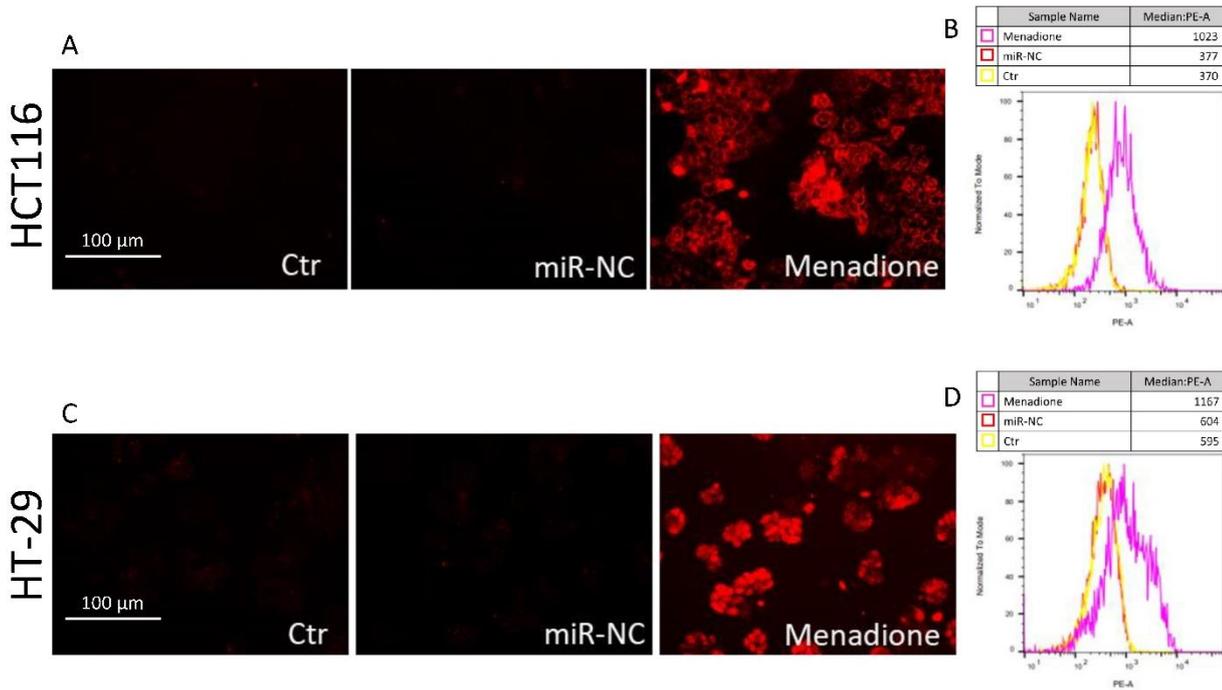
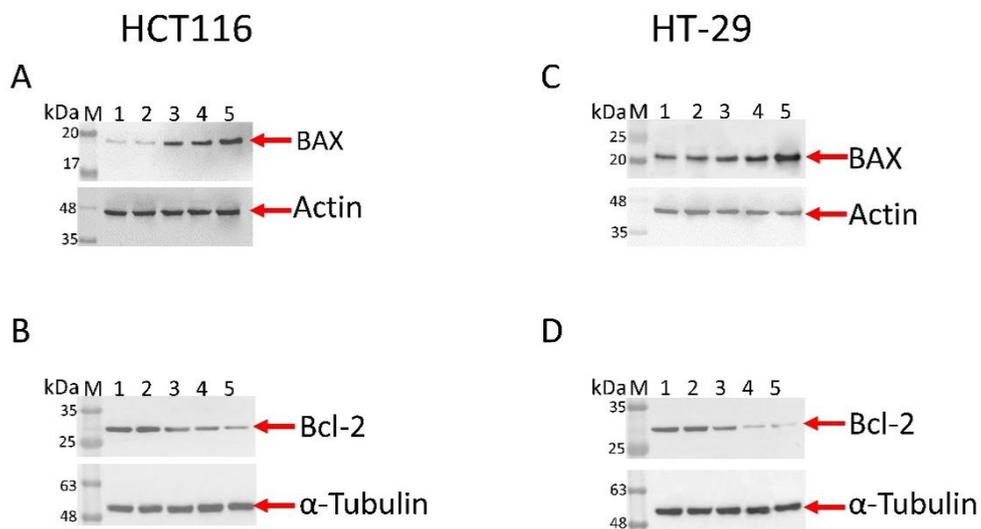


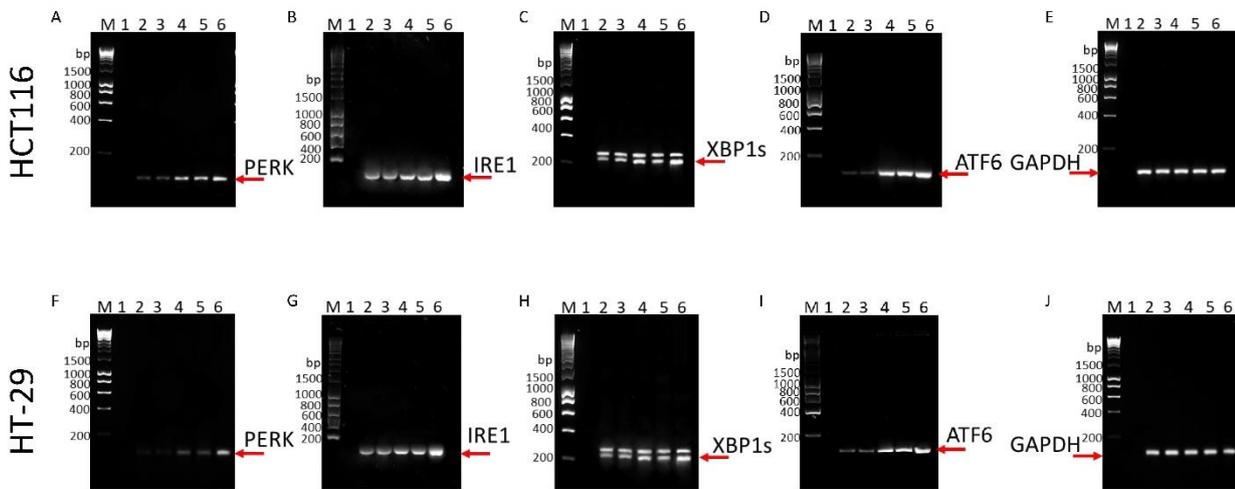
Supplementary Figure S1: Milk-derived miRNA cytotoxicity. (A) Flow chart showing milk exosome miRNA isolation and characterization. The relative expression of (B) miR-148a and (C) miR-15b, analyzed by qRT-PCR and normalized with U6 as endogenous control, in HCT116 and HT-29 transfected with 30 nM mimic Negative Control (miR-NC), miR-148a mimic (miR-148a⁺), and miR-15b mimic (miR15b⁺). MiRNA levels are reported as floating bars with a line representing the mean ± SD. (D,E) HCT116 and (F,G) HT-29 cells were transfected with 30 nM mimic Negative Control (miR-NC), miR-148a mimic (miR-148a⁺), and miR-15b mimic (miR15b⁺) and cell viability, assessed using Cell Counting Kit-8 assay, expressed as % of control of n = 4 independent. Control cells (Ctr) were treated with the corresponding highest volume of HBSS-10 mM Hepses. **p* < 0.05 vs. miR-NC.



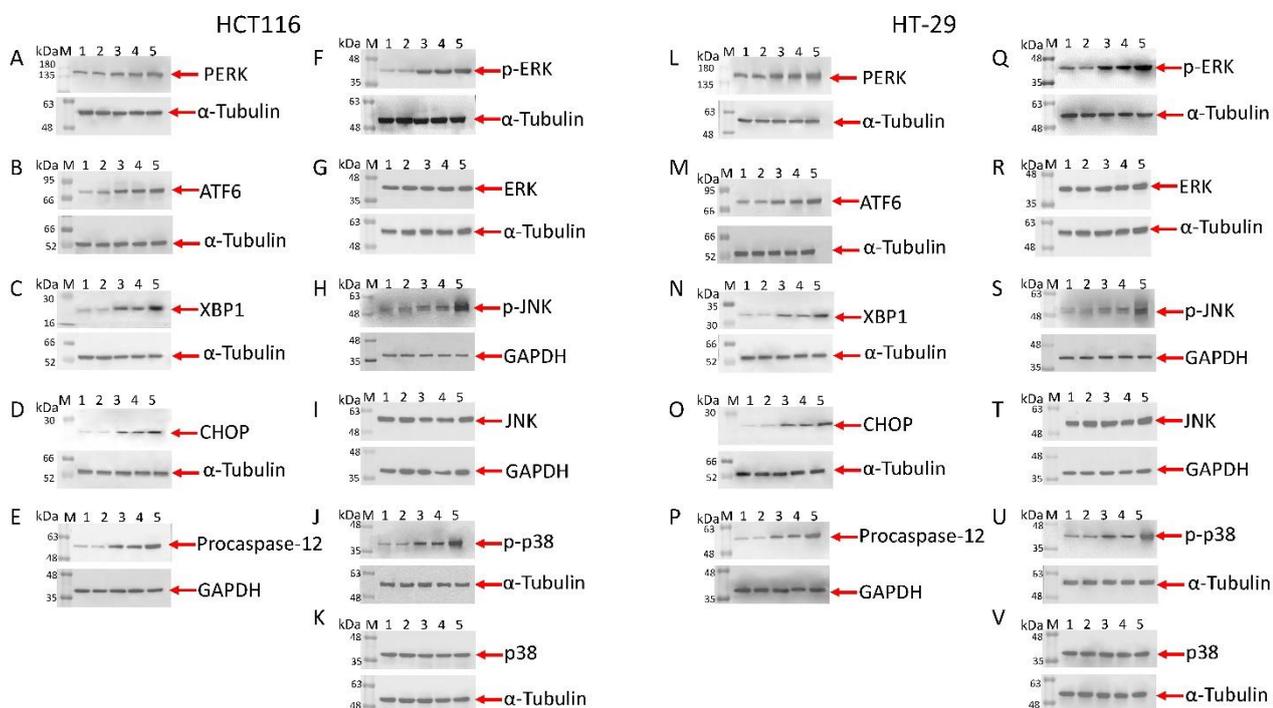
