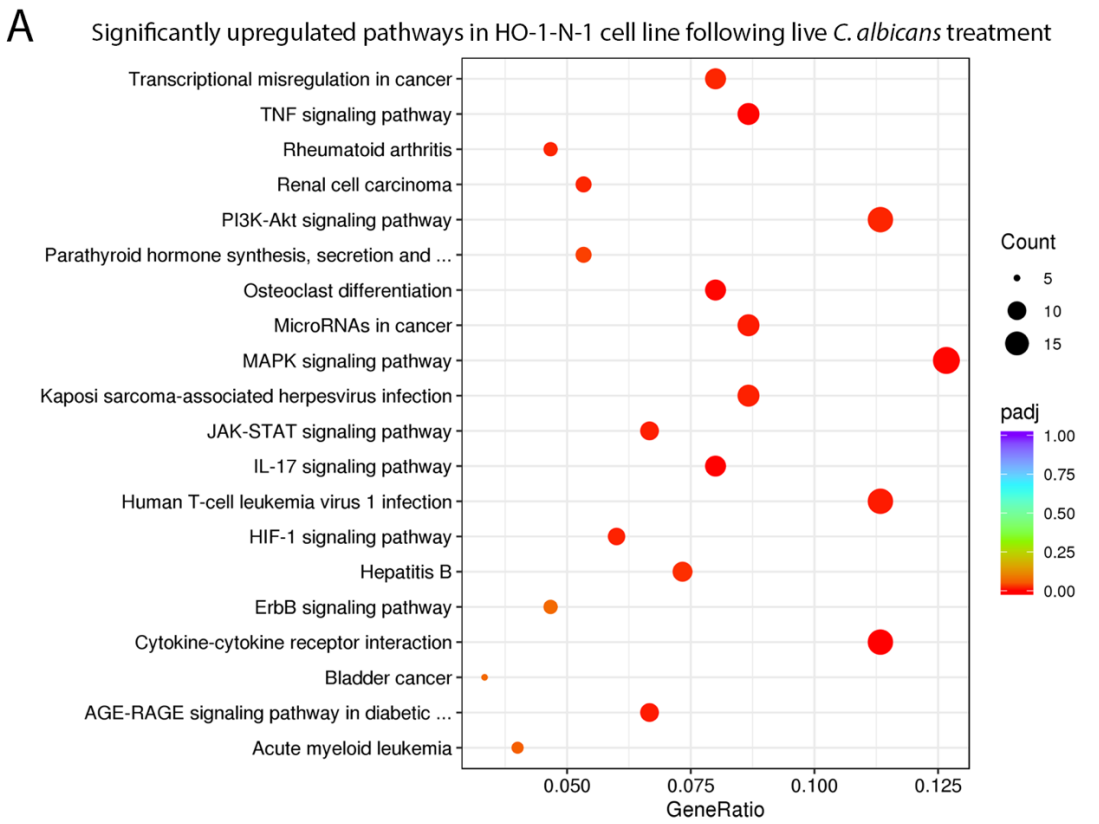


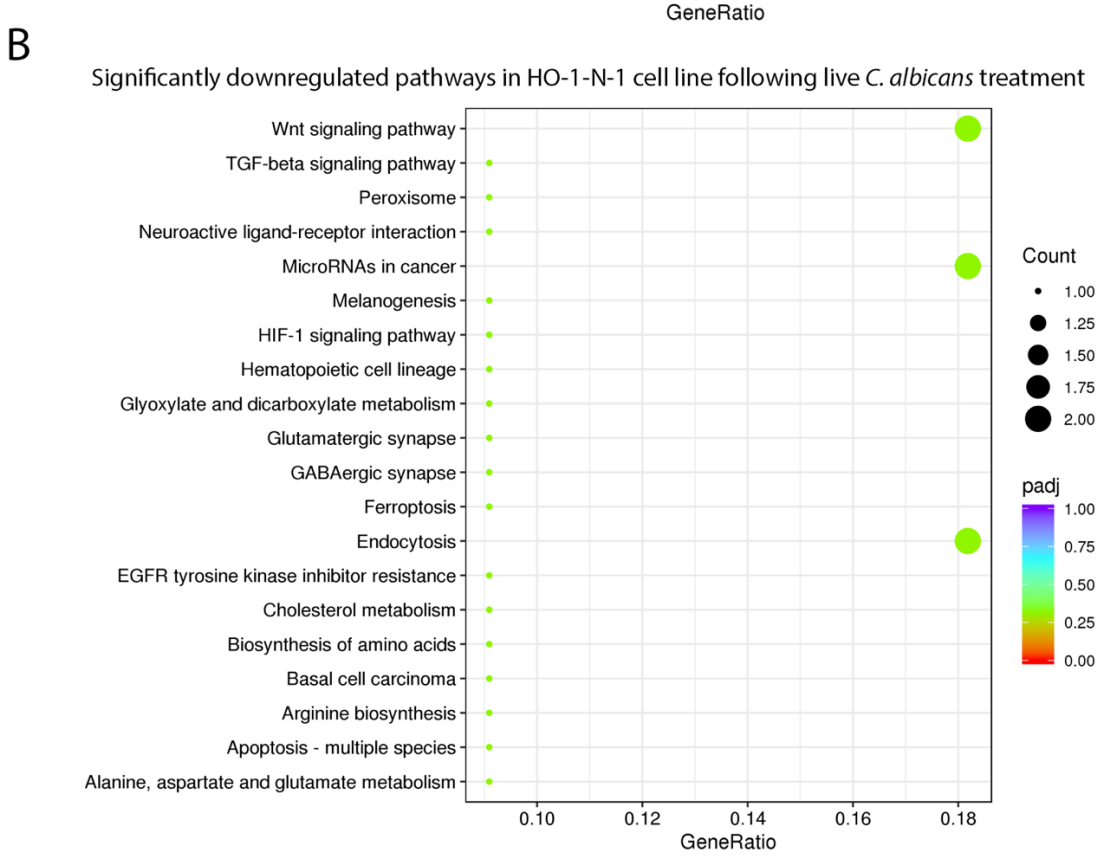


Supp Fig2

(A) Significantly upregulated pathways in HSC-2 cell line induced by *C. albicans*

