

Supplementary data to:

UP-REGULATION OF MIR-381 INHIBITS NAD⁺ SALVAGE PATHWAY AND PROMOTES APOPTOSIS IN BREAST CANCER CELLS

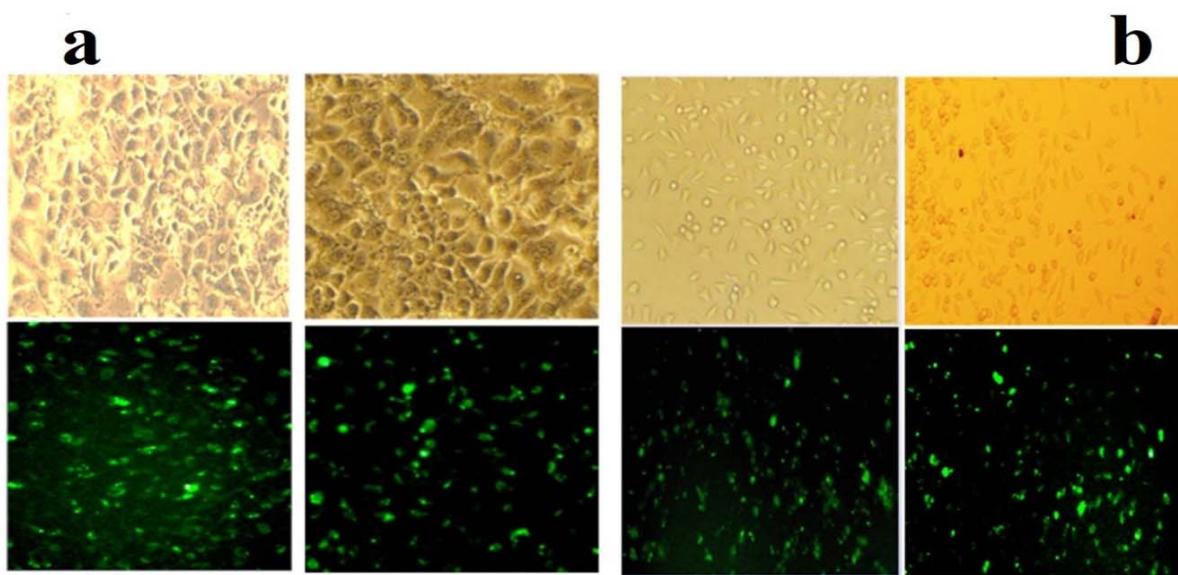
Zahra Bolandghamat Pour^a, Mitra Nourbakhsh^{b,*}, Kazem Mousavizadeh^{a,d,*}, Zahra Madjd^{a,e}, Seyedeh Sara Ghorbanhosseini^b, Zohreh Abdolvahabi^f, Zahra Hesari^{c,g}, Samira Ezzati Mobaser^b

- ^a Department of Molecular Medicine, Faculty of Advanced Technologies in Medicine, Iran University of Medical Sciences, Tehran, Iran
^b Department of Biochemistry, School of Medicine, Iran University of Medical Sciences, Tehran, Iran
^c Laboratory Sciences Research Center, Golestan University of Medical Sciences, Gorgan, Iran
^d Cellular and Molecular Research Center, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran
^e Oncopathology Research Center, Iran University of Medical Sciences, Tehran, Iran
^f Department of Biochemistry and Genetics, Cellular and Molecular Research Center, Qazvin University of Medical Sciences, Qazvin, Iran
^g Department of Laboratory Sciences, Faculty of Paramedicine, Golestan University of Medical Sciences, Gorgan, Iran

* **Corresponding authors:** Mitra Nourbakhsh, MSc, PhD, Department of Biochemistry, Faculty of Medicine, Iran University of Medical Sciences, Hemmat Highway 1449614535, Tehran, Iran, Tel: +98 21 86703109, Fax: +98 21 88622742, Mobile: +98 912 2874740, E-mail: nourbakhsh.m@iums.ac.ir
Kazem Mousavizadeh, Pharm.D, PhD, Department of Molecular Medicine, Faculty of Advanced Technologies in Medicine, Iran University of Medical Sciences, Tehran, Iran. Cellular and Molecular Research Center, Faculty of Medicine, Iran University of Medical Sciences ,Tehran, Iran. Hemmat Highway 1449614535, Tehran, Iran, Tel: +98-21- 86704720, Fax: +98-21- 88622578, Mobile: +98-9369973054, E-mail: mousavizadeh.k@iums.ac.ir

<http://dx.doi.org/10.17179/excli2019-1431>

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>).



Supplementary Figure 1: Evaluation of transfection efficiency under fluorescent (lower panel) and light (upper panel) microscope by FAM-labeled microRNAs in **a)** MCF-7 and **b)** MDA-MB-231 cells

MicroRNA and Target Gene Description:

