Supplemental Titles and Figure Legends

Figures S1-S6. Promoter sequences for DICER1 and selected miRNAs. Promoter sequences were obtained from UCSC website (http://genome.ucsc.edu/) and analyzed using the TFSEARCH software (http://mbs.cbrc.jp/research/db/TFSEARCH.html). P63RE were defined manually using the previously reported consensus sequence.[35] Consensus sequences for transcriptional factors were highlighted in bold with the grey background and boxed. PCR primers used for amplification after ChIP are indicated.

Figure S7. Quantification of ChIP assay. ChIP assay were performed with cross-linked chromatin from 5 x 10^6 cells, treated with control medium (Con) or 10μg/ml cisplatin (CIS) for 24h and either 10 μg of anti-ΔNp63 antibody (Ab-1, EMD-Calbiochem) or 10 μg of anti-phospho-ΔNp63 antibody[32] using ChIP kit (Upstate Biotechnology). The enriched DNA was quantified by qPCR. For each promoter sequence tested, amplification primers described in Figures S1-S6 (below). The amount of immunoprecipitated DNA in each sample is represented as signal relative to the total amount of input chromatin, which is equivalent to one. (A). P63 wild type cells, promoters are: DICER1, Mir-630, and Mir-885-3p. (B). P63 wild type cells, promoters are: Mir-181a, Mir-519a and Mir-374a. (C). P63 mutated cells, promoters are: DICER1, Mir-630, and Mir-885-3p. (D). P63 mutated cells, promoters are: Mir-181a, Mir-519a and Mir-374a.

Figures S8-S16. 3'-UTR sequences for target mRNA bound to specific miRNAs. Selected 3'-UTR sequences are present and potential miRNA bound sequences are boxed

and miRNAs are indicated. Selected 3'-UTR sequences cloned upstream of the luciferase reporter gene [DICER1 3'-UTR (S214311); DDIT1 3'-UTR (S204414); DDIT4 3'-UTR (S206522); YES1 3'- UTR (S211786); HIPK2 3'-UTR (S202331); HMGA1 3'-UTR (S209018), BCL2L2 3'-UTR (S213742) from SwitchGear Genomics and ATM 3'-UTR (SC221017); BCL2 3'-UTR (SC222289), YAP1 3'-UTR (SC220924) from Origene Technologies]. Wild type ΔNp63α cells were transfected with an empty vector and vector with 3'-UTR sequence as indicated. Cells were also transfected with specific miRNA mimics and inhibitors for 24h. Cells were treated with control medium (Con) or 10μg/ml cisplatin (CIS) for an additional 24h and then tested for the luciferase reporter activity. Luciferase activity was normalized for Renilla luciferase activity used as a transfection efficiency control and was also normalized for empty control vector values designated as 1. Numerical values present next to the bars reflect the fold change from values obtained in cells transfected with the 3'-UTR constructs and treated with control medium (Sample 3 for all Figures S8-S16).

Figure S17. Quantitative PCR analysis of expression of selected mRNAs in wild type ΔNp63α cells. Cells were transfected with control vector or specific miRNA mimics and inhibitors for 24h. Cells were treated with control medium (-) or 10μg/ml cisplatin (+) for an additional 24h and then mRNA expression was tested by qPCR assay using the StepOnePlus Real-Time PCR Systems Kit (Applied Biosystems) with SYBR GREEN Universal PCR Master Mix. Data plotted as relative units (RU). Values were normalized for values for GAPDH and values obtained from the control untreated samples were designated as 1. Experiments were performed in triplicate. Numerical values present next to the bars

reflect the fold-change from values obtained in cells transfected with control vector and treated with control medium. The following primers were used: DDIT4 [sense, (+421) 5'-ggatggggtgtcgttgcccg-3'(+440) and antisense, (+781) 5'-tagctccgccaactctccct-3' (+800)], YES1 [sense, (+661) 5'-tagcgcctgcagattccatt-3' (+680) and antisense, (+1201) 5'-taagacatgataaacttgtt-3' (+1220)], DDIT1 [sense, (+421) 5'-agcggccaagctgctcaacg-3' and antisense,(+601) 5'-gctcttggagaccgacgctg-3' (+620)], and BCL2 [sense, (+1081) 5'-tgcctttgtggaactgtacg-3' (+1200) and antisense, (+1741) 5'-gagggttcctgtgggggggaa-3' (+1760)] .