(B) Significantly downregulated pathways in HSC-2 cell line following *C. albicans* treatment

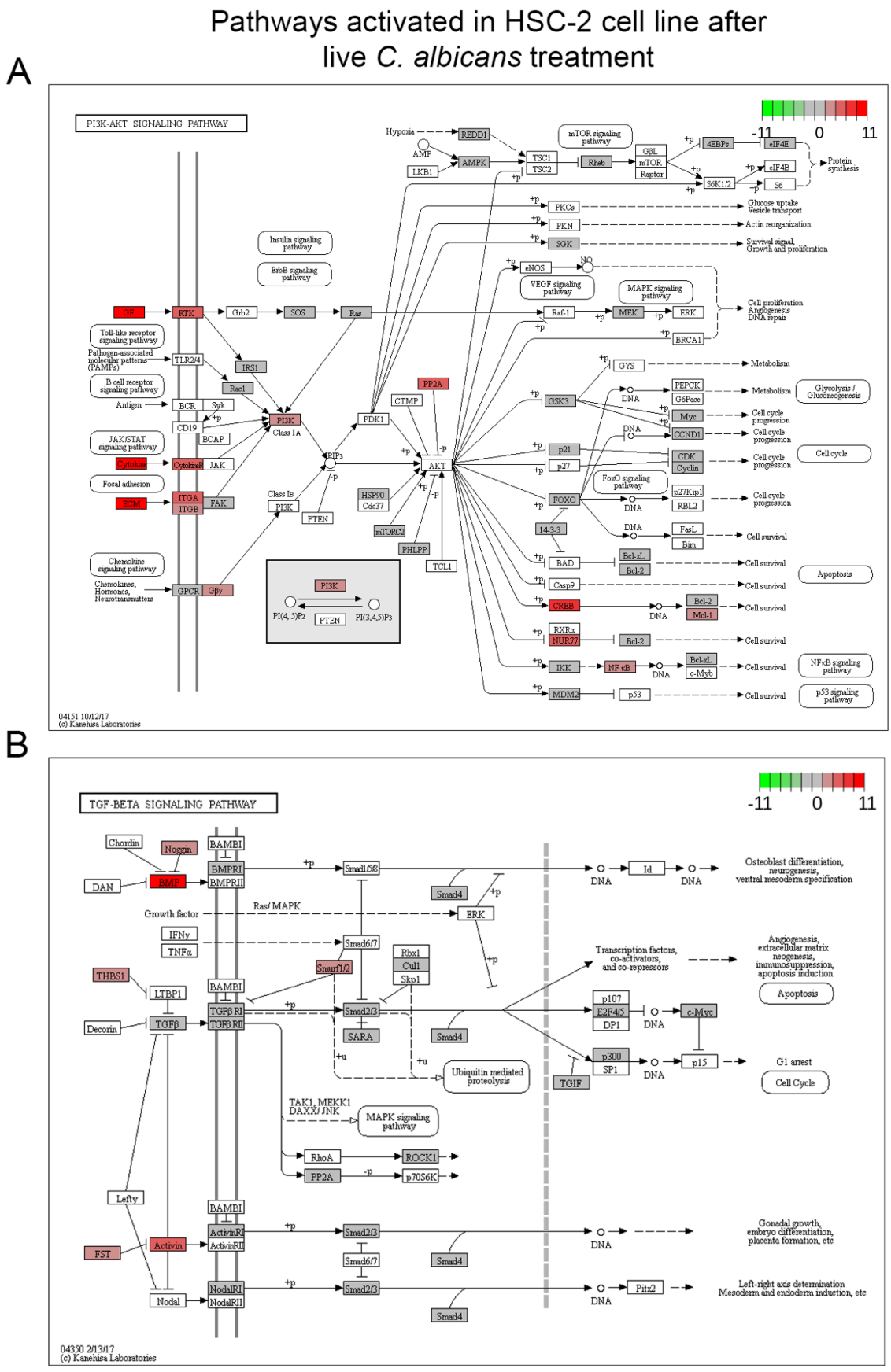




Supp Fig3

(A) Significantly upregulated pathways in HO-1-N-1 cell line induced by *C. albicans*

