Supplementary Materials

Anticancer therapies based on oxidative damage: *Lycium barbarum* inhibits the proliferation of breast cancer cells by activating pyroptosis via endoplasmic reticulum stress

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Figure S1. UV spectra (in range 280 to 400 nm) of LBE (500 µg/mL) alone and in the presence of 40 µM $FeSO_4$, $FeCl_3$ and $CuSO_4$.

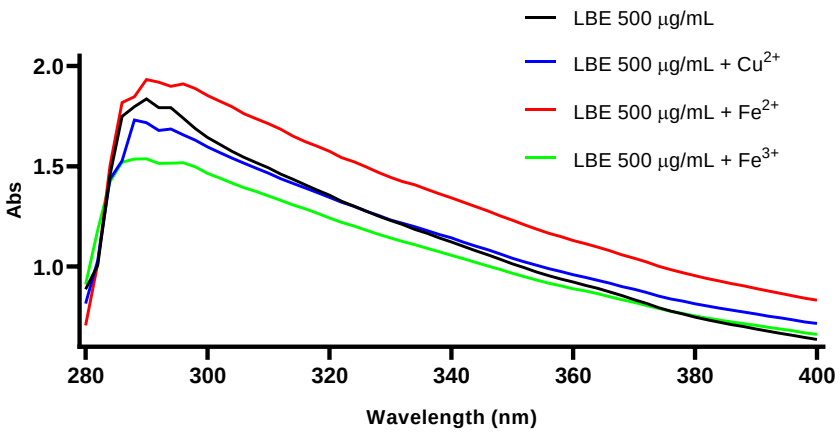


Figure S2. UHPLC-ESI(+)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of N^1-Dihydrocaffeoyl, N^{10}-caffeoyl spermidine hexose.

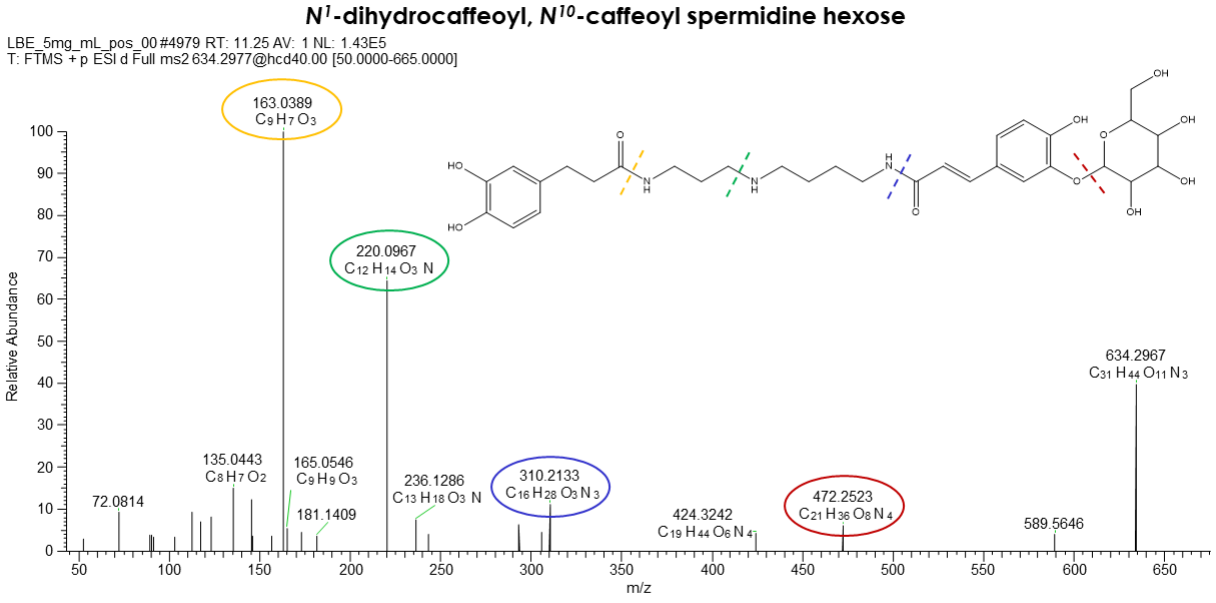


Figure S3. UHPLC-ESI(+)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of *N-p-trans*-coumaroyltyramine.

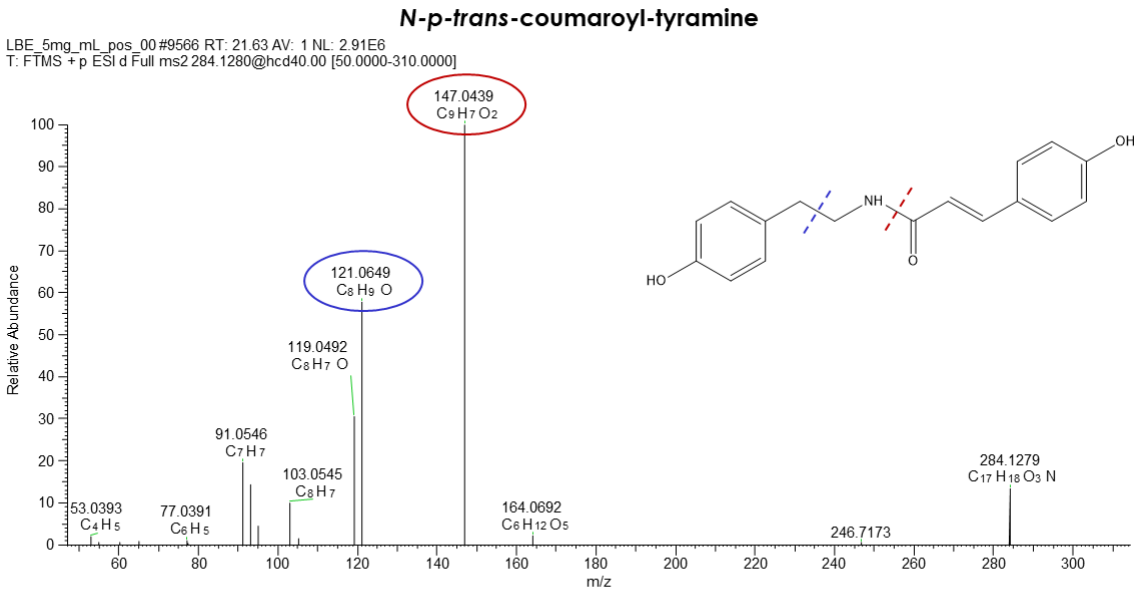


Figure S4. UHPLC-ESI(–)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of a) Caffeic acid, b) p-coumaric acid, c) ferulic acid.

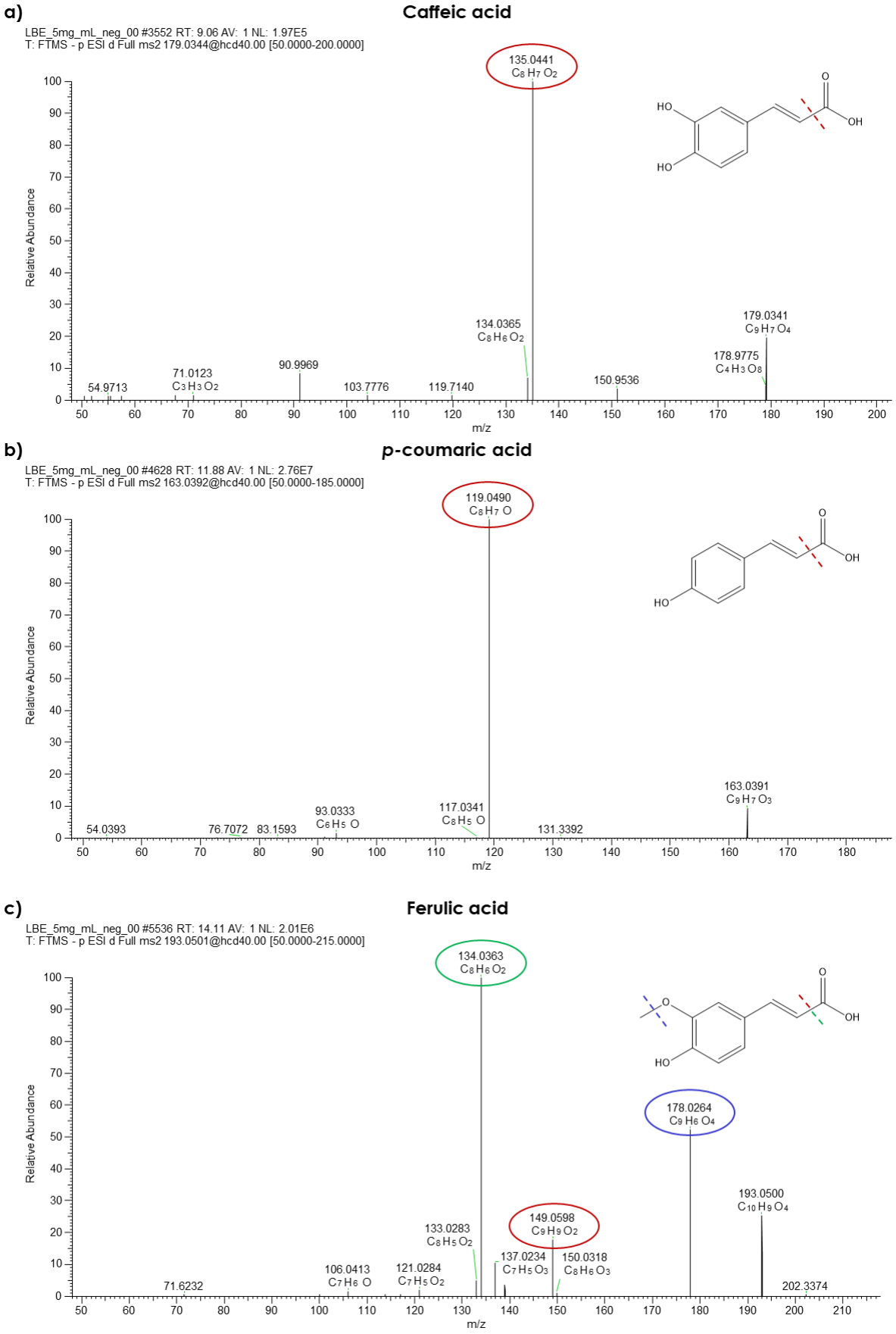


Figure S5. UHPLC-ESI(–)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of Rutin.

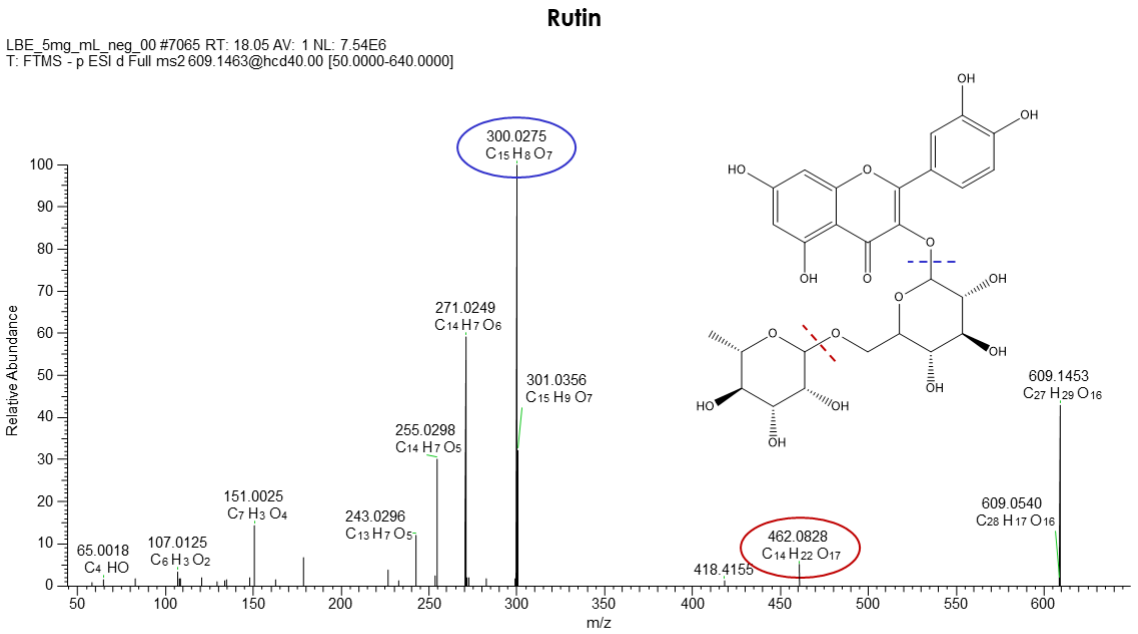


Figure S6. UHPLC-ESI(+)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of Kaempferol 3-O-hexoside-rhamnoside (Nictoflorin).

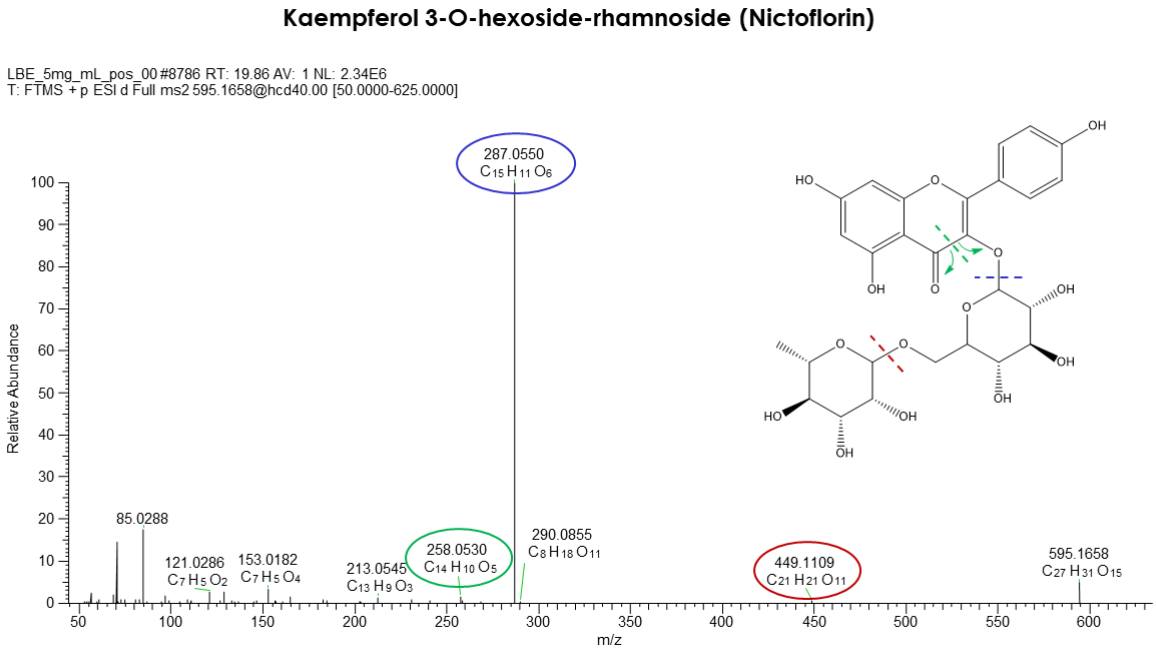


Figure S7. UHPLC-ESI(–)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of Hydroxy octadecadienoic acid (HODE).