Supplementary Figure S2: Oxidative stress controls. Representative images and cytometer analyses, expressed as red fluorescence median, of mitochondrial ROS detection in (A,B) HCT116 and (C,D) HT-29 transfected with 30 nM mimic Negative Control (miR-NC) or treated for 1h with the ROS inducer menadione (100 μ M). Control cells (Ctr) were treated with the corresponding highest volume of HBSS-10 mM Hepes. Scale bars = 100 μ m.



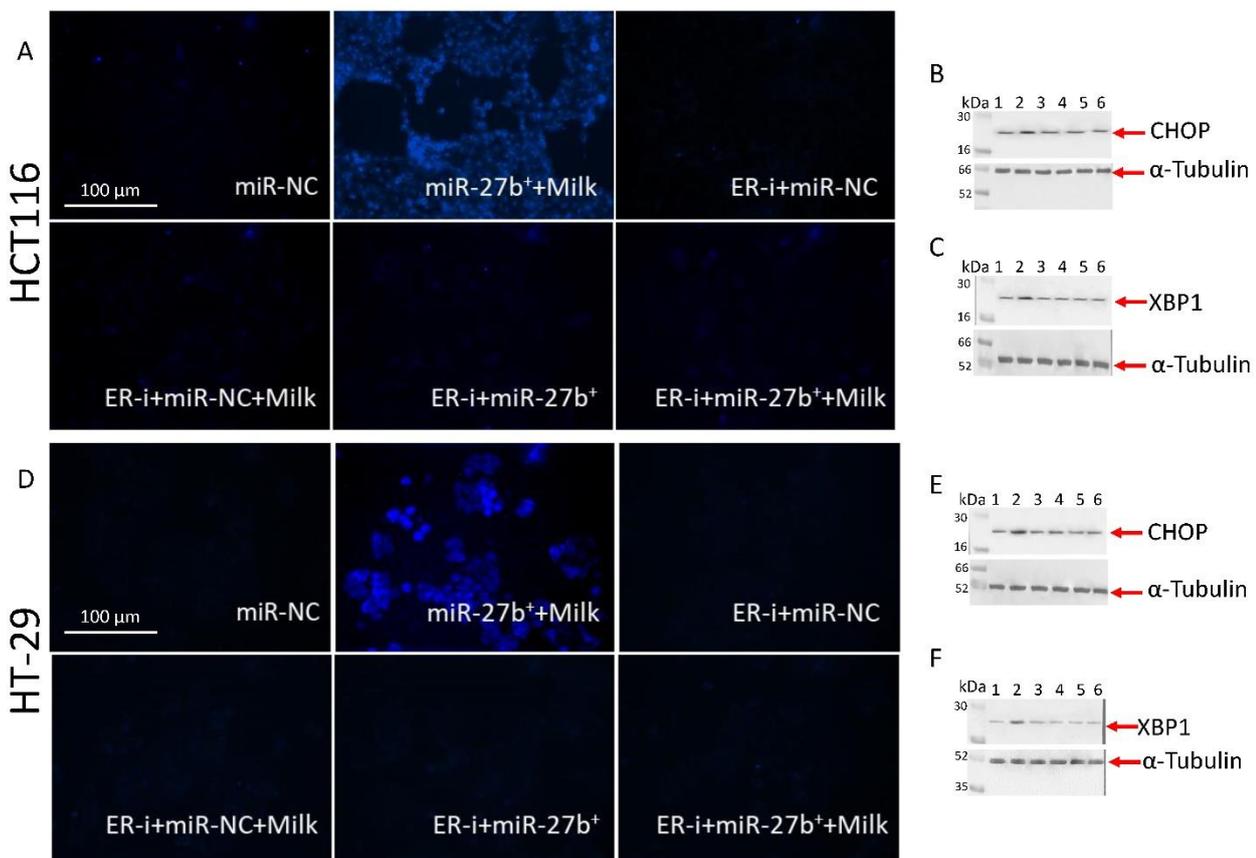
Supplementary Figure S3: Apoptotic markers. Representative cropped blots of BAX, Bcl-2 and their internal controls (actin and α -tubulin) in (A,B) HCT116 and (C,D) HT-29 cells transfected with 30 nM mimic Negative Control (miR-NC) and miR-27b mimic (miR-27b⁺) or with miR-NC and miR-27b⁺ before 72h with 40% v/v milk treatment (miR-NC+Milk and miR-27b⁺+Milk). Control cells (Ctr) were treated with the corresponding highest volume of HBSS-10 mM Hepes. M = weight markers; Lane 1 = Ctr; lane 2 = miR-NC; lane 3 = miR-NC+Milk; lane 4 = miR-27b⁺; lane 5 = miR-27b⁺+Milk.