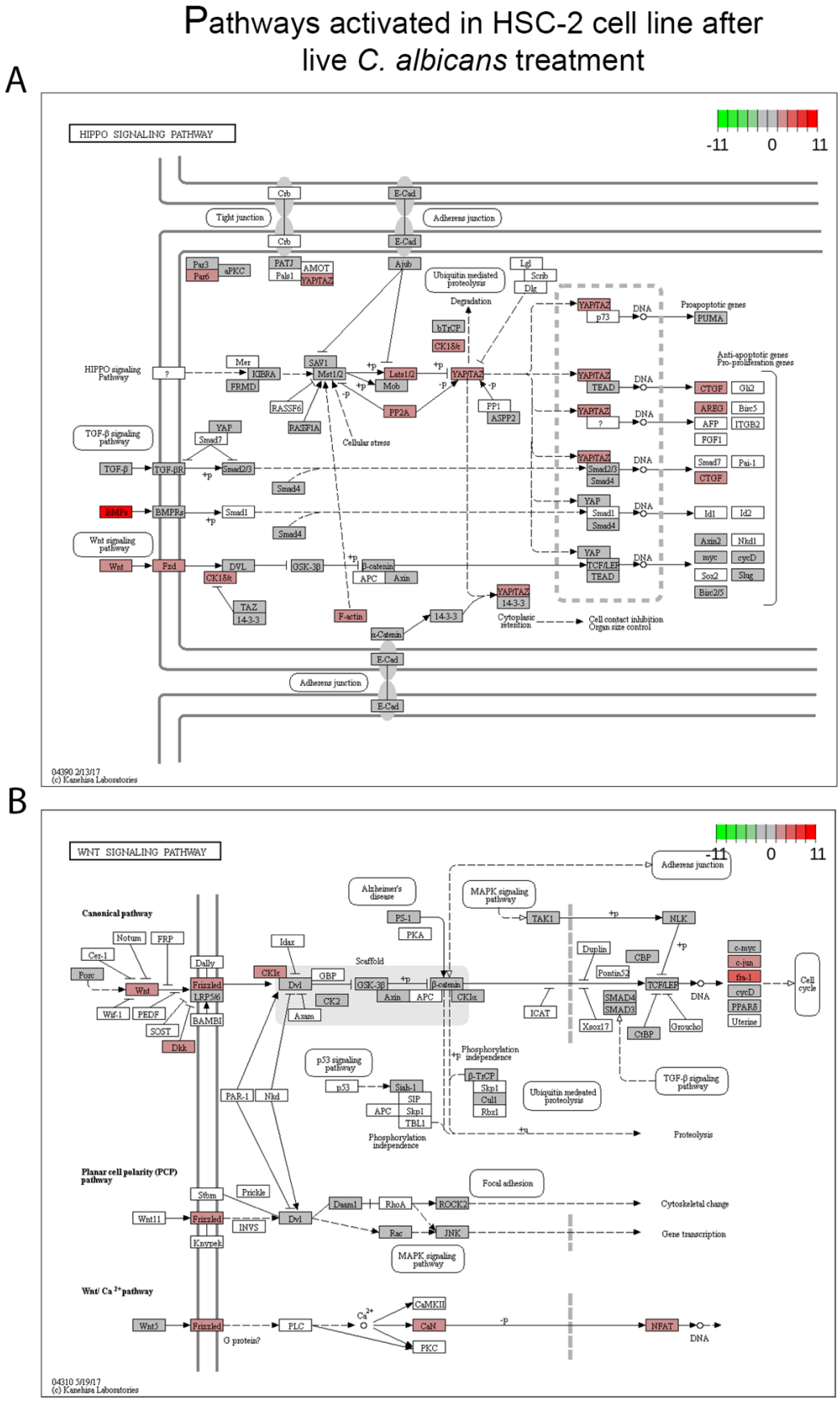
(B) Significantly downregulated pathways in HO-1-N-1 cell line following *C. albicans* treatment



Supp Fig4

(A) PI3K-Akt signaling pathway activated in HSC-2 cell line following live *C. albicans* treatment

(B) TGF- β/SMAD signaling pathway activated in HSC-2 cell line following live *C. albicans* treatment



