

Supplementary tables

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

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**Table S1.** Differentially expressed miRNAs in the paired adjacent normal tissues and cancer tissues

	Adjacent normal tissues		Cancer tissues		p-value (paired t-test)
	Median (min-max)	Mean (S.D.)	Median (min-max)	Mean (S.D.)	
hsa-miR-16	308 (92.8-1709)	435 (331.9)	511 (145.9 - 3952)	628.4 (472.3)	0.006
hsa-miR-21	50117 (10121-196399)	54433 (32501)	248171 (34749-467924)	240079 (87849)	<0.0001
hsa-miR-9	250 (49.1-2628)	414.5 (473)	406.5 (44.7-51986)	3083 (8477)	0.0047
hsa-miR-429	15.1 (0-149.5)	20.9 (21.9)	94.2 (101-436.3)	120.8 (87.4)	<0.0001
hsa-miR-96	3.2 (0-36.2)	4.5 (4.5)	26.8 (2.4-153.9)	41.7 (34.8)	<0.0001
hsa-miR-155	137 (39.9-889.4)	176 (135.4)	294 (91.5-4114)	484 (589.4)	<0.0001
hsa-miR-128	41.3 (24.3-376.9)	49.9 (40.2)	63.0 (23.7-164.3)	71.7 (30.7)	<0.0001

**Table S2.** Evaluation of reference genes for gene expression

Methods	Ranking order (Better-Good-Average)		
	1	2	3
<b>Delta Ct</b>	miR-484	miR-16	let7a-
<b>BestKeeper</b>	miR-484	miR-16	let7a
<b>Normfinder</b>	miR-484	-	let7a
<b>Genorm</b>	miR-484/miR-16	miR-16	let7a

**Table S3.** Function of the selected miRNAs and the expression levels of miRNAs in breast cancer tissues and plasma in TCGA data and review of literature

miRNA	Function <sup>a</sup>	Tissues (clinical samples)		Plasma (clinical samples)	EVs from plasma (clinical samples)
		TCGA data <sup>b</sup>	qPCR validated data <sup>c</sup>		
miR-16	Apoptosis	↑**	↑[1]	↑[14] ↓[24]	↑[22]
miR-21	Tumor growth, drug resistance	↑***	↑[2,3,4]	↑[15,16,17] ↓[18]	↑[23]
miR-9	Metastasis, angiogenesis	↑**	↑[5,6,7]	n.s.[25] ↓[26] ↑[27]	-
miR-429	Proliferation, migration	↑***	↑[8]	↑[19]	-
miR-96	Proliferation, migration	↑***	↑[9,10]	↑[17]	-
miR-155	Proliferation, metastasis	↑***	↑[3,11]	↑[28]	-
miR-128	Apoptosis	↑***	↑[12,13]	↑[30] ↓[29]	-
miR-let7a	Immune response	↓*	-	↑[20,21] ↓ [15]	-

a. Functions of miRNAs based on the breast cancer cell lines in the literature review [1-4].

b. Sources from The cancer genome atlas were obtained (portal.gdc.cancer.gov) and the paired t-tests between primary tumor tissues and paired adjacent normal tissues were performed.

c. The expression levels of miRNAs were obtained from the literature review on breast tumor tissues, plasma, and EVs from plasmas. \*  $p < 0.05$ , \*\*  $p < 0.01$  \*\*\*  $p < 0.001$ , n.s. no significant expression - not validated using clinical samples.

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