Back to article

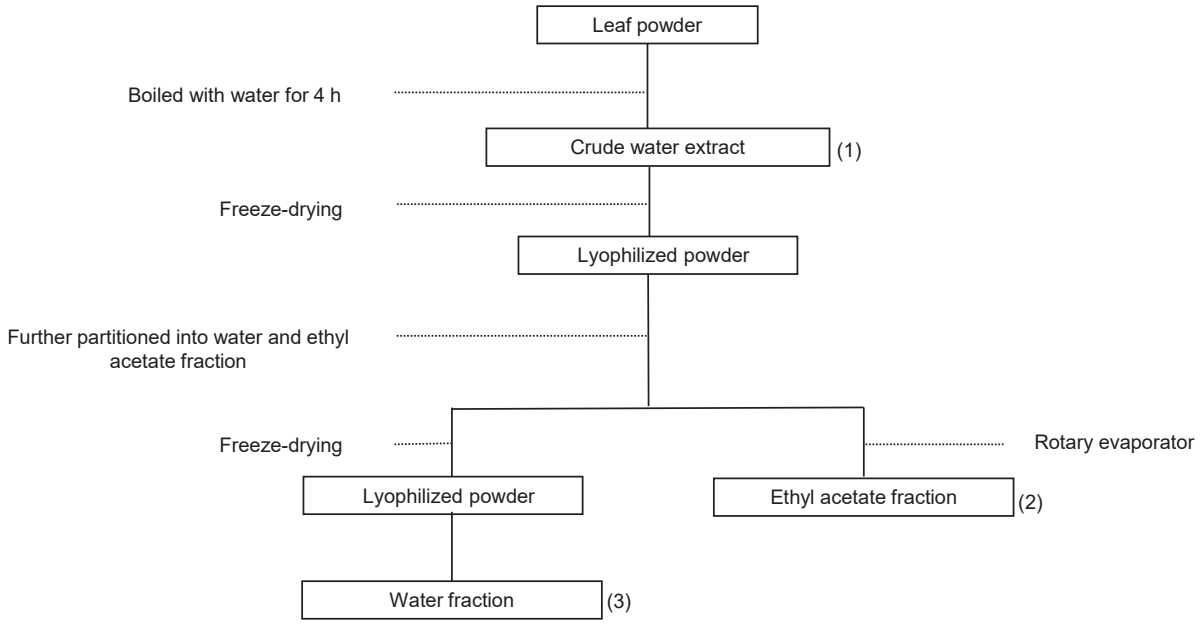


Fig. S1. For each variety of *Ficus deltoidea* leaves, sample preparation results in crude (1), water fraction (2), and ethyl acetate fraction (3)

