Supplementary Materials and Methods

Statistical methods for scoring transcription factors and analysis of oridonin activity and gene expression data

Transcription factor-miRNA regulation data were obtained from the TransmiR Database (1) for those miRNAs that showed differential expression upon oridonin treatment with log2-fold changes greater than 1 or less than -1. A total score (TFscore) was calculated for each transcription factor that has been reported to regulate any of these miRNAs using the following formula:

$$\text{TFscore}_i = \sum_{j=1}^{n} F_j \times R_{ij}$$

where $F_j$ is the log2-fold change of each miRNA upon oridonin treatment obtained from miRNA expression profiling, and $R_{ij}$ reflects the regulatory effect of the $i$th transcription factor on the $j$th miRNA, with positive regulation being assigned as 1, negative regulation as -1, and no regulation as 0.

The correlation between oridonin activity and the gene expression patterns was evaluated as previously described (2). Briefly, IC$_{50}$s of oridonin (NSC 637458) against the NCI-48 cell panel were obtained from the DTP screen (http://dtp.nci.nih.gov) and the drug activity was expressed as $-\log_{10}$IC$_{50}$, whereas the gene expression patterns were assessed using data from studies with HG-U133 Affymetrix chips. The Pearson correlation coefficients ($r$) and Spearman correlation coefficients ($\rho$) between the activity of oridonin and the gene expression levels were computed using SPSS (SPSS Inc.) with the $P$ values provided.
References:
