

Supplementary materials

Table 1. Statistical analyses. (A) Logistic regression of the indicated miRNAs in a Study population of 46 healthy donors (CTR) and 64 BC subjects. * miRNA that significantly ($p < 0.05$) estimates the probability to have a tumor. (B) Logistic stepwise regression. * miRNA that significantly ($p < 0.05$) estimates the probability to have a tumor.

A

Logistic regression			
miRNAs	Estimate	Std. Error	<i>p</i> -value
miR-125b-5p *	8.99381	3.91189	0.02350
miR-143-3p *	9.57245	4.51353	0.03631
miR-145b-5p	-1.47815	4.16086	0.72312
miR-100-5p *	-0.32904	5.40945	0.95161
miR-23a-3p	0.22855	0.42577	0.59257

B

Logistic stepwise regression			
miRNAs	Estimate	Std. Error	<i>p</i> -value
miR-125b-5p *	9.72750	2.55870	0.000239
miR-143-3p *	8.46748	2.88744	0.004113

Table S2. Correlation analysis among the indicated miRNAs and hormonal receptor status of the lesions in a cohort of 77 BC patients. $p < 0.05$ was considered statistically significant.

	miR-125b-5p	miR-143-3p	miR-145-5p
Estrogen Receptor	p-value = 0.8322	p-value = 0.4848	p-value = 0.648
Progesteron Receptor	p-value = 0.6328	p-value = 0.4121	p-value = 0.4218
HER2	p-value = 0.6856	p-value = 0.7519	p-value = 0.6828
Lesion size	p-value = 0.8288	p-value = 0.5154	p-value = 0.8559

HER2: Human epidermal growth factor receptor

Table 3. Array Layout.

hsa-let-7a-5p A01	hsa-miR-1 A02	hsa-miR-100-5p A03	hsa-miR-106b-5p A04	hsa-miR-10b-5p A05	hsa-miR-122-5p A06	hsa-miR-124-3p A07	hsa-miR-125b-5p A08	hsa-miR-126-3p A09	hsa-miR-133a A10	hsa-miR-133b A11	hsa-miR-134 A12
hsa-miR-141-3p B01	hsa-miR-143-3p B02	hsa-miR-146a-5p B03	hsa-miR-150-5p B04	hsa-miR-155-5p B05	hsa-miR-17-5p B06	hsa-miR-17-3p B07	hsa-miR-18a-5p B08	hsa-miR-192-5p B09	hsa-miR-195-5p B10	hsa-miR-196a-5p B11	hsa-miR-19a-3p B12
hsa-miR-19b-3p C01	hsa-miR-200a-3p C02	hsa-miR-200b-3p C03	hsa-miR-200c-3p C04	hsa-miR-203a-5p C05	hsa-miR-205-5p C06	hsa-miR-208a-5p C07	hsa-miR-20a-5p C08	hsa-miR-21-5p C09	hsa-miR-210-5p C10	hsa-miR-214-3p C11	hsa-miR-215-5p C12
hsa-miR-221-3p D01	hsa-miR-222-3p D02	hsa-miR-223-3p D03	hsa-miR-224-5p D04	hsa-miR-23a-3p D05	hsa-miR-25-3p D06	hsa-miR-27a-3p D07	hsa-miR-29b-5p D08	hsa-miR-29a-3p D09	hsa-miR-30d-5p D10	hsa-miR-34a-5p D11	hsa-miR-375-5p D12
hsa-miR-423-5p E01	hsa-miR-499a-5p E02	hsa-miR-574-3p E03	hsa-miR-885-5p E04	hsa-miR-9-5p E05	hsa-miR-92a-3p E06	hsa-miR-93-5p E07	hsa-let-7c E08	hsa-miR-107-5p E09	hsa-miR-10a-5p E10	hsa-miR-128-5p E11	hsa-miR-130b-3p E12
hsa-miR-145-5p F01	hsa-miR-148a-3p F02	hsa-miR-15a-5p F03	hsa-miR-184-5p F04	hsa-miR-193a-5p F05	hsa-miR-204-5p F06	hsa-miR-206-5p F07	hsa-miR-211-5p F08	hsa-miR-26b-5p F09	hsa-miR-30e-5p F10	hsa-miR-372-5p F11	hsa-miR-373-3p F12
hsa-miR-374a-5p G01	hsa-miR-376c-3p G02	hsa-miR-7-5p G03	hsa-miR-96-5p G04	hsa-miR-103a-3p G05	hsa-miR-15b-5p G06	hsa-miR-16-5p G07	hsa-miR-191-5p G08	hsa-miR-22-3p G09	hsa-miR-24-3p G10	hsa-miR-26a-5p G11	hsa-miR-31-5p G12
cel-miR-39-3p H01	cel-miR-39-3p H02	SNORD61 H03	SNORD68 H04	SNORD72 H05	SNORD95 H06	SNORD96A H07	RNU6-2 H08	miRTC H09	miRTC H10	PPC H11	PPC H12