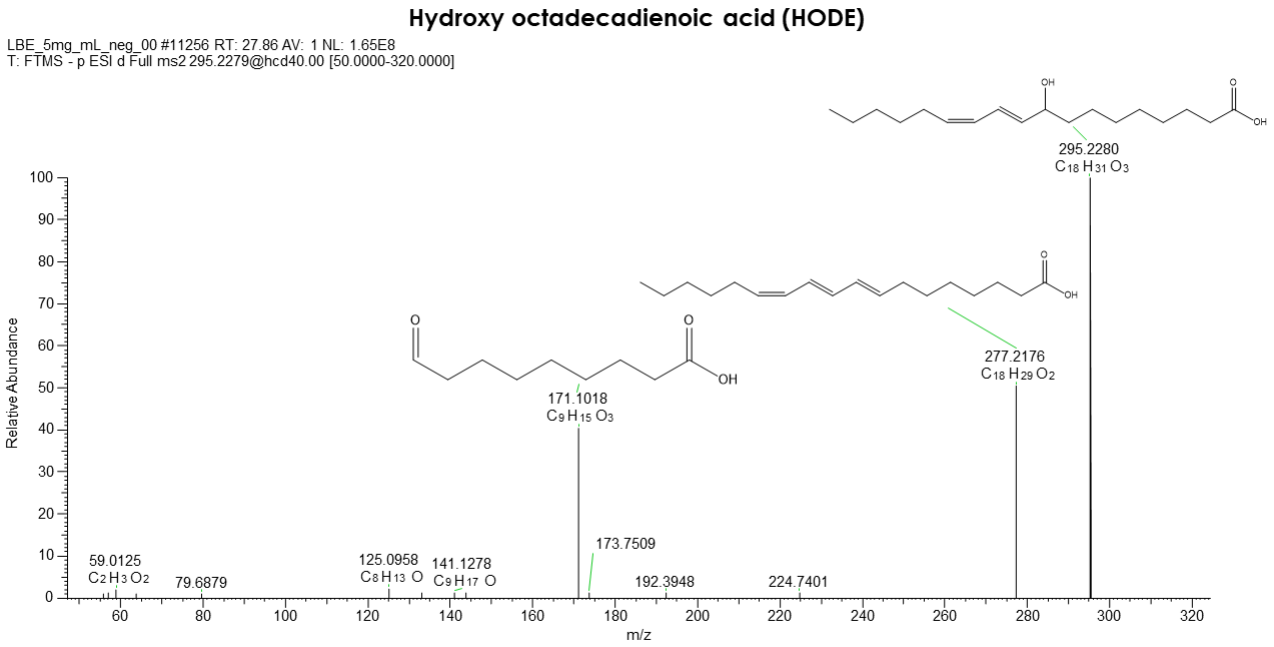


Figure S8. UHPLC-ESI(–)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of Trihydroxy octadecadienoic acid (TriHODE).

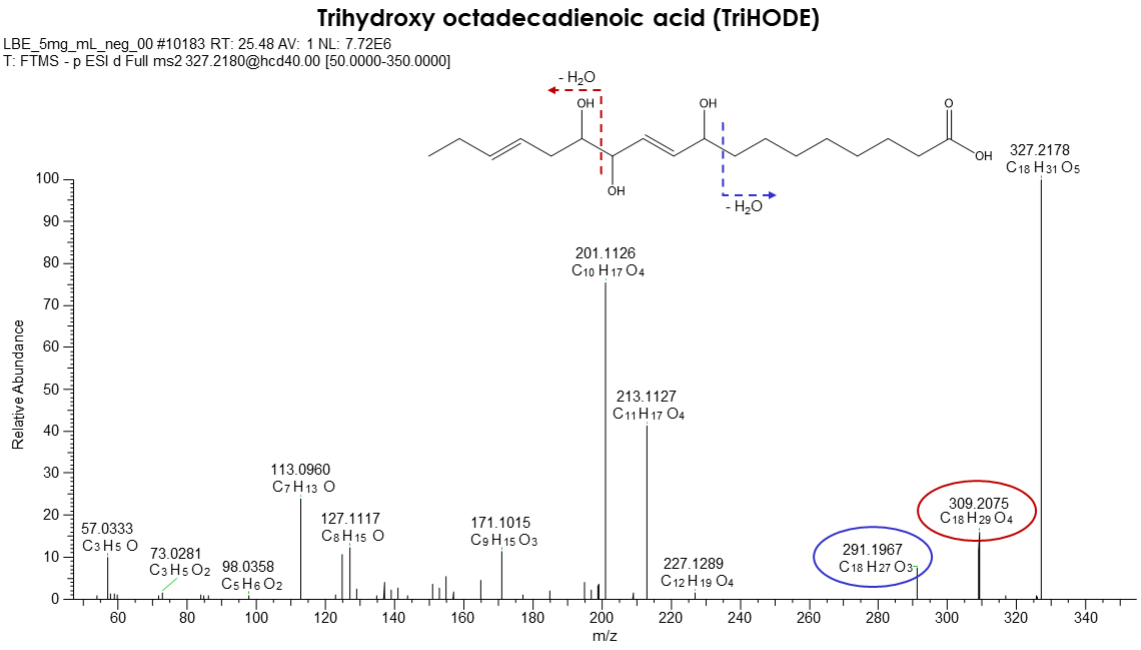


Figure S9. UHPLC-ESI(+)-Orbitrap-MS/MS spectra and proposed fragmentation pathway of Oleamide.

