## Supplementary Information



## Supplementary Fig. S1. Clustering analysis of

 microRNAs expression in TGF- $\boldsymbol{\beta 1}$-induced HT-29cells. Up- and down-regulated genes are represented in red and green colors, respectively. A subset of differential genes was selected for clustering analysis, and the number of genes clustered was 122 .

| Comparison | Up-regulated | Down-regulated |
| :---: | :---: | :---: |
| TGF- $\beta 1 /$ Control | 88 | 7 |
| OXY /Control | 3 | 2 |
| OXY /TGF- $\beta 1$ | 9 | 83 |

Supplementary Table S1. Number of differentially expressed genes in TGF- $\beta 1$-induced HT-29 cell. HT-29 cells were treated with OXY $(70 \mu \mathrm{M})$ with TGF- $\beta 1(10 \mathrm{ng} / \mathrm{mL})$. After 24 h , total RNA was extracted and subjected to analyze the expression for miRNAs. The number of differentially expressed genes for each comparison is shown in the table above. Standard selection criteria to identify differentially expressed genes are established at $\log _{2} \mid$ Fold change $\mid \geq 0.8$ and $p<0.05$.

| Has- | TGF- $\boldsymbol{\beta 1 / C o n t r o l}$ $\log _{2}$ (up ratio) | Has- | OXY /TGF- $\boldsymbol{\beta 1}$ <br> $\log _{2}$ (down ratio) | Has- | TGF- $\boldsymbol{\beta 1 / C o n t r o l}$ $\log _{2}$ (down ratio) | Has- | $\begin{aligned} & \hline \mathbf{O X Y} / \mathbf{T G F - \beta} 1 \\ & \log _{2} \text { (up ratio) } \\ & \hline \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| let-7d-3p | 2.14 | miR-3687 | -1.79 | miR-3612 | -1.72 | miR-3612 | 1.85 |
| miR-301a-3p | 1.71 | miR-301a-3p | -1.67 | miR-6866-5p | -1.13 | miR-6850-5r | 1.15 |
| miR-19b-3p | 1.69 | miR-181a-5p | -1.51 | miR-6850-5p | -1.07 | miR-6866-5r | 1.09 |
| miR-181b-5p | 1.58 | let-7d-3p | -1.44 | miR-4278 | -1.01 | miR-4278 | 1.02 |
| miR-181a-5p | 1.55 | miR-92a-3p | -1.35 |  |  |  |  |
| miR-25-3p | 1.39 | miR-92b-3p | -1.34 |  |  |  |  |
| miR-664b-5p | 1.34 | miR-25-3p | -1.33 |  |  |  |  |
| miR-5100 | 1.29 | miR-664b-5p | -1.32 |  |  |  |  |
| miR-196b-5p | 1.09 | miR-19b-3p | -1.32 |  |  |  |  |
| miR-21-5p | 1.01 | miR-181b-5p | -1.23 |  |  |  |  |
| let-7i-5p | 0.99 | miR-196b-5p | -1.10 |  |  |  |  |
| miR-92b-3p | 0.95 | miR-5100 | -1.08 |  |  |  |  |
| miR-193b-3p | 0.91 | miR-21-5p | -0.99 |  |  |  |  |
| miR-3687 | 0.90 | let-7i-5p | -0.98 |  |  |  |  |
| miR-361-5p | 0.88 | miR-193b-3p | -0.96 |  |  |  |  |
| miR-92a-3p | 0.87 | miR-361-5p | -0.85 |  |  |  |  |

Supplementary Table S2. Oxyresveratrol regulates microRNAs expression in TGF- $\boldsymbol{\beta 1} 1$-induced HT-29 cell. The listed genes at the table above were changed significantly by OXY $(70 \mu \mathrm{M})$ treatment in TGF- $\beta 1$-induced HT-29 cells, $p<0.05$.