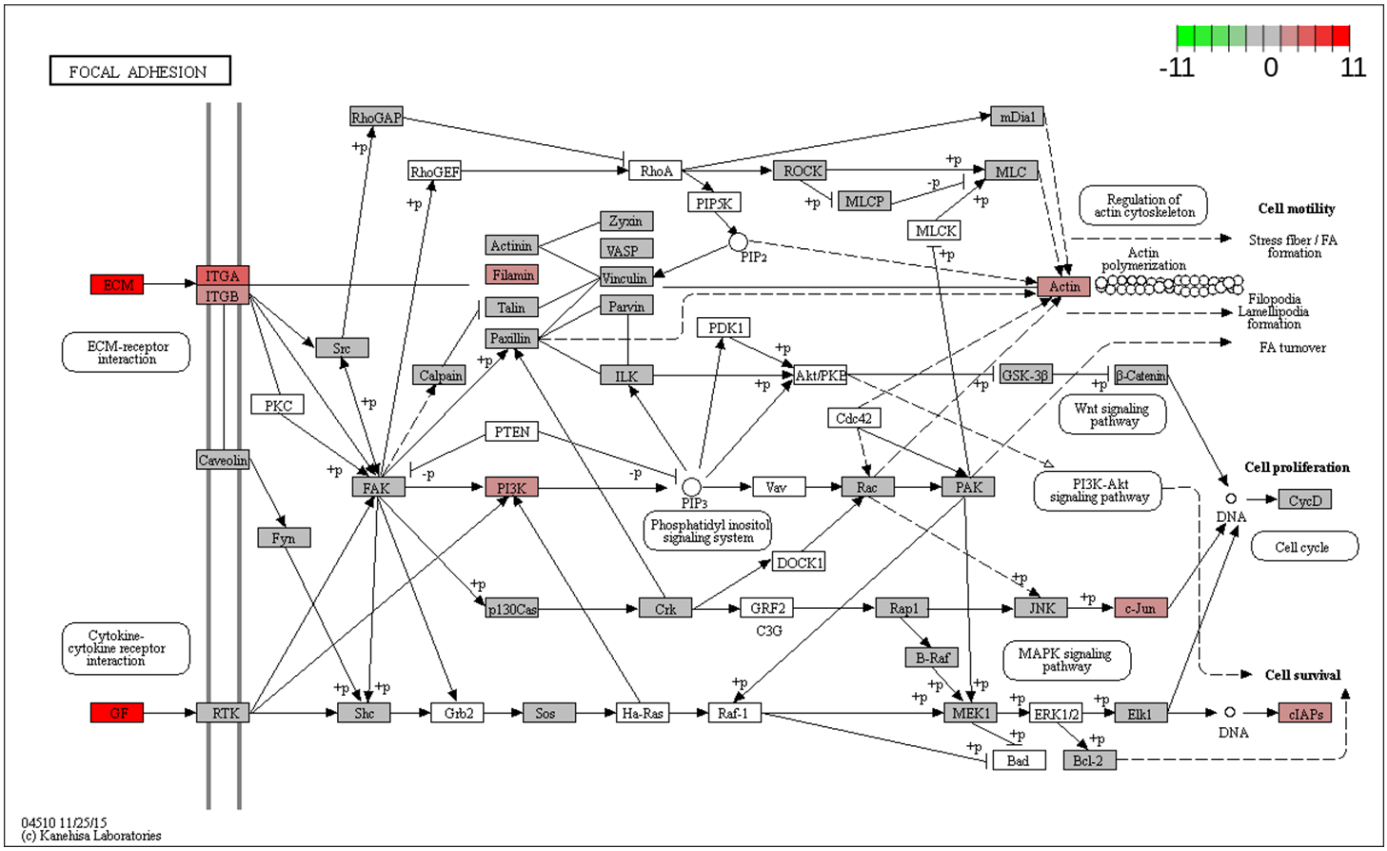
Supp Fig5

(A) Hippo signaling pathway activated in HSC-2 cell line following live *C. albicans* treatment

(B) Wnt signaling pathway activated in HSC-2 cell line following live *C. albicans* treatment

Pathways activated in HSC-2 cell line after live *C. albicans* treatment

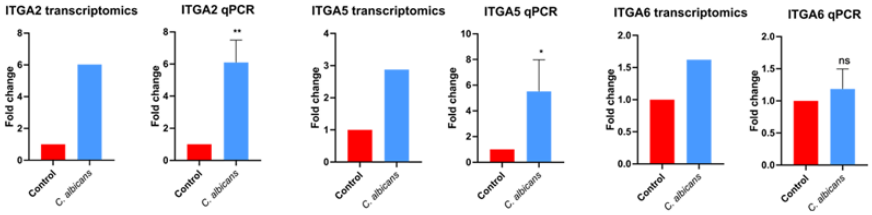
A



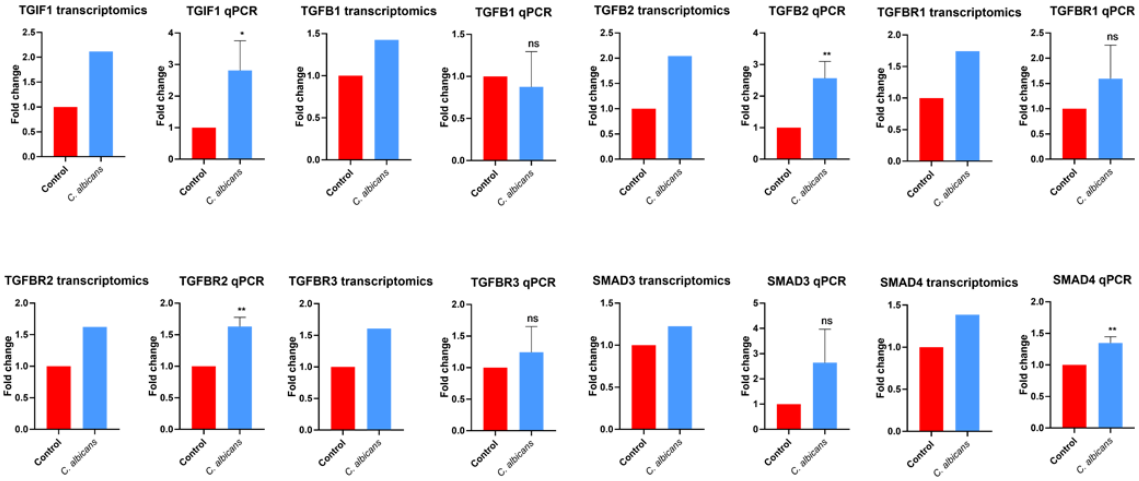
Supp Fig6

(A) Focal adhesion pathway activated in HSC-2 cell line following live *C. albicans* treatment

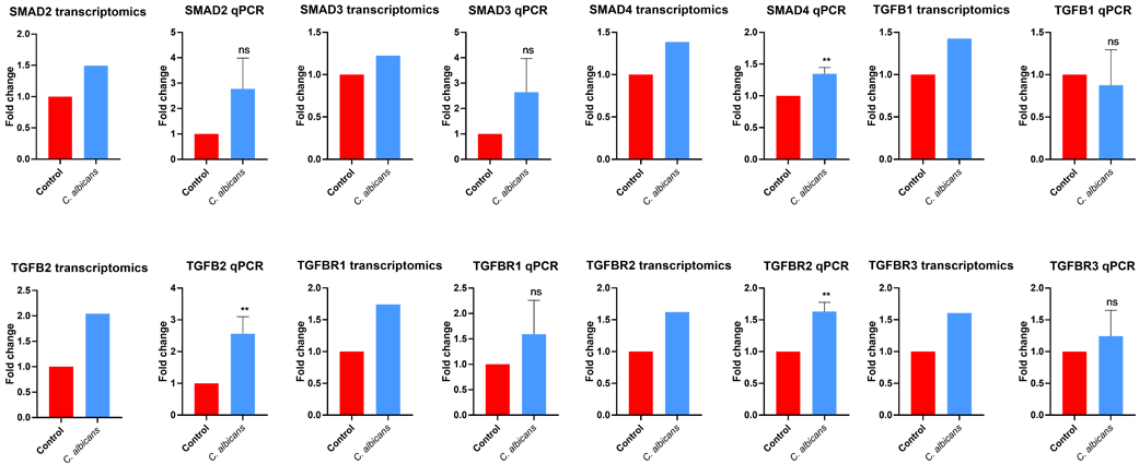
A: validation of PI3K-Akt pathway components by qPCR