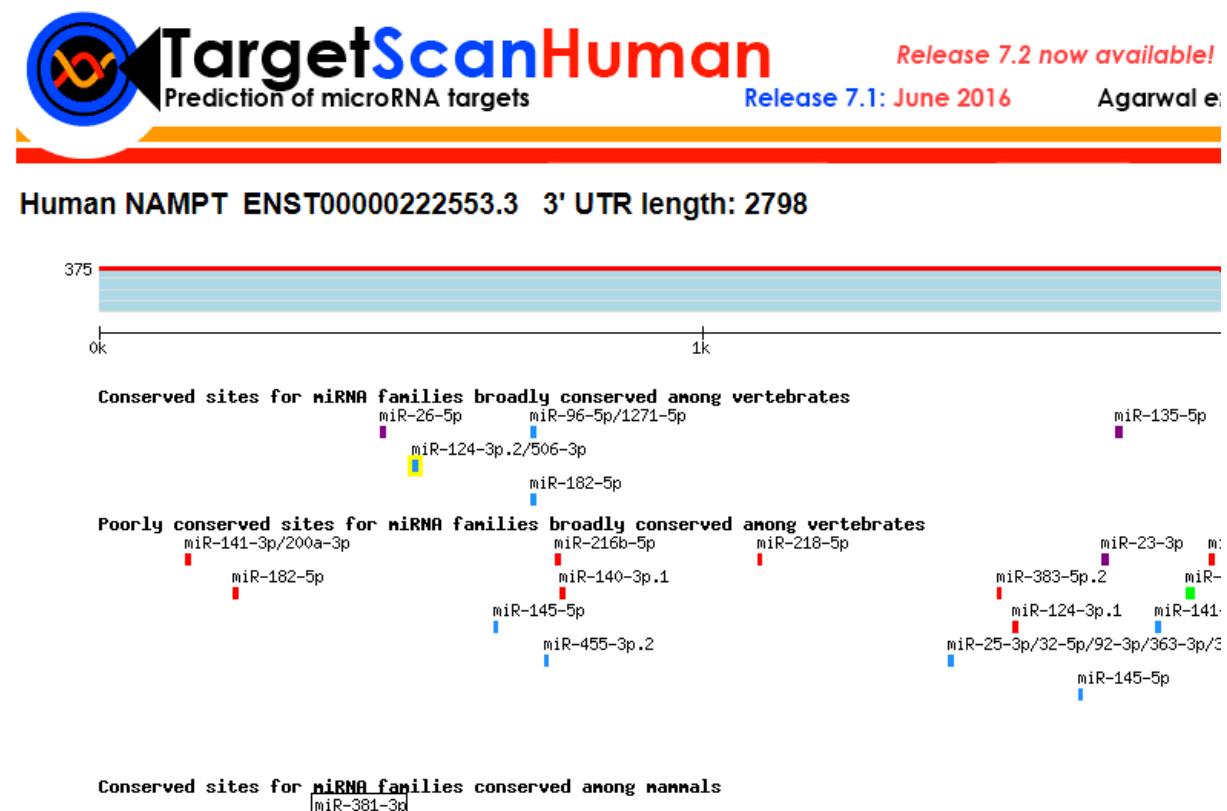
miRNA Name	hsa-miR-381-3p	miRNA Sequence	UAUACAAGGGCAAGCUCUCUGU
Previous Name	hsa-miR-381		
Target Score	69	Seed Location	359
NCBI Gene ID	10135	GenBank Accession	NM_005746
Gene Symbol	NAMPT	3' UTR Length	2809
Gene Description	nicotinamide phosphoribosyltransferase		

3' UTR Sequence

```
1 gctttatgac tgggtgtgt ttgtgttat gtaatacata atgtttattt tacagatgtg
 61 tggggtttgtt gttttatgtt acattacaggc caaaatttattt gttggtttat ggacatactg
121 cccttcatt ttttttcttt tccagtgttt aggtgatctc aaatttaggaa atgcattaa
181 ccatgtaaaa gatgagtgct aaagtaagct ttttagggcc ctttgccaat aggttagtcat
241 tcaatctggt attgatcttt tcacaataaa cagaactgag aaacttttat atataactga
301 tgatcacata aaacagattt gcataaaaattt accatgattt ctttatgttt atatthaact
361 tgtatttttt tacaacaag attgtgttga atatatttga agtttcagtg atttaacagt
421 ctttccaact tttcatgatt tttatgagca cagacttca agaaaataact tgaaaataaa
481 ttacattgcc ttttgcatt taatcagcaa ataaaacatg gccttaacaa agttgtttgt
541 gttattgtac aatttggaaa ttatgtcggtt acatacccta tagaattact aaccttactg
601 ccccttggtag aatatgtattt aatcattcta cattaaagaa aataatggtt cttaactggaa
661 tgtctaggca ctgtacagttt attatataatc ttgggtgttg tattgtacca gtgaaatgcc
721 aaatttggaaa ggcctgtact gcaattttat atgtcagaga ttgcctgtgg ctctaatatg
781 caccaaga ttttaaggag ataattttt tagagagaat ttctgcttcc actatagaat
```

Supplementary Figure 2: The 3'-UTR of NAMPT as a target of NAMPT and miR-381 response element in the 3'UTR of NAMPT as found in miRDB database (http://mirdb.org/cgi-bin/target_detail.cgi?targetID=1808567)

a.



b.

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length
Position 359-365 of NAMPT 3' UTR hsa-miR-381-3p	5' ...UAUGUUUUAUUUAACUUGUAUU... 3' UGUCUCUCGAACGGGAACAUAU	7mer-m8	-0.16	97	-0.16	3.038

Supplementary Figure 3:

- a) Targeting of NAMPT 3'UTR by miR381-3p as presented by Target Scan database (http://www.targetscan.org/cgi-bin/targetscan/vert_71/view_gene.cgi?rs=ENST00000222553.3&taxid=9606&members=miR-381-3p&showcnc=1&shownc=1&subset=1). miR-381 is indicated in frame.
- b) Pairing of miR-381-3p with its seed sequence and its position in the NAMPT 3'UTR presented by the same database

hsa-miR-381/NAMPT Alignment

<pre>3' ugucucucgAACGGGAACAUu 5' hsa-miR-381 345:5' auguuuaauUUUAACUUGUAUu 3' NAMPT</pre>	mirSVR score: -1.3122 PhastCons score: 0.8936
---	--

Supplementary Figure 4: Alignment of miR-381 with NAMPT and its mirSVR score as presented by www.microRNA.org (last update 2010.11.01) (<http://www.microrna.org/microrna/home.do>)