Supplementary Figure S4: mRNA levels of ER-stress markers. Representative PCR products of GAPDH (internal control), PERK, XBP1s, IRE1, and ATF6 in (A–E) HCT116 and (F–J) HT-29 cells transfected with 30 nM mimic Negative Control (miR-NC) and miR-27b mimic (miR-27b⁺) or with miR-NC and miR-27b⁺ before 72h with 40% v/v milk treatment (miR-NC+Milk and miR-27b⁺+Milk). Control cells (Ctr) were treated with the corresponding highest volume of HBSS-10 mM Hepes. M = molecular markers; Lane 1 = negative control lacking cDNA template; Lane 2 = Ctr; lane 3 = miR-NC; lane 4 = miR-NC+Milk; lane 5 = miR-27b⁺; lane 6 = miR-27b⁺+Milk. The amplified transcripts are shown with the expected sizes on 2.0% agarose gels.



Supplementary Figure S5: ER-stress markers. Representative cropped blots of PERK, ATF6, XBP1, CHOP, procaspase-12, phospho-ERK, ERK, phospho-JNK, JNK, phospho-p38, p38, and their internal controls (GAPDH and α -tubulin) in (A–K) HCT116 and (L–V) HT-29 cells transfected with 30 nM mimic Negative Control (miR-NC) and miR-27b