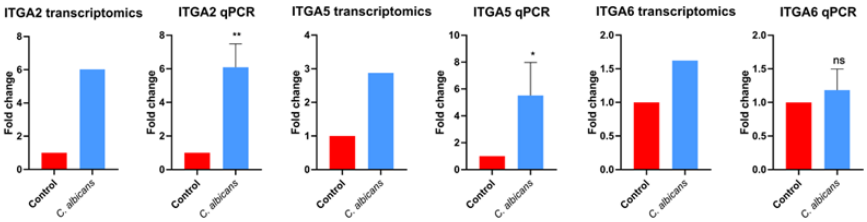
B: validation of TGFB/SMAD pathway components by qPCR



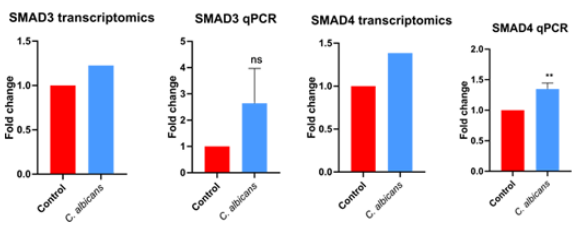
C: validation of HIPPO pathway components by qPCR



D: validation of Focal adhesion pathway components by qPCR



E: validation of Wnt pathway components by qPCR

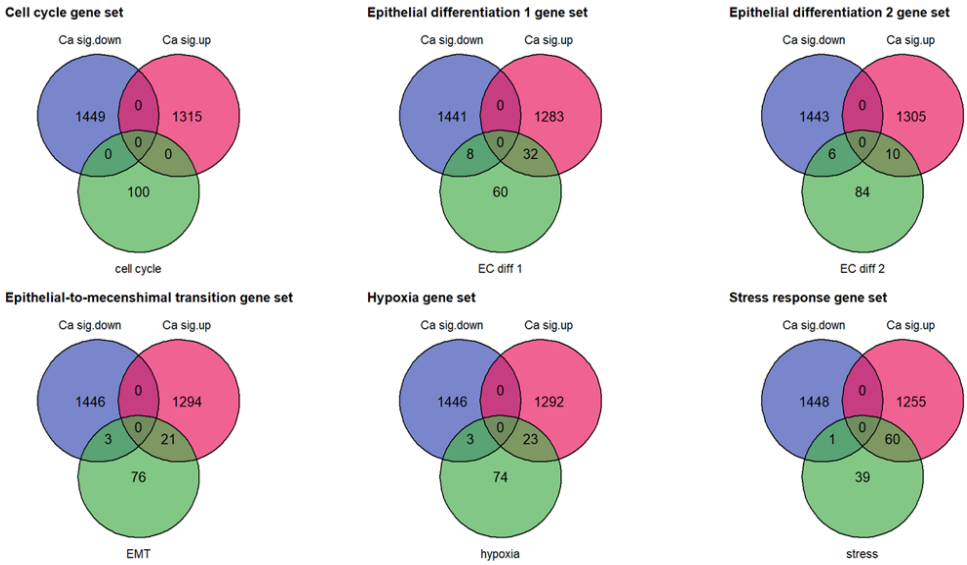


Supp Fig7

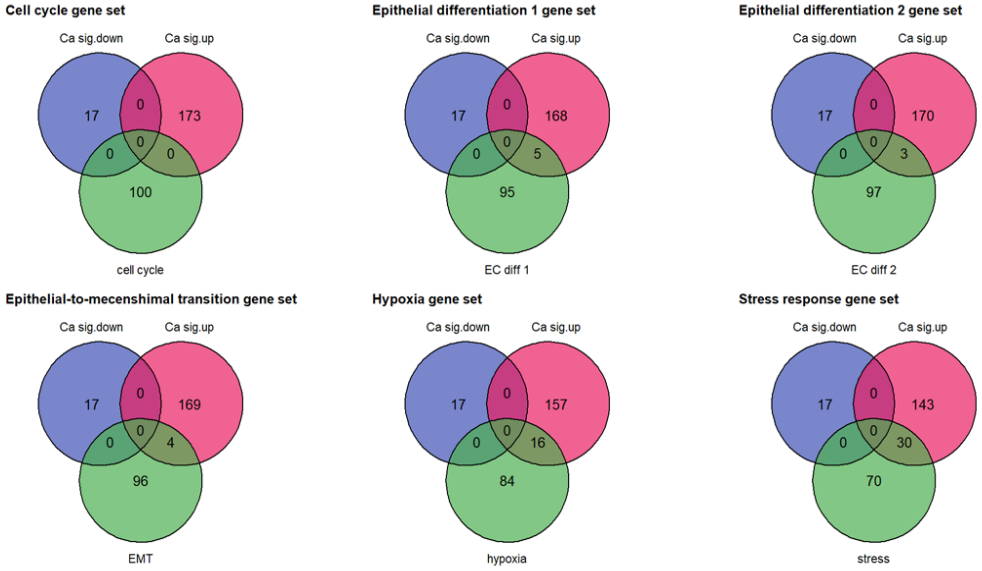
Validation of *C. albicans* activated signaling pathways. Validation was performed by qPCR analysis of pathway components.

