

Supplementary Data

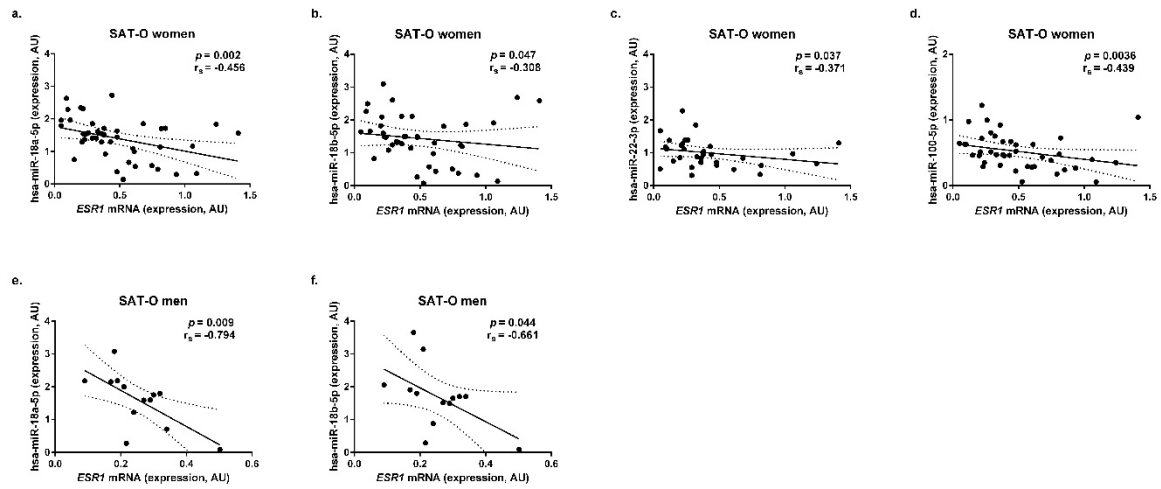


Figure S1. Correlations of *ESR1* mRNA concentrations with *hsa-miR-18a-5p* (a), *hsa-miR-18a-5p* (b), *hsa-miR-22-3p* (c), and *hsa-miR-100-5p* (d) levels in the subcutaneous adipose tissue (SAT) of female obese study participants and with *hsa-miR-18a-5p* (e), and *hsa-miR-18b-5p* (f) in the SAT of male obese study participants.