Back to article

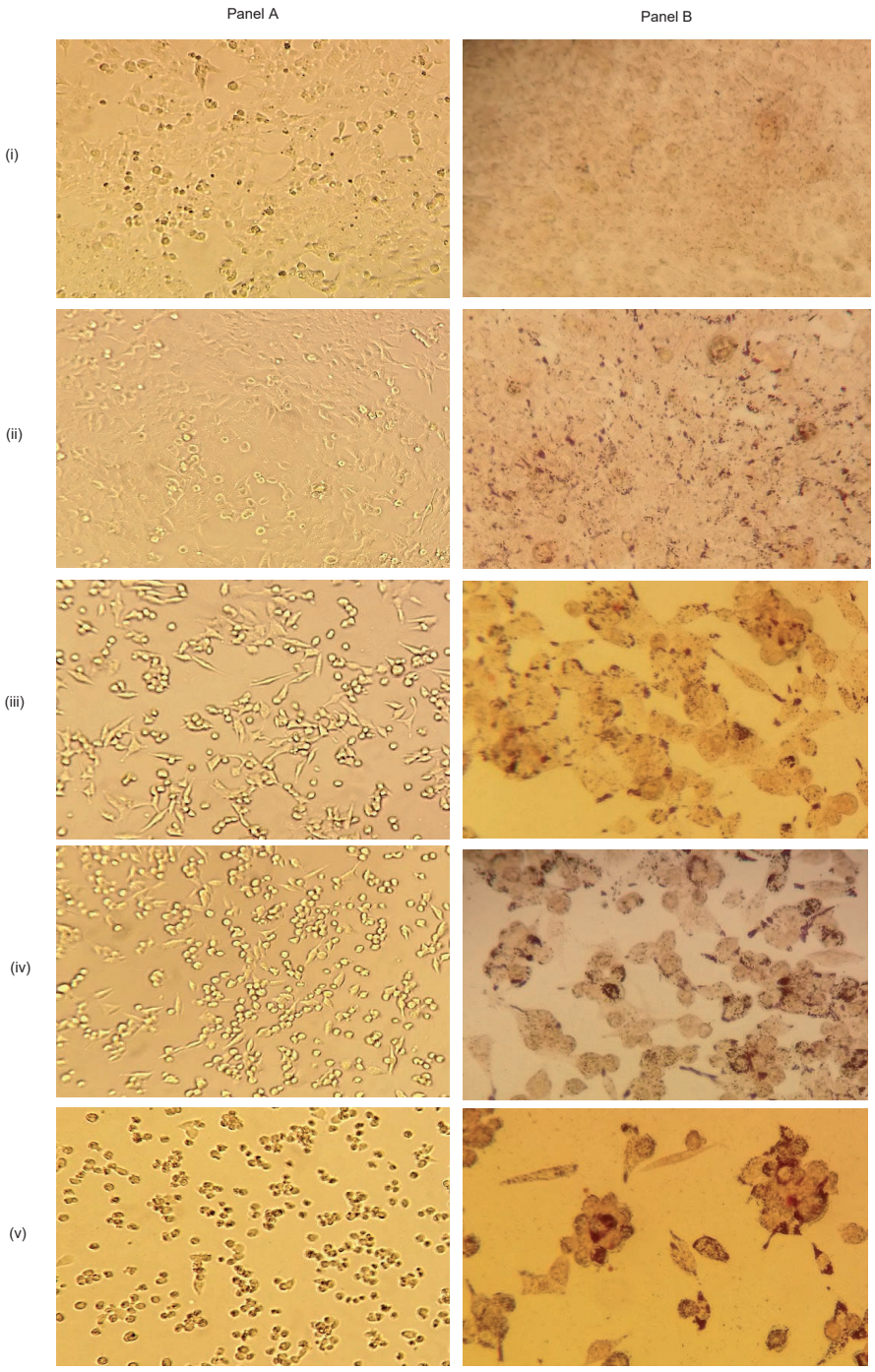


Fig. S2. Images of the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) and Oil Red O assays of WRL68 cells treated with vehicle (bovine serum albumin) (i), and *c*(palmitic acid)=100 μM (ii), 200 μM (iii), 400 μM (iv), and 800 μM (v) are shown in panels A (10× magnification) and B (20× magnification), respectively

Back to article

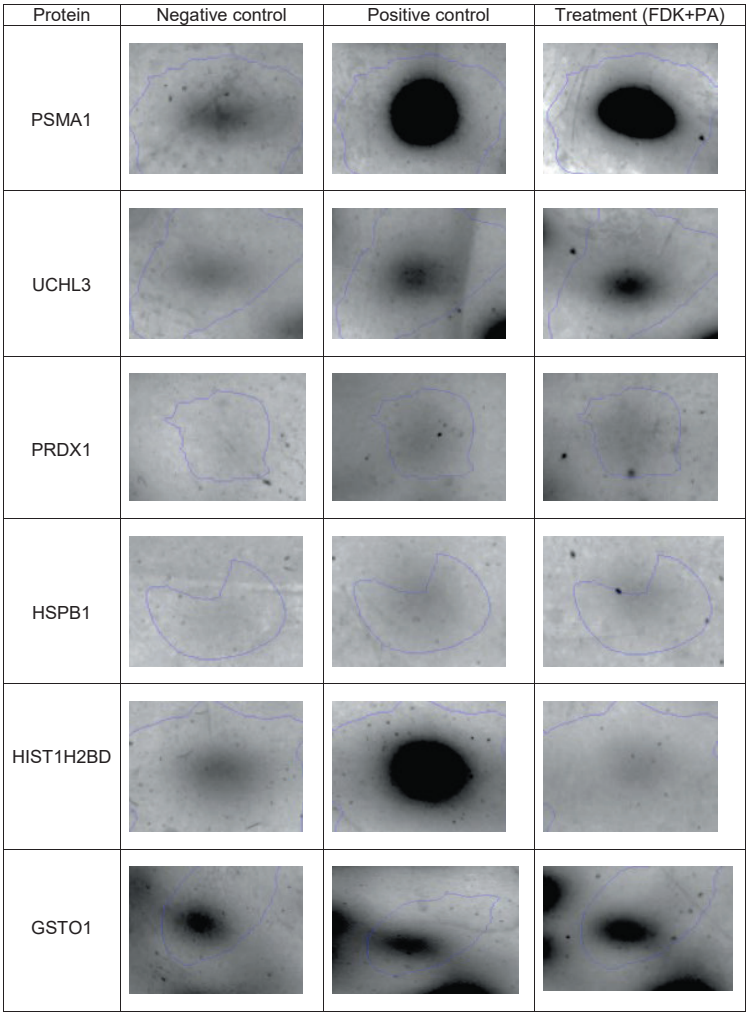


Fig. S3. The differential expression in the negative control (cells incubated without the presence of palmitic acid or FDK), positive control (cells incubated with palmitic acid), and treatment (γ(FDK)=200 μg/mL+PA) in WRL68 cells was highlighted using enlarged pictures of the 2DE gel spots. FDK=*Ficus deltoidea* var. *kunstleri*, PA=palmitic acid