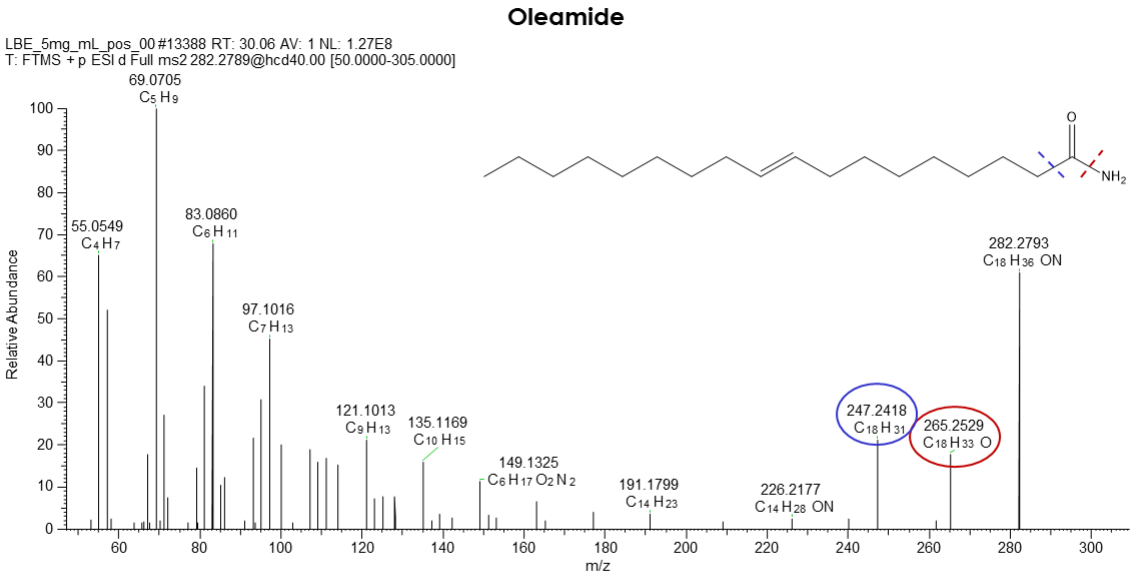
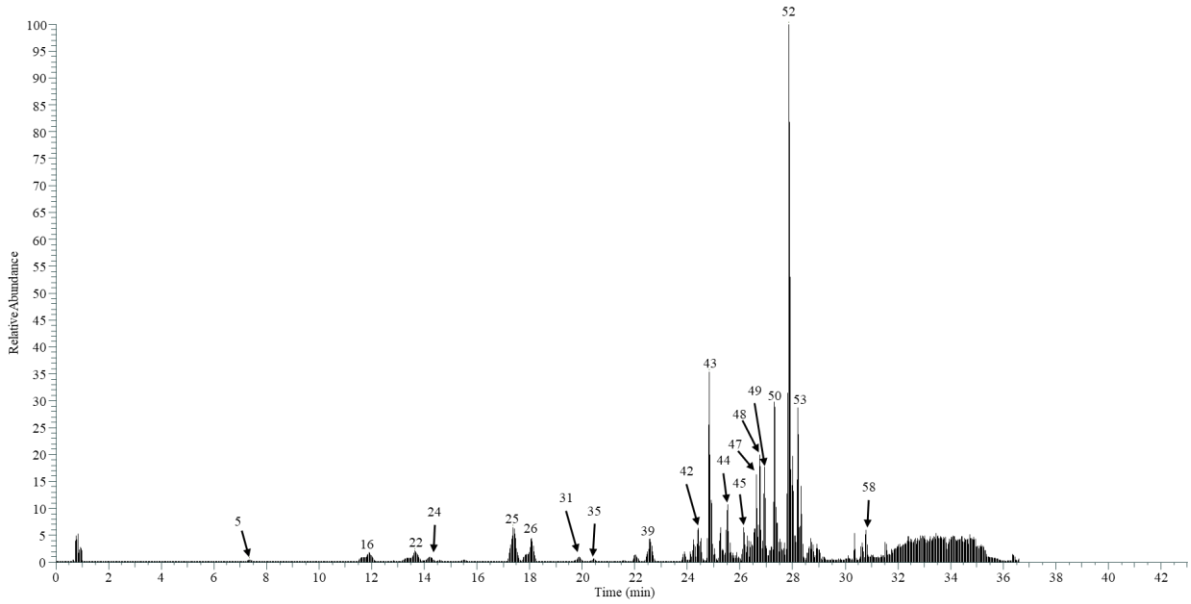


Figure S10 and S11. Total Ion Chromatogram (TIC) profiles, in negative and positive ionization modes, respectively, of polyphenolic compounds isolated from *Lycium barbarum*.



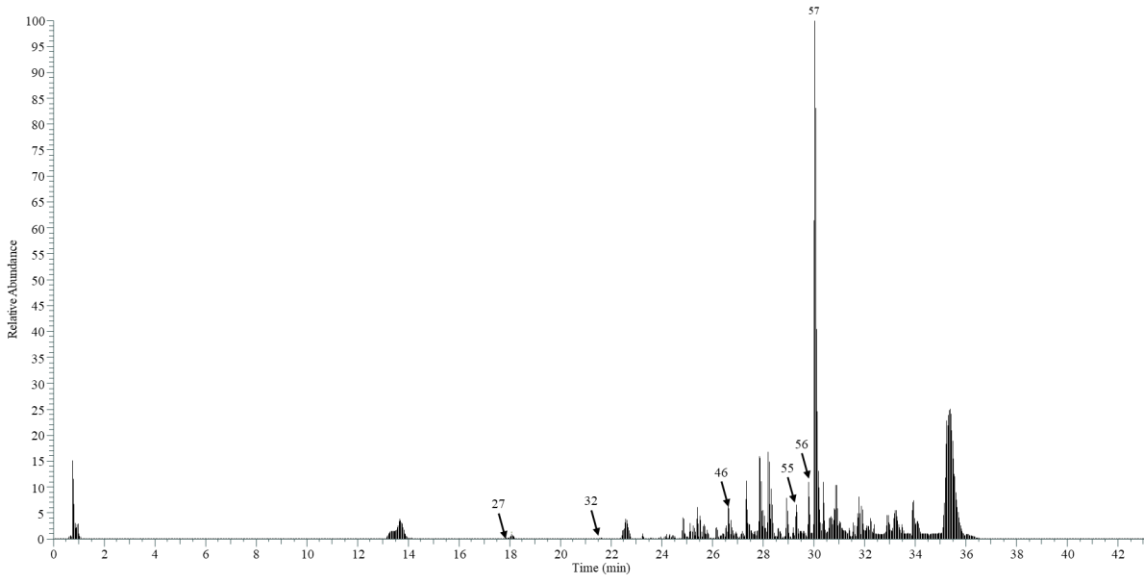
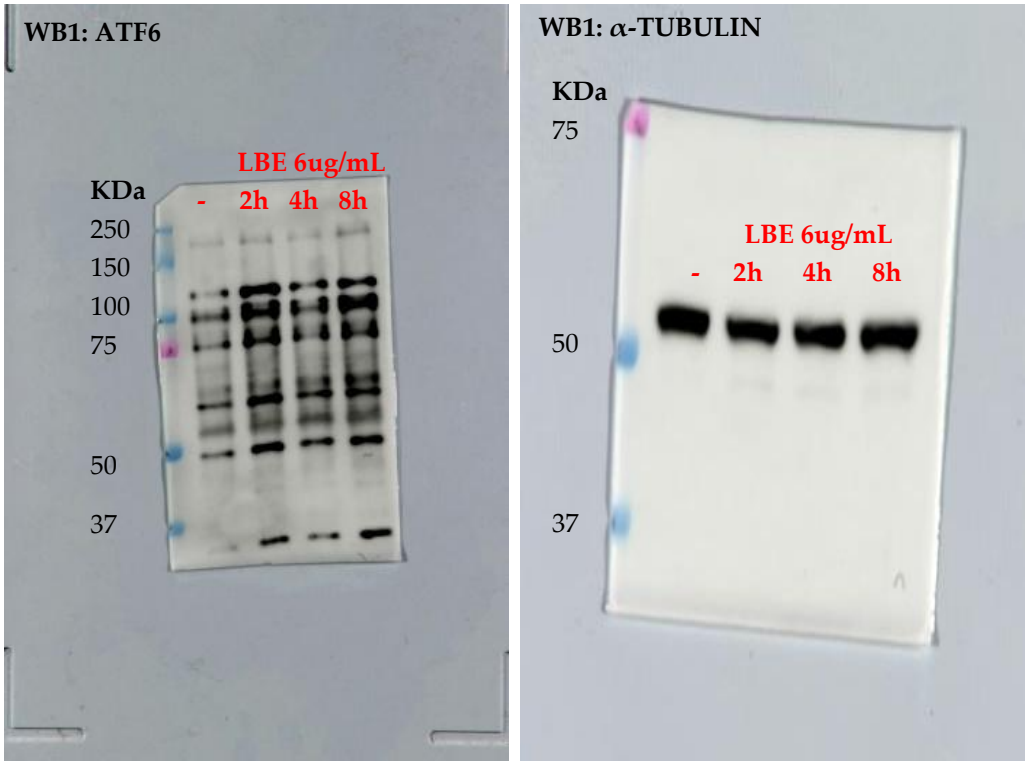
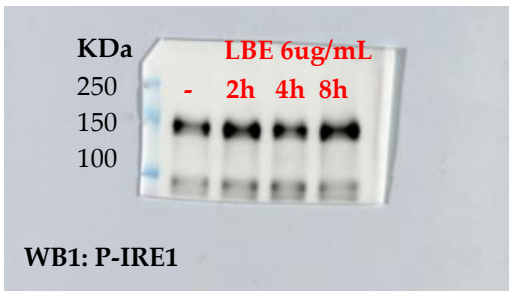