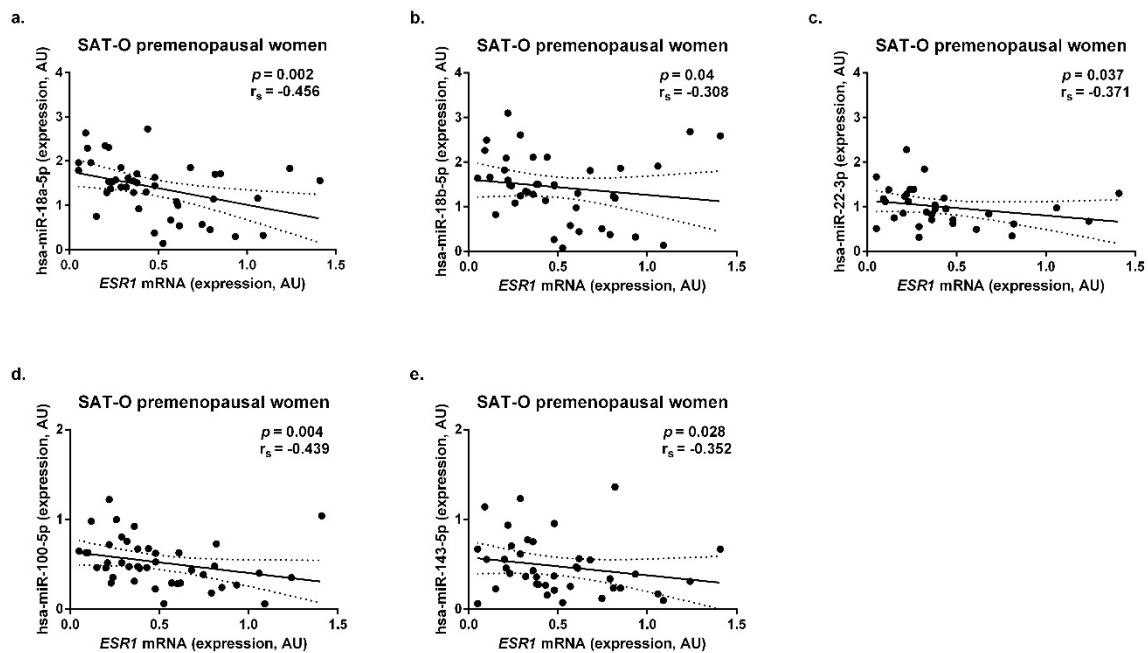


Figure S2. Correlations between *ESR1* mRNA concentrations and *hsa-miR-18a-5p* (a), *hsa-miR-18b-5p* (b), *hsa-miR-22-3p* (c), *hsa-miR-100-5p* (d), and *hsa-miR-143-5p* (e) levels in the subcutaneous adipose tissue (SAT) of premenopausal female obese (O) study participants.

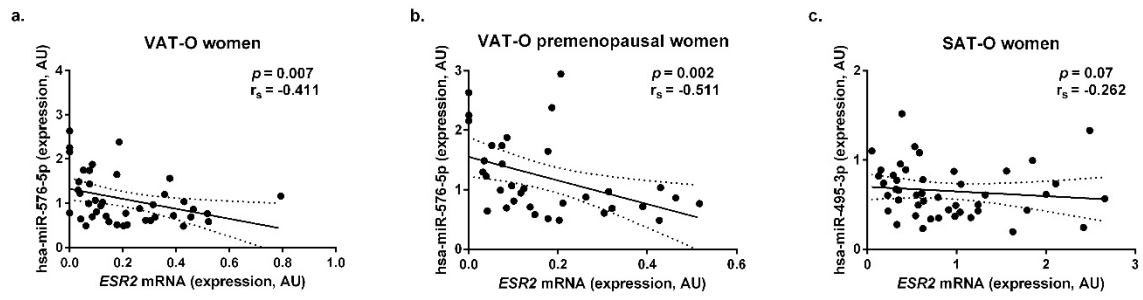


Figure S3. Correlations of *ESR2* mRNA concentrations with hsa-miR-576-5p levels in the visceral adipose tissue (VAT) of obese (O) female study participants (a), hsa-miR-576-5p levels in VAT of obese (O) premenopausal female study participants (b), and hsa-miR-495-3p levels in subcutaneous adipose tissue (SAT) of obese (O) female study participants (c).

Table S1. Primers used for the mRNA, miRNA and methylation analysis.