Back to article

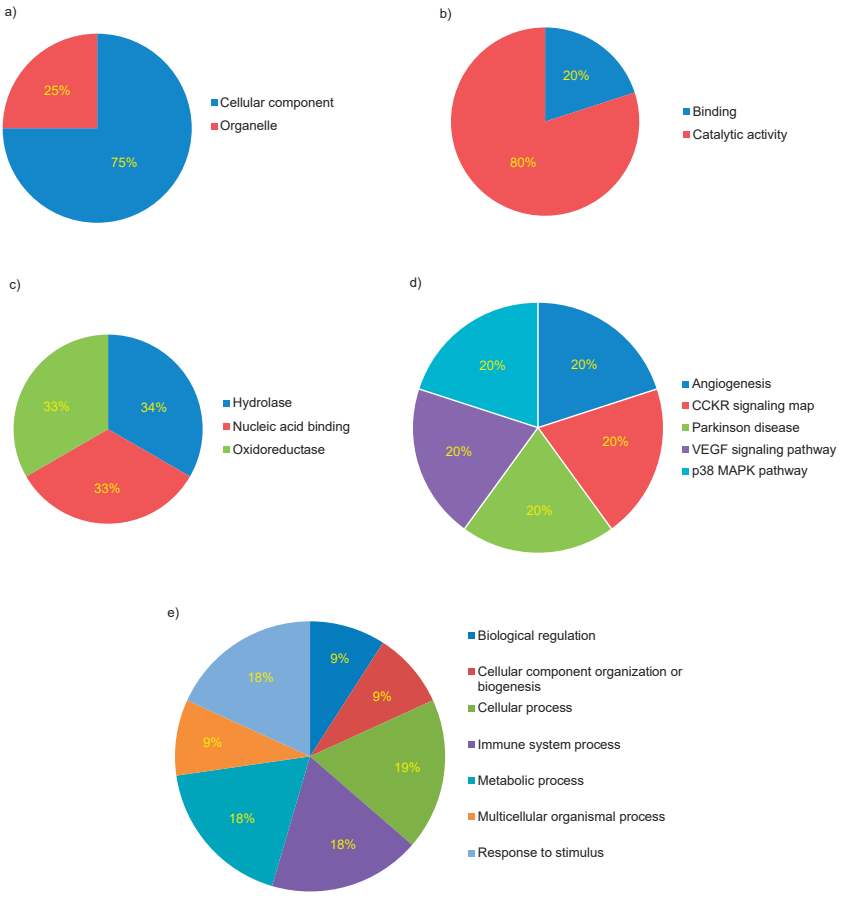


Fig. S4. Pie charts representing the: a) cellular localization, b) molecular functions, c) protein classes, d) pathways, and e) biological processes of the identified proteins obtained from PANTHER database (*17*). The number of genes annotated to a particular category is inversely correlated with a sector's area

Back to article

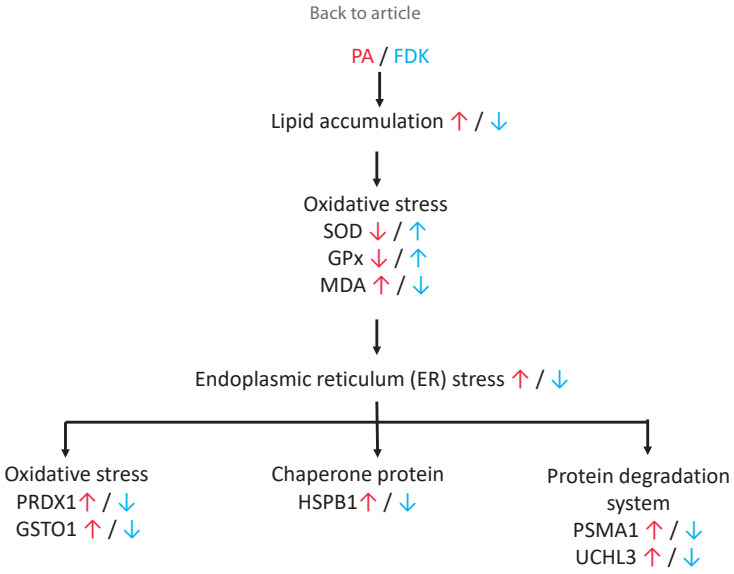
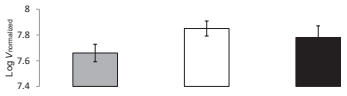
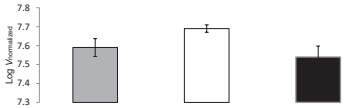
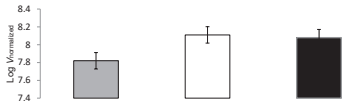
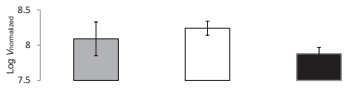
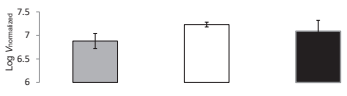