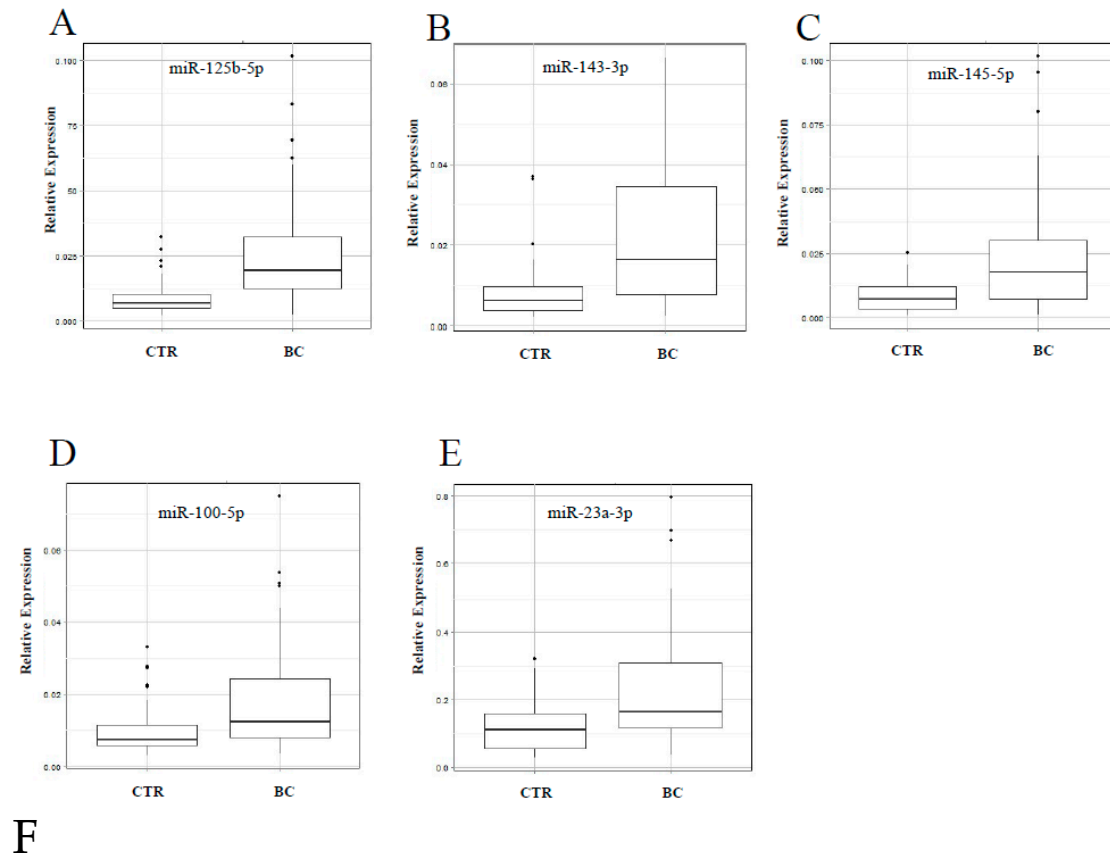


Figure S1. Validation I: Relative expression of the selected miRNAs in a study population of 46 healthy donors (CTR) and 64 BC subjects. Box plot analyses performed to show the relative expression of circulating (A) miR-125b-5p, (B) miR-143-3p, (C) miR-145-5p, (D) miR-100-5p and (E) miR-23a-3p. (F) Statistical analyses. Table includes: p-value; median value; 25th-75th percentiles; and fold change of each miRNAs up-regulated in plasma of BC patients vs CTR.