miRNA ▾	Gene ▾	ΔG open ▾	Probability exact ▾	Conservation PhyloP ▾	miRmap score ▾																																																																																																																																																					
hsa-miR-381-3p	NAMPT	93.65	38.59	71.68	88.55																																																																																																																																																					
Links																																																																																																																																																										
ENSG00000105835 hsa-miR-381-3p																																																																																																																																																										
Target site(s)																																																																																																																																																										
<table border="1"> <tr> <td>105890487 (chr 7) 1842</td> <td>TargetScan AU content</td> <td>86.74</td> <td>105890825 (chr 7) 784</td> <td>TargetScan AU content</td> <td>74.12</td> </tr> <tr> <td>5' (mRNA) AAAAAAUAAAUAUUGGAUAAAUAUUGGAACAUCAU </td> <td>TargetScan 3' UTR position</td> <td>31.11</td> <td>5' (mRNA) ACAGUUAUUAUUAUCUUGGUUGUUGUACCAGU </td> <td>TargetScan 3' UTR position</td> <td>53.63</td> </tr> <tr> <td>UGUCUCUGAACGGGAACAUAU</td> <td>TargetScan 3' pairing</td> <td>20.00</td> <td>UGUCUCUGAACGGGAACAUAU</td> <td>TargetScan 3' pairing</td> <td>35.00</td> </tr> <tr> <td></td> <td>ΔG duplex</td> <td>8.55</td> <td></td> <td>ΔG duplex</td> <td>18.49</td> </tr> <tr> <td></td> <td>ΔG binding</td> <td>7.05</td> <td></td> <td>ΔG binding</td> <td>34.37</td> </tr> <tr> <td></td> <td>ΔG duplex seed</td> <td>16.55</td> <td></td> <td>ΔG duplex seed</td> <td>16.55</td> </tr> <tr> <td></td> <td>ΔG binding seed</td> <td>3.61</td> <td></td> <td>ΔG binding seed</td> <td>3.61</td> </tr> <tr> <td></td> <td>ΔG open</td> <td>94.65</td> <td></td> <td>ΔG open</td> <td>67.07</td> </tr> <tr> <td></td> <td>ΔG total</td> <td>67.77</td> <td></td> <td>ΔG total</td> <td>56.67</td> </tr> <tr> <td></td> <td>Probability exact</td> <td>38.98</td> <td></td> <td>Probability exact</td> <td>38.98</td> </tr> <tr> <td></td> <td>Probability binomial</td> <td>16.61</td> <td></td> <td>Probability binomial</td> <td>16.61</td> </tr> <tr> <td></td> <td>Conservation Branch Length Score</td> <td>25.58</td> <td></td> <td>Conservation Branch Length Score</td> <td>25.58</td> </tr> <tr> <td></td> <td>Conservation PhyloP</td> <td>49.67</td> <td></td> <td>Conservation PhyloP</td> <td>72.09</td> </tr> <tr> <td></td> <td>miRmap score</td> <td>56.07</td> <td></td> <td>miRmap score</td> <td>56.34</td> </tr> </table> <table border="1"> <tr> <td>TargetScan AU content</td> <td>74.83</td> <td>105891163 (chr 7) 366</td> <td>TargetScan AU content</td> <td>99.30</td> </tr> <tr> <td>TargetScan 3' UTR position</td> <td>94.00</td> <td>5' (mRNA) AUUGCUUUAUUGUUUAUAAAACUUGGUUUUUGUACA </td> <td>TargetScan 3' UTR position</td> <td>76.15</td> </tr> <tr> <td>TargetScan 3' pairing</td> <td>30.00</td> <td>UGUCUCUGAACGGGAACAUAU</td> <td>TargetScan 3' pairing</td> <td>20.00</td> </tr> <tr> <td>ΔG duplex</td> <td>19.88</td> <td></td> <td>ΔG duplex</td> <td>12.72</td> </tr> <tr> <td>ΔG binding</td> <td>38.38</td> <td></td> <td>ΔG binding</td> <td>19.45</td> </tr> <tr> <td>ΔG duplex seed</td> <td>16.55</td> <td></td> <td>ΔG duplex seed</td> <td>35.25</td> </tr> <tr> <td>ΔG binding seed</td> <td>3.61</td> <td></td> <td>ΔG binding seed</td> <td>17.32</td> </tr> <tr> <td>ΔG open</td> <td>65.06</td> <td></td> <td>ΔG open</td> <td>73.02</td> </tr> <tr> <td>ΔG total</td> <td>57.96</td> <td></td> <td>ΔG total</td> <td>47.95</td> </tr> <tr> <td>Probability exact</td> <td>38.98</td> <td></td> <td>Probability exact</td> <td>30.47</td> </tr> <tr> <td>Probability binomial</td> <td>16.61</td> <td></td> <td>Probability binomial</td> <td>21.06</td> </tr> <tr> <td>Conservation Branch Length Score</td> <td>25.58</td> <td></td> <td>Conservation Branch Length Score</td> <td>25.58</td> </tr> <tr> <td>Conservation PhyloP</td> <td>49.67</td> <td></td> <td>Conservation PhyloP</td> <td>77.99</td> </tr> <tr> <td>miRmap score</td> <td>61.62</td> <td></td> <td>miRmap score</td> <td>79.97</td> </tr> </table>	105890487 (chr 7) 1842	TargetScan AU content	86.74	105890825 (chr 7) 784	TargetScan AU content	74.12	5' (mRNA) AAAAAAUAAAUAUUGGAUAAAUAUUGGAACAUCAU 	TargetScan 3' UTR position	31.11	5' (mRNA) ACAGUUAUUAUUAUCUUGGUUGUUGUACCAGU 	TargetScan 3' UTR position	53.63	UGUCUCUGAACGGGAACAUAU	TargetScan 3' pairing	20.00	UGUCUCUGAACGGGAACAUAU	TargetScan 3' pairing	35.00		ΔG duplex	8.55		ΔG duplex	18.49		ΔG binding	7.05		ΔG binding	34.37		ΔG duplex seed	16.55		ΔG duplex seed	16.55		ΔG binding seed	3.61		ΔG binding seed	3.61		ΔG open	94.65		ΔG open	67.07		ΔG total	67.77		ΔG total	56.67		Probability exact	38.98		Probability exact	38.98		Probability binomial	16.61		Probability binomial	16.61		Conservation Branch Length Score	25.58		Conservation Branch Length Score	25.58		Conservation PhyloP	49.67		Conservation PhyloP	72.09		miRmap score	56.07		miRmap score	56.34	TargetScan AU content	74.83	105891163 (chr 7) 366	TargetScan AU content	99.30	TargetScan 3' UTR position	94.00	5' (mRNA) AUUGCUUUAUUGUUUAUAAAACUUGGUUUUUGUACA 	TargetScan 3' UTR position	76.15	TargetScan 3' pairing	30.00	UGUCUCUGAACGGGAACAUAU	TargetScan 3' pairing	20.00	ΔG duplex	19.88		ΔG duplex	12.72	ΔG binding	38.38		ΔG binding	19.45	ΔG duplex seed	16.55		ΔG duplex seed	35.25	ΔG binding seed	3.61		ΔG binding seed	17.32	ΔG open	65.06		ΔG open	73.02	ΔG total	57.96		ΔG total	47.95	Probability exact	38.98		Probability exact	30.47	Probability binomial	16.61		Probability binomial	21.06	Conservation Branch Length Score	25.58		Conservation Branch Length Score	25.58	Conservation PhyloP	49.67		Conservation PhyloP	77.99	miRmap score	61.62		miRmap score	79.97
105890487 (chr 7) 1842	TargetScan AU content	86.74	105890825 (chr 7) 784	TargetScan AU content	74.12																																																																																																																																																					
5' (mRNA) AAAAAAUAAAUAUUGGAUAAAUAUUGGAACAUCAU 	TargetScan 3' UTR position	31.11	5' (mRNA) ACAGUUAUUAUUAUCUUGGUUGUUGUACCAGU 	TargetScan 3' UTR position	53.63																																																																																																																																																					
UGUCUCUGAACGGGAACAUAU	TargetScan 3' pairing	20.00	UGUCUCUGAACGGGAACAUAU	TargetScan 3' pairing	35.00																																																																																																																																																					
	ΔG duplex	8.55		ΔG duplex	18.49																																																																																																																																																					
	ΔG binding	7.05		ΔG binding	34.37																																																																																																																																																					
	ΔG duplex seed	16.55		ΔG duplex seed	16.55																																																																																																																																																					
	ΔG binding seed	3.61		ΔG binding seed	3.61																																																																																																																																																					
	ΔG open	94.65		ΔG open	67.07																																																																																																																																																					
	ΔG total	67.77		ΔG total	56.67																																																																																																																																																					
	Probability exact	38.98		Probability exact	38.98																																																																																																																																																					
	Probability binomial	16.61		Probability binomial	16.61																																																																																																																																																					
	Conservation Branch Length Score	25.58		Conservation Branch Length Score	25.58																																																																																																																																																					
	Conservation PhyloP	49.67		Conservation PhyloP	72.09																																																																																																																																																					
	miRmap score	56.07		miRmap score	56.34																																																																																																																																																					
TargetScan AU content	74.83	105891163 (chr 7) 366	TargetScan AU content	99.30																																																																																																																																																						
TargetScan 3' UTR position	94.00	5' (mRNA) AUUGCUUUAUUGUUUAUAAAACUUGGUUUUUGUACA 	TargetScan 3' UTR position	76.15																																																																																																																																																						
TargetScan 3' pairing	30.00	UGUCUCUGAACGGGAACAUAU	TargetScan 3' pairing	20.00																																																																																																																																																						
ΔG duplex	19.88		ΔG duplex	12.72																																																																																																																																																						
ΔG binding	38.38		ΔG binding	19.45																																																																																																																																																						
ΔG duplex seed	16.55		ΔG duplex seed	35.25																																																																																																																																																						
ΔG binding seed	3.61		ΔG binding seed	17.32																																																																																																																																																						
ΔG open	65.06		ΔG open	73.02																																																																																																																																																						
ΔG total	57.96		ΔG total	47.95																																																																																																																																																						
Probability exact	38.98		Probability exact	30.47																																																																																																																																																						
Probability binomial	16.61		Probability binomial	21.06																																																																																																																																																						
Conservation Branch Length Score	25.58		Conservation Branch Length Score	25.58																																																																																																																																																						
Conservation PhyloP	49.67		Conservation PhyloP	77.99																																																																																																																																																						
miRmap score	61.62		miRmap score	79.97																																																																																																																																																						