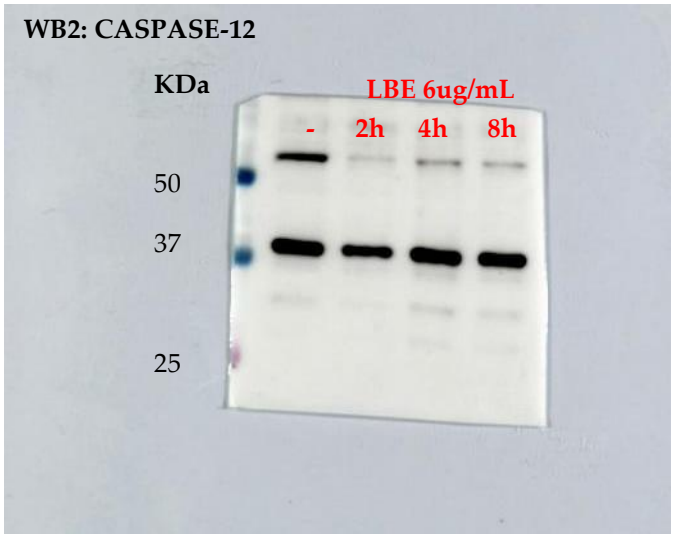
Figure S12. Western blots and PCR raw data