mimic (miR-27b⁺) or with miR-NC and miR-27b⁺ before 72h with 40% v/v milk treatment (miR-NC+Milk and miR-27b⁺+Milk). Control cells (Ctr) were treated with the corresponding highest volume of HBSS-10 mM Hepes. M = weight markers; Lane 1 = Ctr; lane 2 = miR-NC; lane 3 = miR-NC+Milk; lane 4 = miR-27b⁺; lane 5 = miR-27b⁺+Milk.



Supplementary Figure S6: ER-i effects. Representative images by fluorescence microscopy and cropped blots of CHOP, XBP1, and the internal control (α -tubulin) in (A–C) HCT116 and (D–F) HT-29 cells transfected with 30 nM mimic Negative Control (miR-NC) and miR-27b mimic before 72h with 40% v/v milk treatment (miR-27b⁺+Milk) or incubated for 1h with 2 μ M GSK2606414 (ER-i) and then transfected with miR-NC (ER-i+miR-NC) or with miR-27b⁺ (ER-i+miR-27b⁺) before milk incubation (ER-i+miR-NC+Milk and ER-i+miR-27b⁺+Milk). Scale bars = 100 μ m. M = weight markers; Lane 1 = miR-NC; lane 2 = miR-27b⁺+Milk; lane 3 = ER-i+miR-NC; lane 4 = ER-i+miR-NC+Milk; lane 5 = ER-i+miR-27b⁺, lane 6 = ER-i+miR-27b⁺+Milk.