Supplementary Figure 5: Alignment of miR-381-3p with the 3'-UTR of NAMPT and its properties as presented by miRmap (<https://mirmap.ezlab.org/app/>)

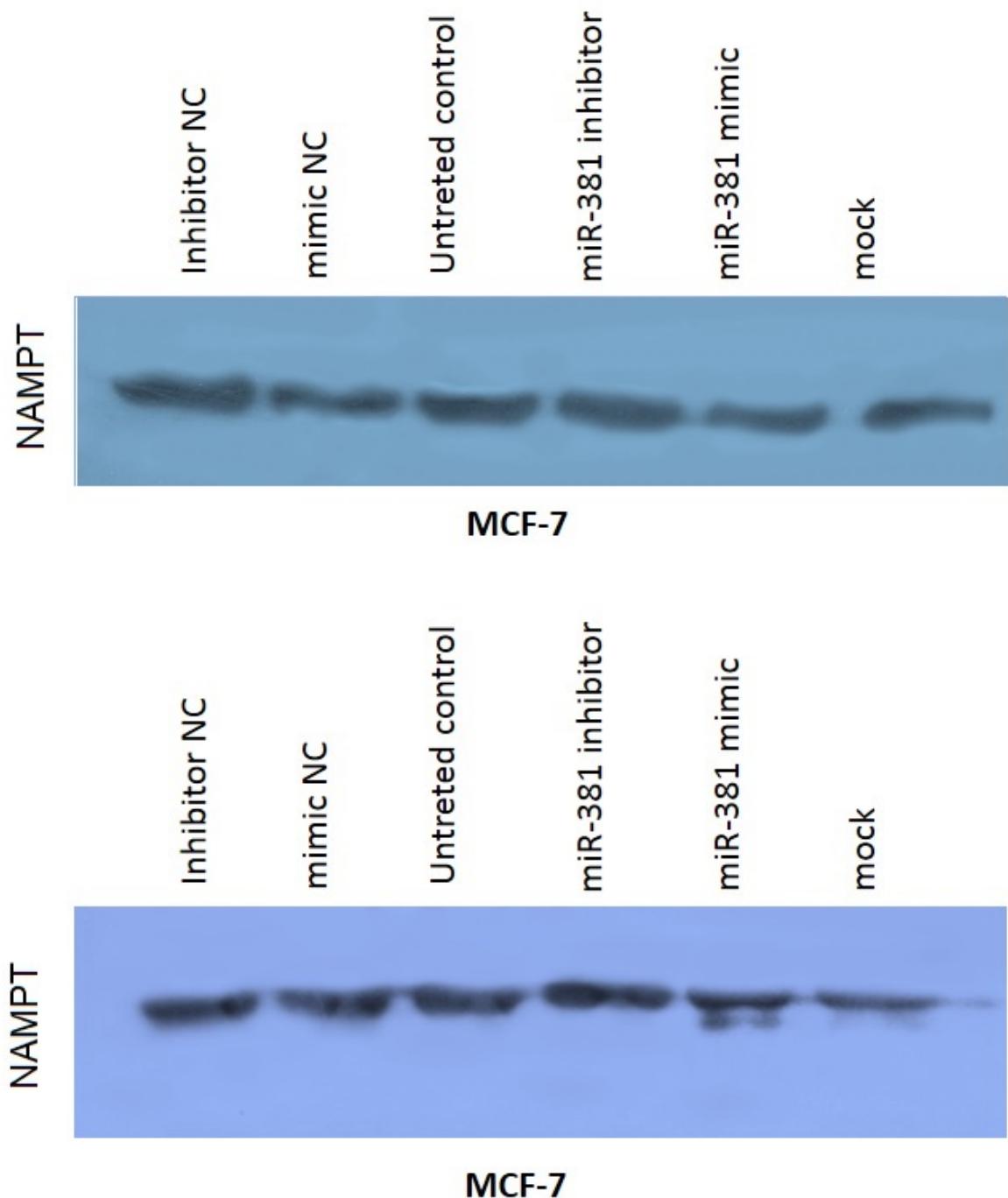
Expression values (RPM) of hsa-miR-381-3p in breast