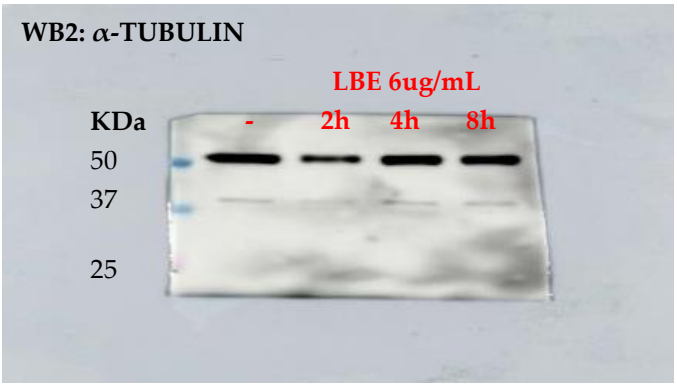
WB1: ATF6/P-IRE1/α-TUBULIN



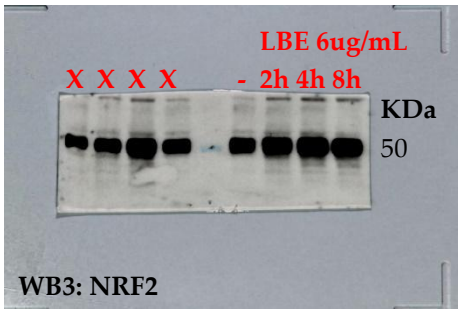


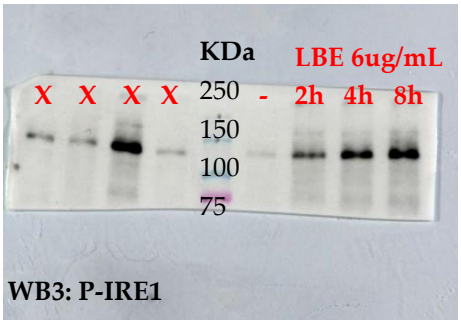
WB2: CASPASE-12/α-TUBULIN

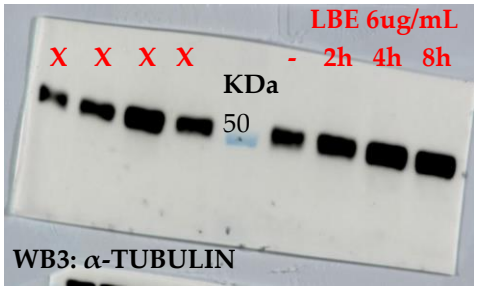


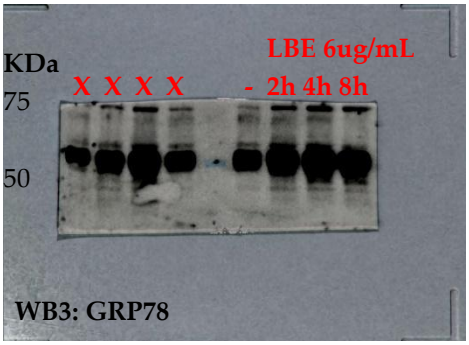


WB3: GRP78/NRF2/P-IRE1/α-TUBULIN

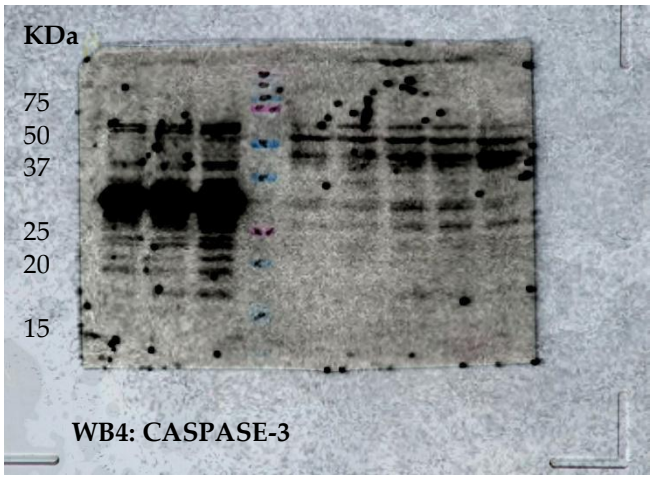


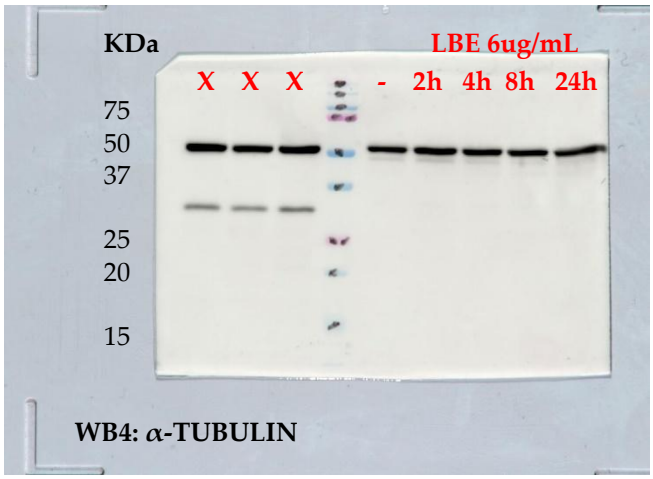


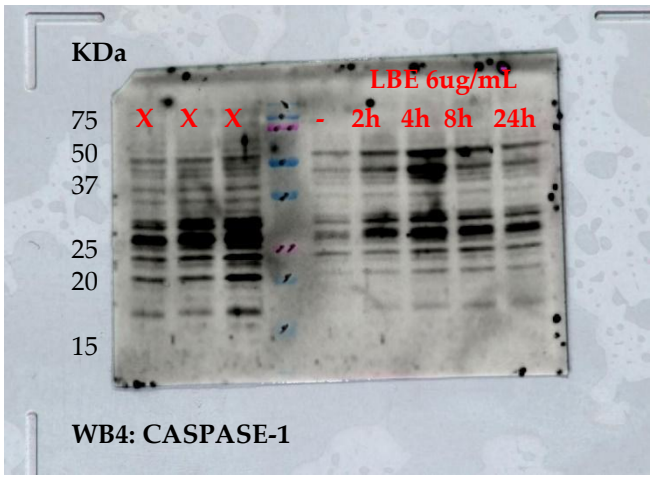


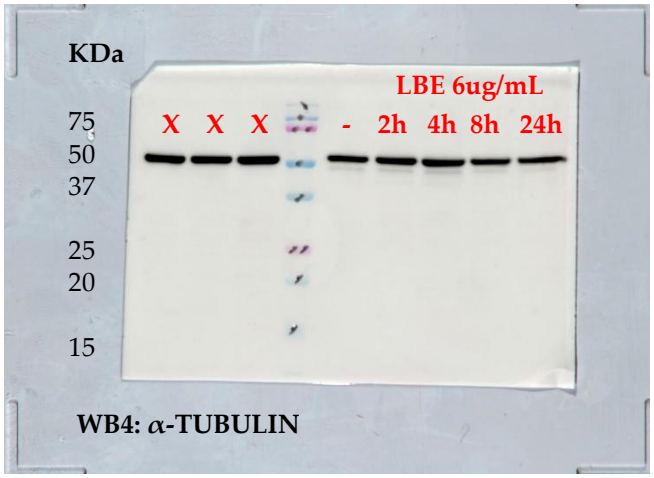