(A) PI3K-Akt signaling pathway (B) TGF- β/SMAD (C) Hippo signaling pathway (D) Wnt signaling pathway (E) Focal adhesion pathway

A HSC-2 cell line *C. albicans* treatment in vitro; scSec data vs. *C. albicans* induced gene set

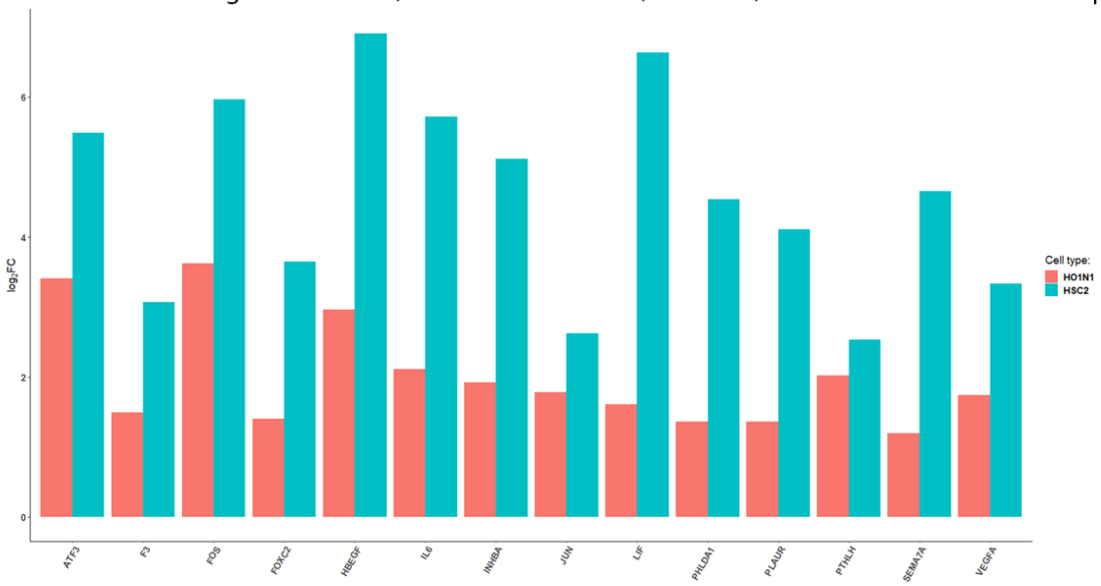


B HO-1-N-1 cell line *C. albicans* treatment in vitro; scSec data vs. *C. albicans* induced gene set



C

Live *Candida albicans* induced genes in both (HSC-2 and HO-1-N-1) cell lines, which are involved in OSCC progression

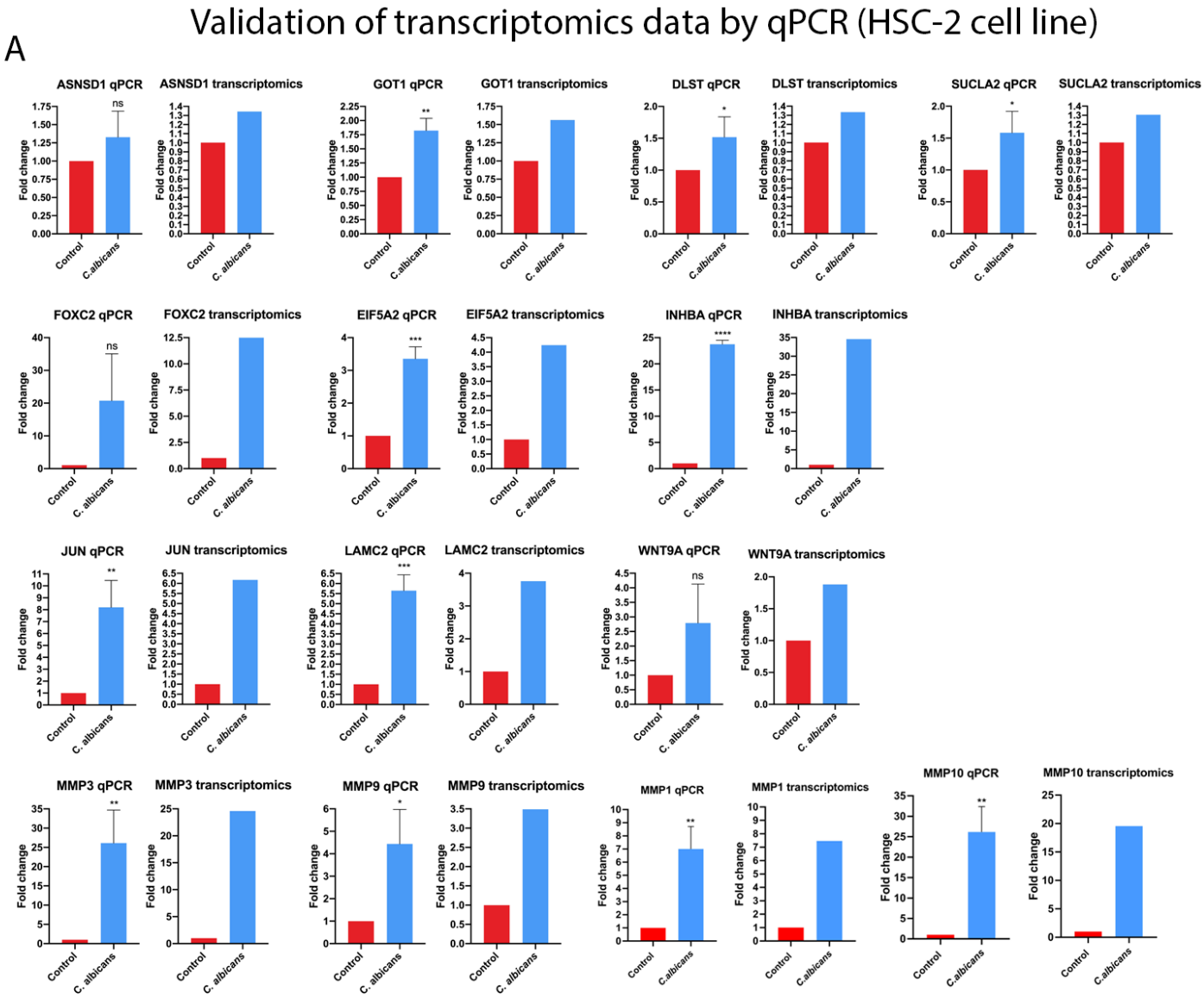


Supp Fig8

(A) Comparison of *Candida induced* genes in HSC-2 cell line to genes involved in different tumor progression processes. Differentially expressed gene list derived from an OSCC single cell sequencing study.