Tissue	Description	Disease	Sex	PubMed ID
Breast	Serum from healthy woman control	Normal		24904649
Breast	Tumor serum	Breast cancer		24904649
Breast	Tumor tissue	Breast cancer		24904649
Breast	Normal tissue	Normal		24904649

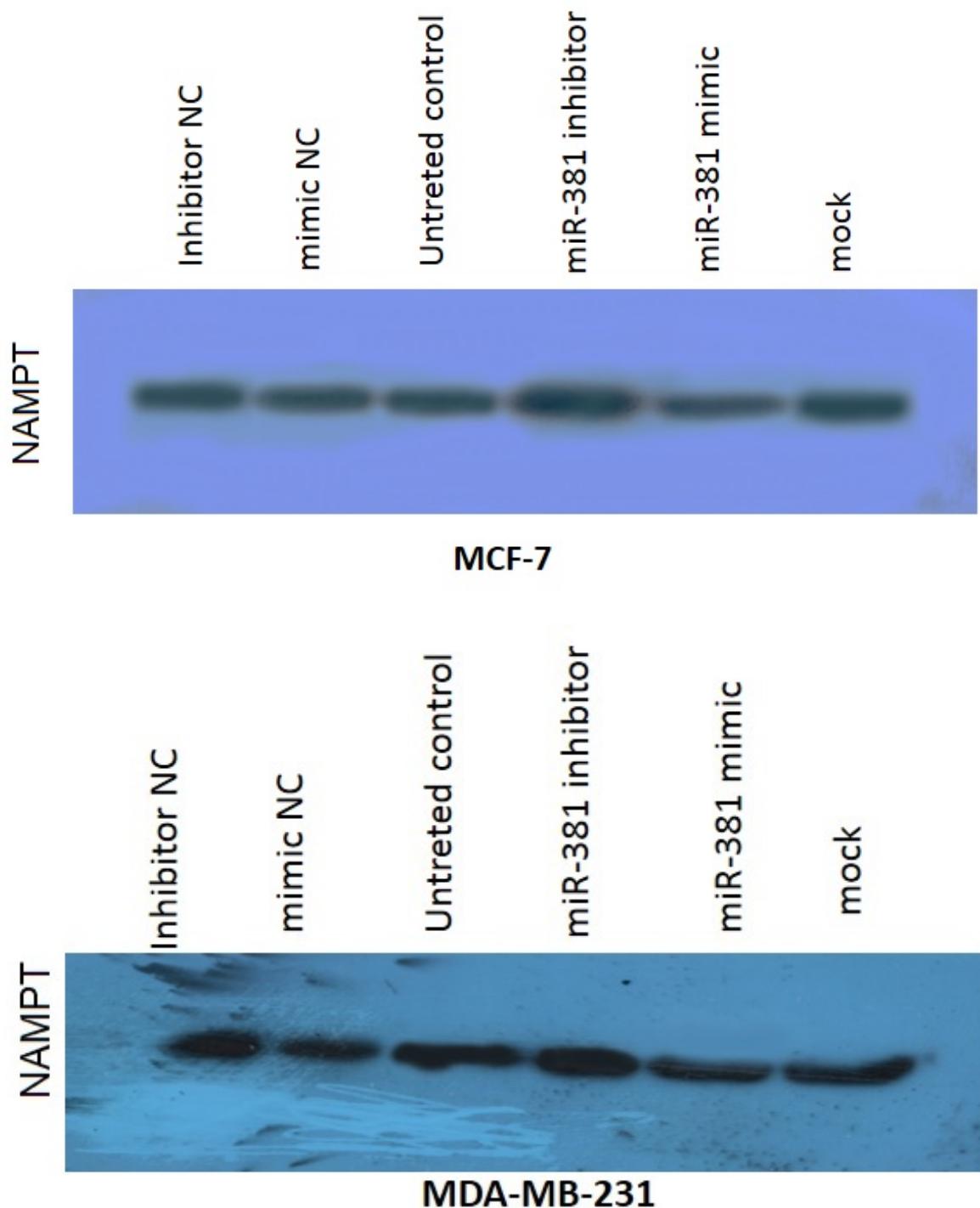
Supplementary Figure 6: Expression of miR-381-3p in normal and tumor tissue of breast (<http://guanlab.ccmb.med.umich.edu/mirmine/single.php?mirna=hsa-miR-381-3p&tissue=breast&cline=>)