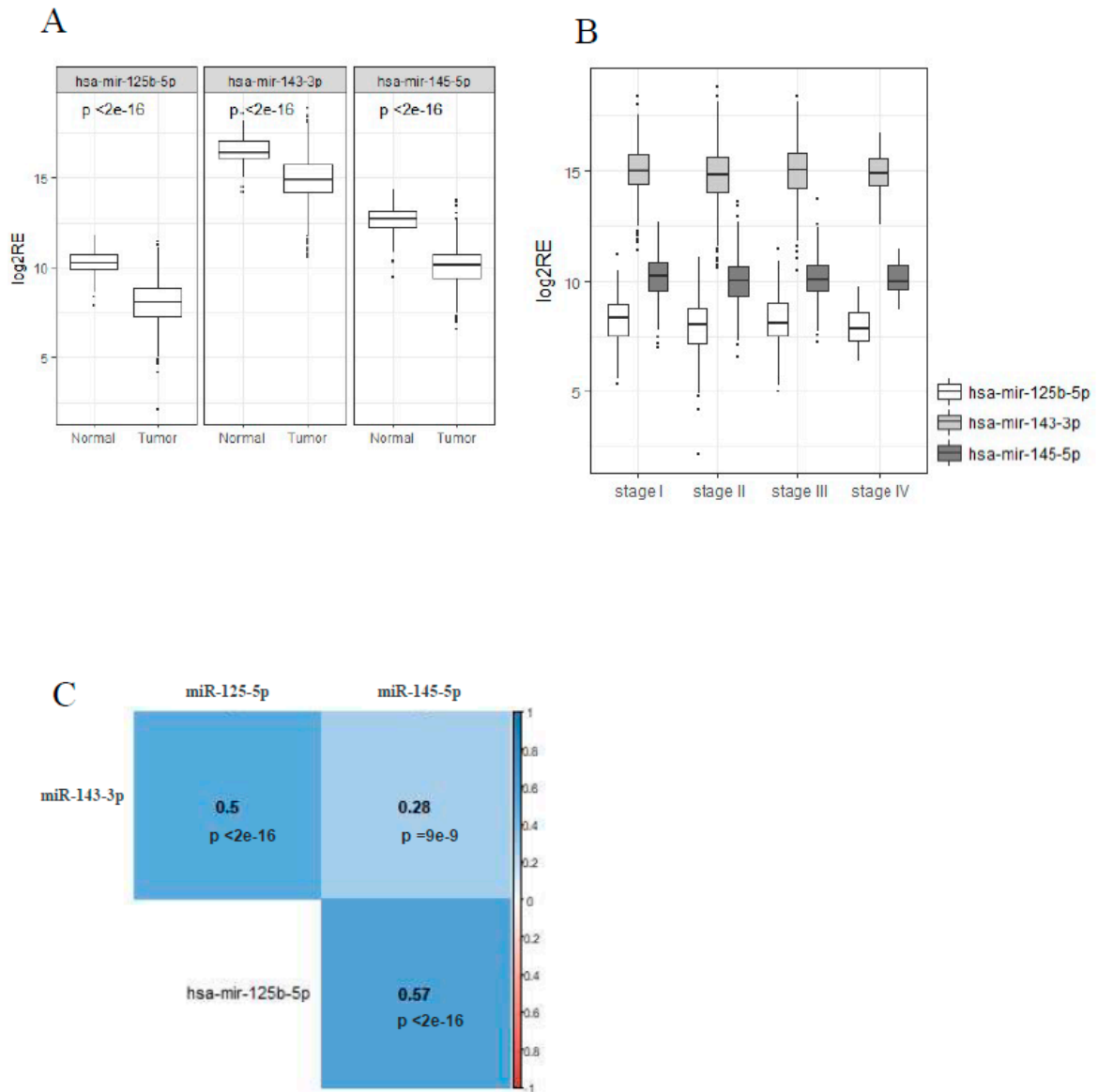


Figure S2. Expression analysis of miR-125b-5p, miR-143-3p and miR-145-5p by using the The Cancer Genome Atlas database (TCGA). Expression levels of the indicated miRNAs in breast tissue samples (normal = 104, and tumor = 1076) (A), trend of miRNAs profile with staging of the disease (B), and among them (C).