(B) Comparison of *Candida induced* genes in HO-1-N-1 cell line to genes involved in different tumor progression processes. Differentially expressed gene list derived from an OSCC single cell sequencing study.

(C) Live *C. albicans* induced genes in both (HSC-2 and HO-1-N-1) cell lines, which are involved in OSCC progression. OSCC progression marker gene list derived from literature and OSCC single cell sequencing study.



Supp Fig9

(A) Histopathological samples of *Candida*-colonized and *Candida*-free tumors, analysed and scored manually by a pathologist after H&E staining.

(B) Causal analyses of the genes which expression changed in OC-OSCC xenograft samples.

(C) Weight loss of the animal groups of OSCC xenograft and OC-OSCC xenograft.

(D) p63 staining of OSCC xenograft and OC-OSCC xenograft sections.

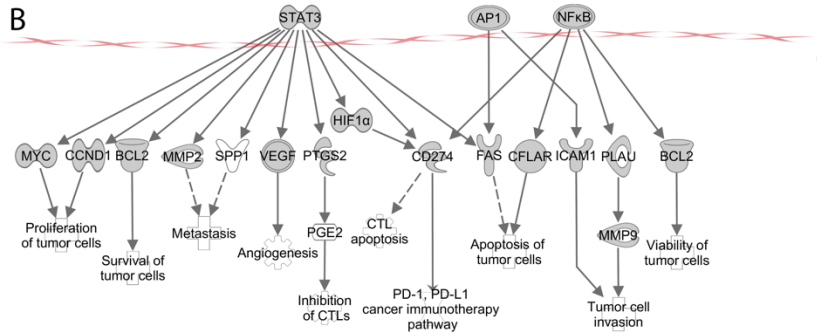
(E) E-cadherin staining of OSCC xenograft and OC-OSCC xenograft sections.

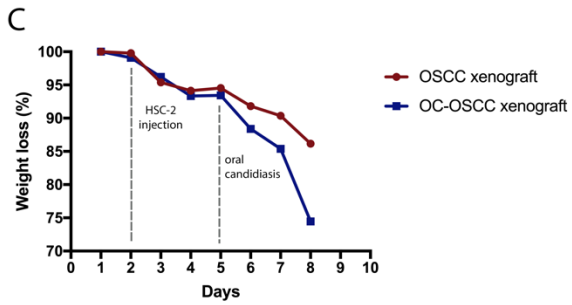
(F) Vinentin staining of OSCC xenograft and OC-OSCC xenograft sections.

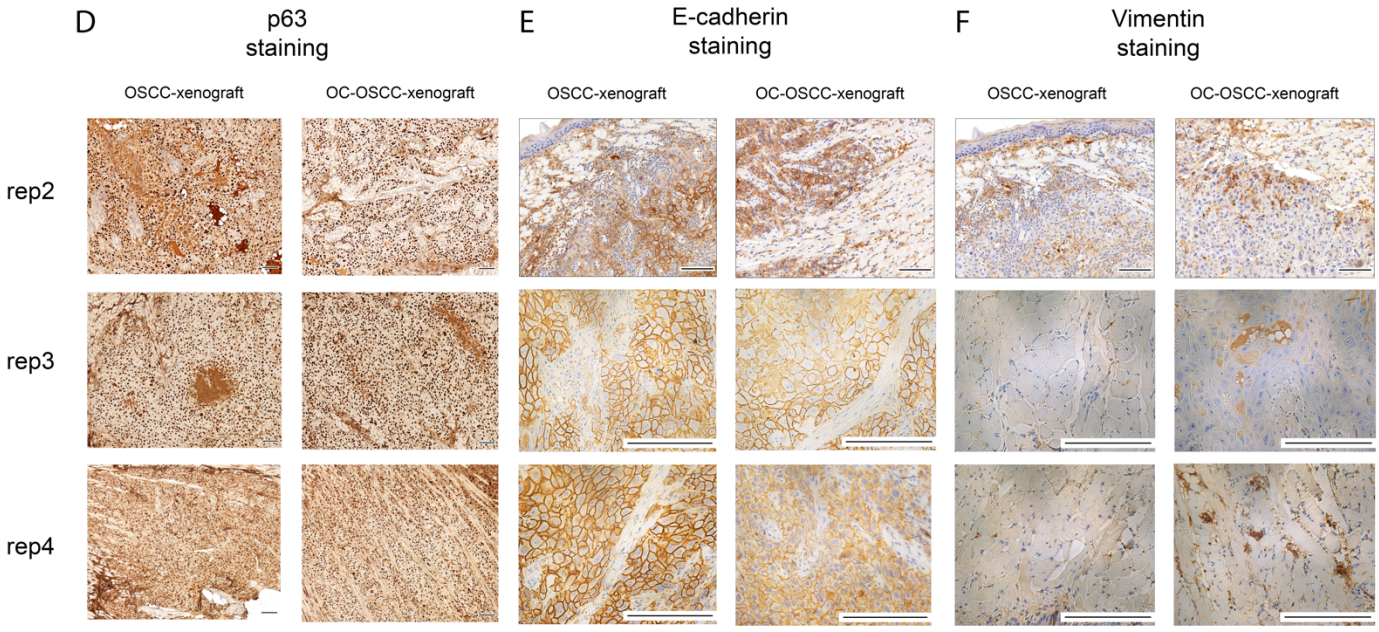
A

	OSCC Xen.1	OC-OSCC Xen.1	OSCC Xen.2	OC-OSCC Xen.2	OSCC Xen.3	OC-OSCC Xen.3	OSCC Xen.4	OC-OSCC Xen.4
Inflammation in surface epithelium	0	1	0	3	0	2	0	2
Necrosis	0	1	1	1	1	1	1	1
Pushing (P) or invasive (I) tumor edge	I	P/I	P	I	I	I	P	I
Budding / EMT	1	1	2	1	1	2	1	2
Invasion	1	1	1	1	1	1	2	2
Thrombosis	0	1	1	2	0	1	0	0
Peritumoral inflammation	3g	1l/g	1l/g	1l/g	1l/g	1l/g	1l/g	2l/g

