

Supplementary Table 1. The primers used for expression and methylation analysis.

Primer	Sequence
<i>hsa-miR-16</i> -RT	GTCGTATCCATGGCAGGGTCCGAGGTATTCGCCATGGATACGACCGCCAAT
<i>hsa-miR-371a-5p</i> -RT	GTCGTATCCATGGCAGGGTCCGAGGTATTCGCCATGGATACGACAGTGCC
<i>hsa-miR-371b-5p</i> -RT	GTCGTATCCATGGCAGGGTCCGAGGTATTCGCCATGGATACGACAAAGTG
<i>hsa-miR-372-3p</i> -RT	GTCGTATCCATGGCAGGGTCCGAGGTATTCGCCATGGATACGACACGCTC
<i>hsa-miR-373-3p</i> -RT	GTCGTATCCATGGCAGGGTCCGAGGTATTCGCCATGGATACGACACACCC
<i>hsa-miR-16</i> -F	GCGGTAGCAGCACGTAATATT
<i>hsa-miR-371a-5p</i> -F	AGGGACTCAAACCTGTGGGGG
<i>hsa-miR-371b-5p</i> -F	CGACTCAAAAGATGGCGGC
<i>hsa-miR-372-3p</i> -F	GGGAAAGTGCTGCGACATTTG
<i>hsa-miR-373-3p</i> -F	GAAGTGCTTCGATTTGGGGTG
universal reverse	TGGCAGGGTCCGAGGT
<i>GAPDH</i> -F	GCACCGTCAAGGCTGAGAAC
<i>GAPDH</i> -R	TGGTGAAGACGCCAGTGGA
<i>NF2</i> -F	CGGTGTCCTTGATCGTGACTG
<i>NF2</i> -R	TCAATTGCGAGATGAAGTGGAA
<i>LATS2</i> -F	CAGAGATTTCTCATCAATGTTCTTC
<i>LATS2</i> -R	ATTAACTTTGACAAATCATGCTGC
<i>TAZ</i> -F	CGTGAAGTGGCCGTTCCC
<i>TAZ</i> -R	AGGTGGTTCATGTACTTGGTCC
<i>OXR1</i> -F	TACCTTGCCATTTCTTTGC
<i>OXR1</i> -R	TGGAGGTTGATTCAGGAAGG
<i>JNK</i> -F	GTCAGGCAAGGGATTTGTTAT
<i>JNK</i> -R	TCTTGGTTCTCTCCTCCAAGTC
<i>CASP9</i> -F	CGCCACCATCTTCTCCCTG
<i>CASP9</i> -R	CCAACGTCTCCTTCTCCTCC
<i>MiR-373-3p</i> -MF	CGGGGAGTAGTATGGAGTCGGCG
<i>MiR-373-3p</i> -MR	AACTTCGTCCTCCAAAATCGCCCCG
<i>MiR-373-3p</i> -UF	GGGAGTAGTATGGAGTTGGTGGTG
<i>MiR-373-3p</i> -UR	CTTCATCCTCCAAAATCACCCAC

RT:reverse transcription; F:forward; R:reverse; GAPDH:glyceraldehyde-3-phosphate dehydrogenase; NF2: neurofibromatosis type 2; LATS2:large tumor suppressor2; TAZ:transcriptional co-activator with PDZ-binding

motif; OXR1:oxidation resistance 1; JNK:Jun Kinase; CASP9:caspace 9; miR:microRNA; M:methylated; U:unmethylated.

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OXR1      5' ugAUUGCCAGGUUGCUUAUAGCACUUu 3'
           |:: | |::|:| | | | | | | |
has-miR-373 3' ugUGGGGUUUUAGC---U-UCGUGAAg 5'

LATS2     5' acAGUUUAGAA--AGAGCACUUa 3'
           | ::: |:| | :| | | | | | |
has-miR-373 3' ugUGGGGUUUUAGCUUCGUGAAg 5'
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Figure S1. Target gene prediction of miR-373-3p. Target genes were predicted using TargetScan and PicTar. The alignment of miR-373-3p and putative binding sites in the 3'-UTRs of OXR1 and LATS2 are presented. OXR1:oxidation resistance 1; LATS2:large tumor suppressor2.