



Representative real-time PCR profiles for detection of miRNAs. Validation of real-time transcript data was carried out by assessing microRNA expression in cell populations of varying numbers/single cells. To achieve this, multiples of 1, 10, 100, 1000, or 3000 cells were picked up using a PALM Microbeam 4 laser catapulting microscope as described. RNA was isolated and miR-21 specific primers were used to generate cDNA, which was analyzed by TaqMan-based quantitative PCR as described. Each 10-fold increase in cell number accounts for a ~3.3-fold decrease in Ct value. Each curve represents a different biological sample.