Search result for miRNA = 'hsa-miR-381' Or cancer = " Total: 13 relations found.				
mirId	Family/Cluster	Cancer	Profile	PubMed Article
hsa-mir-381		breast cancer	down	miR-381 suppresses C/EBP β -dependent Cx43 expression in breast cancer cells.
hsa-mir-381		breast cancer	down	Analysis of miR-205 and miR-155 expression in the blood of breast cancer patients.
hsa-mir-381		colon cancer	down	Down-regulation of MicroRNA-381 promotes cell proliferation and invasion in colon cancer through up-regulation of LRH-1.
hsa-mir-381		colon cancer	down	[Expression and proliferative regulation of miR-204 related to mitochondrial transcription factor A in colon cancer].
hsa-mir-381		colorectal cancer	down	MIR-381 functions as a tumor suppressor in colorectal cancer by targeting Twist1.
hsa-mir-381		endometrial cancer	down	MicroRNA-381 inhibits cell proliferation and invasion in endometrial carcinoma by targeting the IGF-1R.
hsa-mir-381		esophageal squamous cell carcinoma	down	MicroRNA-381 enhances radiosensitivity in esophageal squamous cell carcinoma by targeting X-linked inhibitor of apoptosis protein.
hsa-mir-381		gastric cancer	down	MicroRNA-381 inhibits the metastasis of gastric cancer by targeting TMEM16A expression.
hsa-mir-381		gastric cancer	down	MIR-381 inhibits migration and invasion in human gastric carcinoma through downregulated SOX4.
hsa-mir-381		hepatocellular carcinoma	down	MicroRNA-381 suppresses cell growth and invasion by targeting the liver receptor homolog-1 in hepatocellular carcinoma.
hsa-mir-381		lung adenocarcinoma	down	MicroRNA-381 represses ID1 and is deregulated in lung adenocarcinoma.
hsa-mir-381		non-small cell lung cancer	down	microRNA-381 suppresses the growth and increases cisplatin sensitivity in non-small cell lung cancer cells through inhibition of nuclear factor- κ B signaling.
hsa-mir-381		osteosarcoma	down	MicroRNA-381 suppresses the proliferation of osteosarcoma cells through LRH-1/Wnt/ β -catenin signaling pathway.

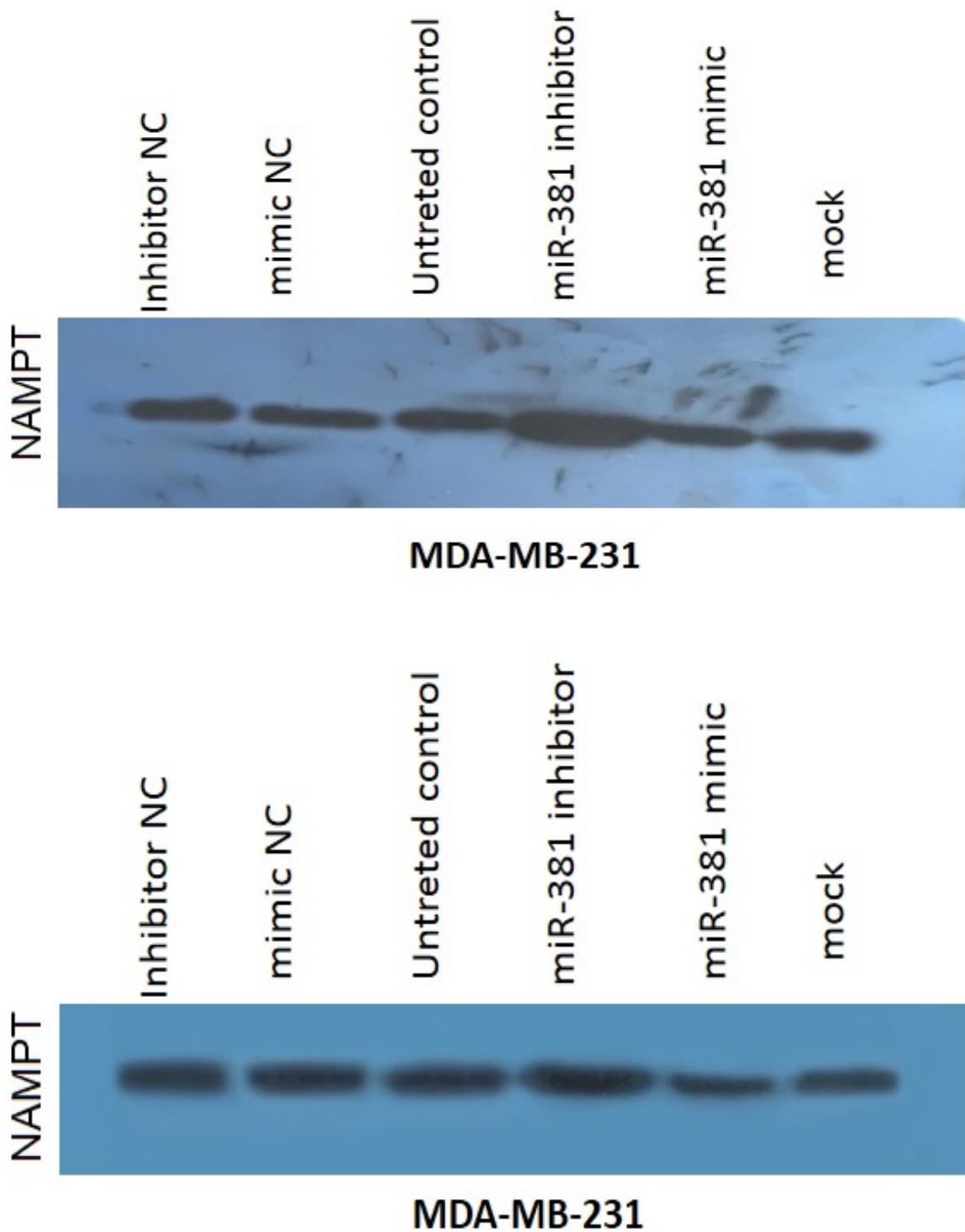
Supplementary Figure 7: The expression status of miR-381 in breast and other cancer types (<http://mircancer.ecu.edu/search.jsp?mirId=hsa-miR-381&logic=&condition=Or&cancerName=&buttonSearch=>)



Supplementary Figure 8: Individual images of each Western blot experiment. The cell line in which the experiment was performed is stated under each blot.



Supplementary Figure 8 (cont.): Individual images of each Western blot experiment. The cell line in which the experiment was performed is stated under each blot.



Supplementary Figure 8 (cont.): Individual images of each Western blot experiment. The cell line in which the experiment was performed is stated under each blot.