WB4: CASPASE-1/CASPASE-3/α-TUBULIN

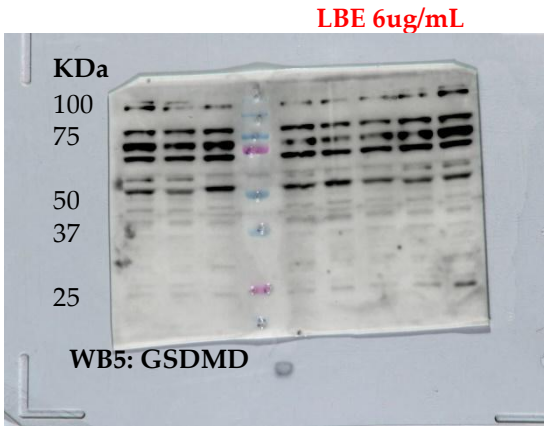


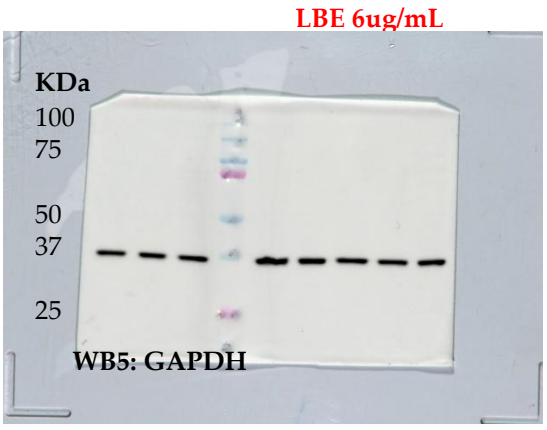




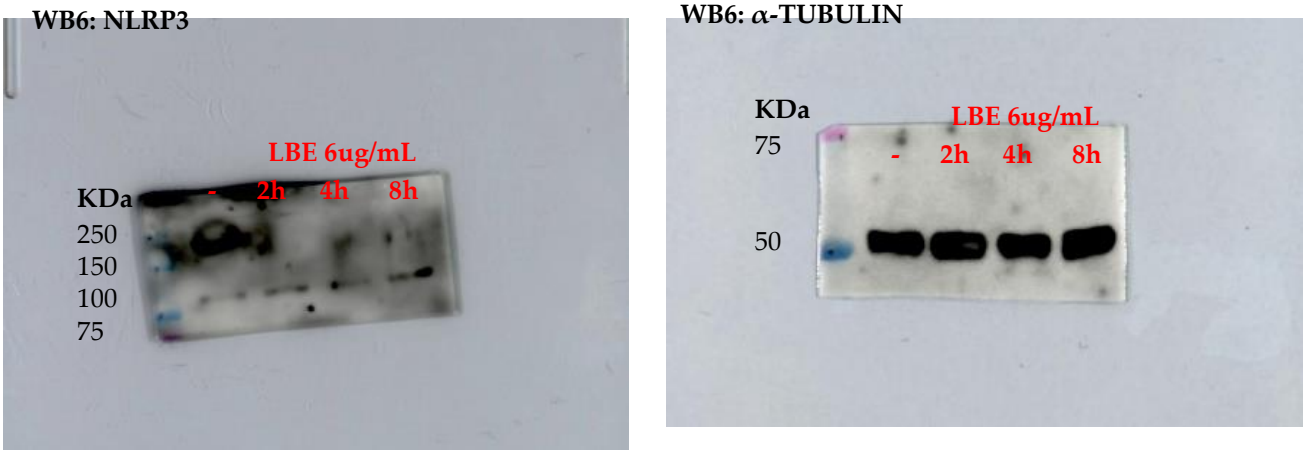


WB5: GSDMD/GAPDH

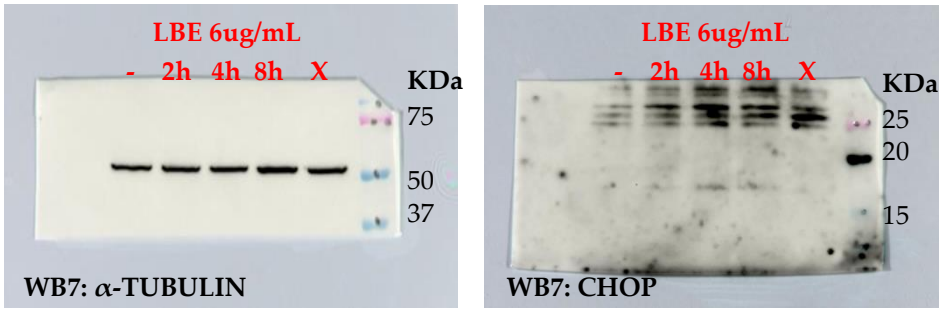




WB6: NLRP3/α-TUBULIN



WB7: CHOP/α-TUBULIN



Xbp1 SPLICING

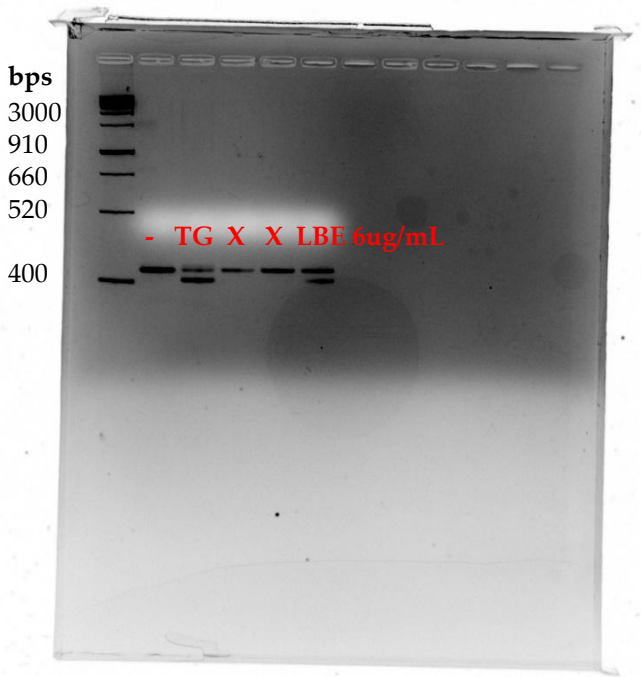
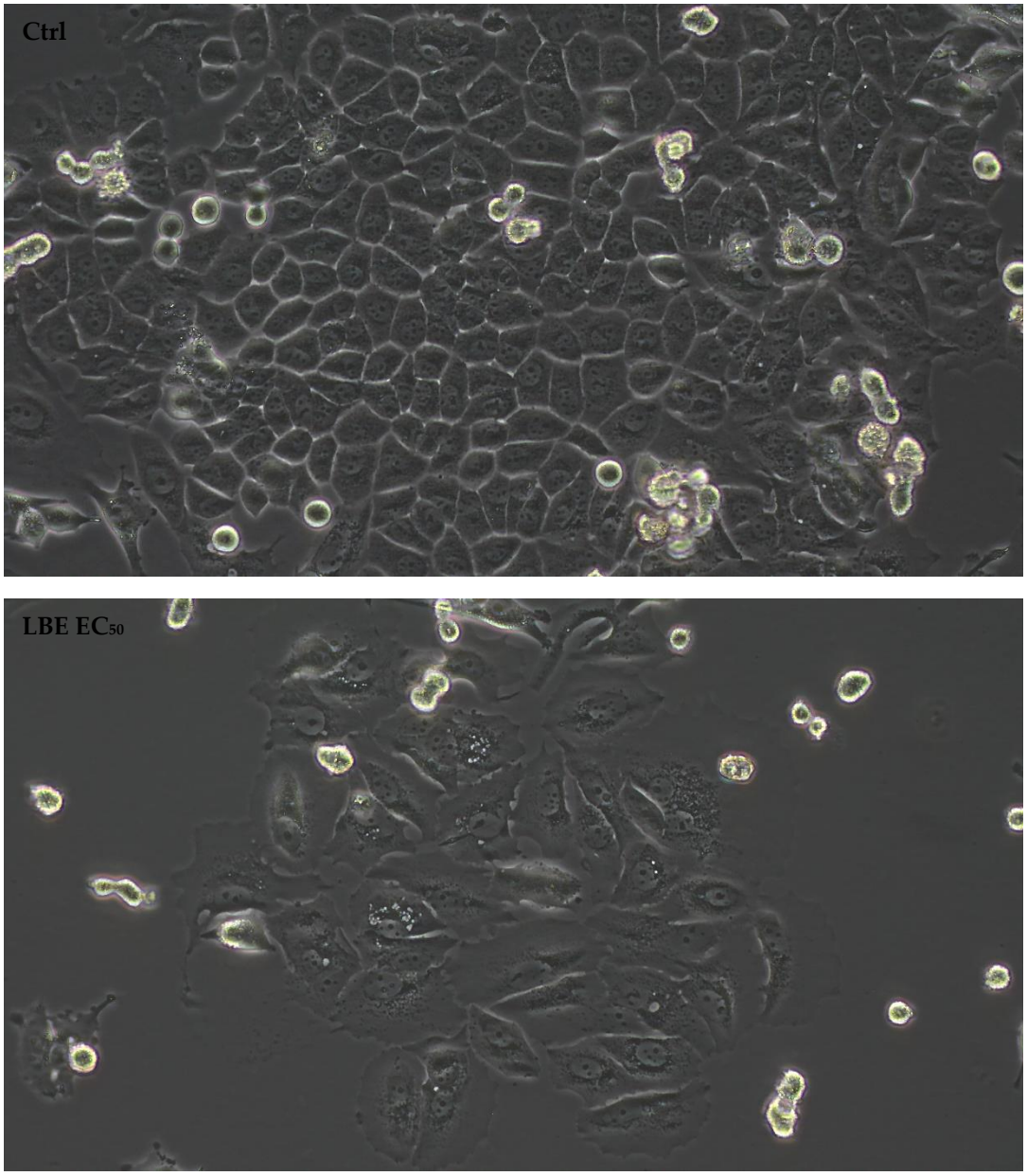
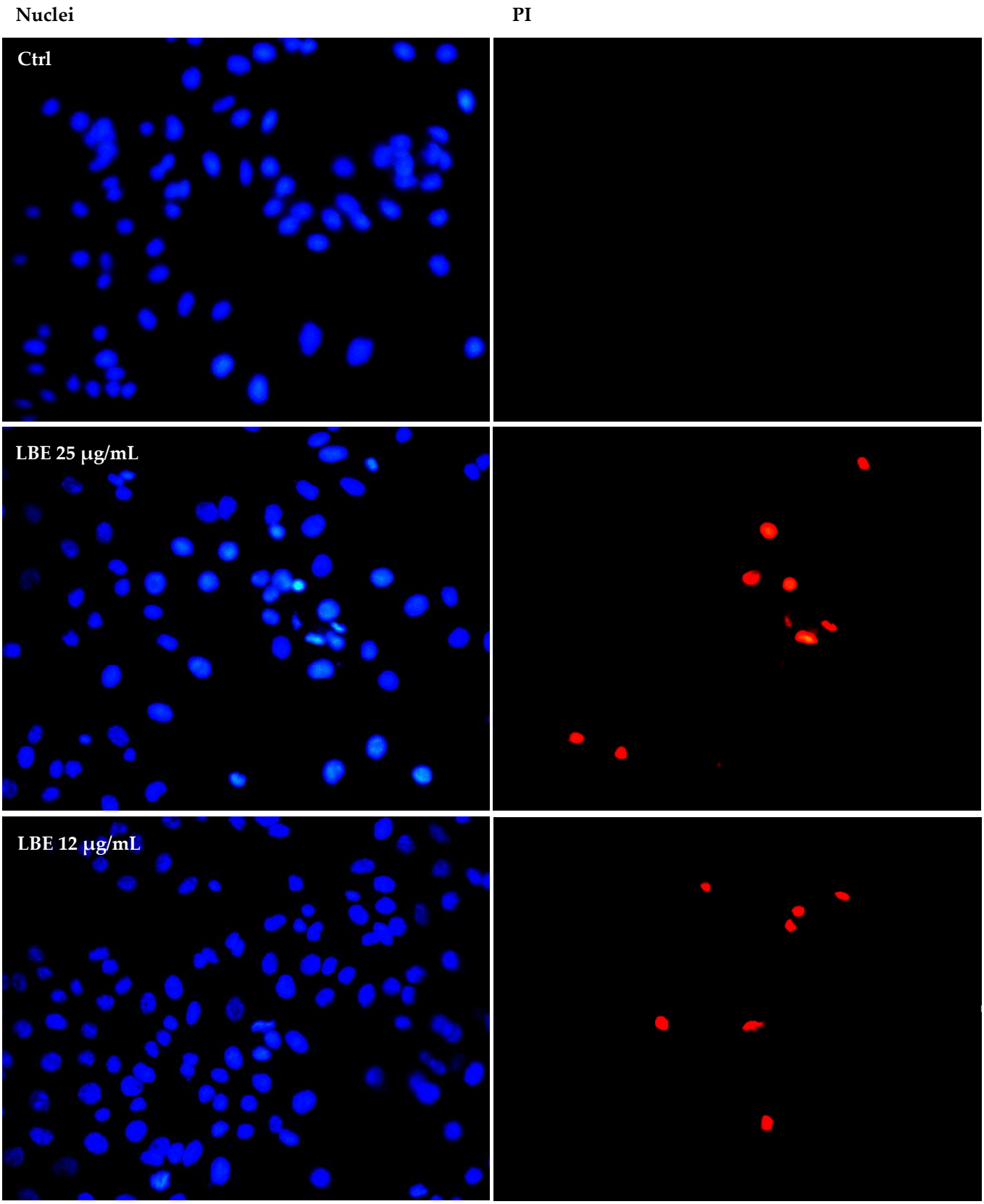
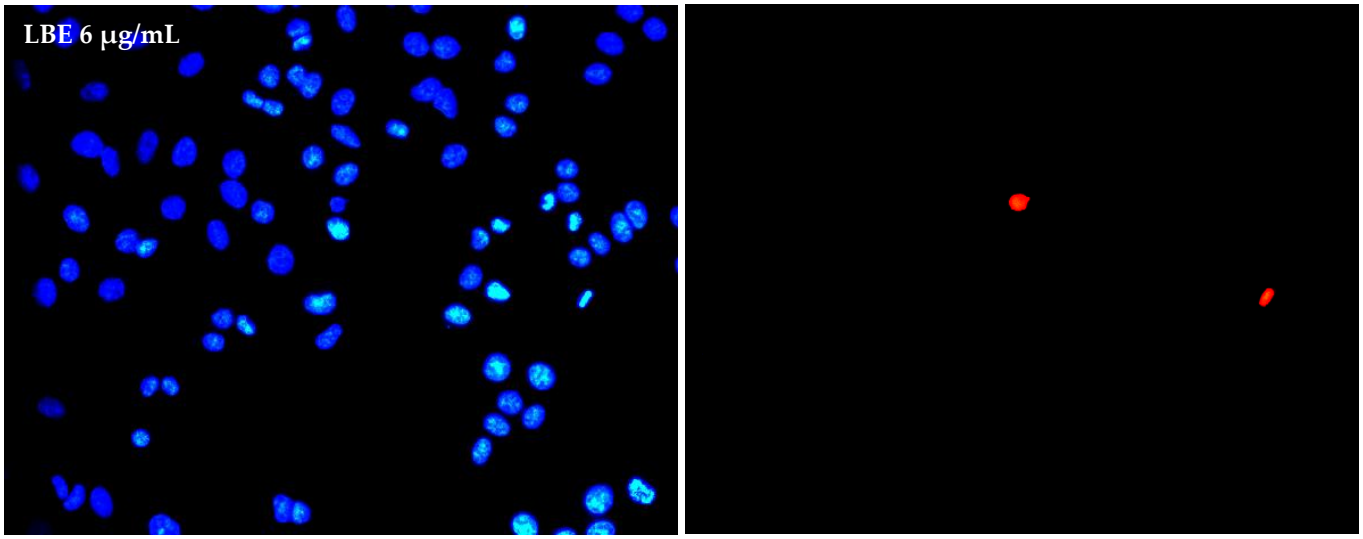


