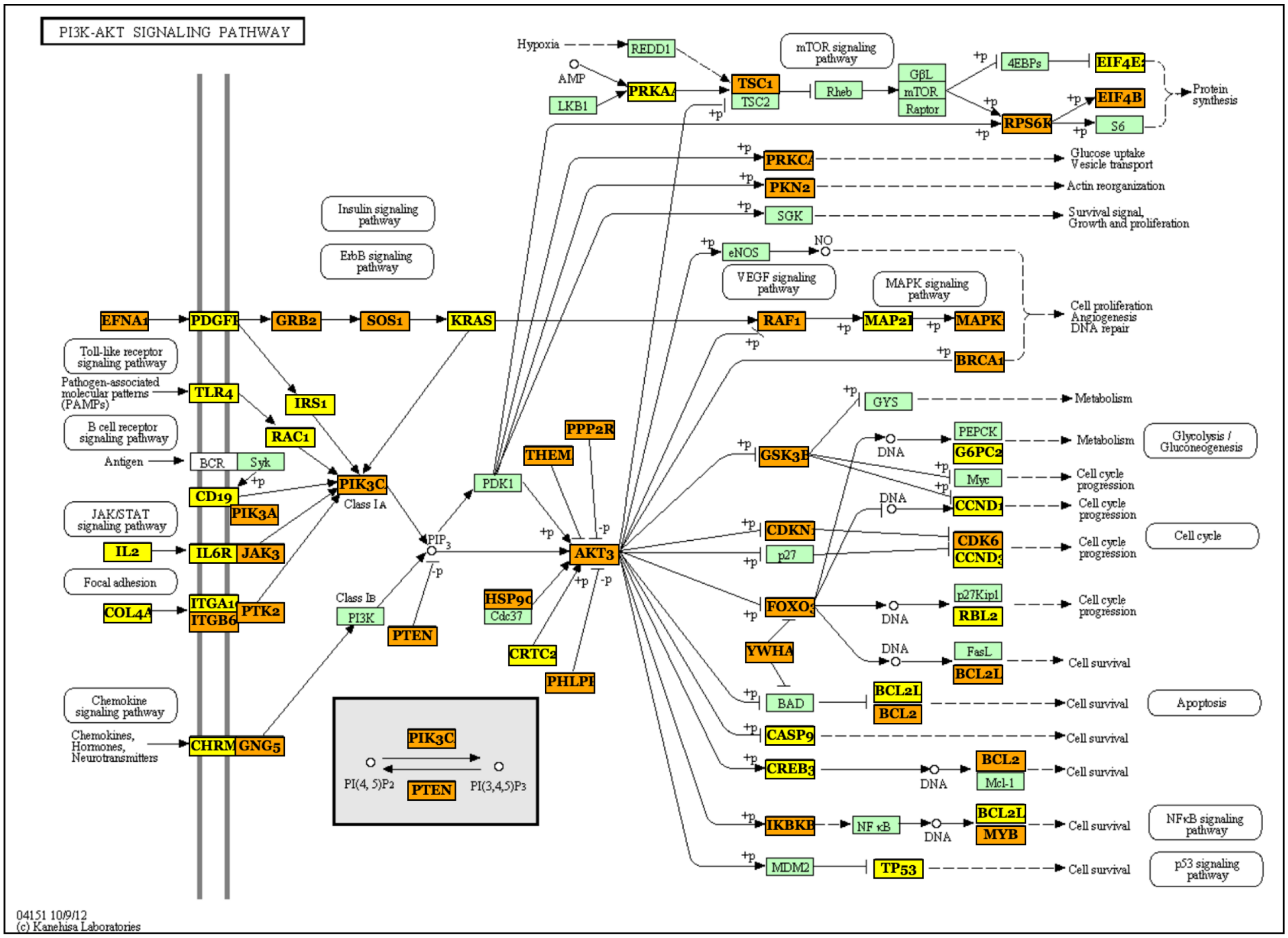
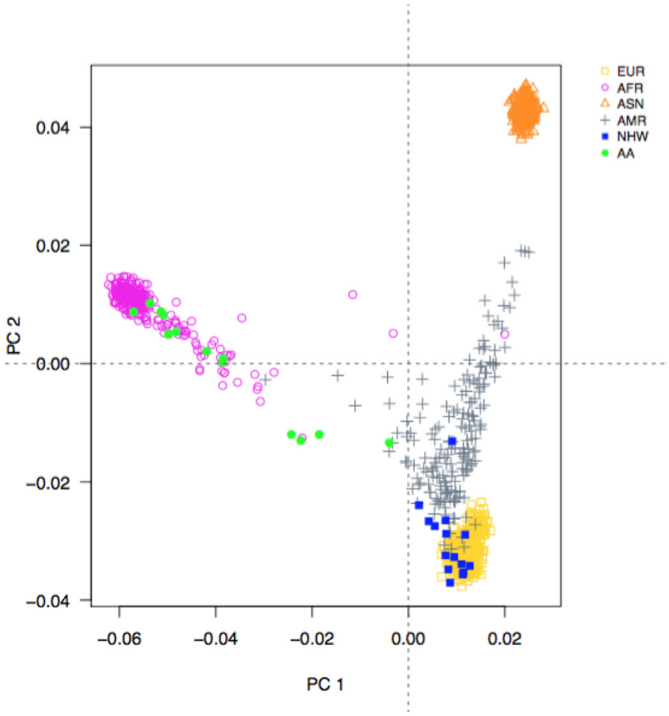
Differentially expressed miRNAs in triple negative breast cancer between African-American and non-Hispanic white women