Supplementary Table 1: Sequences of primers used for measuring miRNA and NAMPT expression, synthesis of NAMPT 3'-UTR and NAMPT MRE tandem mutant

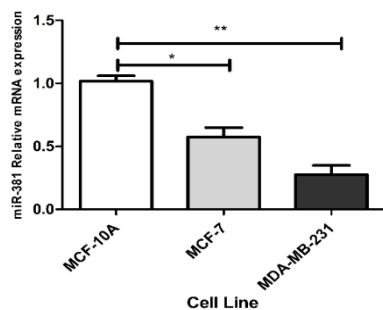
Template	Primer	Sequence (5'→3')
<i>miRNA</i>		
<i>miR-381</i>	Forward	AGTATACAAGGGCAAGCTCTGT
	Universal	GCGAGCACAGAATTAATACGACTC
	Reverse	
<i>U6-snRNA (Internal Control)</i>	Forward	CTCGCTTCGGCAGCACA
	Reverse	AACGCTTCACGAATTGCGT
<i>Reverse Transcription Genes</i>		
<i>NAMPT</i>		GCGAGCACAGAATTAATACGACTCAC-TATAGGTTTTTTTTAG
<i>GAPDH (Internal Control)</i>	Forward	GGTTCTTGGTGGAGGTTGCTAC
	Reverse	GAAGACGTTAACCCAAAGGCC
	Forward	GGGAAGGTGAAGGTCGGAGT
	Reverse	TCCACTTACCAGAGTTAAAAGCAG
<i>NAMPT-3'-UTR</i>	Forward	CCGCTCGAGCGGGTACAGATGTGTGGGGTTGTG
	Reverse	AAATATGCGGCCGCGCTGACATTCTCCACTGAATGGG
<i>NAMPT MRE Tandem Mutant</i>	Forward	CCGCTCGAGCGCTTCACTTCACTTCTCTTTCCAC-TTTCACTTCTCTCTCTCTCCGTCC
	Reverse	ATAAGAATGCAGGCCAGGGAGGGAAAATGAGGAC-GGAAGAGAG

Supplementary Table 2: Raw data of luciferase assay analysis

	NAMPT-3'UTR			NAMPT MRE tandem mutant			psiCHECK2 vector		
	Mean	SD	N	Mean	SD	N	Mean	SD	N
Untreated control	1	0	3	1	0	3	1	0	3
miR-381 mimic	0.693267	0.0814	3	1.033333	0.057735	3	1.02	0.026457	3
miR-381 inhibitor	1.276667	0.032145	3	0.955	0.031225	3	0.972333	0.010786	3
mimic NC	0.993333	0.030551	3	0.986667	0.037859	3	1.036667	0.083267	3
inhibitor NC	0.999333	0.077468	3	1.033667	0.057449	3	0.983333	0.047258	3
mock	0.960333	0.069573	3	0.953333	0.037859	3	0.948	0.037041	3

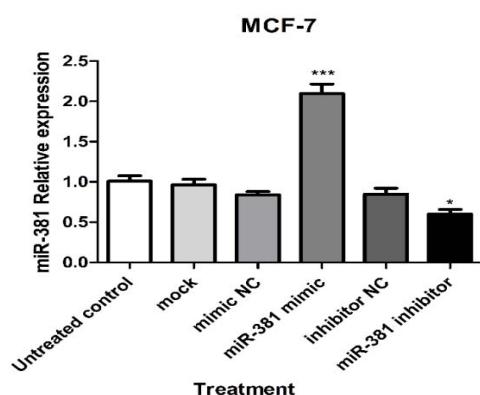
Supplementary Table 3: Raw data of real-time PCR analysis. miR-381 expression in MCF-7, MDA-MB-231 and MCF-10 cells and their comparison

			ΔCt Value	ΔΔCt	Expression Fold Change ($2^{\Delta\Delta Ct}$)
MCF10-A	U6	21.97	33.49	11.52	0.2934 0.815976778
		21.78	33.03	11.25	0.0234 0.983911186
		20.66	31.78	11.12	-0.1066 1.076687814
	miR-381	24.12	36.52	12.4	1.1734 0.443375206
		24.97	36.81	11.84	0.6134 0.653654418
		25.65	37.74	12.09	0.8634 0.549655657
MCF-7	U6	23.51	36.22	12.71	1.4834 0.357644956
		22.47	35.57	13.1	1.8734 0.272929454
		24.53	37.98	13.45	2.2234 0.214136109
MDA-MB-231	miR-381				



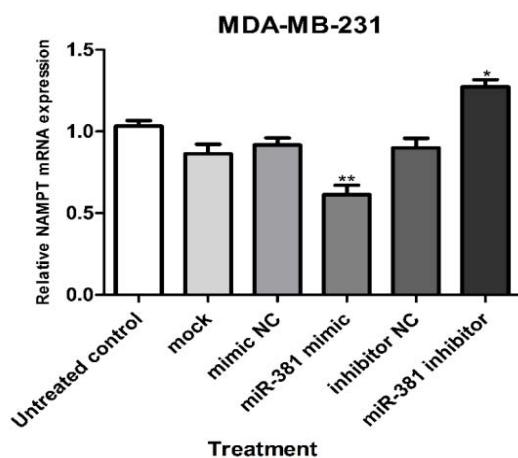
Supplementary Table 4: Raw data showing miR-381 relative expression after transfection of MCF-7 cells with the mimic or inhibitor of miR-381 or their corresponding negative control.

	U6	miR-381	ΔCt Value	ΔΔCt	Expression Fold Change ($2^{\Delta\Delta Ct}$)
untreated control	21.48	32.54	11.06	-0.123	1.088997015
	20.19	31.44	11.25	0.067	0.954621014
	21.83	32.97	11.14	-0.043	1.030253954
	22.71	33.7	10.99	-0.193	1.143138335
	24.02	35.21	11.19	0.007	0.995159722
	23.65	34.94	11.29	0.107	0.928516852
mock	24.81	36.22	11.41	0.227	0.854409741
	23.97	35.37	11.4	0.217	0.860352631
	24.03	35.28	11.25	0.067	0.954621014
mimic NC	19.29	29.25	9.96	-1.223	2.334316204
	18.75	28.86	10.11	-1.073	2.103803558
	20.54	30.81	10.27	-0.913	1.882956929
inhibitor NC	22.19	33.88	11.69	0.507	0.703684188
	23.54	34.87	11.33	0.147	0.90312651
	24.01	35.21	11.2	0.017	0.988285652
miR-381 inhibitor	25.57	37.45	11.88	0.697	0.616853585
	25.96	37.97	12.01	0.827	0.563700206
	24.53	36.15	11.62	0.437	0.738669032



