Supplemental Figure Legends

Figure S1. Pri-miR-7-1 and -7-2 harbor QREs.

Sequences of pri-miR-7-1 and pri-miR-7-2 are shown. Green denotes the pri-miR-7-1 host gene *hnRNPK* exons, dark and light green represent alternative spliced exons. Red denotes miR-7-1 steam-loop sequences. Putative QREs (light blue) are boxed with hatched lines.

Figure S2. Pri-miR-7-1, but not pri-miR-7-2 and pri-miR-7-3, is expressed in U343 cells.

Real time RT-PCR was performed on RNA isolated from siCTL and siQKI transduced U343 cells.

Figure S3. Increased miR-7 expression in QKI deficient U343 cells as detected by Northern blotting.

(A) RNA from siCTL and siQKI transduced U343 cells was isolated and mature miR-7 was detected by Northern blotting.

(B) Semi-quantitative RT-PCR with primers spanning intron pri-miR-7-1, intron-exon boundaries at exon hnRNPK pre-mRNA. U343 cells were transfected with siCTL and siQKI at 0h and 48h, cells were collected at 72 h post-transfection for analysis.

Figure S4. QKI deficient U87 cells have reduced EGFR expression, EGF-dependent ERK activation. (A) U87 cells were transiently transfected with mimic-miR negative

control (miR CTL), mimic-miR-7 (miR-7), siCTL or siQKI RNAs and 48 h later the cells were left untreated or stimulated with EGF for 15 min. The cells were lysed and immunoblotted with anti-EGFR, anti-pan-QKI and -β-tubulin antibodies as indicated. The molecular mass markers are shown in kDa on the left.

(B) siCTL and siQKI transduced U87 cells were starved overnight at 72 h post-transfection, and were stimulated with 20 ng/ml EGF 15 min. Protein extracts were prepared and pERK, ERK, QKI, and β-tubulin were detected by immunoblotting. The ratio of the relative quantification of pERK/ERK is shown.

Figure S5. Depletion of QKI isoforms or the overexpression of miR-7 in U343 cells lead to cell cycle arrest.

U 343 cells were transfected with 40 nM synthetic small RNAs: mimic miR negative control (miR CTL), mimic miR-7, siLuciferase (siCTL), and two siQKI siRNAs (siQKI-1 and siQKI-2), respectively, and cell cycle analysis were performed as described in the "Materials and Methods". Two independent experiments were performed and the represented FACS graphs from one experiment were shown in (A) and the average percentage of cells at G0/G1, S and G2/M phases from the two experiments is presented in (B). ** $p < 0.01$; *** $p < 0.001$; student t-test.