Supplementary figures

Multi-miRNAs panel of tumor-derived extracellular vesicles as promising diagnostic biomarkers of early-stage breast cancer

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Figure S1. Nanoparticle tracking analysis (NTA) quantification of extracellular vesicles (EVs) released from media of breast cancer cell lines. (A) NTA distribution of MCF-7 EVs. (B) NTA distribution of BT-474 EVs. (C) NTA distribution of SK-BR-3 EVs. (D) NTA distribution of MDA-MB-231 EVs. (E) Measurement of EVs amounts by NTA. (F) Western blot analysis of EpCAM, CD49f, CD9, CD81, and Alix on EVs.



Figure S2. Evaluation of endogenous controls for comparing microRNA (miRNA) expression levels between breast cancer cells (BT-474, MCF-7, SK-BR-3, and MDA-MB-231) and their EVs. (A) Heat map of correlations between miRNA expression in cell lines and cell-derived EVs for miR-16, miR-21, miR-9, miR-429, miR-96, miR-155, miR-128, and miR-let-7a normalized by miR-484, miR-let7a, and miR-16. A darker red color represents a stronger positive correlation (Pearson correlation coefficients closer to 1). (B) A darker green color represents significant correlations. The miR-16, miR-21, miR-9, and miR-429 of extracellular vesicles normalized by miR-484 were significantly correlated with those of breast cancer cells. *p < 0.05, **p < 0.01.



Figure S3. Evaluation of hemolysis of plasma samples prior to isolation of EVs to minimize the hemolysis-induced miRNA expression inhibition. (A) Standard curve of hemolysis at 414 nm of absorbance. (B) Condition of rule-out by RBC concentration in 32 representative plasma samples from total population.