Figure S13. Microscopy images raw data




Nuclei
PI
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LBE 25 µg/mL
LBE 12 µg/mL


LBE 6 µg/mL

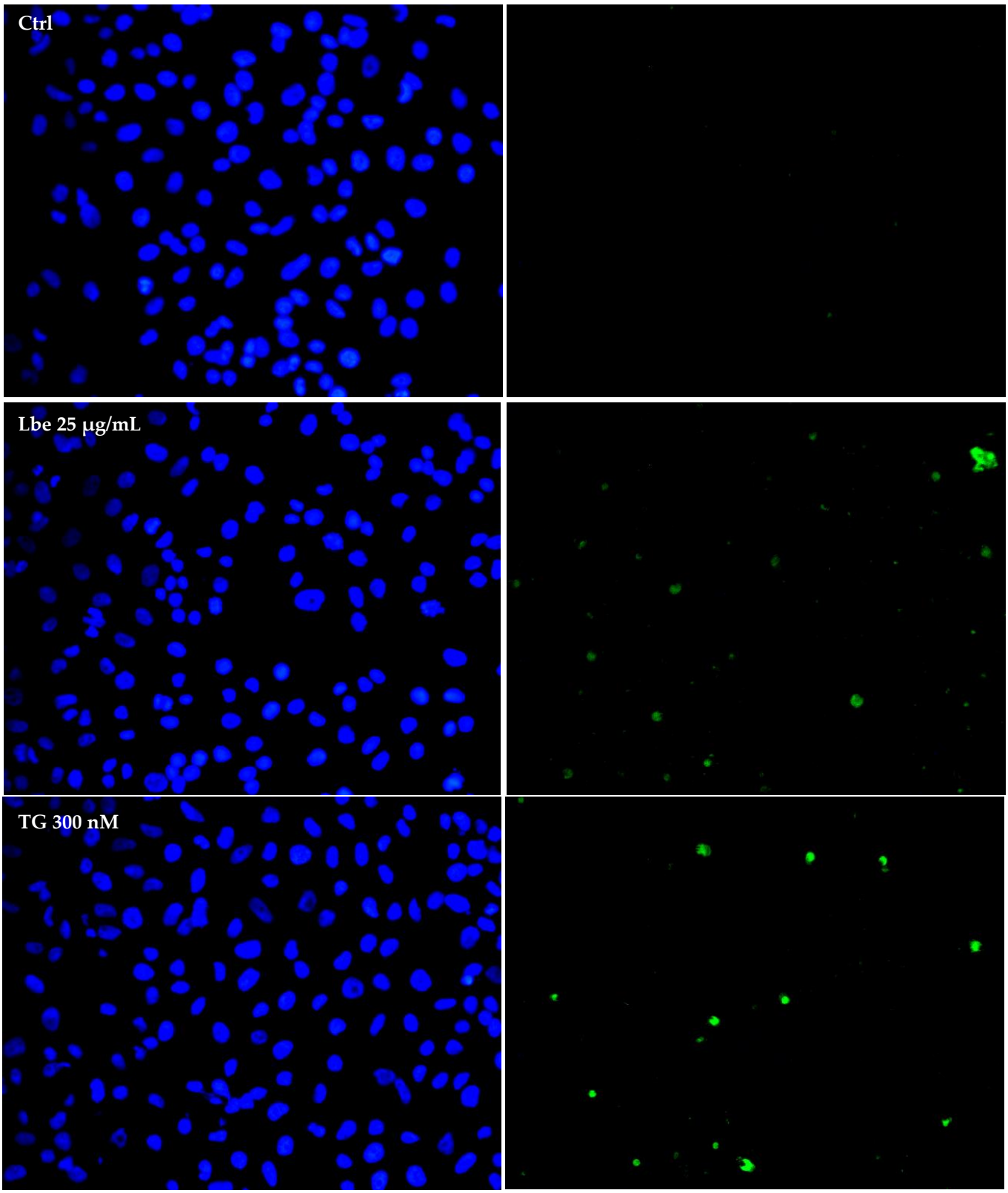

Nuclei
Tht
Ctrl
Lbe 25 µg/mL
TG 300 nM

Table S1. Method validation parameters for quantitative assay.

Parameters	Caffeic acid	Rutin	Oleic acid
Retention time (min) ± dev. st. (n = 4)	8.9425 ± 0.0096	17.1625 ± 0.0096	33.6850 ± 0.0058
Regression equation	y = 3.63E-09x -4.72E-02	y = 7.31E-09x -1.68E-01	y = 1.73E-06x -1.50E+01
Linear range	0.03-4 μg mL^{-1}	0.06-15.63 μg mL^{-1}	15.63-2000 μg mL^{-1}
Correlation coefficient (R^2)	≥ 0.9979	≥ 0.9989	≥ 0.9996
Intraday (n = 3)	0.98 : 91.68	1.95 : 90.77	62.5 : 92.19
Analyte concentration (μg mL^{-1}):	1.95 : 95.63	3.91 : 91.35	125 : 93.34
Accuracy (%)	3.91 : 101.91	7.81 : 100.31	250 : 95.03
Interday (n = 3)	0.98 : 90.42	1.95 : 105.57	62.5 : 97.48
Analyte concentration (μg mL^{-1}):	1.95 : 94.81	3.91 : 100.76	125 : 109.11
Accuracy (%)	3.91 : 102.41	7.81 : 104.48	250 : 92.28
LOQ (μg mL^{-1})	0.0008	0.0053	9.3185
LOD (μg mL^{-1})	0.0003	0.0017	3.0751