Supplementary Materials



Supplementary Figure S1: PIK3-AKT and other signaling related pathways affected by the 26 miRNAs of our panel (DIANA miRPath v.2.0). White boxes indicate gene entries in non-metabolic pathways or enzyme and reaction entries in metabolic pathways (Reference Pathway). Green boxes indicate presence of the gene in the genome (Organism-specific pathway). Yellow boxes indicate genes targeted by one miRNA. Orange boxes indicate genes targeted by two or more miRNAs.



Supplementary Figure S2: Principal component analysis (PCA) showing that a subset genotype dataset of African American (AA) and Non-Hispanic White (NHW) patients of this study, distinctly clustered with the European (EUR) and African (AFR) main ethnic groups from the 1000 Genome Project (phase 1). ASN: East Asian, AMR: Latin American.

Supplementary Table S1: Top 15 miRNAs (based on log2FC) observed up- and down-regulated in the TNBC subtype in comparison to the non-TNBC subtype of the AA group of patients

MiRNAs up-regulated	Log2 FC	*P*-value	FDR	MiRNAs down-regulated	Log2 FC	*P*-value	FDR
hsa-miR-384	2.559	4.05E-05	7.20E-04	hsa-miR-497-5p	–4.079	1.89E-08	1.51E-05
hsa-miR-135b-5p	2.360	9.31E-04	0.004433157	hsa-miR-145-5p	–3.251	1.28E-06	1.28E-04
hsa-miR-1277-3p	2.358	5.79E-05	8.91E-04	hsa-miR-29c-3p	–3.105	1.75E-07	7.00E-05
hsa-miR-1185-5p	2.304	7.74E-06	3.10E-04	hsa-miR-143-3p	–3.036	1.47E-06	1.31E-04
hsa-miR-626	2.245	2.08E-06	1.19E-04	hsa-miR-26a-5p	–2.976	3.20E-06	1.70E-04
hsa-miR-219-5p	2.194	7.87E-06	3.00E-04	hsa-miR-1253	–2.879	4.51E-04	0.0027133
hsa-miR-576-5p	2.190	1.69E-06	1.23E-04	hsa-miR-199b-5p	–2.825	1.65E-06	1.32E-04
hsa-miR-606	2.164	2.79E-07	7.43E-05	hsa-miR-342-3p	–2.785	4.42E-07	7.07E-05
hsa-miR-499a-3p	2.132	4.86E-05	7.94E-04	hsa-miR-1290	–2.763	7.36E-06	3.10E-04
hsa-miR-548al	2.093	8.52E-06	2.96E-04	hsa-miR-29b-3p	–2.742	8.27E-05	0.001050187
hsa-miR-522-3p	2.091	1.72E-06	1.15E-04	hsa-miR-30a-5p	–2.720	1.41E-04	0.001429822
hsa-miR-516a-5p	2.029	7.06E-05	9.57E-04	hsa-miR-196a-5p	–2.668	4.62E-05	7.69E-04
hsa-miR-659-3p	2.020	4.01E-05	7.29E-04	hsa-miR-195-5p	–2.631	3.72E-07	7.45E-05
hsa-miR-568	2.016	1.43E-05	4.08E-04	hsa-miR-451a	–2.613	8.64E-05	0.001063546
hsa-miR-518c-3p	1.993	1.91E-05	4.50E-04	hsa-miR-30b-5p	–2.555	3.15E-05	6.45E-04