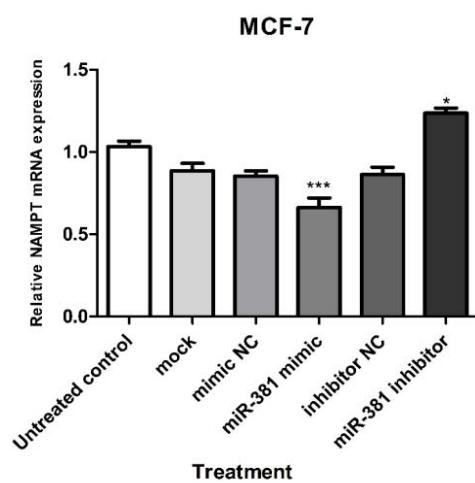
Supplementary Table 5: Raw data showing miR-381 relative expression after transfection of MDA-MB-231 cells with the mimic or inhibitor of miR-381 or their corresponding negative controls (NC)

MDA-MB-231	GAPDH	NAMPT	ΔCt Value	ΔΔCt	Expression Fold Change ($2^{-\Delta\Delta Ct}$)
untreated control	12.88	23.62	10.74	-0.21	1.156688184
	11.89	22.58	10.69	-0.26	1.197478705
	12.28	23.13	10.85	-0.1	1.071773463
	13.01	24.22	11.21	0.26	0.835087919
	12.37	23.65	11.28	0.33	0.795536484
	12.18	23.18	11	0.05	0.965936329
mock	13.37	24.89	11.52	0.57	0.673616788
	13.18	24.28	11.1	0.15	0.901250463
	14.88	26.11	11.23	0.28	0.823591017
miR-381 mimic	14.48	25.98	11.5	0.55	0.683020128
	14.18	26.09	11.91	0.96	0.514056913
	15.09	26.71	11.62	0.67	0.628506687
inhibitor NC	12.76	23.87	11.11	0.16	0.895025071
	13.01	24.11	11.1	0.15	0.901250463
	13.17	24.11	10.94	-0.01	1.00695555
miR-381 inhibitor	11.25	21.76	10.51	-0.44	1.356604327
	10.67	21.25	10.58	-0.37	1.292352831
	10.68	21.25	10.57	-0.38	1.301341855



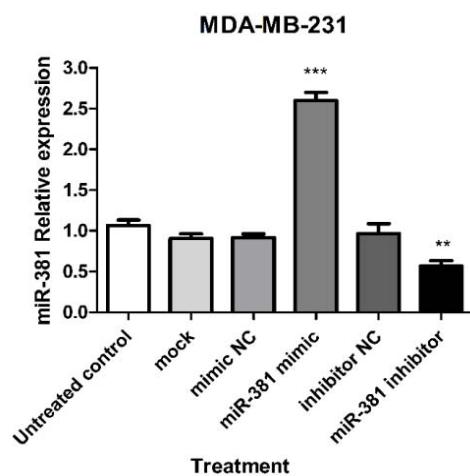
Supplementary Table 6: Raw data showing relative expression of NAMPT mRNA in MCF-7 cells after transfection with miR-381 mimic, inhibitor or NCs

MCF-7	GAPDH	NAMPT	ΔCt Value	ΔΔCt	Expression Fold Change (2 ^{Δ-ΔCt})
untreated control	16.87		27.87	11	-0.11
	16.09		27.21	11.12	0.01
	17.08		28.15	11.07	-0.04
mock	19.11		30.35	11.24	0.13
	18.81		29.97	11.16	0.05
	19.15		30.58	11.43	0.32
	16.88		28.04	11.16	0.05
	17.87		29.01	11.14	0.03
mimic NC	17.35		28.65	11.3	0.19
miR-381 mimic	19.32		30.87	11.55	0.44
	18.25		29.89	11.64	0.53
	18.77		30.46	11.69	0.58
inhibitor NC	16.57		27.82	11.25	0.14
	16.44		27.81	11.37	0.26
	17.64		28.96	11.32	0.21
miR-381 inhibitor	16.88		27.65	10.77	-0.34
	17.25		28.01	10.76	-0.35
	15.48		26.15	10.67	-0.44



Supplementary Table 7: Raw data showing relative expression of NAMPT mRNA in MDA-MB-231 cells after transfection with miR-381 mimic, inhibitor or NCs

	U6	miR-381	ΔCt Value	ΔΔCt	Expression Fold Change ($2^{\Delta\Delta Ct}$)
untreated control	25.96		36.97	11.01	-0.093
	26.21		37.37	11.16	0.057
	21.83		32.97	11.14	-0.043
mock	24.81		35.97	11.16	0.057
	23.02		34.21	11.19	0.087
	25.87		37.24	11.37	0.187
mimic NC	28.18		39.25	11.07	-0.033
	27.19		38.36	11.17	0.067
	26.82		38.18	11.36	0.257
miR-381 mimic	16.58		26.36	9.78	-1.323
	17.41		27.01	9.6	-1.503
	16.85		26.58	9.73	-1.373
inhibitor NC	25.36		36.74	11.38	0.277
	24.67		35.87	11.2	0.097
	25.39		36.28	10.89	-0.213
miR-381 inhibitor	24.18		36.15	11.97	0.867
	23.68		35.67	11.99	0.887
	24.39		36.08	11.69	0.507



Supplementary Table 8: Raw data of viability assay analysis in MCF-7 and MDA-MB-231 cells respectively

MCF-7							
0.416	0.504	0.46	0.46	0.36	0.854295	85.42952	inhibitor NC
0.546	0.542	0.561	0.549667	0.549667	1.304383	130.4383	miR-381 inhibitor
0.541	0.537	0.524	0.534	0.434	1.0299	102.99	mock
0.435	0.551	0.548	0.511333	0.411333	0.976111	97.61114	mimin NC
0.435	0.418	0.324	0.392333	0.292333	0.693719	69.37193	miR-381 mimic
mda-mb-231							
0.236	0.254	0.233	0.241	0.141	0.79661	79.66102	inhibitor NC
0.212	0.315	0.268	0.265	0.165	0.932203	93.22034	mimin NC
0.252	0.235	0.253	0.246667	0.146667	0.828625	82.86252	miR-381 mimic
0.277	0.247	0.253	0.259	0.159	0.898305	89.83051	mock
0.332	0.287	0.367	0.328667	0.228667	1.291902	129.1902	miR-381 inhibitor