Inflammation in surface epithelium: 0 / 1 / 2 / 3
Necrosis : 0 / 1
Budding / EMT: 0 / 1 / 2
Invasion: 0 / 1 / 2 / 3
Thrombosis: 0 / 1
Peritumoral inflammation: 0 / 1 /2 /3
(g=granulocyte; l=lymphocyte)







Supp Fig10

(A) Scoring OSCC and OC-OSCC xenograft samples manually by a pathologist.

(B) Causal analyses of the genes which expression changed in OC-OSCC samples after oral candidiasis.

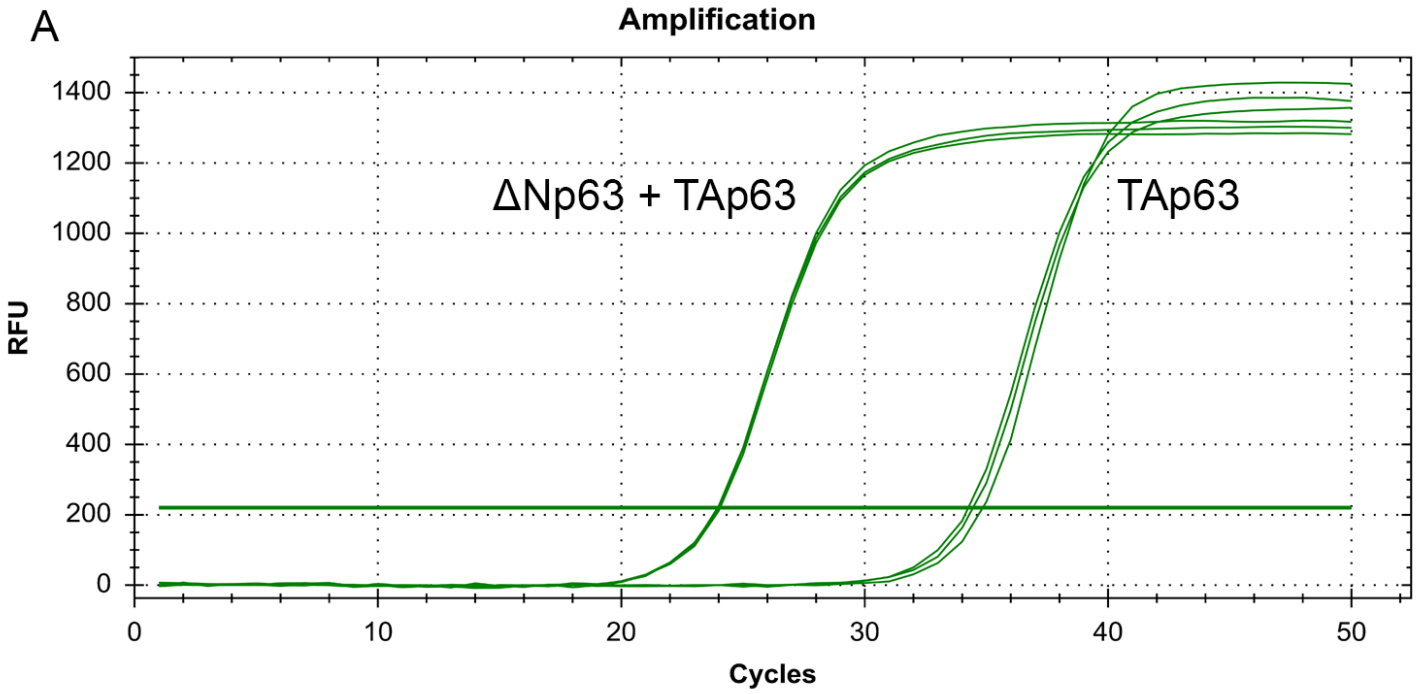
(C) Weight loss of the animals after HSC-2 tumor cell injection (OSCC xenograft) and HSC-2 injection combined with oral candidiasis (OC-OSCC xenograft).

(D) p63 staining of the histopathological samples (animal 2, 3, 4)

(E) E-cadherin staining of the histopathological samples (animal 2, 3, 4)

(F) vimentin staining of the histopathological samples (animal 2, 3, 4)

A



B

	qC
ΔNp63+TAp63	24.02
ΔNp63+TAp63	23.96
ΔNp63+TAp63	24.06
TAp63	34.45
TAp63	34.26
TAp63	34.85

Supp Fig11

(A) qPCR curve of TAp63 and ΔNp63+TAp63 splice variants. First primer pair was designed colse to C-terminal region, second primer pair in the N-terminal region. First primer pair amplifies both splice variant group (ΔNp63+TAp63), secon primer pair amplifies only splice variant posessing N-terminal region (TAp63).

(B) qC value of the transcript variants.

Supp Table 1

The precursor mass, fragment ion mass, polarity, retention time and fragmentation energy of the metabolites

Supp Table 2

Differentially expressed genes. *In vitro* and *in vivo* sequencing data.

Supp Table 3

qPCR primer list of the genes which were validated

Supp Table 4

120 genes derived from literature data (25 papers) which are involved in OSCC progression.