FC = fold change, FDR = false discovery rate.

Supplementary Table S2: Top 15 KEGG pathways (based on P value) mostly affected by the differentially expressed miRNAs in the TNBC and non-TNBC subtypes of the AA group of patients (DIANA miRPath v.2.0)

#	KEGG pathway	*P*-value	# Genes	# MiRNAs
1	Pathways in cancer	8.22E-34	190	49
2	PI3K-AKT signaling pathway	1.49E-33	206	49
3	MAPK signaling pathway	1.43E-26	155	46
4	Endocytosis	1.24E-21	118	45
5	Focal adhesion	3.00E-21	127	47
6	Regulation of actin cytoskeleton	1.10E-20	116	45
7	WNT signaling pathway	4.65E-18	98	47
8	Chemokine signaling pathway	1.87E-17	102	47
9	Hepatitis B	3.58E-17	90	45
10	Axon guidance	5.81E-16	82	44
11	Ubiquitin mediated proteolysis	1.09E-14	84	44
12	Insulin signaling pathway	1.09E-14	85	49
13	RNA transport	1.69E-14	82	43
14	Neurotrophin signaling pathway	1.69E-14	82	46
15	Measles	1.92E-14	79	43

KEGG = Kyoto Encyclopedia of Genes and Genomes.

Supplementary Table S3: Top 15 and 12 miRNAs observed up- and down-regulated, respectively, in the TNBC subtype in comparison to the non-TNBC subtype of the NHW group of patients

MiRNAs Up-regulated	Log2 FC	*P*-value	FDR	MiRNAs down-regulated	Log2 FC	*P*-value	FDR
hsa-miR-522-3p	8.41	1.46E-18	0	hsa-miR-1253	–4.45	2.99E-07	2.78E-06
hsa-miR-451a	7.12	8.63E-12	8.63E-10	hsa-miR-1469	–3.26	1.84E-07	1.82E-06
hsa-miR-150-5p	6.68	2.61E-09	6.14E-08	hsa-miR-548aa	–2.74	1.18E-08	2.01E-07
hsa-miR-126-3p	6.53	3.38E-10	1.18E-08	hsa-miR-520d-5p+ miR-518a-5p+miR-527	–2.52	1.79E-07	1.81E-06
hsa-miR-223-3p	6.41	3.29E-10	1.20E-08	hsa-miR-1234	–2.25	5.18E-06	2.82E-05
hsa-miR-374a-5p	6.01	1.00E-10	6.17E-09	hsa-miR-877-5p	–1.89	2.01E-05	9.20E-05
hsa-miR-125a-5p	5.98	8.25E-12	9.42E-10	hsa-miR-376a-3p	–1.81	1.33E-06	8.87E-06
hsa-miR-651	5.95	1.79E-13	4.78E-11	hsa-miR-874	–1.50	3.11E-04	9.73E-04
hsa-miR-182-5p	5.75	4.61E-13	9.22E-11	hsa-miR-1224-5p	–1.50	8.42E-04	0.002
hsa-miR-762	5.70	2.31E-12	3.07E-10	hsa-miR-940	–1.49	0.001	0.003
hsa-miR-34a-5p	5.60	1.78E-10	7.50E-09				
hsa-miR-185-5p	5.55	2.84E-14	1.14E-11				
hsa-miR-181a-5p	5.19	8.43E-09	1.57E-07				
hsa-miR-18a-5p	5.16	5.85E-11	4.68E-09				
hsa-miR-191-5p	5.13	2.56E-09	6.20E-08				