Gene		Primers	
<i>ESR1</i>	F	5' CCGGCTCCGCAAATTGCT 3'	
	R	5' AGCGGGTTGGCCAAAGGTT 3'	
<i>ESR2</i>	F	5' GACAGCGCAGAAGTGAGCATC 3'	
	R	5' AAGCCGTGATGTAAAGGGTG 3'	
<i>ACTB</i>	F	5' CAGCCTGGATAGCAACGTAC 3'	
	R	5' TTCTACAATGAGCTGCGTGTG 3'	
miRNA			
hsa-miR-18a-5p	F	5' GTAAGGTGCATCTAGTGCAG 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTCTATC 3'	
hsa-miR-18b-5p	F	5' GTAAGGTGCATCTAGTGCAG 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTCTAAC 3'	
hsa-miR-20b-5p	F	5' GCAAAGTGCTCATAGTGCAG 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTCTAC 3'	
hsa-miR-22-3p	F	5' GAAGCTGCCAGTTGAAGA 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTACAGT 3'	
hsa-miR-100-5p	F	5' CAGAACCCGTAGATCCGA 3'	
	R	5' GTCCAGTTTTTTTTTTTTTTTCCACAAG 3'	
hsa-miR-142-3p	F	5' CGCAGTGTAGTGTTCCT 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTCCA 3'	
hsa-miR-143-5p	F	5' TGCAGTGCTGCATCTCT 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTACCA 3'	
hsa-miR-146b-3p	F	5' GCCCTGTGGACTCAGT 3'	
	R	5' GTCCAGTTTTTTTTTTTTTTTACCAGA 3'	
hsa-miR-335-3p	F	5' CGCAGTTTTTCATTATTGCTCCT 3'	
	R	5' GGTCCAGTTTTTTTTTTTTTTTGGT 3'	
hsa-miR-495-3p	F	5' CGCAGAAACAAACATGGTG 3'	
	R	5' GTCCAGTTTTTTTTTTTTTTTAAGAAGTG 3'	
hsa-miR-576-5p	F	5' GCAGATTCTAATTTCTCCACGTC 3'	
	R	5' CAGGTCCAGTTTTTTTTTTTTTTTAAAG 3'	
Gene			
<i>ESR1</i> 1 st fragment (-34 bp to +255 bp)	F	5' TCCTCCAGCACCTTTGTAATG 3'	
	R	5' GTGTGGAGGGTCATGGTCAT 3'	
<i>ESR1</i> 2 nd fragment (+255 to +615 bp)	F	5' ATGACCATGACCCTCCACAC 3'	
	R	5' TCCAGGTAGTAGGGCACCTG 3'	
<i>ESR2</i> P0K 1 st fragment (-56 044 to -55 433 bp)	F	5' CTCCTGTGGTCCAACATTCC 3'	
	R	5' TCCACGTTTTCCTTGTCTC 3'	
<i>ESR2</i> P0K 2 nd fragment (-56 044 to -55 433 bp)	F	5' GACTGGCTGAAGGGGATGAT 3'	
	R	5'GCCCTCACACTTCTGCAC 3'	
<i>ESR2</i> P0N 1 st fragment (-11 532 to -10 258 bp)	F	5' TTCTCAGGCCCTACTCCAGA 3'	
	R	5' CAGCAGCTGGAGAACTGAA 3'	
<i>ESR2</i> P0N 2 nd fragment (-11 194 to -10 891 bp)	F	5' AACTGCCTCTTGAACTTGC 3'	
	R	5' CAGGATTTCAAACAAAATGAGACA 3'	

bp – base pairs, F – forward, P0K – distal promoter, P0N – central promoter, R – reverse

Table S2. The mean percentage of the methylated CG pairs in the *ESR1* and *ESR2* regulatory regions

Analysed gene fragment	Length (bp)	CpG (N)	VAT-O	SAT-O	VAT-O MS	SAT-O MS	VAT-O NOMS	SAT-O NOMS	VAT-N	SAT-N
<i>ESR1</i> 1 st fragment	289	28	63.2%	51.6%	60.9%	50.1%	65.5%	53.2%	62.4%	54.7%
<i>ESR1</i> 2 nd fragment	360	34	58.8%	53.5%	59.7%	54.6%	57.9%	52.4%	65.1%	59.9%
<i>ESR2</i> P0K 1 st fragment	275	21	3.5%	1.8%	2.6 %	1.9%	4.4%	1.7 %	2.2%	1.8%
<i>ESR2</i> P0K 2 nd fragment	322	28	1.7%	1.7%	1.8%	1.9%	1.6%	1.5%	1.6%	1.6%
<i>ESR2</i> P0N 1 st fragment	277	16	15.3%	14.0%	14.5%	16.0%	16.1%	12.1%	15.2%	17.4%
<i>ESR2</i> P0N 2 nd fragment	303	25	11.6%	12.2%	10.6%	12.0%	12.1%	12.4%	11.5%	11.4%

bp – base pairs, MS – metabolic syndrome (patients with metabolic complications of obesity), NOMS – no metabolic syndrome components (metabolically healthy), N – number, P0K – distal promoter, P0N – central promoter,