Fig. S5. An overview of *Ficus deltoidea* var. *kunstleris* (FDK) effects in palmitic acid-induced WRL68 cells. The results of pretreatment with a crude water extract of FDK are shown in blue, while those caused by PA are shown in red. PA=palmitic acid, SOD=superoxide dismutase, GPx=glutathione peroxidase, MDA=malondialdehyde

Back to article

Table S1. Crude extract of *Ficus deltoidea* var. *kunstleri* (FDK) alters protein abundance in steatotic WRL68 cells. Six significantly altered proteins were identified by MALDI-ToF/ToF in negative control (grey bar), positive control (white bar) and treatment (black bar) in steatotic WRL68 cells

Accession number	UniProt ID	Fold-change	pI	Mascot score	*N*(peptide match), *A*(coverage)/%	Matched sequences	Protein expression		
							Negative control	Positive control	Treatment (γ(FDK)=200μg/mL +palmitic acid)
P04792|HSPB1_HUMAN	Heat shock protein beta-1 (HSPB1)	1.39	5.98	67	3 , 12	R.DWYPHSR.L R.QDEHGYISR.C R.LFDQAFGLPR.L			
A0A087WTB8|A0A087WTB8_HUMAN	Ubiquitin carboxyl-terminal hydrolase L3 (UCHL3)	1.54	4.85	95	3 , 11	K.FLEESVSMSPEER.A K.FLEESVSMSPEER.A R.YLENYDAIR.V			
B2R983|B2R983_HUMAN	Glutathione S-transferase omega 1 (GSTO1)	1.42	6.23	151	4 , 17	K.GSAPPGPVPEGSIR.I R.FCPFAER.T K.VPSLVGSFIR.S K.EDYAGLKEEFR.K			
A0A109NGN6|A0A109NGN6_HUMAN	Proteasome subunit alpha type 1 (PSMA1)	1.93	4.74	59	1 , 4	R.GVNTFSPEGR.L			
A0A024QZZ7|A0A024QZZ7_HUMAN	Histone H2B (HIST1H2BD)	2.32	10.31	113	5 , 38	K.QVHPDTGISSK.A K.AMGIMNSFVNDIFER.I R.LAHYNKR.S R.EIQTAVR.L R.LLLPGELAK.H			
A0A0A0MRQ5|A0A0A0MRQ5_HUMAN	Peroxiredoxin-1 (PRDX1)	2.22	8.79	72	2 , 20	K.IGHPAPNFK.A R.QITVNDLPVGR.S			

Negative control=cells incubated without the presence of palmitic acid or FDK, positive control=cells incubated with palmitic acid

Back to article

Table S2. Alteration of protein abundance by the crude extract of *Ficus deltoidea* var. *kunstleri* (FDK) is associated with multiple pathways in steatotic WRL68 cells. The list shows the most significant pathways that involve the identified proteins sorted according to p-value ($p<0.05$). This data was obtained through the Reactome database (*18*)

	Pathway name	Found entity*	Identified protein	p-value	FDR
1	ABC-family protein mediated transport	2/161	HSPB1, PSMA1	0.005	0.143
2	UCH proteinases	2/172	PSMA1, UCHL3	0.005	0.143
3	G2/M checkpoints	2/194	PSMA1, HIST1H2BD	0.006	0.143
4	AUF1 (hnRNP D0) binds and destabilizes mRNA	3/198	HSPB1, PSMA1, GSTO1	0.007	0.143
5	RUNX1 regulates transcription of genes involved in differentiation of HSCs	2/230	PSMA1, HIST1H2BD	0.009	0.143
6	Apoptosis induced DNA fragmentation	1/17	HSPB1	0.011	0.143
7	Protein ubiquitination	2/275	UCHL3, HIST1H2BD	0.013	0.143
8	Deubiquitination	4/808	PSMA1, UCHL3, HIST1H2BD, PRDX1	0.013	0.143
9	Neddylation	2/292	PSMA1, UCHL3	0.014	0.143
10	Cellular response to stress	4/1650	PSMA1, HSPB1, PRDX1, HIST1H2BD	0.016	0.143

*The numbers of identified proteins from this study over total proteins that are related to that pathway. FDR=false discovery rate