FC = fold change, FDR = false discovery rate.

Supplementary Table S4: Top 15 KEGG pathways (based on P value) mostly affected by the differentially expressed miRNAs in the TNBC and non-TNBC subtypes of the NHW group of patients (DIANA miRPath v.2.0)

#	KEGG pathway	*P*-value	# Genes	# MiRNAs
1	Pathways in cancer	5.02E-43	191	43
2	PI3K-AKT signaling pathway	2.95E-38	181	44
3	MAPK signaling pathway	2.27E-34	159	45
4	HTLV-I infection	5.00E-30	137	45
5	Endocytosis	1.37E-27	119	39
6	Regulation of actin cytoskeleton	1.44E-27	124	39
7	Epstein-Barr virus infection	1.92E-24	109	37
8	Focal adhesion	1.46E-23	110	41
9	Transcriptional misregulation in cancer	2.08E-21	102	43
10	WNT signaling pathway	2.38E-21	93	41
11	Chemokine signaling pathway	4.49E-21	97	40
12	Axon guidance	1.40E-20	82	38
13	Hepatitis B	2.68E-20	80	38
14	Neurotrophin signaling pathway	1.27E-18	83	41
15	Ubiquitin mediated proteolysis	3.19E-18	82	40

KEGG = Kyoto Encyclopedia of Genes and Genomes.

Supplementary Table S5: Area Under the Curve (AUC) values of the individual 26 miRNAs differentially expressed between the AA and NHW-TNBC group of patients

MiRNA	AUC (95% CI)
hsa-miR-1225-3p	0.89 (0.81–0.98)
hsa-miR-216a-5p	0.88 (0.78–0.97)
hsa-miR-532-3p	0.87 (0.77–0.97)
hsa-miR-580-3p	0.87 (0.77–0.97)
hsa-miR-599	0.86 (0.75–0.96)
hsa-miR-769-5p	0.86 (0.75–0.98)
hsa-miR-18a-5p	0.84 (0.73–0.95)
hsa-miR-28-5p	0.83 (0.70–0.95)
hsa-miR-182-5p	0.83 (0.71–0.94)
hsa-miR-183-5p	0.83 (0.72–0.94)
hsa-miR-205-5p	0.82 (0.69–0.94)
hsa-miR-4284	0.83 (0.72–0.95)
hsa-miR-4458	0.83 (0.71–0.95)
hsa-miR-614	0.82 (0.70–0.94)
hsa-miR-940	0.80 (0.67–0.92)
hsa-miR-1263	0.80 (0.68–0.93)
hsa-miR-4431	0.80 (0.68–0.92)
hsa-miR-15b-5p	0.79 (0.66–0.91)
hsa-miR-17-5p	0.79 (0.67–0.92)
hsa-miR-93-5p	0.79 (0.66–0.91)
hsa-miR-548ad-3p	0.79 (0.66–0.92)
hsa-miR-661	0.79 (0.65–0.92)
hsa-miR-23a-3p	0.78 (0.64–0.91)
hsa-miR-200c-3p	0.78 (0.64–0.91)
hsa-miR-3934-5p	0.78 (0.65–0.91)
hsa-miR-150-5p	0.75 (0.61–0.89)
Score 1 (combined panel)	**0.88 (0.78–0.99)**